GENETICS SOCIETY OF NIGERIA

IN COLLABORATION WITH THE

FEDERAL UNIVERSITY OF AGRICULTURE, ABEOKUTA

CONFERENCE PROCEEDINGS OF THE

45th

ANNUAL CONFERENCE OF
THE GENETICS SOCIETY OF NIGERIA

OGUN 2023

DATE:
26-30
MARCH
2023

THEME:

GENETICS AND AGRICULTURAL TRANSFORMATION: PATHWAY TO FOOD SECURITY

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PROCEEDINGS OF THE

ANNUAL CONFERENCE OF THE
GENETICS SOCIETY OF NIGERIA

THEME:

GENETICS AND AGRICULTURAL TRANSFORMATION: PATHWAY TO FOOD SECURITY

DATE:

SUNDAY 26TH – THURSDAY 30TH MARCH, 2023

VENUE:

INTERNATIONAL SCHOLAR CENTRE,
CENTRE OF EXCELLENCE IN AGRICULTURAL DEVELOPMENT AND SUSTAINABLE ENVIRONMENT (CEADESE),
FEDERAL UNIVERSITY OF AGRICULTURE, ABEOKUTA (FUNAAB), OGUN STATE

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This book contains the edited and unedited abstracts/manuscripts of all special talks, invited talks and oral presentations at the Gnetics Society of Nigeria 45th Annual Conference held form 26th – 30th of March, 2023 at the International Scholar Centre, Centre of Excellence in Agricultural Development and Sustainable Environment (CEADESE), Federal University of Agriculture, Abeokuta (FUNAAB), Ogun State, Nigeria.

Organizers are not responsible for the accuracy of the content of this book.

45TH ANNUAL CONFERENCE GENETIC SOCIETY OF NIGERIA, OGUN'23

PROGRAMME OF EVENTS

Venue: International Scholars Centre, Federal University of Agriculture, Abeokuta

DAY 1: SUNDAY, MARCH 26, 2023

S/No	Time (Hrs)	Event	Officials concerned
1.		Arrival & Registration	LOC Members

DAY 2: MONDAY, MARCH 27, 2023

S/No	Time (Hrs)	Event	Officials concerned
2.	0700- 0900	Arrival of guests, participants and Registration	Participating Members
3.	0930-0940	Arrival of GSN NEC, BOT Members, Paper presenters, VC, Principal Officers, Deans, Directors, Head of Centres and Departments.	Master of Ceremony (MC)
4.	0940-1000	Arrival of the Executive Governor of Ogun State and other Invited Guests	MC
5.	1000-1005	National Anthem and FUNAAB Anthem	ICTREC
6.	1005-1015	Welcome Address by the Ag. Vice Chancellor, FUNAAB	Prof. O. B. Kehinde
7.	1015-1025	Address by National President GSN	Prof. S. A. Olakojo
8.	1025-1035	Remarks by HE Governor of Ogun State	Prince Dapo Abiodun
9.	1035- 1100	Investiture of GSN Fellows	Prof. S. A. Olakojo
10.	1100-1120	Presentation from National Seed Council (NASC), Abuja	NASC Representative
11.	1120-1125	Reading of Citation of Keynote Speaker	
12.	1125-1145	Keynote address: Genetics and agricultural transformation: Pathway to food security	**Prof. M. O. Akoroda** Prof of Agronomy, UI, Ibad an
13.	1145-1200	Goodwill messages and presentations	VC, DGs, MDs and all invited guests
14.	1200-1205	Vote of thanks	Prof. M. O. Ozoje
15.	1205-1210	Announcements	MC
16.	1210-1215	FUNAAB Anthem and National anthem	ICTREC
17.	1215-1230	Group Photographs	Invited Guests and All Participants
18.	1230-1300	Tea break	Catering Unit
19.	1300-1320	Lead paper 1	**Prof. Olufunmilayo A. Adebambo** Emeritus Prof. of Animal Breeding & Genetics, FUNAAB
20.	1320-1340	Lead paper 2	**Prof. M. A. B. Fakorede** Prof of Plant Breeding & Genetics, O.A.U., Ile-Ife

21.	1340-1400	Lead paper 3	**Prof. Chiedozie Egesi** Prof of Plant Breeding & Biotechnology, NRCRI, Umudike
22.	1400-1420	Lead paper 4	**Prof. Olubode Olufegba** Prof. of Fisheries, MAOU
23.	1420-1440	Lead paper 5	**Prof. Bolanle Oboh** Prof. of Genetics, UNILAG
24.	1440-1455	Vote of thanks	Chairman, LOC
25.	1445-1545	Lunch	All participants

Monday, 27 March, 2023

Technical/Scientific Session 1

Time: 1600 - 1800

Venue: Seminar Rooms A and B, International Scholars Centre, FUNAAB

S/No	Time (Hrs)	Event	Officials concerned
1.	1600 - 1800	Paper presentation	Participants
2.	1800	Closing	Chairman
3.	1800 - 1900	Cocktail party	

Parallel Session	Area of Specialization	Chairman	Rapporteur
A	Plant Breeding and Genetics	Prof. C. O. Alake, Prof. F. A. Sowemimo	Dr. J. B. O. Porbeni, Dr. E. O. Idehen, Dr. O. A. Oduwaye,
B	Animal Breeding and Genetic	Prof. M. N. Bemji, Prof. Agbebi, Prof. A. O. Adebambo	Dr. A. J. Sanda, Dr. M. Wheto, Dr. A. S. Oyelakin

Tuesday, 28 March, 2023

Technical/Scientific Session 2

Time: 0900 - 1800

Venue: Seminar Rooms; A and B, International Scholars Centre, FUNAAB

S/No	Time (Hrs)	Event	Officials concerned
1.	0900 - 1300	Paper presentation	Participants
2.	1300 - 1400	Lunch	Catering Unit
3.	1400 - 1800	Paper presentation	Participants
4.	1800	Closing	Chairman

Parallel Session	Area of Specialization	Chairman	Rapporteur
A	Plant Breeding and Genetics	Prof. C. O. Alake, Prof. F. A. Sowemimo	Dr. J. B. O. Porbeni, Dr. E. O. Idehen, Dr. O. A. Oduwaye,
B	Animal Breeding and Genetic	Prof. M. N. Bemji, Prof. Agbebi, Prof. A. O. Adebambo	Dr. A. J. Sanda, Dr. M. Wheto, Dr. A. S. Oyelakin

Wednesday, 29 March, 2023

Scientific Session 3
Time: 0900 - 1800
Venue: Seminar Rooms; A and B, International Scholars Centre, FUNAAB

S/No	Time (Hrs)	Event	Officials concerned
1.	0900	Paper presentation	Participants
2.	1300	Lunch	Catering Unit
3.	1400	Paper presentation	Participants
4.	1600	Annual General Meeting (AGM)	GSN President
4.	18.00	Closing	Chairman
4.	1800	Cocktail party	

Parallel Session	Area of Specialization	Chairman	Rapporteur
A	Plant Breeding and Genetics	Prof. C. O. Alake, Prof. F. A. Sowemimo	Dr. J. B. O. Porbeni, Dr. E. O. Idehen, Dr. O. A. Oduwaye,
B	Animal Breeding and Genetic	Prof. M. N. Bemji, Prof. Agbebi, Prof. A. O. Adebambo	Dr. A. J. Sanda, Dr. M. Wheto, Dr. A. S. Oyelakin

THURSDAY 30th March, 2023:

EXCURSION AND DEPARTURE

ACKNOWLEDGEMENTS OF DONORS

- Cocoa Research Institute of Nigeria (CRIN)
- Dr. S. Aladele of NACGRAB
- Federal University of Agriculture, Abeokuta
- NextgenCassava, International Institute of Tropical Agriculture (IITA), Abuja
- INQABA BIOTECH
- National Centre for Genetic Resources and Biotechnology (NACGRAB)
- National Horticultural Research Institute (NIHORT)
- National Agricultural Seed Council (NASC)

WELCOME ADDRESS BY THE VICE-CHANCELOR OF THE FEDERAL UNIVERSITY OF AGRICULTURE ABEOKUTA

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ADDRESS BY THE NATIONAL PRESIDENT OF THE GENETICS SOCIETY OF NIGERIA

I humbly and warmly welcome us to the 45th Annual Conference of the Genetic Society of Nigeria, holding in the Ancient and beautiful City of Abeokuta. If my memory will not fail me, the last time this conference was held in this University was 2004, about 19 years ago. This Campus was not as large and as developed as this. A lot of changes and transformation had taken place structurally, academically and administratively in the University. In this same vein, GSN had since evolved through thick and thin of our contemporary time and challenges as people, and as a Nation. These include but not limited to security challenge, COVID-19, Pandemic, longest academic industrial strike and cashless economic crisis that characterized the nation presently. I, therefore, need to sincerely appreciate those are present and those who will still be able to make it here. In spite of the above challenges, the Society is still surviving and able to stay above board. Permit me to enumerate some of our modest achievements since we came on board in October, 2022 as NEC.

Our Modest Accomplishments in The Last One Year

1. The GSN through NEC was able to organize the Grantsmanship workshop in July 2022 in order to build the capacity of members both at home and abroad, through hybrid presentations and discussion. The resource persons were drawn from Nigeria and abroad who are of high profile in grants attraction, grant management and track record of deliverables. Those who attended physically and virtually can testify to the gains, network built and contacts of funding organizations shared among participants. I encourage the participants to please utilize the knowledge acquired to improve their skill for grant attraction to better their chosen career especially the early career members
2. Re-design of our collapsed website to make it more robust, relevant and of good attraction to those who are visiting the website either for journal articles, and other useful information including bloggings. The website is now live, while upload of information is still in progress to populate it and make it more educative. Volumes of Journals earlier published are presently been scanned and uploaded to enhance open access of the articles for use anywhere across the globe. The present website will also enable us to submit, review, track and publish online, thereby reducing cost, time and stress of publishing our articles as a Society of professionals and academia.
3. The effort of our indefatigable Editor-in Chief had resulted to processing, reviewing and publishing of articles, in volume 36, and made available at this conference. The Nigerian Journal of Genetics is one of the most regular, current and of high standard Journals, not only in Nigeria but in the world. My deep appreciation is to the Editor-in-Chief and his team of reviewers and Associate.
4. All statutory functions at the level of Government policies such as crop and livestock release committee, bill on PVP, and, review of Seed Law that was recently approved by Federal Government were carried out as your representative in these committees.

Proposed Projects in View

1. Launching of Endowment Fund for GSN activities: The Society is planning to Launch the endowment fund for the Society in the fourth coming 46th annual conference in Abuja come September, 2023 this year. Details of this will be made available before the time. We therefore, urge our Ministries, Agencies of Government, NGOs, Universities and Industries, and other individuals to come to our aid. This shall be formally communicated to you soonest.
2. The Editorial Board of Nigerian Journal of Genetics will identify credible, relevant and indexing firms to abstract and make the Societies better visible.
3. Resuscitation of Zonal Branches of the GSN: The Zonal coordinators will be elected at this conference; they will be responsible for coordinating and managing activities of the Zones for better participation at the grass root. They will be encouraged to organize symposium, conferences, meetings and debate with the collaboration and approval of the NEC.
4. Resuscitation of New bulleting to be published quarterly by the office of the Vice President electronically, to keep people abreast of necessary information for members and the general public.
5. There is a great need as a society to publish a Book on Genetics and Changing environment occasioned by Global warming. We cannot afford to wait on until the environment will no longer

support and sustain crops and livestock production, which are essentials for human existence before we package, harness and document relevant findings that can mitigate the production constraints imposed by global warming and climate change. We need to make the results of coping strategies available to teach our students, and, to be proactive in further challenges of our tropical environment. I, therefore, challenge our senior colleagues to put their thought together and submit chapters in the book which is to be made available in the coming Conference in September. NEC had identified sub editors to handle processing, submission and editing of different sections of the Book. These Editors shall be formally commissioned for this noble task before we leave the conference. Submission and collation of chapters will be due by June ending, while final editing will be concluded by July 15, while final electronic version shall be available in July ending. All things being equal, printing will commence in August for copies to be available in September.

6. Membership Directory is urgently needed to know the real Geneticists, where they are located, their status, contacts, and disciplines. This became necessary to curb some situation where non-geneticists do conduct external post-graduate exams, carry out assessment of candidates for promotion to Professorial cadres, thereby graduating poor quality students. Similarly, such directory will help in constituting accreditation team during university course accreditation visits. The PRO, Associate Editor and the Assistant Secretary shall be responsible for this task and should conclude this by June ending. This will be uploaded in the website by July ending for people to access.
7. Production of customized seal of full professor of Genetics and Breeding with their Membership reference number is becoming necessary to apply to all thesis examined before putting signatures as a control measure against the abuse of our professionalism by non-members. This is a suggestion if approved by AGM of this year's conference.

Conclusion: This annual conference is unique in all situations. The LOC had worked seriously to make sure things come out as scheduled for good outing, please let us cooperate with them for hitch-free conference. The Communique drafting committee should please be sensitive to necessary messages to be made available for the general public from this conference.

Let me use this opportunity to once again congratulate Prof. O. B. Kehinde on his appointment as the Vice Chancellor of this prestigious University, the hard-working LoC committee members for putting in place befitting conference, the B o T members for the approval of new Fellows and to GSN members for the active participation in this year conference. I urge all of us to use this period to build a better network, exchange contacts, and follow all suggestions from senior colleagues during paper presentations especially the early career Geneticists, Breeders, and students so as to build a strong academic and performing career life for a better future. To my NEC team members, thank you for supporting me always. To our Moslem Colleagues, Ramadan Kareem.

God bless you all.

Prof. S. A. Olakojo
National President, GSN

CITATION ON PROFESSOR OLUSOLA BABATUNDE KEHIND FOR INVESTITURE AS FELLOW OF THE GENETICS SOCIETY OF NIGERIA (FGSN) ON MONDAY, MARCH 27, 2023 AT THE FEDERAL UNIVERSITY OF AGRICULTURE, ABEOKUTA, NIGERIA

Prof. Kehinde, Olusola Babatunde, a Professor of Plant Genetics and Breeding was born in Abeokuta, Ogun State on December 22, 1964. He attended the University of Ibadan where he obtained a B. Sc degree in Agricultural Biology (second class honours, upper division) in 1987; M. Sc in 1990 and a Ph.D. in 1994.

He began his academic career at the University of Agriculture, Abeokuta in March, 1994 as Assistant Lecturer in the Department of Plant Breeding and Seed Technology and rose through the ranks to become a Professor in 2007.

Prof Kehinde has served the University in various capacities which included: Ag. Head, Department of Plant Breeding and Seed Technology (2004-2008); Director, Graduate Records and Career Centre (2008-2009); Dean, College of Plant Science and Crop Production (2009-2011); Director, Institute for Human Resources Development (2011-2013); member, FUNAAB Governing Council (2009-2013). He has also been chairman/member of many notable committees in the University. He was the Deputy Vice-Chancellor (Development) between Nov 7, 2021 and October 31, 2022. He became the Acting Vice-Chancellor on November 01, 2022, a position he held until March 7, 2023 when he was appointed as the 7th Substantive Vice-Chancellor.

He was the National Secretary, Genetics Society of Nigeria (2004 -2006). He is a recipient of many fellowships and grants, both personally and for the university, some of which are: Graduate Fellowship Programme at IITA, Ibadan; Chinese Fellowship Programme at the Chinese Academy of Agricultural Sciences, Beijing; grants for research studies and the establishment of Centre of Excellence in Agriculture. He was a Visiting Lecturer at the Mendel University in Brno, Czech Republic. He has attended leadership courses at the Galillee International Management Institute (GIMI), Israel; London Business School, London; and Graceland College, Kansas, USA.

Prof. Kehinde was a member of the National Technical Working Group (Agriculture) of the Vision 20:2020, as well as the Study Group that reorganised the National Agricultural Cooperative and Rural Development Bank into the Bank of Agriculture.
He was the pioneer Ag. Dean, School of Agriculture, Lagos State University (2016-2019).

He is a consultant to several international and national organisations and agricultural farms. He has attended many conferences, workshops and exhibitions nationally and internationally.

Prof. Kehinde is well published Locally and Internationally and has graduated several doctorate degree holders and numerous undergraduate students. He belongs to several professional associations and is a Fellow, Institute of Health and Safety, Canada (FIHS) and Fellow, Applied Information Management Professionals (FAIMP)

Professor Kehinde exemplifies town and gown relationship and was conferred with the title of Akinfimogbayi of Oke-Ona, Egba Kingdom.

He is happily married to Prof (Mrs) Iyabode Kehinde and they are blessed with children.

CITATION ON PROFESSOR EMMANUEL HALA KWON-NDUNG FOR INVESTITURE AS FELLOW OF THE GENETICS SOCIETY OF NIGERIA (FGSN) ON MONDAY, MARCH 27, 2023 AT THE FEDERAL UNIVERSITY OF AGRICULTURE, ABEOKUTA, NIGERIA

Prof. Emmanuel Hala Kwon-Ndung was born in Ganawuri, Riyom LGA of Plateau State on the 17th December 1964. He attended EKAN Primary School Ganawuri (1973-1978) and later Boys' Secondary School Gindiri from 1978 to 1983. He enrolled at Ahmadu Bello University, Zaria in 1984 and graduated in 1988. After the compulsory NYSC in Akwa Ibom State in 1989, he proceeded to the University of Jos and by January 1991, he bagged a Master of Science degree in Cytogenetics and Plant breeding and a Ph.D from the same University in 1999.

He started his research career at the National Root Crops Research Institute in 1991 as Research Officer 1 (Potato breeding) before moving to the National Cereals Research Institute (NCRI), Badeggi Niger State in 1992 on the same rank. He worked in NCRI as a breeder in the Sugarcane Research Programme and successfully delivered on the mandate of the Institute. He introduced an innovative modified area cross in 1994 which produced promising seedlings and later initiated the novel research work on mutation breeding which later led to the release of three outstanding indigenous smut resistant industrial sugarcane varieties for commercial cultivation in Nigeria. Along with his colleagues, 7 other varieties of sugarcane with different traits were released by Prof. Kwon-Ndung while in NCRI. He joined the services of the Nasarawa State University in 2005 as an Associate Professor (subject to favorable external assessment) and he became a full Professor in 2008. He later joined the Federal University of Lafia in September 2012 where he is currently serving as the Director, Centre for Energy Studies.

He has previously served as the pioneer Resident Scientist of NCRI at the Savanah Sugar Company Numan, Adamawa State, Head of NCRI out station in Bacita, Kwara State, REFILS Team leader for Taraba State, National Coordinator for the NCRI-IPGRI Acha project and has been a many-tenure Head of Department, Dean of the Faculty, Chairman Committee of Deans and Directors, two-term member of Governing Council representing Senate. He has also served as a member of the Board of Trustees (BOT) of Bingham University Karu (2014 to 2019). Outside the University, he has served as Chairman of the Governing Council of Emergency Crisis and Risk Management Institute, Sub-Committee Chair on Biotechnology for the National Science, Technology and Innovation Policy of the Federal Ministry of Science and Technology, member of National Biosafety Technical Committee and is a current member of the TETFUND Standing Committee on Research and Development.

He is a member of several Professional Societies including Genetics Society of Nigeria, where he is the Immediate Past President, Biotechnology Society of Nigeria, Agricultural Society of Nigeria, Botanical Society of Nigeria, African Crop Science Congress, West Africa Plant Genetic Resources Network, American Society of Plant Biologists and Global Facility Network for Underutilised Species and founding member of African Plant Breeders Association.

He joined the Genetics Society of Nigeria in 1987 as student member at the Ahmadu Bello University Zaria and has served the Society in many capacities as member of Constitution Review Committee, member Electoral committee, Vice-President from 1997 to 1999, and as a two-term President from 2016 to 2021. His tenure witnessed a transformative leadership in GSN and of note is the incorporation of the Society with CAC on 24th April 2018.

Prof. Kwon-Ndung, a well published scientist has accessed a number of research grants in his career and is also a winner of the Third World Academy of Sciences postdoctoral fellowship (2004-2005) and is a Fellow of the Academy of Science for the Developing World (TWAS).

CITATION ON DR. PHILLIP OLUSEGUN OJO FOR INVESTITURE AS FELLOW OF THE GENETICS SOCIETY OF NIGERIA (FGSN) ON MONDAY, MARCH 27, 2023 AT THE FEDERAL UNIVERSITY OF AGRICULTURE, ABEOKUTA, NIGERIA

Dr. Phillip Olusegun Ojo, the Director General of National Agricultural Seeds Council (NASC), is an astute seed expert trained both nationally and internationally in Seed Science and Seed Industry development. He attended the Mississippi State University and Iowa State University, USA. Dr Ojo holds a Bachelor of Science (BSc) and Master of Science (MSc) in Agriculture from University of Ife now Obafemi Awolowo University, Ile-Ife and Ph.D. in Policy Analysis from University of Abuja, Nigeria and was appointed the DG, NASC in May, 2015 and reappointed as Director General by Mr President on the 26th of May 2019.

Dr. Ojo started as Seed Certification Officer from the year 1985 to 1986 and rose through the rank to become Regional Seed Certification and Quality Control Officer, and later Director Seed Certification, Quality Control, Crop Registration and Release for many years before he was appointed the Director General.

He has superintended over many agricultural innovations and technologies in the Seed Sector ranging from the development of Seed Policy, introduction of Plant Variety Protection –PVP, coordinated several Bill and Melinda Gates interventions including: BASIC -the National Seed Tracker, third party certification scheme, introduction of Molecular diagnostics techniques certification, IMAGE Project, YIIFSWA etc. He mentored many seed experts in Nigerian seed industry and beyond.

He is leading the transformation of the NASC in Nigeria to becoming the Centre of Excellence for Seed Industry in West Africa and has presented several technical papers on seed quality control, seed industry development and attended several international workshops globally.

Dr. Ojo is a member of the International Seed Testing Association (ISTA); Governing Board Member of AfricaSeed -African Union, member of West Africa Seed Committee (WASC/COASem), the Chair of National Seed Committee, Nigeria, member National Agricultural Seeds Council Governing Board, member of Agricultural Society of Nigeria, member Board of Trustees of Nigerian Plant Breeders Association (NPBA), a member of the Association of Seed Scientists of Nigeria (ASSN).

He has authored over 20 international academic journals on seed production, processing, quality control and seed industry development.

As NASC DG, he is charged with the responsibility of supervising the regulation and development of the Nigerian seed industry.

Dr Phillip Olusegun Ojo is married to Mrs Comfort Ojo and their marriage is blessed with four lovely children.

CITATION ON PROFESSOR CHRISTIAN OBIORA NDUBUISI IKEOBI FOR INVESTITURE AS FELLOW OF THE GENETICS SOCIETY OF NIGERIA (FGSN) ON MONDAY, MARCH 27, 2023 AT THE FEDERAL UNIVERSITY OF AGRICULTURE, ABEOKUTA, NIGERIA

Professor Christian Obiora Ndubuisi Ikeobi was born to the family of Sir Dennis Chukwuemeka and Lady Virginia Akuoma Ikeobi (both of blessed memories). He hails from Ozubulu in Anambra State.

Christian Ikeobi attended several primary schools for his primary education first because his parents were school teachers and were always being transferred, and secondly due to the exigencies of the Nigerian Civil War. He finished his primary education in 1971 at St. James' School, Uga. In Anambra State obtaining the First School Leaving Certificate with Distinction.

Christian thereafter proceeded to the Dennis Memorial Grammar School, Onitsha for his secondary education and completed this in 1976, passing the West African School Certificate examination in Division One.

Christian was admitted into the then University of Ife, Ile-Ife in 1977 for a five-year degree programme in Animal Science and graduated in 1982 with a Bachelor of Agriculture degree in the Second Class Honours, Upper Division.

After the mandatory National Youth Service Corps programme which he did in Ogun State, Christian proceeded to the University of Ibadan, Ibadan for his postgraduate studies in 1983. He obtained the degrees of Master of Science in Animal Science in 1984 and Doctor of Philosophy (PhD) in Animal Breeding and Genetics in 1990.

Christian Ikeobi was employed as Lecturer II in the Department of Animal Breeding and Genetics, University of Agriculture Abeokuta in 1990 and through the ranks to become a Professor in 2003.

He has held several administrative positions in the University such as:

1. Coordinator, Department of Animal Breeding and Genetics, 1990 - 1993.
2. Ag. Head, Department of Animal Breeding and Genetics, 1996 - 1997.
3. Head of Department, Department of Animal Breeding and Genetics, 2009 - 2011.
4. Dean, Student Affairs, 2005 - 2008.
5. Dean, College of Animal Science and Livestock Production, 2011 - 2015.
6. Director, Institute of Food Security, Environmental Resources and Agricultural Research, August 2021 to January 2022.
7. Deputy Vice-Chancellor (Academic), January 2022 to date.

In addition, Professor Christian Ikeobi has served as Chairman of over 40 committees in the University and member of more than 60 committees. For example, he has served as Chairman of the following committees Time-Table Committee, Student Welfare and Hostel Management Committee, Student Disciplinary Committee, University Sports Committee, Senate Committee on Examination Results, Senate Coordinating Committee on Examination Results, Examination Committee, Senate Academic Planning and Curriculum Committee, FUNAAB Schools Management Board, among several others.

A member of the University Senate, Professor Christian Ikeobi has served as a Senate Representative in the Governing Council (2014 - 2018), a Senate Representative in the Joint Council / Senate Selection Board for the Appointment of Vice-Chancellor (2006], and a Senate Representative in the Staff Disciplinary Committee. He has also served as a member of several Council Committees such as Finance and General Purposes Committee, Appointment and Promotions Committee for Academic Staff, Appointment and Promotions Committee for Non-Teaching Staff, etc.

Prof Ikeobi has successfully supervised more than 150 final-year students' projects, 36 M. Agric. dissertations and 20 PhD theses. Many of his former proteges have risen to the rank of Professor in several universities.

Prof. Ikeobi has more than 180 publications in reputable journals, conference proceedings and technical reports.

He has received several awards such as

1. CIDA Young Scientists Award for the World Congress on Genetics Applied to Livestock Production. GUELPH, CANADA, 1994.
2. Commonwealth Fellowship Award tenable in Roslin Institute, UK, 2000 - 2001.
3. ILRI Fellowship, Kenya, 2001 - 2003.
4. Fellowship of the Nigerian Institute of Animal Science, (FNIAS), 2014.
5. Fellowship of the College of Animal Scientists of Nigeria. (FCASN), 2015.
6. Fellowship of the Nigerian Society for Animal Production, (FNSAP), 2016.
7. Fellowship of the Animal Science Association of Nigeria (FASAN), 2018.
8. TETFund Research Grants (Several years ago)

Prof. Ikeobi is a member of several professional bodies and Academic associations.

He is happily married to Mrs. Elizabeth Olubamike Ikeobi and they both have three wonderful and gifted children.

CITATION ON PROFESSOR ANDREW SABA GANA FOR INVESTITURE AS FELLOW OF THE GENETICS SOCIETY OF NIGERIA (FGSN) ON MONDAY, MARCH 27, 2023 AT THE FEDERAL UNIVERSITY OF AGRICULTURE, ABEOKUTA, NIGERIA

Professor Andrew Saba Gana, is a Professor of Crop Production with specialization in Plant Breeding and Genetics. He hails from Emindayisa in Edati Local Government area of Niger state. He had his primary and secondary education at LEA Primary School, Bologi (1970-1976) and Government Science College, Kutigi (1976-1981) respectively. He graduated from University of Sokoto now Usmanu Danfodio University, Sokoto for his B Sc. Agriculture in 1987. He won the University prize for the best graduating student of the Faculty and Sokoto River Basin Development's prize for the best graduating student in Animal Science. After the National Youth Service, he took appointment with Niger state Government as Education Officer and served at Government Science College Kagara, where he was Head of Department; and coordinated Agricultural Science Examinations in all the Science Schools in Niger state. Both his MSc and PhD were from University of Ilorin.

He took appointment with National Cereals Research Institute Badeggi, as Research Officer 1 and rose through the ranks to become Chief Research Officer. He worked as a rice breeder in the institute and was at a time head of the breeding unit. While at National Cereals Research Institute Badeggi, he worked variously on different aspects of rice improvement especially targeting African Rice Gall midge, iron toxicity and drought tolerant cultivars. He had a working collaborative research work with West African Rice Development Association (WARDA) now African Rice Center. He participated in the rice breeding activities of both lowland and upland rice ecologies. He was part of the Regional Rice Research group of WARDA, known as ROCARIZ. These activities led to the commercial release of the following rice varieties to farmers: FARO 54, 55, 56. Also he participated in the breeding and commercial release of FARO 62 which is currently being cultivated by farmers. He participated in the training of farmers across the country on rice related topics and guest lecturer to several Agricultural trainings. He was also involved in the supervision of outgrowers farms on seed production. He also trained seed officers from Agricultural Development Projects, National Agricultural Seed Council and farmers groups on good agricultural practices (GAP). He has served as consultant and facilitator to International Fund for Agriculture Development Value Chain Development Program Niger state (IFAD/VCDP - Niger state) on various intervention programs.

He joined the services of the Federal University of Technology, Minna as a Senior Lecturer and became a Professor in October, 2014. He has served as Head of Department of Crop Production, and also held responsibilities in committees and units of the University. He has supervised a total of 15 PhD students (seven as major supervisor and eight as co-supervisor). He is a member of Genetics Society of Nigeria, Crop Science Society of Nigeria and Association of Seed Scientists of Nigeria; he is currently serving as editorial member of the association. He has published about 112 articles in journals, book chapters, conference proceedings and technical papers. His Google scholar citation at present is 721. He has also served as external examiner to Universities at both undergraduate and postgraduate levels and assessed people for the rank of Associate Professor and Professor. He has won research grants that include University Base Research, TETFUND- National Research Fund and World Bank- African Center of Excellence- African Center for Mycotoxins and Food Safety. He is an Academic Board member of the Center. He is a Board member to some Non- Governmental Organizations and Private institutions. He is married to Mrs. Rachel L. Gana and is blessed with two children: Jude Boye and Hosea Soko Aminci

CITATION ON SULEIMAN DANGANA ABDUL FOR INVESTITURE AS FELLOW OF THE GENETICS SOCIETY OF NIGERIA (FGSN) ON MONDAY, MARCH 27, 2023 AT THE FEDERAL UNIVERSITY OF AGRICULTURE, ABEOKUTA, NIGERIA

Suleiman Dangana Abdul came into this world on the 17th Day of July 1963. He had his primary and secondary education in the present-day Niger State, where he obtained his primary and secondary school certificates in 1975 and 1980, respectively. He proceeded to the University of Jos in the same year where he stayed for four years and had his first degree in Botany graduating with second class upper division. He also, graduated from Ahmadu Bello University with M.Sc. Crop Breeding in 1990. In the same year he proceeded to University of Cambridge where he obtained MPhil and PhD degrees in Plant Breeding in 1991 and 1994, respectively.

After his National Youth Service year (1984-1985) he immediately started work as a Graduate Assistant with the then Abubakar Tafawa Balewa College, Ahmadu Bello University, Zaria, formerly Federal University of Technology, Bauchi. The College was demerged from ABU, Zaria and made autonomous in 1988 still maintaining the name Abubakar Tafawa Balewa University, Bauchi (ATBU, Bauchi). He remained with ATBU, Bauchi and rose to the position of Professor of Genetics and Plant Breeding in 2007. During his stay in ATBU, Bauchi he attended more than 21 courses and workshops towards improving his skills. Over the period of his academic career, he has taught 17 undergraduate courses and 11 postgraduate courses. His research areas include genetic improvement of wheat, cowpea, fonio (Acha), sesame with emphasis on biotic and abiotic stress and conservation of plant genetic resources. He has successfully supervised 13 PhDs and six (6) MScs. He is currently supervising six (6) PhDs and ten (10) MScs. Nine (9) of those that he successfully supervised for PhD are now Professors.

He has more than 60 published papers, a chapter contribution and accepted textbook for publication to his credit. In addition to these are five technical reports. He attended several scientific conferences within and outside Nigeria. He is a member of Genetic Society of Nigeria (GSN), a life member of Botanical Society of Nigeria (BOSON), a member of British Society of Plant Pathology (BSPP) and Botanical Society of America (BSA).

Abdul was a beneficiary of the TETfund National Research Fund award in 2015 and a member of the TETFund National Research Fund Screening and Monitoring Committee since 2016. He was external examiner at both undergraduate and postgraduate level to various universities in Nigeria. He was a beneficiary of the Cambridge Commonwealth/ODA Award (1990 –1991), Cambridge Commonwealth Trust Bursary (1992), British Society for Plant Pathology Award (1992), Alice Evans Memorial Award, Wolfson College, University of Cambridge (1990 – 1993), Association of African Universities' s Senior Executive attachment on Technology uptake, National University of Science and Technology Bulawayo, Zimbabwe (2015). He is a Fellow, Cambridge Commonwealth Society since 1991.

At various times he was Director, Industrial Training, Director Research & Innovation, and Dean, School of Postgraduate Studies all in ATBU, Bauchi. He was a member of the University Governing Council and its various committees for 14 years, representing Congregation and Senate at different times. Abdul was at various times the Deputy Branch Chairman, Branch Chairman, National Internal Auditor, and member and Convener of several Committees of the Academic Staff Union of Universities (ASUU) from 1996 to date. Presently, Abdul is the Convener, University Transparency and Accountability Solution (UTAS) an Enterprise Resource Planning Software developed by ASUU. At various times he was the Protem Chairman, University of Jos Alumni Association, Bauchi Chapter (1995-2008), Secretary General, Cambridge University Nigeria Society (1990-1991).

Abdul is happily married and blessed with children.


GSN CONFERENCE - OGUN 2023
GENETICS SOCIETY OF NIGERIA
45
ANNUAL
GENETICS AND AGRICULTURAL TRANSFORMATION:
PATHWAY TO FOOD SECURITY
MALACHY O. AKORODA

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KEYNOTE ADDRESS DELIVERED AT THE 45TH ANNUAL CONFERENCE OF GENETICS SOCIETY OF NIGERIA

GENETICS AND AGRICULTURAL TRANSFORMATION: PATHWAY TO FOOD SECURITY

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ANIMAL BREEDS IN AGRICULTURAL TRANSFORMATION FOR FOOD SECURITY

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INTRODUCTION

ANIMAL BREEDS A NATIONS HERITAGE

Animal genetic resources for Food and Agriculture (**AnGR**), also known as **Farm Animal Genetic Resources** or **Livestock Biodiversity**, are genetic resources (i.e., genetic material of actual or potential value) of avian and mammalian species, which are used for food and agricultural purposes. AnGR is a subset of and a specific element of agricultural biodiversity.

AnGR can be embodied in live populations or in conserved genetic materials such as cryoconserved semen or embryos. The diversity of animal genetic resources includes diversity at species, breed and within-breed level. Known are currently 8,800 different breeds of birds and mammals within 38 species used for food and agriculture. The main animal species used for food and agriculture production are cattle, sheep, goats, chickens and pigs. In the livestock world, these species are often referred to as "the big five". Some less-utilized species include the dromedary, donkey, bactrian camel, buffalo, guinea pig, horse, rabbit, yak, goose, duck, ostrich, partridge, pheasant, pigeon, and turkey.

One of the greatest threats to livestock diversity is pressure from large-scale commercial production systems to maintain only high-output breeds. Recent molecular studies have revealed that the diversity of today's indigenous livestock populations greatly exceeds those found in their commercial counterparts

Despite the importance of animal genetic resources, their diversity has been continually decreasing over time due to genetic erosion caused by:

- (Indiscriminate) cross-breeding
- Introduction/increased use of exotic breeds
- Lack of/weak AnGR management policies, programmes or institutions
- Use of breeds that are not profitable/competitive or have poor performance
- Intensification of production or decline of traditional production systems or small farms
- Disease/disease management
- Loss/lack of grazing land or other elements of the production environment
- Inbreeding or other problems in the management of breeding
- Migration from countryside/uptake of alternative employment
- Changes to consumer/retailer demand/ habits
- Mechanization
- Unappreciated value of locally adapted breeds
- Unspecified economic/market factors
- Climate change
- Globalization, trade liberalization or imports
- Lack of infrastructure or support for production, processing or marketing

And majorly by aging farmers or lack of interest among the young generation"

The State of the World's Animal Genetic Resources.

The Food and Agriculture Organization of the United Nations (FAO) took the initiative and published two global assessments of livestock biodiversity: *The State of the World's Animal Genetic Resources for Food and Agriculture* (2007) and *The Second Report on the State of the World's Animal Genetic Resources for Food and Agriculture* (2015).

Although many diverse species and breeds of animals are currently available for food and agricultural production, there is more work to be done on classifying their risk of extinction. In 2014, 17% of the World's farm animal breeds are at risk of extinction and 58% are of unknown risk status, meaning that the problem may be underestimated. The world's pool of animal genetic resources is also currently shrinking, with rapid and uncontrolled loss of breeds and conjointly their often uncharacterized genes. Nearly 100 livestock breeds have gone extinct between 2000 and 2014 (FAO 2015). With the loss of these breeds comes the loss of their unique adaptive traits, which are often under the control of many different genes and complex interactions between the genotype and the environment. In order to protect these unique traits, and the diversity they allow, collaborative global efforts towards the characterization and management of these genetic resources must be made. Unlike plants, which can be easily conserved in seed banks, a large portion of livestock genetic diversity relies on live populations and their interactions with the environment.

With recent advances in molecular genetics providing data on the history and current status of animal genetic resources, progress is being made in the characterization and management of animal genetic resources for food and agriculture. Genetic markers and molecular studies are being used to characterize livestock diversity and to reconstruct the events that have shaped the present diversity patterns, which includes ancestry, prehistoric and historical migrations, admixture, and genetic isolation, with the exploration of the past in order to understand the trends and to better characterize the current state of animal genetic resources. In 2009, cattle became one of the first livestock species to have a fully mapped genome and that was six years after the completion of the human genome project,

Policy for animal genetic resources

In May 1997, a body of the FAO, the Commission on Genetic Resources for Food and Agriculture (CGRFA) established an Intergovernmental Technical Working Group on Animal Genetic Resources for Food and Agriculture (ITWG-AnGR). The ITWG-AnGR's objectives are to review the situation and issues related to agrobiodiversity of animal genetic resources for food and agriculture. The body is expected to make recommendations and advise the Commission on the agrobiodiversity, and consider progress resulting from proposed interventions. With many partners in different countries, the group successfully produced the First Report on the State of World's Animal Genetic Resources, which served as the basis for creating the Global Plan of Action for Animal Genetic Resources (GPA).

Characterization of animal genetic resources

For proper management, characterization of animal genetic resources is a prerequisite. With recent advances in molecular genetics, many technologies capable of determining genetic profiles have provided us with tools to better understand livestock origin and diversity. These technologies include the whole genome sequencing, shotgun sequencing, RNA sequencing and DNA microarray analysis. These techniques allow us to map genomes and then analyze their implications through bioinformatics and statistical analysis. Molecular genetic studies, especially Genome-wide association Studies (GWAS) and whole-genome sequencing allow adaptive traits to be linked to genomic regions, genes, or even solve mutations. For example, in cattle, single genes with polymorphic effect had been found to be responsible for most phenotypic traits such as horn size, meat quality, gait, and prenatal growth.

Genes that affect observable traits with statistically detectable associations with those traits are found on specific regions of DNA, such genes are localized as Quantitative Trait Loci (QTL). However, DNA polymorphisms that are not linked to specific traits are now more commonly used as markers for genetic diversity studies. Different levels of genetic diversity information

can be obtained from different kinds of genetic markers. For example, autosomal polymorphisms are used for population diversity estimates, estimation of genetic relationships and population genetic admixture, whereas mitochondrial DNA polymorphisms are used to detect geographic regions of domestication, reconstructing migration routes and the number of female founders. Drawing such inferences is possible because mitochondrial DNA sequences are transferred only through egg cells of the female.

From recent molecular studies, it has been shown that individual breeds within species show variation at only about 1% of the genome, whereas the variation between species is about 80%. Additionally, breeds with well-defined and appreciated traits tend to be inbred and have low genetic diversity, while non-descript local populations tend to have high molecular genetic diversity.

NIGERIA'S ANIMAL POPULATION (000,000)

Animal specie	Population	Import ($)
Cattle	20.6	254 mi
Sheep	48.0	12.3 mi
Goats	84.0	9.0 mi
Pigs	9.0	11.2 mi
Poultry	305.0	18.2 mi
Rabbits	5.4	???

FAOSTAT 2020

THE BREEDERS' ASSIGNMENT FOR ENHANCED FOOD SECURITY:

- Increased animal protein production
- Increased body weight
- Increased milk production-----1000 kg to 20,000 kg /305 days
- Increased egg production----100 to 250/280 /ann
- In order to increase animal protein consumption ----5 g/c/d to 25/50 g/c/d

ADEQUATE REQUIREMENT

For better understanding of breeds and within specie classification, Nigeria requires additional specialized:

- Animal Research Centres
- Improved environment for sustainability---Feed, housing, drugs (herbal or regular)
- Extension workers
- Veterinary Officers

FOR BREEDS TO BE TRANSFORMED

- General collection
- Characterization
- Selection
- Crossbreeding for traits of interest.
    * higher body size
    * Improved reproduction
    * better Adaptation
    * acceptability
    * marketability

Nigeria needs to reduce her foreign exchange flight on food importation such as with:

- Milk and Eggs

Reduce importation for animal protein consumption such as for:

- Poultry and meat animals

Stem rural urban migration

- From initial 30 to current 75%
- Emphasize use of contract growers in the rural and semi-urban areas around projects.

FOR RESILIENCE AND SUSTAINABILITY

- We have to develop our local resources
- Use both conventional and biotechnology tools for rapid selection
- Concentrate on the best genes for production and reproduction

BREED DEVELOPMENT;

- Genetic progress depends on generation interval
    - Poultry 5 - 8 months
    - Pigs 8 months to 1 year
    - Small ruminants 1 year to 18 months
    - Cattle 3 to 4 years

In Nigeria the registration format required 6 to 9 generation of crossing and selection for sustainable animal breed development and registration. As an example:

FIRST CROSS (F_1)	E X L -----50:50--EL
SECOND CROSS (F_2)	E X EL----75:25 EEL
THIRD CROSS (F_3)	L X EEL--- 37.5: 62.5 EELL
FOURTH CROSS (F_4)	E X EELL---68.75: 31.25 EEELL
FIFTH CROSS (F_5)	L X EEELL----34.375: 65.625 EEELLL

It is highly essential and highly desirable that the constitution of the locally bred stocks should not be lower than 65% of the indigenous component. This therefore will not only involve backcrossing but also crisscrossing to ensure stability.

ESSENTIALS

Major essentials are the use of only local female line which is widely available locally. In combination with only a few exotic males/Semen to local males in a criss-cross or back crossing fashion.

BIOTECH. APPLICATION

To date, Biotechnology tools are available for reproduction, growth evaluation, efficient feed utilization, health and disease control for rapid food production and security in animal development. For example, there is currently:

- Use of Fecundity genes for reproductive efficiency
- Genomics selection for growth factors IGF I & II genes
- Nutrigenomics for efficient feed utilization
- Use of Probiotics for improved feed consumption
- Selection for Immune genes for adaptability
- Gene Editing
- Somatic Cell Nuclear Transfer SCNT

For animals that are genetically engineered through the targeted modification of the somatic cells

CURRENT TRENDS IN ANIMAL IMPROVEMENT - GENE EDITING:

What is Gene/Genome Editing?

In livestock, genome editing has the potential of bringing about significant improvements in productivity, health and welfare. The industry is facing an increasing demand for animal-based foods to feed the increasing human population, this means there is a need for a more sustainable approach to animal production that considers climate change, deforestation, conservation of biodiversity at the same time ensuring the animal health and welfare. Genome editing technology is a set of tools that precisely modifies an organism's genetic components in four basic procedures:

- Use of mega nucleases such as Zinc Finger Nucleases (ZFNs),
- Transcription Activator-like Effector Nucleases (TALENs),
- Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR),
- Somatic Cell Nuclear Transfer (SCNT).

These methods are used to cut the DNA at specific places to trigger a repair mechanism which can either be used to rejoin broken ends of the DNA with or without the use of a template and also allows the insertion of new sequences within the normal gene of the organism.
While the CRSPR technique is most widely used due to its simplicity, efficiency and low cost, its application in ruminants still requires advanced reproductive technologies for the delivery of editing components into reproductive cells or zygotes.

In chickens, scientists have used genome editing to introduce growth hormone genes resulting in birds that grow faster and produce more meat. In pigs it has been used to improve efficiency of feed conversion into meat resulting in higher meat per kilogram of feed. It has been used to knock out the Myostatin gene in cattle and sheep resulting in the double muscling phenotypes for superior meat production (Tait-Burkard et.al. 2019).

- The technologies have therefore created new changes for:
    - Increased genetic gain
    - Efficiency of production
    - Removal of lethal genetic variants
    - Introduction of desirable phenotypes
        - Such as for disease resistance
        - Thermo-tolerance
        - Hornlessness

*Inactivation or repairs of undesirable genes.

THE GLOBAL PLAN OF ACTION FOR ANIMAL GENETIC RESOURCES (GPA)

In 2007, the GPA was adopted by 109 countries as the first agreed international framework for the management of livestock biodiversity. The implementation of the GPA is overseen, monitored and evaluated by the CGRFA. The funding for this program arrives from a wide range of actors, under the guidelines of the *Funding Strategy for the Implementation of the Global Plan of Action for Animal Genetic Resources.*

In 1992 there was the Convention on Biological Diversity. which focuses on the access and benefit sharing of animal genetic resources. In October 2014, an agreement was signed to provide a legal framework for the fair and equitable distribution of benefits arising from the utilization of all genetic resources, including animal genetic resources for food and agriculture. The agenda is currently known as the Nagoya Protocol which entered into force on 12 October 2014.

Within the Agenda 2030 for Sustainable Development, AnGR are addressed under the target 2.5 which stated that: *"By **2020, countries must maintain the genetic diversity** of seeds, cultivated plants and farmed and domesticated animals and their related wild species, including through soundly managed and diversified seed and plant banks at the national, regional and international levels, and promote access to and fair and equitable sharing of benefits arising from the utilization of genetic resources and associated traditional knowledge, as internationally agreed."*
This is to be monitored by the following indicators:

- Number of plant and animal genetic resources for food and agriculture to be secured in either medium or long term conservation facilities.
- Proportion of local breeds to be classified as being at risk, not at risk or unknown level of risk of extinction.

Although these policies can have some negative consequences, they are nonetheless important. Lack of adequate policies can lead to the insufficient capacity to manage AnGRs, further the loss of genetic diversity and marginalization of relevant stakeholders, such as pastoralists, who are valuable players in maintaining livestock diversity.

To help regulate the ownership of genetic resources and control their utilization is one example where policies are necessary. Patenting of genetic resources is one approach that has been applied. Patenting of animal genetic resources reached its apex in the late 1990s, focusing on Expressed Sequence Tags (ESTs) and Single Nucleotide Polymorphisms (SNPs) with associations in economically important traits. SNPs are important in Marker-Assisted Breeding, for the identification of traits such as meat or milk quality. At the same time, patenting activity involving transgenic livestock also increased. However, work on patents and characterization of AnGR declined sharply from 2001, caused by a combination of factors including an increasingly restrictive approach to the patentability of DNA sequences by patent offices and a lack of markets for food products from Transgenic animals. However, trends in activity arising from genome sequencing projects merit careful attention with regard to their implications (positive or negative) for animal genetic resources management.

FUNAAB's involvement in SNP utilization and regulation has focused on the IGF1 and 11 genes which had been registered for our FUNAAB-Alpha birds with its eventual utilization as Genetic Marker for our animal growth and reproductive abilities. We have successfully Sequenced and submitted FUNAAB Alpha Insulin-Like Growth Factor 1(IGF1) gene to the International GeneBank with the accession numbers GenBank MK439387-MK439419 January 2019 for the following sequences: Bank It 2186795 seq1 to 20 and BankIt 2186460 seq1 to 13 Accessible at International GeneBank gb-admin@ncbi.nlm.nih.gov, Bethesda, Maryland USA.

CONCLUSION

- Policies are necessary to help regulate the ownership of genetic resources and control their utilization.
- Patenting of genetic resources is one approach that has been applied. Patenting of animal genetic resources reached its apex in the late 1990s, focusing on expressed sequence tags (ESTs) and single nucleotide polymorphisms (SNPs) with associations in economically important traits such as meat or milk quality.
- Livestock and their products should be used sustainably, developed and ultimately conserved.
- National planning should integrate "consumer affairs, human health matters, and the management of new biotechnologies, as well as physical and spatial planning of animal production in the context of urban expansion and protected areas.

- There is the need to have Nigeria's animal online database such as FAOLEX, one of the largest online databases run by FAO for monitoring policies, national laws, treaties and regulations on food, agriculture and renewable natural resources, including animal genetic resources in Nigeria.

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PLANT GENETICS AND BREEDING: A PANACEA FOR FOOD SECURITY

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ABSTRACT

Starting with a proper definition of panacea and security, the paper assured the reader that geneticists and breeders are being supported as far as possible with interventions from the government, international donors, and individual philanthropists to carry out their functions in universities and research institutes, most especially from 1960 to date. Plant breeders play a critical role in crop improvement and they must have a deep knowledge of introductory and advanced plant breeding, statistics, and basic genetics, quantitative genetics, as well as experiences and skills in practical breeding, experimental design, and field work. All geneticists and breeders need to be trained in scientific writing. A brief review is also presented on how the contribution of geneticists and breeders to abiotic and biotic stress resistance has continued to increase yield thereby sustaining the drastically increasing population – a kudos to the plant geneticists and breeders. The population rose from 47 million in 1961 to 163 million in 2011 at an estimated rate of 232,000 per annum and proportion of people that had no access to food drastically reduced, although food still had to be imported to subsidize the shortages here and there. Crop yields have improved drastically in research stations and on-farm demonstration fields supervised by scientists but lags behind in farmers' farms – a yield gap. The Federal Government of Nigeria finally solved the problem of availability of quality seed by providing the initial capital for hybrid maize research which, in turn, led to the establishments of private seed companies about 40 years ago. Other areas that need urgent support include general agronomic practices, particularly timing and rate of fertilizer application. Many publications have been sent out which, if reviewed and the findings and recommendations applied properly, Nigeria would have arrived in a panacea. To reach a panacea and food security quickly, interventions must reach the farmers both financially and by proper training. Unfortunately, interventions so far has not reached the grass root; that is farmers. The author discussed three examples of interventions reaching the grass root, which are (i) IITA Youth Agripreneurs (IYA) and the Start Them Early Project (STEP) for secondary school students, (ii) Tony Elumelu Entrepreneurs Project (TEEP), and (iii) Youth Farmers Cooperatives. These and perhaps several others are already revolutionizing agriculture all over Africa with Nigeria in the lead. The author ended the paper by suggesting areas that could hasten reaching a panacea for food security.

INTRODUCTION

One important keyword in the title of this presentation that needs clarification for proper understanding is *panacea*. Panacea is a medical term used to describe a solution or remedy for all difficulties or diseases; for example, panacea of all corporate ills. Some other meanings are universal cure for all ills, universal remedy, sovereign remedy, heal all, elixir, perfect solution, something that can solve all problems of people. Where and when a panacea occurs, there is complete cure, relief or remedy from a disease or, by extrapolation, a difficulty. The other important word in this title is *security*. It means to feel safe, confident, and free from worries. We are here to examine the extent to which Genetics and Plant Breeding (or, Geneticists and Plant Breeders) have solved the 'difficulty or disease' of food insecurity or instability in Nigeria. We all understand that the solution to the problem of food security does not rest solely with plant geneticist and breeders, but they have a central, crucial role to play in it. Other important

players in it are research institutes, universities, seed companies, along with farmers for whom all the other players are working. We shall review the creation of research institute, universities, and seed companies in Nigeria. Subsequently, we shall look at the population versus food production and how the geneticists and breeders have tackled the challenge of feeding the Nigerian population. We conclude by giving some suggestions on the bottom-up approach to research and extension, specifically in genetics and plant breeding.

Creation of Research Institutes, Universities, and Seed Companies

Geneticists and Plant Breeders have not been abandoned in Nigeria. They are called upon by government officials to attend to one problem or another from time to time. In response to the yearnings of these scientists, the Federal Government has established many research institutes to cater for the many crops of the nation. Among the institutes are: Cocoa Research Institute of Nigeria (CRIN), Nigeria Institute for Oil Palm Research (NIFOR). National Cereals Research Institute (NCRI), Institute of Agricultural Research-Zaria (IAR-Zaria), Institute of Agricultural Research & Training (IAR&T), Nigeria Horticultural Research Institute (NIHORT), Rubber Research Institute of Nigeria (RRIN), and Lake Chad Research Institute (LCRI). Each institute was created primarily to conduct research on specific crops, including genetics and plant breeding. Furthermore, universities were established all over the country to conduct training, research, and community service. The efforts of university dons include both basic and applied research. Both research institutes and universities support their staff by sending them for higher degree training, visiting scientist positions, learned conferences, exchange visits to other universities and research institutes, etc. That way, the universities and research institutes keep abreast of latest developments, both within and outside the country, particularly their mandate crops.

Formation and establishment of seed companies – Of special interest to all crop scientists in Nigeria is the establishment of seed industry in the country. Hybrid maize, the handiwork of geneticists and plant breeders, prompted private seed industry development in Nigeria and the history of the two go hand in hand (Fakorede et al., 2022). Good quality seed of appropriate, high-yielding variety is the key to profitable modern farming. Improved seed is the cheapest, most cost-effective agricultural input for increasing yield per hectare of land. It makes farming more profitable and sets the limits to the economic benefits and production potential derivable from other agricultural inputs such as fertilizer, herbicide, pesticide and other components of good crop management. The attainment of increased productivity of a farmer's crop depends largely on the quality of the seed planted. Good management cannot produce good yields from a genetically low-yielding crop variety. Nigerian farmers gradually became seed-conscious and are willing to pay higher prices for quality seeds of improved varieties (Fajemisin, 2014).

The need for a coordinated and integrated national seed system, entirely under public sector management, was advocated by the Federal Government in 1969. It came to effect in 1976 named the National Seed Service (NSS), with the technical and financial assistance of FAO-UNDP. Dr. Adeyemi Joshua was the Nigerian co-leader. He nurtured the NSS with bold initiatives for manpower and infrastructural development across the national landscape. The headquarters, first located at Iwo Road, Ibadan was equipped with essential seed processing facilities as well as modest seed testing laboratories and improvised warehouses. The personality of Dr. Joshua inspired impressive working relationship with colleagues at research, ministry (state and federal), and parastatal levels while his co-workers were among the most motivated and devoted in the public sector. The NSS succeeded in decentralizing seed production with the creation of zonal headquarters at Zaria, Umudike and Jos where all the operations that were hitherto carried out at Ibadan headquarters (contract seed production and

seed processing) were also done. Additional federal government-assisted seed processing plants were also provided in Sokoto, Borno, Niger and Kwara States. Seed testing laboratories were completed and modestly equipped at the zonal headquarters as well as in Abuja. Many of the State ADPs (Kano, Ondo, and Kaduna) also had processing plants in their seed multiplication units (Fajemisin, 2014).

The National Seed Service, as the sole national agency responsible for the provision of good quality seed to farmers, produced foundation seed through contract seed growers. It also provided State Seed Multiplication Units and the ADPs with foundation seed for the production of certified seeds. NSS had to resort to the appropriate research institute for the provision of breeder's seed. Of course, NSS also has the responsibility for quality assurance through its seed certification unit. There was no strict rule guiding the marketing and sale of certified seed. This was done through the NSS directly, or through the State seed multiplication units or the ADPs, all at highly subsidized rate.

Despite the nation-wide framework for seed production, the seed system in Nigeria was never able to meet the requirement of supplying the seed needs of the farmer at the right time and place. The constraints militating against meeting the national seed requirements were many. Among the major ones were: absence of reliable information on effective demand for good quality seed, inadequate supply of breeder and foundation seed, inadequate funding of the largely public sector agencies, cumbersome financial procedures for the disbursement of the limited available funds, ad-hoc seed policy without due consideration to cost of production and marketing costs, and a weak national seed certification and quality control system.

The development of hybrid maize varieties adapted to the productive potentials of Nigeria exposed the stark inadequacy of our national seed system to embrace and sustain this new technology. Since the potential of this novel technology cannot be ignored, something had to happen to our seed production and delivery system

Sequel to a request by the Federal Government through the Technical Sub-Committee of the Green Revolution Council for advice on ways to implement the setting up of Seed industry in Nigeria, the Action Committee on Hybrid Maize Production met on March 16, 1982 to deliberate on the issue. The following people were present at the meeting: Dr. J. M. Fajemisin (Chairman), Dr. S.K. Kim (Maize Breeder, IITA), Dr. M. A. B. Fakorede (Maize Breeder, Obafemi Awolowo University), Dr. A. O. Obajimi (Maize Breeder, IAR&T), Dr. J. E. Iken (Maize Breeder, NCRI), Mr. Amir Singh (Project Manager, NSS), Mrs. K. A. Agbaje (Seed Technologist, NSS), Mr. O. A. Odegbaro (Agronomist, Federal Ministry of Science & Technology) and Mr. E. O. Matuluko (Extension Officer/Agronomist, Federal Department of Agriculture). Although Drs. A. Joshua and A. Tunde Obilana could not attend the meeting, their views were subsequently sought before writing the final report.

The Committee appraised the status of seed activities in Nigeria and confirmed that the only formal organization dealing with seed production in the country was the National Seed Service (NSS), a unit within the Federal Department of Agriculture. NSS produced foundation seed of some crops and distributed this to State Ministries of Agriculture for further multiplication. On its part, the NSS had, hitherto, encouraged morally, materially and financially the development of a Seed Multiplication Unit in each State. Unfortunately, the State Multiplication Units had not performed as effectively and efficiently as expected. Foundation seed sent to the States from NSS was most often not planted on time; the seed was often stored in unfavorable environments forgetting that seed is a living entity. Thus, when it was eventually planted, it had lost viability and, as such, the resources spent in producing the first stage foundation seed were wasted and the expectation that seed produced would be made available to the farmers was frustrated.

The Committee, therefore, strongly agreed that there was a need to develop a Seed Industry that would be directed towards getting enough seeds produced and used. This presumed that such an industry would find the most suitable ways of determining the real demand of the farmers for seed. It should also ensure that seed was produced, processed, stored and marketed in the most proper manner. It must be oriented towards serving the farmers. The Committee suggested that the government should look seriously into the setting up of Seed Enterprise(s) that would have effective hold on the farming situation of the country.

The Committee enunciated three broad forms of Seed Enterprise, stating clearly their advantages and disadvantages. They are: (i) Private Seed Companies, (ii) Government Enterprises, and (iii) Joint Public-Private Enterprises. After a rather exhaustive discussion of these forms of seed enterprise, the committee reached the following conclusions/recommendations (Fajemisin, 2014):

1. In order to salvage the country from impending danger of food production seriously lagging behind population, increased emphasis should be given to the production and distribution of improved seed/planting stock of our important crops. The Seed Industry is a lot more than seed production *per se*; it must be ensured that such seed is used which implies knowledge of the demand for such seed and good marketing facilities.
2. Considering the inadequacy of the present seed activities particularly the weakness in distribution, the government should encourage the setting up of commercial seed enterprise whose survival will be determined by the confidence it builds up with the farmer-consumers in terms of production and sale of verifiable good quality seed of high yielding crop varieties.
3. Such companies could be Joint Public-Private venture or be owned privately either by renowned foreign seed companies or by committed Nigerians who are aware of the special management problems of the Seed Industry, chief of which are (i) both production and marketing are seasonal, (ii) not most of the processes are under complete control of the operators; for instance, frequent changes of varieties, different climatic conditions, varying disease and pest threats all force sudden modification in production technology; and (iii) seed, the end product is a living material and must be handled carefully and used before it dies. If government wishes to remain in the seed industry, the relevant organization/unit must be accorded autonomous status and allowed to operate as a viable company in a competitive environment.
4. In order to develop a healthy, stable, and sustained seed industry, any seed enterprise interested in the development of proprietary crop (through the setting up of its own research unit) should not be prevented from doing so. Also, publicly developed cultivars or lines should be available to the privately owned company provided that (i) such company pays for the seed acquired and such seed is not restrictively made available to only one company. The money realized must be passed on to the Institution that developed such line, and (ii) the breeder must characterize the line/cultivars made available to the seed companies so that professional ethics can be protected. The proprietary cultivars developed by the Seed Company must be channeled through the Nationally Coordinated Trials and Variety Release Committee before seed of such varieties could be offered for sale to the farmers.
5. The role of the government should be that of encouraging the growth of viable commercial seed production. Loans could be made available to genuinely interested Nigerian individual/group who intends to go into seed enterprise. Such prospective body must show convincing evidence of expertise and commitment. Furthermore, the government should help in the provision or acquisition of land and granting some import concessions for the required machineries.
6. Finally, in view of the importance of the Seed Industry to the success of the current special projects being sponsored by the Federal Government such as the hybrid maize and

sorghum, the Committee strongly recommends that the Government should ensure that commercial seed enterprises are set up to a functioning level before 1985. In order to avoid monopoly and its attendant disasters, more than one such enterprise should be encouraged to be established.

The Director-General of IITA, Dr. Ermond H. Hartmans, was proactive. In June, 1982 he invited Mr. V. H. Verbought as a consultant to advise us in this regard. Mr.Verbought was, for many years, the Managing Director of Kenya Seed Company. He spent 10 days in Nigeria. He was charged to survey the situation in Nigeria as far as agricultural seed was concerned and make recommendation as to the future policy to be followed and actions to be taken to establish an efficient operating seed industry in Nigeria.

The followings are among his major recommendations:

1. He recommended that development of private enterprise operating in the seed industry should be encouraged and the policy should be made very clearly known both within the country and beyond its borders to attract the enterprises which will be interested and have the knowledge to invest in the seed industry. Once established, government should allow the seed industry the greatest possible freedom in the running of its commercial operations, that is, refrain from interference with its management organization, staffing, contracts, pricing policy, marketing and distribution.
2. The conditions for these companies should be made reasonably attractive so that a number of companies will be operating or start their operations within the near future and will then be free to develop and compete within, of course, the laws of the land.
3. Breeding material and seed of existing varieties developed by public institutions should be made available to these companies at reasonable terms and with the least possible restrictions. The terms and conditions at which this material is made available should be uniform to all parties concerned.
4. Private research by these companies should be very much encouraged and supported since industry operating in the "market-place" and having to make a return on investment is usually quite well geared to judge farmers' demand. Also, if a company is prepared to set up its own research facility, this does imply that the commitment is of a long-term nature and this must be considered as a big advantage.
5. After having strongly recommended charging private enterprise with the task to initiate and run the seed industry, a comprehensive package of duties remain to be carried out by publicly owned and funded institutions. One of the vital services which ought to be provided by government is quality control. It is also important that quality control service should not be mixed with a seed production unit.
6. The subject of seed testing and quality control is rather emphasized because of the extreme importance which ought to be attached to the quality of seed which the farmers are offered. It is of overriding importance that the seed of improved varieties not only contain high genetic potential, but is also of the highest physical quality. Once the new seed gets a bad reputation it may take many years to recover from this kind of setback.
7. Apart from quality control, public institutions will have to carry out the research which is required in a vast range of crops and under the various ecological regimes which exist in the country. Private research will always be concentrated on a few crops only and will be mainly concerned with grain crops which can be multiplied by seed.
8. Research workers ought to concentrate on research only and should not be charged with the job of seed multiplication and seed distribution apart from the initial stages of breeders' seed multiplication, otherwise the real research work may become of secondary importance.

In view of the progress being made in the hybrid maize project and the seriousness and commitment of the key players in the project, the Consultant proposed, as at June 1982, the following time table:

> 1982: The policy of private industry is made known to potential candidates and local investors. As soon as applications are received, negotiations can start to find a suitable formula for the companies to operate and for the government to be satisfied that the policies are properly executed.
>
> 1983: The seed company(s) get themselves established in the country and start making arrangements for the necessary facilities to be acquired.
>
> 1984: The first fields of crops to be multiplied will be planted and the industry will establish its marketing policies.
>
> 1985: The first commercial marketing of seed produced in 1984 will be put on the market. Experience has taught that the initial years of production, processing and marketing are difficult ones and one can therefore expect the quantities of seed sold by the industry during the second half of the 1980s to be relatively small. The real take-off will come during the early nineties and this shows that no time ought to be lost.

With all of these efforts in place, the call for establishment of private seed companies went public. The successful development of appropriate and superior high-yielding hybrid maize varieties triggered the establishment of the first Nigerian private seed company—Agricultural Seeds Ltd (a subsidiary of Leventis Plc) in 1984. The headquarters and processing facilities were based in Zaria. The first Managing Director was Mr. Hazeldin, former Managing Director of Kenya Seed Company. He was later replaced by Dr. Adeyemi Joshua, a long-term Project Manager of the National Seed Service. The major commodity of the company was hybrid maize; cowpea, soybeans and cotton seeds were also produced and sold. In 1988, AgSeed (the acronym of Agricultural Seeds Ltd) established a department for research and development with Dr. Y. Efron, former Director of IITA Maize Program as its pioneer Director. The purpose was to supplement the research done by public research institutions in Nigeria. Two sites—Zaria and Ilesa—representing the savanna and forest ecologies, respectively, were used for the purpose. Pioneer Hi-bred Seed Company of USA started operation in Nigeria in 1989 and in 1992 bought the Agricultural Seeds Ltd. Unfortunately, owing to non-favorable economic and political environment, Pioneer dropped out and sold its assets to Retired General Olusegun Obasanjo, who renamed the company Premier Seeds Ltd.

Soon after the establishment of the erstwhile Agricultural Seeds Ltd, many organizations, individuals, as well as multinational, ventured into the seed industry with most of them swiftly folding up. The Nigerian Grain Production Company registered as a Seed Company in 1988. It was located in Niger State and owned by the Federal Government. Although it was able to produce as much as 50 tons of hybrid maize seed in 1989, it soon thereafter ceased operation. Total Agric also registered as a Seed Producing Company in 1985 and was at 1989 producing 20 tons of hybrid maize seed. It was financed by the Total Company and based its operation in Kwara State. It closed down in 1990. M'Billa Farms was established as a seed company in Gongola in 1988. It was financed by SCOA, a French group and was able to produce 30 tons of hybrid maize seed in 1989. It is, however, no longer in operation.

UAC Seeds which is a Division of UAC of Nigeria Plc started seed production in Kaduna in 1989. That year, it produced 100 tons of hybrid maize seed and 20 tons of open-pollinated varieties. It made serious attempts to survive. It had strong technical support and collaboration with PANNAR Seeds of South Africa. UAC Seeds benefitted from IITA support for gemplasm supply, follow-up visit by Dr. Kim and human resource development in association

with IITA training program. UT Seeds, a division of UTC Plc was established in 1989 in Jos after several years of collaboration with IITA's research efforts on developing improved maize germplasm for the mid-altitude ecology. It was the major producer of TZMSR, developed by IITA and which UT Seeds sold as Plateau No. 1. It was operational till the mid-1990s.

As there was a high rush into seed company formation, there was also a high drop-out rate of the private seed companies after formation. The news of the establishment of Agricultural Seeds Ltd as the first private seed company was greeted with a lot of excitement and euphoria as a landmark in the agricultural development of this highly endowed country. Up to 1,000 tons of hybrid maize seeds were sold out annually in 1986 and 1987. Hybrid maize cultivation in Nigeria increased from 5,000 ha in 1985 to 100,000 ha in 1989. Unfortunately, from 1990 onwards, seed demand of hybrid maize declined. Up to 500 tons of high-quality seeds were carried over to the following year owing to lack of patronage. Such seed would lose viability and economic value resulting in high financial loss to the company.
Among the reasons for this scenario are:

1. Lack of good promotion campaign including negative notion of extension agents about hybrids resulting in loss of confidence in improved seeds amongst farmers. For instance, the perception that there are no hybrids that would produce better yields than open-pollinated varieties under a sub-optimal fertilizer treatment was not generally true for some of the hybrids developed under Nigerian conditions.
2. Companies, on their own, did not mount sufficiently aggressive and pervasive promotion campaigns for hybrid use.
3. Collapse of large-scale farms which were the prospective major users of high-quality hybrid seeds because fertilizers became more difficult to access owing to increased cost.
4. Private companies were increasingly unable to compete with the subsidized seed prices of government such as those produced through the State ADPs.
5. High interest rates were in vogue whereas the seed industry is a venture with slow rate of returns to investment. The high expectation from the company promoters that the seed business was a money-spinning venture apparently led to deep frustration.
6. Lack of appropriate expertise required by this high-tech industry
7. Lack of appropriate legislation to protect privately bred gemplasm which could have benefited the seed industry.

No wonder, Dr. Kim, in a paper in May 1995 at Cotonou, Benin Republic on the "Achievement, challenges and future direction of hybrid maize research and production in West and Central Africa" lamented "why the World No.1 company, Pioneer, could not survive in Nigeria after a big investment of about 3 million US dollars?"
However, through the implementation of the *Agricultural Transformation Agenda* (ATA), there is a resurgence of seed companies. In order to empower the predominantly peasant farmers, the provision of 20 kg of free seed of improved recommended varieties of some selected crops together with 50% subsidy in fertilizer cost, was the central theme of the agricultural transformation agenda of the Federal Government since 2012. The annual registration of farmers and the assemblage of proven input suppliers facilitated this scheme, the Growth Enhancement Scheme (GES), using the now largely affordable mobile telephone contact with the beneficiary registered farmers.

The operation of the GES helped in streamlining many things in our agricultural system. First, it ensured that our researchers must, of necessity, prepare an up-to-date list of the varieties of the specific crop that can be described as recommended for farmers' use. Secondly, there must be a plan for the chain increase or multiplication of seed of the varieties available with the breeder (breeder's seed) so that adequate quantity of certified seed is eventually made available to the farmers. Obviously, the National Agricultural Seeds Council (NASC) must be at the driver's seat. The Council must, in the first instance, ensure that adequate quantity of

foundation seed is generated by appropriate, reliable agencies. After that, the seed production industry will be charged with the production of adequate quantity of good quality certified seed that will be purchased by the Government through the GES for timely distribution to the farmers.

With the implementation of this scheme, unprecedented quantum of seeds of improved crop varieties was made available to the farmers. For instance, in 2012, 61,000 tons of maize, 51,000 tons of rice, and 70,000 tons of sorghum were distributed to the farmers directly, rather than through any government or other agencies. Using a growth rate of 5% in land area, the corresponding estimates for 2015 and 2016 were 62,000 and 67,000 tons of maize, 76,500 and 102,000 tons of rice, and 840,000 and 980,000 tons of sorghum, respectively (Ajala, 2013). This represents, by any standard, a phenomenal departure from the past.

Obviously, the volume of improved seed required for this scheme went beyond the carrying capacity of Premier Seeds and the few other private seed companies that survived the drop-out episode of the 1990s. This led to what can aptly be described as virtual sprouting of Seed Companies. This was understandable because contract for large quantities of seed of some prescribed varieties were given to any seed company deemed qualified. Appropriate quantities of foundation seed of such varieties were provided by the NASC which has the responsibility to inspect such seed production fields for certification. To assist NASC in this task, a 6-member committee was mandated in 2013 to critically examine the seed value chain for maize and rice, and also review associated issues militating against the adequacy of seed supply for the two crops. Members of the committee were Dr. S.O. Ajala – *Team Leader Maize* – Chair, Dr. O. Osiname – *Team Leader Rice*, Dr. J.M. Fajemisin – *Consultant Maize,* Dr. J. Odeyemi – *FDA*, Pst. O. Olatokun – *NASC*, and Dr. P. Ojo – *Certification - NASC*

Undoubtedly, the implementation of the Transformation Agenda has increased the awareness of farmers for improved seed. Farmers are gradually recognizing that it is not proper to go to the market and purchase grains and use as seed. They know that seeds of their choice varieties are specially produced and appropriately treated with chemicals.

But unfortunately, there have been many instances of delivery of poor quality seed by some seed companies. Some of them have been known to buy grains, dress them with chemical and deliver as seed. However, we are gradually having a few discerning farmers who now recognize poor seed and thus decide not to take seed from such companies in future transactions. The problem is that the undiscerning clients will be unable to discover the actual performance of the authentic variety and will, therefore, have a wrong perception which may take a long time to change. For this reason, the scheme for the provision of free seed which encourages this kind of corruption should be reconsidered; otherwise, it would kill the seed industry. When farmers are able to choose to buy the seed of their cherished varieties from companies that deliver good quality seeds, such companies would be able to sell more seed and remain in business. On the other hand, poor quality seed producers will not have steady and sufficient customers to keep them in business and will eventually die off. Plant geneticists and breeders would feel more comfortable with a few transparent seed companies rather than a large number that continuously damage the reputation of the country. Such efficient companies can grow, remain sustainable and will add value to our agricultural development.

Nigerian population *versus* food production

The population of Nigeria has continued to increase at an alarming rate (Table 1). It rose from 47 million in 1961 to 163 million in 2011; an estimated annual rate of 232,000 per annum (Fig. 1). Many things occurred in Nigeria during this period, including training of many geneticists and breeders, establishment of more universities, coups and counter coups, establishment of the International Institute of tropical Agriculture (IITA), and many more that have led us to

where we are today. That is when we were all trained, a time this society (GSN) as well as many professional societies was formed – a difficult time indeed. Despite the difficult times, which have continued to grow worse, we geneticists and plant breeders continue to work as hard as the situation allows. Many publications have been sent out which, if reviewed and the findings and recommendations applied properly, Nigeria would have arrived in a panacea.

A closer look at Table 1 reveals some interesting findings. Land area for cereals (maize, rice, sorghum, millet, etc) is much more than that for root and tuber crops (yam, cassava, cocoyam, etc) but the yield per hectare and the total production are exact opposite of that trend.

Table 1. Nigerian population, yield of cereals and root and tuber crops, and yield index from 1961 to 2011

	1961	1970	1980	1990	2000	2011	Index[1]
Population, *millions*	47	57	76	98	124	163	346
Area of harvested crop, *million ha*							
Cereal	10.6	12.4	7.2	15.4	18.2	16.6	157
Root & tuber	1.4	2.4	1.8	3.1	7.6	8.4	592
Average yield, *t/ha*							
Cereal	0.7	0.7	1.1	1.1	1.2	1.3	179
Root & tuber	8.6	9.8	9.6	10.9	8.6	11.5	135
Total basic food production, *million tons*							
Cereal	7.9	9.0	7.8	17.7	21.4	22.2	281
Root & tuber	12.2	23.8	17.1	33.6	65.2	97.2	797
Food energy value of crop, *kcal/kg*							
Cereal	2969	2983	3012	3123	3051	3069	103
Root & tuber	833	872	827	847	858	895	107
Potential energy value, *kcal/capita/day*							
Cereal	1367	1279	850	1550	1443	114.6	84
Root & tuber	593	988	512	799	1237	146.5	247

[1]Index = 2011 value/1961 value

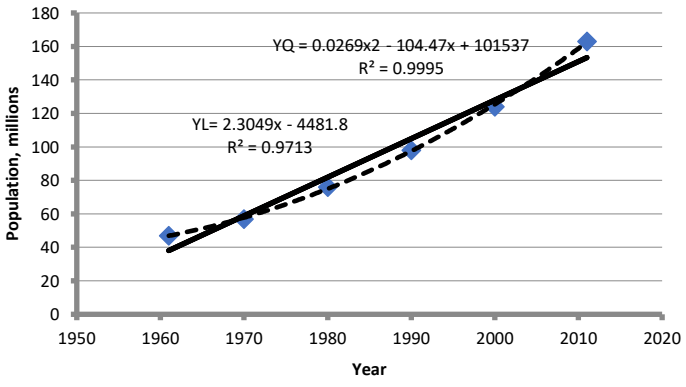


Fig. 1. Population of Nigeria from 1961 to 2010

The food and potential energy values of cereals, however, are much higher than those of root and tuber crops.

Research vs Actual production – Yield gaps. The objectives of plant breeders working on food crops (including cassava, yam, maize, banana/plantain, soybean, and cowpea, etc) are many but may be summarized as follows:

(i) Increased yield of major staple food crop,
(ii) Increased average farm income,
(iii) Lift poor households above the poverty line (over 11 million Africans)
(iv) Reduce the number of malnourished children, and
(v) Restore farms to sustainable resource management (revitalizing of degraded farmlands)

For more than 50 years, breeders have carried out research on these objectives and have made a lot of progress. In **soybean**, for example, following are some of the achievements:

Early maturity (ii) High promiscuous nodulation (iii) Resistance to rust, leaf spot and bacterial pustule (iv) High grain and fodder yield (v) Shattering resistance (vi) Good seed storability (Plate 1). For **maize** (Plate 2), the breeders have also attained the following achievements: (i) High grain yield (ii) Drought tolerance (iii) Adaptation to sub-optimal soil nitrogen (iv) Tolerance to lodging (v) Resistance to major foliar diseases and maize streak virus (vi) Maturity (late, medium, early, or extra early) (vii) Tolerance to *Striga hermonthica (viii)* Resistance to stem borers (*Sesamia calamistis* and *Eldana sacharina*) (ix) High pro-vitamin A content (x) Quality protein maize (QPM) containing high lysine and tryptophan contents (xi) Resistance to aflatoxin contamination. In **cassava** (Plate 3), breeders have developed (i) high and stable root yield (ii) high root dry matter (starch) content (iii) drought tolerance (iv) high root pro-vitamin A content (v) early maturity (vi) low cyanogenic potential of roots (vii) disease resistance (cassava mosaic, anthracnose, bacterial blight).

Plate 1. Clean grains of soybean

Plate 2. Maize at the grain-filling stage

Plate 3. Cassava in the field

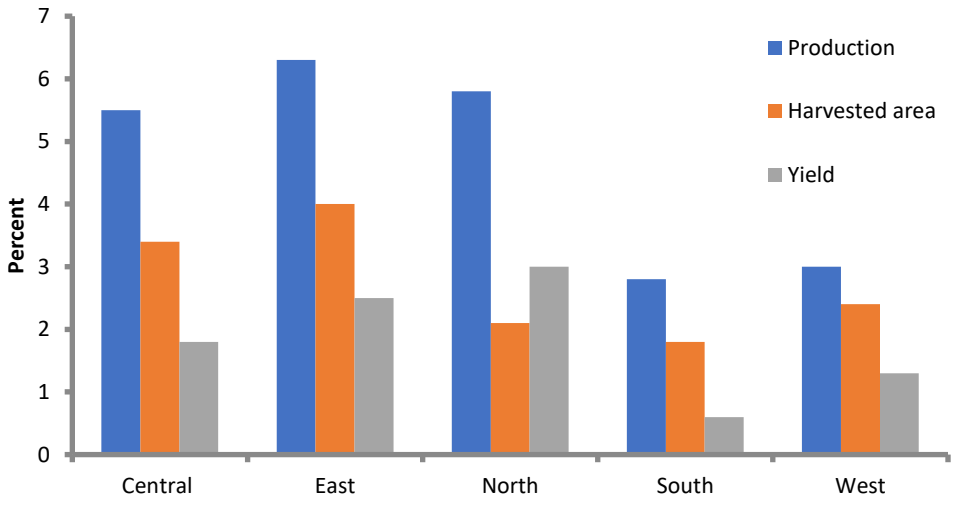


Fig. 2. Percent growth in cereal production (2000-2012) in Africa sub-regions

Despite these encouraging trends found in the improvement of Nigerian crops, proportion of the population earning less than US $1.25 (about ₦500-600) per day was 33.7% in 2005-2012 and over 50.2% of the population earned less than US $2.00 per day in the same period of time. Furthermore, the % increase in production, area harvested, and yield of cereal crops were much higher in Central, Northern, and Eastern Africa than Southern and Western Africa (Fig. 2).

In Nigeria, there was a sharp reduction in the proportion of the population having inadequate access to food in 2011-2013 compared with 1990-1992 (Table 2).

Table 2. People having inadequate access to food in 1990-1992 compared with 2011-2013 in Nigeria relative to West Africa, Africa, and the world.

Part of the world	Undernourishment prevalence, %		Number, millions		Food deficit, kcal/capita/day		Prevalence of food inadequacy, %	
	1990-92	2011-13	1990-92	2011-13	1990-92	2011-13	1990-92	2011-13
World	18.9	12.0	1015.3	842.3	128	83	26.2	18.4
Africa	27.3	21.2	177.6	226.4	179	145	34.4	27.0
Western Africa	24.0	10.8	45.2	34.5	156	67	32.5	15.9
Nigeria	21.3	7.3	21.3	12.1	133	42	29.7	18.4

Maize, a major food crop in sub-Saharan Africa (SSA) is deficient in vitamin A, an important vitamin which cannot be synthesized by the human body but sourced from external food supplements. Because maize can be eaten in many forms, it exposes human populations in SSA to the risk of health challenges associated with vitamin A deficiency such as night blindness, retarded growth and depressed immune system. Approximately one third of children under the age of five are at risk of Vitamin A deficiency (VAD), the leading cause of childhood blindness. Normal-endosperm maize, which is widely consumed in SSA, lacks two amino acids, lysine and tryptophan thereby making the maize protein of low quality. Development, promotion and deployment of maize varieties with elevated levels of provitamin A (PVA), lysine, tryptophan, and multiple stress tolerance/resistance is the most ideal and sustainable option for mitigating malnutrition and food insecurity in SSA. With the support of the HarvestPlus Challenge Program, both CIMMYT in Mexico and IITA in Nigeria have screened thousands of entries in the maize germplasm available to the breeders in form of inbred lines, OPVs and hybrids into which tolerance to some or all of the stresses and/or quality protein had been incorporated. At IITA, the maize scientists screened the germplasm for PVA, subjected them to quantitative genetic studies and molecular approaches for PVA enhancement, and conducted extensive multi-environment trials (MET) in West and Central Africa (WCA). The results of the MET led to the release of several varieties in four countries of West Africa (Table 3).

Table 3. Released early and extra-early maize hybrids and OPVs in DTMA Partner Countries, 2007-2015

Country	Number of varieties released		Year of release	Institution	Total
	OPVs	Hybrids			
Benin	6	0	2007-2015	INRAB/IITA	6
Ghana	5	2	2010-2012	CRI/SARI/IITA	7
Mali	2	7	2009-2014	IER/IITA	9
Nigeria	6	4	2009-2013	IAR/IAR&T/IITA	10
Total	19	13			

The PVA breeding target, which was set at 15 μg g^{-1}, have been surpassed by several newly developed synthetics, inbred lines, single-cross, and three-way hybrids (Badu-Apraku and Fakorede, 2017). Examples are extra-early inbred lines TZEEIOR 202 (23.98 μg g^{-1}) and TZEEIOR 205 (22.58 μg g^{-1}),

and the early inbred line, TZEIORQ 55 (15.1 μg g^{-1}). Ife maizehyb-3 and Ifemaizehyb-4 are not only higher yielding than Oba Super 5 but also have higher PVA (Table 4).

Table 4. Mean pro-vitamin A content and grain yields of hybrids maize released in Nigeria in 2012.

Hybrids	Mean pro-vitamin A, (μg/g)		Mean grain yield, kg/ha	
	2009	2011	2010	2011
Ife maizehyb-3	8.8	7.2	5440	5744
Ife maizehyb-4	8.1	7.4	5121	5198
Oba Super 2 (Check)	5.3	3.5	4636	4867
Mean	5.8	5.2	5026	4889
LSD (0.05)	0.7	1.0	1093	673
CV	13	16	15	16

Many more hybrids have been released while others are in the pipeline for release in SSA. Results of quantitative genetic studies showed that PVA is controlled more by additive than non-additive genetic variance; therefore, heritability and response to selection are quite high. PVA is amenable to recurrent selection and both synthetic and hybrid varieties may be developed for commercial production of high PVA maize. Few studies on the genetic versus agronomic factors responsible for the gains in Nigerian crops are available in the literature. A study was conducted to quantify genetic gains in yield and associated traits of open pollinated maize cultivars released from 1970 to 1999 in the West African savannas (Kamara et al., 2004). The results showed genetic gain in grain yield was 0·41% per year for a total of 12.3% increase in three decades. This gain was associated with increases in total biomass, kernel weight, and reductions in plant height, days to anthesis and silk emergence. There was no significant change in harvest index of the cultivars. Kim et al. (1993) obtained gains of 20-25% from hybrids evaluated in nearly 200 field trials in several sites across Nigeria. Ogunremi (1987), Akintunde *et al.*, (1993), and Alofe *et al.* (1993) reported similar results.

How geneticists and breeders arrived at this stage
Education and training of geneticist and breeders

Statistics and experimental design and analysis -

Extensive and intensive research with support from Government and international donors
Research is very expensive to conduct reasonably well. Therefore, researchers have to depend on some form of input of funds from within and/or outside the organization. Universities and research institutes obtain certain annual allocation for research from the government. In most cases this funding is not enough; therefore, researchers have to look outside for more support. Whenever there is a call for proposals in their field of specialization, they develop, write, and submit the proposals as specified by the intending donor. In some cases, the donor keeps an open door throughout the year. Intending researchers can submit applications at any time of the year. A proposal jointly written by junior and senior colleagues stands a better chance of being accepted than one written singly, especially by an inexperienced young person. It is better for a senior colleague to write the proposal with younger colleagues. The senior person will be assumed as the principal investigator and will be held responsible for overseeing the execution of the project. Some universities, such as OAU, Ile-Ife have project funds earmarked for junior colleagues under the supervision of a senior person. This is laudable. At present, globally known ***International donors*** include USAID, USDA-ARS, IDRC, Africa Development Bank (AfDB), Foundations such as Ford, Rockefeller, Kellogg, Bill & Melinda Gates (BMG), etc. ***Regional donors*** include CORAF, AGRA, FARA, crop research networks e.g., West and Central Africa Maize Research Network (WECAMAN); etc. ***Donor-sponsored special projects,*** such as DTMA/STMA funded by BMG Foundation, and SARD-SC funded by the AfDB. ***National donors*** are: Government MANR, R&T Inst., Universities, Parastatals, etc. Strictly, Donor-sponsored special projects, R&T Institutes, universities, and parastatals are not donor but they can co-opt any scientist on the funds they received for project. ***Community-Based Projects*** sponsored by CBOs, NGOs, and commodity-based organizations such as Maize Association of Nigeria (MAAN). More donor can be found on the internet *(www.htps.//donor)*
Funded genetic and plant breeding research projects are expected to be extensive and intensive. The researcher needs a lot of funds for such projects. Plant breeding is a game of numbers – large number

of individual plants to pollinate, pollination equipment, large number of entries in field trials, several or many locations for 2 or more years, harvesting bags, vehicles to carry harvested materials to the building, and, of course, large number of human beings at different stages of skill expertise, and so on. All of these and many more will need funds for purchase of items, running the equipment, maintenance, and be paid salaries for the work they are hired to perform. Funds are also needed for publishing the results of the research. Any research done and the results kept in the researcher's drawer in the office is equivalent to no work done.

Research to solve specific biotic and abiotic problems

To increase and improve food crop production and crop management for sustainable agricultural development, nearly all programs at IITA, in partnership with national and international organizations, focused attention on the genetic improvement of the individual crops for tolerance/resistance to abiotic and biotic stresses constraining crop production. For example, the abiotic stresses for maize include drought, low soil nitrogen, and heat stress. The biotic stresses are diseases, insect pests, and weeds, specifically, *Striga hermonthica* ((Del.) Benth., the witch weed. Each of the stresses had specific research projects and, in most cases specific scientists executing the research. We shall discuss briefly only one of the stresses. Others may be found in Badu-Apraku and Fakorede (2017).

Abiotic stresses – Nitrogen – Low soil nitrogen has been one of the abiotic stresses into which new technologies have been established for crop protection and sustainable natural resource management in maize. Nitrogen, an important plant nutrient required for growth and productivity, is not readily available and little quantity or none is applied by farmers for maize grain production. Because of long periods of bush fallow, the absence of N was not noticeable at the initial stages of maize production in West and Central Africa (WCA). However, with the fallow period gradually reducing and totally disappearing, it has become imperative for external supply of N in maize production. Taking a cue from CIMMYT, IITA has been breeding low-N tolerant maize and several low-N-tolerant maize varieties and hybrids have been released.

Field Trips and Field Days

Field Trips and Field Days are effective means of demonstrating and transferring technologies to farmers because they see and do what they are taught practically on the field. IITA started yield trials in northern Nigeria in 1980 and soon discovered the extent, advantages, and limitations of the agricultural land in the northern parts of Nigeria. Therefore, the scientist planned *ab initio* to organize and support field trips to monitor field trials in all ecological zones in the northern parts of Nigeria as frequently as possible. One such trip was undertaken from the 26 to 29 July 1988. The objectives of trip included i) ensuring that top agronomic practices are strictly adhere to in every location, ii) investigating any problems the farm managers and technicians might be having, and iii) disbursing some money as needed for the maintenance of the trials. Within the few days of the trip, visits were made to Mokwa Experiments Station, NGPC site near Mokwa, Funtua, Kaduna, Samaru, Bagauda, BARC Farm-Zalaki Jos, Vom, and UTC Farm in Tenti Baba. Driving from Zaria through Bagauda to Jos, there was a lot of beautiful maize fields mostly planted to hybrids and they were at the flowering stage. In general, the northern locations were satisfactory. The team recommended that Mokwa be elevated to the position of the major breeding station for *Striga* resistance, and headed back through Keffi-Abuja-Suleja-Bida-Mokwa-Ibadan, arriving around 10.30 p.m. Similar trips were msde to Owo in Ondo State and Agenegbode in Bendel State on 18 and 19 August 1988 to i) monitor the spread of downy mildew on the maize trials, ii) visually screen the maize plants for susceptibility for the disease, iii) visit the Leventis Farm at Agenegbode for possible infestation of *Striga*, and iv) visit one Dr. Ezumah's maize trials at Ohusu, on the Ore-Benin Freeway in Bendel State. On each visit, every block and plot was visited in search for diseases and the best materials. Overall, the field visits were very informative about what was being done well, what needed to be improved upon, and what should be stopped right away.

Farmers' Field Days – Unlike the Field Trips, Farmers' Field Days were organized for farmers to see and probably rate the varieties or technologies being displayed so they could select the best for possible seed production for their own farms. Number of participants is usually very large and they are treated to some form of snacks or feeding as far as possible. Also, proper pre-arrangement would have been made in the community, State, or country so that nothing would be lacking. In 1988, for example, several field days were organized and each had its own characteristics. Three field days were held: (i)

Hybrid Maize Village, Orunwa, Ogun State on July 20, (ii) West Africa Milk Company (WAMCO) Farm, Vom, Jos, Plateau State on the 9th of November, and (iii) IITA on November 16. Generally, the field days were a huge success and it was expected that maize production in the zones visited would increase.

It is quite unfortunate that mounting field days has stopped since 1989, except for a few of them mounted during the execution of PIDOM.

THE FUTURE

To end this paper, I like to share with you my recent experience. Figure 9 shows the progress we have been making in crop yield in Nigeria. This is quite encouraging.

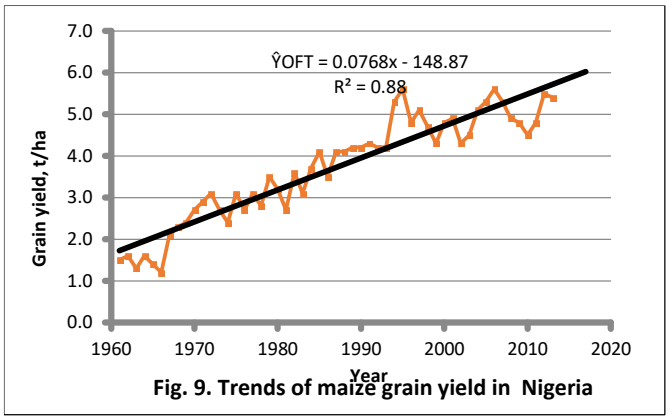


Fig. 9. Trends of maize grain yield in Nigeria

That was OFT most of which was monitored by the researcher, in this case, maize breeders. In Fig. 10 is presented grain yield in farmers' fields. Clearly, this shows some progress but it lags far behind what happened in Fig. 9. Figure 10 shows a curvilinear fit with R^2=94, better than the linear trend (R^2=84).

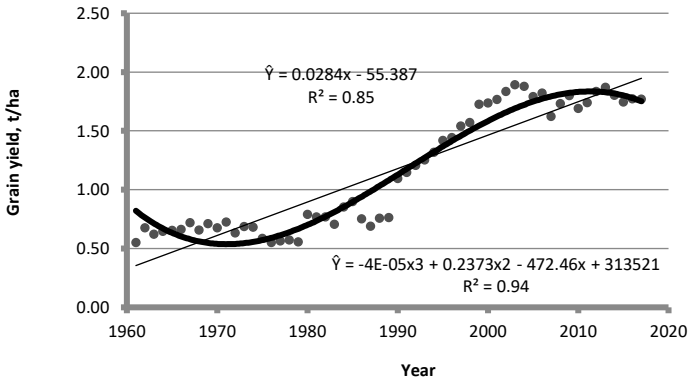


Fig. 10. Trend of maize grain yield in Nigerian farmers' fields, 1961-2017.

In Table 5 are shown more traits with progress from breeders. These values were obtained from a study involving 50 entries for unimproved land races and 50 improved cultivars evaluated in four field trials.

Table 5. Means of agronomic traits in traditional and improved cultivars of maize.

Trait	Traditional	Improved	LSD	% Impvt.
Grain yield, t /ha	1.8	3.3	0.12	83.3
Ear per plant	0.8	0.9	0.02	12.5
Anthesis, days	57	57	NS	0.0
Silking, days	60	59	0.3	-1.7
ASI, days	2.4	1.7	0.2	-29.2
Plant height, cm	176	169	2.6	-4.0
Stalk lodging, %	11.5	6.1	1.2	-47.0
Plant aspect	3.1	2.4	0.1	-22.6
Rust score	2.3	1.9	0.1	-17.4
E. turcicum blight	1.7	1.4	0.1	-17.6
Curvularia leaf spot	2.0	1.6	0.1	-20.0

In another study, the traits were again measured in OFT in farmers' fields and the results are as follows:

- Grain yield was improved by 45%
- Ear placement, 19%
- Ear aspect, 40%
- Stalk standability, 88%
- Anthesis-silking interval, 41%
- Ear length, 16%.
- Resistance to *Puccinia polysora* 37%
- *Exserohilum turcicum* 36%
- *Curvularia* spp. 42%.

These results are direct efforts of plant geneticists and breeders for which I heartily commend their efforts. But still, there are Problems!!!

Problem # 1 - Yield plateau in the farmer's field relative to researcher's field.

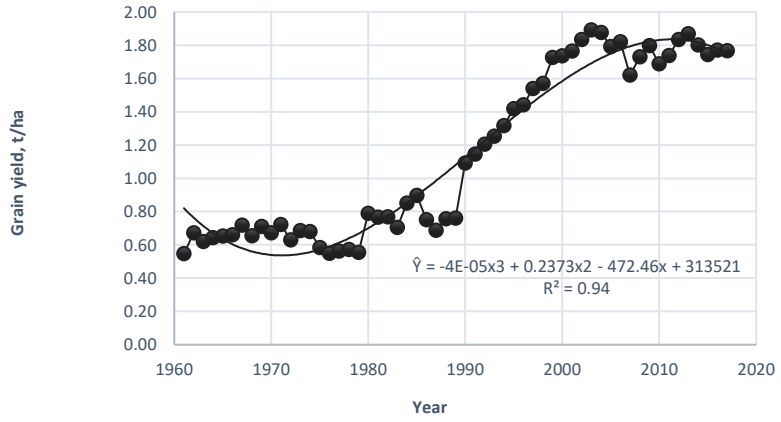


Fig. 11. Trend of maize grain yield in Nigerian farmers' fields, 1961-2017.

Can you identify the plateau?

Problem # 2 – Increasing yield gap between research and farmer's production.

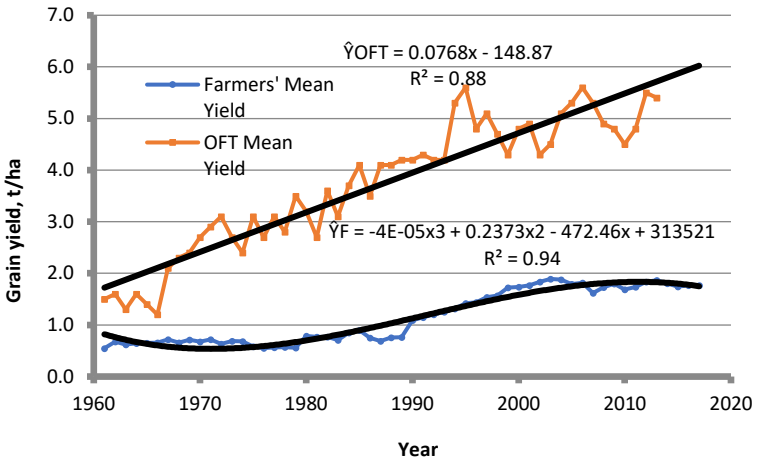


Fig. 12. Trends of maize grain yield in SSA farmers' fields and OFT, 1961-2017.

This is clearer in Figure 13, with R^2 of 81 for the curvilinear fit.

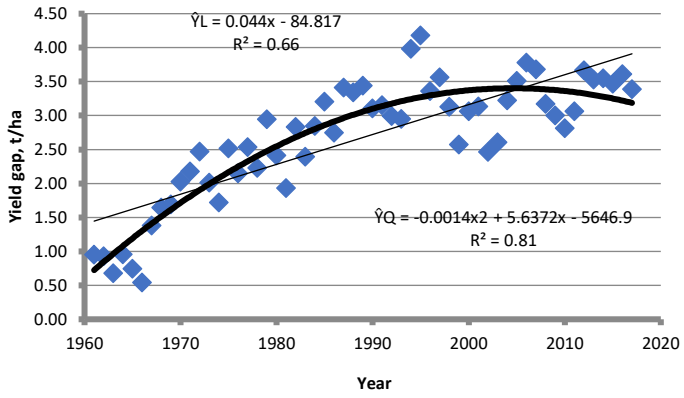


Fig. 13. Maize grain yield gap between Nigerian farmers' fields and OFT, 1961-2017.

Table 6. Grain yield (t ha^{-1}) of SG-2000 farmer MTPs vs. farmer practices and their yield gap, 1993-1997

Year	Area harvested, ha	SG-2000 farmers (MTPs)	Farmer practices	Yield gap	
				t ha^{-1}	%
1993	58	3.8	1.9	1.9	100.0
1994	187	4.3	2.2	2.1	95.5
1995	64	5.4	2.7	2.7	100.0
1996	235	5.6	2.1	3.5	166.7
1997	250	4.8	2.6	2.2	84.6

Possible reasons for the yield gap are as follows:

Interventions have

- been top down
- sparingly reached the grass root (producers)
- mostly emphasized
  - ➢ research

- education
- training of farmers (to a limited extent) indoors
- technology transfer (to a much more limited extent)

Financial empowerment of producers (farmers) has been grossly neglected!!!!
There is, therefore, an urgent need for paradigm shift in interventions.

Please permit me to support this suggestion with some examples of on-going projects along this paradigm shift scenario.

Example # 1 - IITA Youth Agripreneurs (IYA) Initiative

- A youth-in-agribusiness model
- Initiated in 2012 to train graduates in agricultural production
- Addresses the issue of unemployment
- Provides a platform along the agricultural value chain for unemployed youth
- Trains the participants to generate wealth and create jobs in agriculture
- Participants go thru 18-month incubation program during which they are
  - trained, mentored, coached, and exposed to the business opportunity in
  - exposed the production and value chain of crops (cassava, maize, soybean, etc)
  - trained in fishery, piggery, poultry, raising rabbits, snails, etc
  - taught technology adoption for best practices to obtain top yields with best marketing strategy
  - exposed to what can differentiate them from competitors in the market;
  - encouraged to embrace agriculture as a business and to create jobs to employ the unemployed youth.
- Youth Agripreneurship has spread widely in West, Central, East and Southern Africa
- Youth Agripreneur Groups are operating in Nigeria, DR Congo, Kenya, Tanzania, Uganda, and Zambia
- IYA also partners with the public and private sectors to offer training and consultancy services to youth farmers.

INTERNATIONAL INNOVATION AWARD
FOR SUSTAINABLE FOOD AND AGRICULTURE

- The award is the first of its kind
- Funded by the Government of Switzerland
- Presented during the 41st conference of the FAO in Rome on June 26, 2019.
- *It is very important to showcase positive results and concrete ways in which we can work together* – FAO DG, José Graziano da Silva's remark at the event
- IYA won the Award

in recognition of its commitment to improving both agribusiness opportunities and credit worthiness of youth across Africa**.**

Plate 4. Evelyn Ohanwusi (*Head of the program*)

Example # 1-1 - IITA's *Start Them Early Program* (STEP)

To the young African, agriculture is

- undesirable to create wealth
- a punishment
- dirty occupation
- for those without western education (illiterates)

STEP was initiated to

- transform the mindsets of the African youth to see agriculture as a viable source of income
- work in partnerships with secondary schools
- raise a generation of young African leaders with education in agribusiness
- merge training in agribusiness with the school curriculum.
- STEP currently carried out its activities in DR Congo, Kenya, and Nigeria.

Example # 2 - Tony Elumelu Entrepreneurship Project (TEEP)

- Tony Elumelu initiated the Tony Elumelu Foundation which, in 2014, committed $100 million to train and assist 10,000 entrepreneurs across the continent over a 10-year period.
- Beneficiaries are drawn from the 54 African countries
- Applications are thoroughly screened
- Selected individuals are

✓ assigned to volunteer mentors
✓ mentored online for 12 weeks on their chosen business
✓ granted $5,000 based on submission of acceptable business proposal

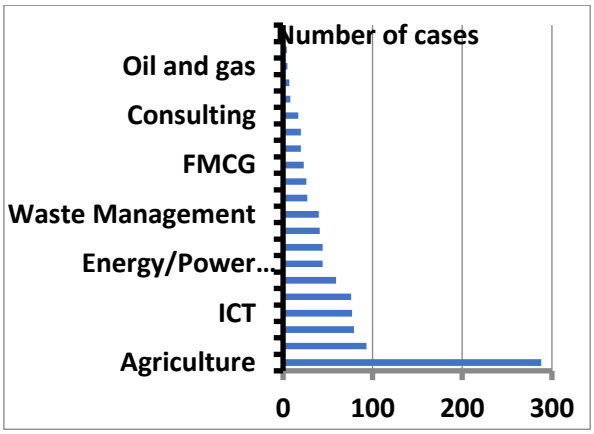
- Date established – 2014
- Capital committed –$100 million over 10 years
- Start-Up goal – 10,000 start-ups
- Job creation goal – 1 million jobs
- Anticipated Revenue growth goal – $10 billion
- Total selected to date – >7,000
- African countries submitting application – 54

❖ Countries with most applications are Nigeria, Kenya, and Ghana

- Top 3 sector are - Agriculture, Education/training, and Commerce
- Gender distribution – 29% female, 70% male
- Age of applicants – 18-27 yrs = 23% ; 28-37 yrs= 54%
- Stage of business – 24% idea, 30% market testing, 24% market entry, 21% growth

Global support for TEEP – *An Example*

- The United Nations Development Program (UNDP) to empower 100,000 young African entrepreneurs in partnership with TEEP
- The TEEP-UNDP MoU was signed in July 2019 at the African Union (AU) Summit in Niamey, Niger
- The Program targets seven Sahel countries including Nigeria (northern parts), Niger, Mauritania, Chad, Mali, Burkina Faso and Cameroon.
- Over 81,000 applications received:
  43% from rural areas, 57% from urban areas; 30% from females, 70% from males.
- Final selection of 2,100 applicants was announced on December 15, 2020
- Beneficiaries who opted to take the business training offline were trained in different locations in the 7 sahel countries.



Example #3 - YOUTH FARMERS COOPERATIVES

MISSION

- Provide exclusive training platforms;
- create opportunities for the youth to benefit from the enormous prospect embedded in agricultural value chain

OBJECTIVES

1] Youth Empowerment and Development
2] Reduction of Unemployment
3] Poverty Alleviation Scheme
4] Socio-cultural Economic Integration

MODUS OPERANDI

- Land is provided in a farm cooperative settlement
- Financial support, primarily in kind, up to N5m (about US $10,000)
- Mechanization, labor, production inputs, etc supplied
- Farm produce purchased after harvest

Plate 5. Youth Farmers Cooperative

Plate 6. A Youth Farmers Cooperative member's maize farm

Conclusions

1. A paradigm shift in agricultural transformation agenda for Africa will likely expedite the attainment of sustainable food security in the continent.
2. The paradigm shift should involve capacity building and financial empowerment of youth in agricultural entrepreneurship.
3. Execution of the paradigm shift is already yielding positive results all over Africa**.**

RECOMMENDATIONS

1. Improvement in grain yield and nutrition traits such as PVA should continue at IITA and national programs in Nigeria, using presently known breeding techniques such as recurrent selection and new, yet unknown techniques such. Sustainability of the PVA program may likely involve the establishment of laboratories and skill acquisition by technicians and scientists. We need funding support for this.
2. Massive creation of awareness of improved technologies. Necessarily, we must revive on-farm trials and demonstrations.
3. How to minimize or totally eliminate the yield gap between research and production should now be a priority. Breeders should seek for research means to reduce their CVs. That way, they are likely to have more reliable new cultivars released for farmer's use.
4. Extensive use of bioinformatics. Bioinformatics could be defined as the storage, retrieval, and analysis of information about biological structure, sequence, or function (Altman, 1998). It relates to information about virtually any biological enquiry – from molecular biology to ecology, including computational biology. However, it is most frequently used in molecular biology or genomic research (Tinker, 2002). Nigeria is far behind in this area.
5. We scientists should call for a paradigm shift in agricultural transformation agenda for Nigeria. This will likely expedite the attainment of panacea for food security in Nigeria. The paradigm shift should involve capacity building and financial empowerment of youth in agricultural entrepreneurship. We can cite the three examples given here or any others we have come across in Africa.

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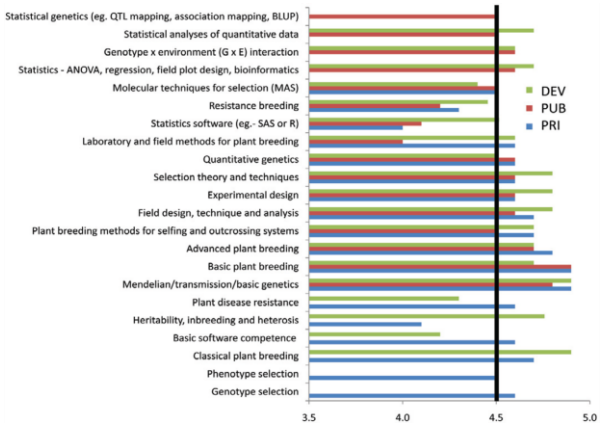
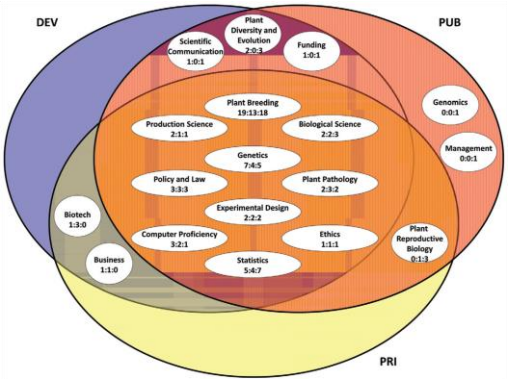
Appendices



Appendix Fig. 1. Mean scores from a survey of developing (DEV), private (PRI), and public (PUB) sector plant breeders. Any figure above the black line (mean rating 4.5 and above) is considered very important.



Appendix Fig. 2. Knowledge categories (small white ellipses) identified by developing nations (DEV), and private (PRI) and public (PUB) sector stakeholders of developed nations

APPLICATION OF BIOTECHNOLOGIES & GENOMICS FOR CULTIVAR DEVELOPMENT: THE CASE OF CASSAVA IN AFRICA

Chiedozie EGESI
Professor of Plant Breeding & Biotechnology
National Root Crops Research Institute, Umudike

Delivered by Dr. Gaby Mbanjo

GENETICS AND AGRICULTURAL TRANSFORMATION: PATHWAY TO FOOD SECURITY (THE CASE OF FISHERIES AND AQUACULTURE)

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INTRODUCTION

According to The World Fish Center (2011), food security is achieved when all people, at all times, have access to sufficient, safe and nutritious food that meets their dietary needs and food preferences for an active life. Worldwide, there is an international concern over food insecurity and this is very common and worrisome especially in the developing world (Thorpe, 2007). This has increasingly manifested itself in recent years, therefore making the theme of this conference "genetics and agricultural transformation: pathway to food security" very timely.

According to FAO (2016), fisheries (capture fisheries) and aquaculture (culture) are known to play important roles in providing food security for the teaming population all over the world. Though fisheries and aquaculture have high potential to contribute to food security and poverty eradication, unfortunately their roles in the achievement of sustainable development goals and food security are often overlooked and poorly documented by experts. This is one of the reasons why data on the socioeconomic characteristics and livelihoods of fishing communities and other households are limited (Bene *et al.*, 2015).

Therefore, there is need to have a better understanding of fishing-related livelihoods by analyzing household survey data which relates to food security, poverty and livelihoods of fishing and non-fishing communities. According to FAO (2011), many countries with many fishing households have a lower probability of falling below the poverty (food insecurity) line showing that fisheries can, indeed, be an important ally in the fight against poverty, hunger, and food insecurity. It was observed by Thorpe (2007) that despite enormous gains in the wellbeing and economic circumstances of hundreds of millions of people, 10% of the world's population still live on less than $2 a day. High population growth is responsible for the reason why many individuals, communities and even entire countries are trapped in poverty. Achieving sustainable population level, locally and globally help people achieve the dignity and standard of living we all deserve.

GENETICS AND FOOD SECURITY

Genetics deals with the study of traits and how traits are transferred from one generation to another. Economically important performance traits are desirable and exploited to improve production to meet human needs (Olufeagba, 2013). Genetic tools (including biotechnology) that utilizes biological systems, living organism or part of this are used in conventional and non-conventional breeding to develop or create different products. Because of the available tools in biotechnology, conventional genetic breeding methods that should ordinarily take years to yield results could be circumvented and result obtained earlier to ensure food security. As a result of changes in DNA sequences, we have variations which could be exploited to improve the performance of organisms. Gene is a segment of DNA containing instructions for building one or more molecules. This new area of biotechnology can facilitate faster agricultural innovation and transformation (FAO 2023)

Geneticists produce new varieties by special treatment of the parental or their gametes e.g., hybrid variety is produced by crossing two lines that are different species or genera. Fish genetic resources conservation has also contributed to food security as they lead to increase

production through improved performance of pure lines and germplasm. Other fish genetic applications with high potential to increase fish production and food security are monosex production through hormonal sex reversal especially in species like Oreochromis niloticus (tilapia) where males are more desirable because of their growth advantage over the females, mutation breeding, chromosome engineering to induce triploids, tetraploid e.t.c., epigenetics, transgenesis where foreign growth gene are introduced principally to improve on their growth

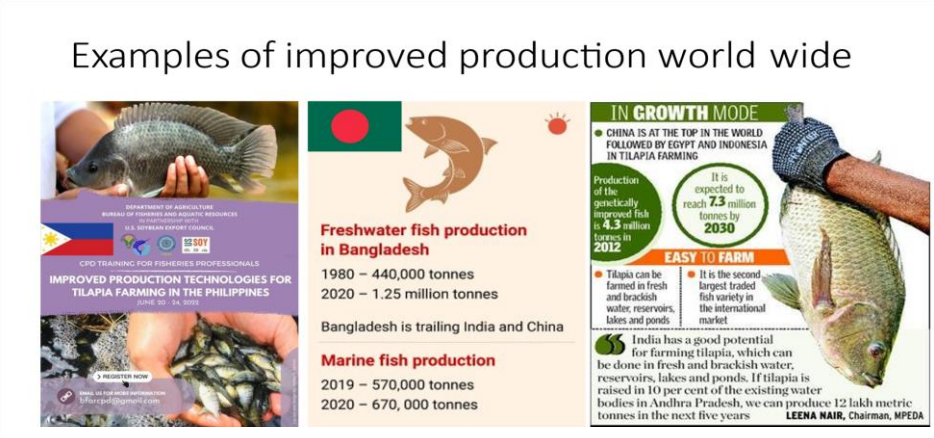


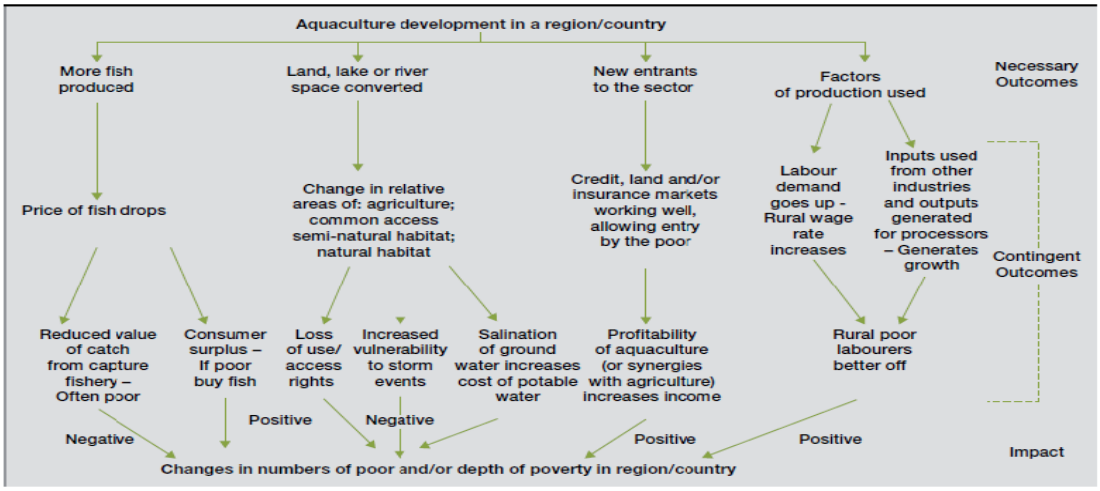
Fig. 1. All male tilapia production through sex reversal

AGRICULTURAL TRANSFORMATION

According to Timmer (1988), agricultural transformation evolves through at least four phases that are roughly definable. The process of agricultural transformation starts when agricultural productivity rises as new technologies are deployed. The increase in productivity which is the result of improvement in production methodologies create a surplus which in the second phase of the transformation could be tapped directly through taxation and factor into the rural-urban terms of trade. This surplus could be exploited to develop the non-agricultural sector and this phase has been the focus of most dual economy model of development. Fisheries and aquaculture which most often are confined as rural business must be transformed and be integrated into the economy to make real impact in food security.

FISHERIES AND AQUACULTURE FOR FOOD SECURITY

According to the report of The WorldFish Centre (2011), fisheries and aquaculture supplied the world with about 142 million tonnes of fish in 2008 and 178 million tonnes in 2020. In 2021, global fish production rose to 178.1 million metric tons and this increased to 184.6 million metric tons in 2022(www.fao.org). The contribution of this to food security is much with continuous increase in aquaculture, food security could be attained. Despite occasional fluctuation in world figure of capture fisheries, culture fisheries support to food security has continued to be on the increase and has outpace population growth with per capital supply increasing from 0.7 kg in 1970 to 7.8 kg in 2008. This has significant impact on food security (FAO, 2011). Fisheries and aquaculture can contribute in several ways to food security and poverty eradication as shown in Figure 2 below.



The following sections expand on the main pathways linking the sector to poverty and food security: - contributions t and economic multipliers, and to nutrition.

Fig. 2: Aquaculture and poverty reduction: potential impact pathways (Source: Stevensen & Irz, 2009). (The following sections expand on the main pathways linking the sector to poverty and food security: - contributions to GDP and trade, employment and economic multipliers, and to nutrition)

Contributions of fisheries and aquaculture to poverty reduction/food security are in the form of many economic multipliers. These according to Bene et al., (2007) and Thorpe et al. (2007) include low manifestation of diseases, increase access to good healthcare, water and sanitation facilities. Disaggregating food security strategies reveal four major interconnecting pathways in global contribution of fisheries and aquaculture. These are (i) nutritional benefits from fish consumption and utilization (ii) income to those employed in the fisheries and aquaculture sectors (iii) multiplier and spillover effects in fishery-dependent regions and (iv) generation of revenues from export, taxation e.t.c. on fisheries and aquaculture trade.

Based on FAO (2011) report, the harvest, sale and processing of fish contribute indirectly to food security by increasing purchasing power at individual or household level and also regionally and nationally. The establishment of 200- nautical mile exclusive economic zones (EEZs) for coastal states following the 1982 United Nations Conference on the Law of the Sea (UNCLOS), coastal nations have access to huge revenue through direct fishing in the EEZ or lease and agreement with foreign countries with potential to exploit and market the fisheries product ant tother natural resources. Agreement saw extensive fisheries growth in many developing coastal countries – to the point where developing economies now supply more than 70 percent of total fish for food production (IFPRI, 1997). As fisheries exports now generate more foreign exchange (either through export earnings or license receipts than the revenues earned from any other traded food commodity such as rice, cocoa, coffee or tea (FAO, 2003b), this provides a firm foundation for integrating fisheries into the national policy formulation process for some countries. Transformation will help to incorporate the revenue generated into the next phase of food security policy and development. Second, in terms of underpinning national nutritional standards, as fish products presently account for 15-16 percent of global animal protein intake (FAO, 2003). The greater the domestic reliance upon fish protein, the greater the opportunity to insert the fisheries sector into national food security strategies (as in many Asian countries, for example). Third, the sector stands to benefit from the new poverty-oriented development programmes in those instances/countries where individuals, groups and communities linked to the sector are identified as inherently poor and/or latently vulnerable (as in Viet Nam, for example) – and therefore, deserving of support.

Finally, the potential for poverty-reducing, fisheries-specific, policies grow in line with the numeric size of the sector. The more [poor] fishers there are, the greater the potential for mobilization – and the more difficult it is for policy-makers to ignore such voices in the participatory dialogues that are increasingly informing national development processes (Thorpe, A. 2004).

CONCLUSIONS

According to Kent (1997), there is no doubt, fisheries and aquaculture are making serious contributions to food security and poverty eradication. Also, according to Bene et al. (2015), about 4.5 billion individuals worldwide are receiving about 15% of their per capital intake of protein directly from fisheries and aquaculture. According to Thorpe (2004), the September 2000 Millennium Development Compact and the subsequent 2002 Monterrey Consensus (emanating from the UN Financing for Development Conference), called for concerted action on the major developmental challenges of the day to further encourage fisheries and aquaculture development. Without missing words, the central concern in all efforts at food security is towards eradicating human poverty (MDG–Goal 1) (World Bank, 2003: 2). Poverty is likely to remain a crucial – if not the fundamental – policy objective in the next couple of years in international development and scientific conference like this.

Genetics has a lot of roles to play in food security. To achieve food security there is need to identify alternatives to fishmeal that could be used in feed formulation for animals. This will reduce the struggle between human and livestock protein demand. Efforts in genetic improvement of fish species and conservation of fish germplasm will also help to increase productivity and bring a food secured world.

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CYTOLOGY AND HUMAN GENETICS

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CYTOLOGY

Variously defined as

- the field that uses the smallest possible tissue sample for diagnosis, reducing criteria as much as possible to the cellular level (McManus and Mitchell, 2014)
- the study of cells as fundamental units of living things (Encyclopaedia Britannica)
- a branch of pathology, the medical speciality that deals with making diagnoses of diseases and conditions through the examination of tissue samples from the body (Stöppler, 2021)
- the study of the microscopic appearance of cells, especially for the diagnosis of abnormalities and malignancies (dictionary.com).
- Also known as cytopathology and defined as involving examining cells from bodily tissues or fluids to determine a diagnosis. This is relating it to the context or focus of the lecture

Cytology use as a diagnostic or screening test

- A diagnostic test is only used for people who have signs, symptoms, or some other reason to suspect that they might have a particular disease (like cancer). A diagnostic test finds out if a disease is present and, if so, it precisely and accurately classifies the disease.
- A screening test is used to find people who might have a certain disease even before they develop symptoms. A screening test is expected to find nearly all people who are likely to have the disease, but a screening test doesn't always prove that the disease is present.

Often, a diagnostic test is used if a screening test result is positive (that is, if something is found on the screening test). Some cytology tests, such as the Pap test, are mainly used for screening, while others can accurately identify cancers (see "Scrape or brush cytology" below). When cytology results show cancer, often a biopsy is also done to be sure before treatment is started.

Cytology as a diagnostic tool

Cytology now emerges as a powerful diagnostic technique, especially since the advent of the fine needle aspiration (FNA) biopsy. This article highlights the use of ancillary techniques, primarily electron microscopy (EM), and immunohistochemistry (IHC).

Body fluids where cytology tests can be accompanied.

Fluids taken from cavities (spaces) in the body can be tested to see if cancer cells are present.

Some of the body cavity fluids tested in this way include:

i. Urine,
ii. Sputum (phlegm), Spinal fluid, also known as cerebrospinal fluid or CSF (from the space surrounding the brain and spinal cord)
iii. Pleural fluid (from the space around the lungs)
iv. Pericardial fluid (from the sac that surrounds the heart)
v. Ascitic fluid, also called ascites or peritoneal fluid (from the space in the belly)

There are two main kinds, or branches of cytology: exfoliative cytology and intervention cytology.

Exfoliative cytology is a branch of cytology in which the cells that a pathologist examines are either "shed" by your body naturally or are manually scraped or brushed (exfoliated) from the surface of your tissue.

Intervention cytology is a branch of cytology in which your healthcare provider has to "intervene" with your body to get a sample of cells to test, meaning they have to pierce your skin in some way to get a sample of cells. The most common type of intervention cytology is fine-needle aspiration (FNA).

GENETICS, on the other hand, is also defined as

- The scientific study of genes and heredity—of how certain qualities or traits are passed from parents to offspring as a result of changes in DNA sequence. A gene is a segment of DNA that contains instructions for building one or more molecules that help the body work. (National Institute of General Medical Science, 2021). It has many branches as depicted below:

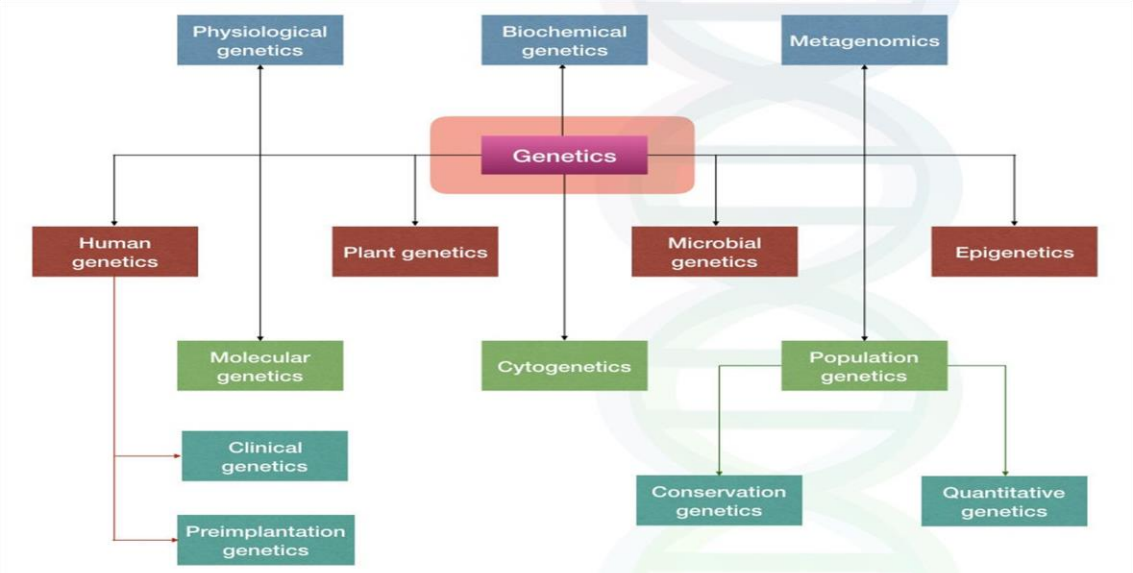

Figure 1: Branches of Genetics

From the figure above, it could be seen that a branch of Genetics is Cytogenetics, which is a combination of Genetics and Cytology.

Medical Genetics is any application of genetic principles to medical practice. This includes studies of inheritance, mapping disease genes, diagnosis and treatment, and genetic counselling.

Pharmacogenetics is the study of how drugs affect the body with respect to specific genetic backgrounds. Medical Genetics is the branch of medicine that involves the diagnosis and management of hereditary disorders. Medical Genetics differs from Human Genetics in that Human Genetics is a field of scientific research that may or may not apply to medicine, while Medical Genetics refers to the application of genetics to medical care.
For example, research on the causes and inheritance of genetic disorders would be considered within both Human Genetics and Medical Genetics, while the diagnosis, management, and counselling people with genetic disorders would be considered part of Medical Genetics.

In contrast, the study of typically non-medical phenotypes such as the genetics of eye color would be considered part of human genetics, but not necessarily relevant to medical genetics (except in situations such as albinism). Genetic medicine is a newer term for medical genetics

and incorporates areas such as gene therapy, personalized medicine, and the rapidly emerging new medical specialty, predictive medicine. Medical Genetics encompasses many different areas, including clinical practice of physicians, genetic counselors, and nutritionists, clinical diagnostic laboratory activities, and research into the causes and inheritance of genetic disorders. Examples of conditions that fall within the scope of medical genetics include birth defects and dysmorphology, intellectual-disabilities, autism, mitochondrial disorders, skeletal dysplasis, connective tissue disorders, cancer genetics, and prenatal diagnosis.

Medical Genetics is increasingly becoming relevant to many common diseases. Overlaps with other medical specialties are beginning to emerge, as recent advances in genetics are revealing aetiologies
for morphologic, endocrine, cardiovascular, pulmonary, ophthalmologist, renal, psychiatric, and
dermatologic conditions. The medical genetics community is increasingly involved with individuals who have undertaken elective genetic and genomic testing.

In some ways, many of the individual fields within medical genetics are hybrids between clinical care and research. This is due in part to recent advances in science and technology (for example, see the Human Genome Project) that have enabled an unprecedented understanding of genetic disorders.

CYTOGENETICS

Based on the definition of the two individual words, Cytogenetics, another field of study could be variously defined as follows:

- According to the National Institute of General Medical Science, 2022, Cytogenetics is a branch of biology focused on the study of chromosomes and their inheritance, especially as applied to medical genetics. Chromosomes are microscopic structures containing DNA that reside within the nucleus of a cell. During cell division, these structures become condensed and are visible with a microscope. Special staining techniques can be used to assess the number and structure of a person's chromosomes as part of diagnostic testing. The number and/or structure of chromosomes are known to be altered in certain genetic diseases.

- Nature.com also defined Cytogenetics as the study of chromosomal structure, location and function in cells. It includes the study of chromosome number and appearance (karyotyping), the physical location of genes on chromosomes, and chromosomal behaviour in processes such as cell division (https://www.nature.com/subjects/cytogenetics).

HUMAN GENETICS?

Human genetics is the study of how parents pass on their traits to their offspring. There are no fundamental differences between human inheritance and that of other creatures. A key area of research in genetics is the study of human heredity. This fascination is mostly motivated by a fundamental curiosity about what makes people tick and what makes them the way they are. Practically speaking, the prediction, diagnosis, and treatment of illnesses with a genetic component depend heavily on our ability to comprehend human heredity
(**https://www.britannica.com/science/human-genetics**).

APPLICATION OF CYTOLOGY IN MODERN MEDICINE

Cytology is the exam of a single cell type, as often found in fluid specimens. It's mainly used to diagnose or screen for cancer. It's also used to screen for foetal abnormalities, for pap smears, to diagnose infectious organisms, and in other screening and diagnostic areas.

KARYOTYPING AND BANDING?

A karyotype is the study of a chromosomal complement's morphology, including its size, shape, centromere location, satellite, distinct uniqueness of its somatic chromosomes, and any other traits. Karyotyping is the process of matching and ordering all of an organism's chromosomes, which produces a genome-wide picture of a specific person's chromosomes. Karyotypes are created using standardised staining techniques that highlight the distinctive structural characteristics of each chromosome.

Methods for chromosomal banding can include colouring chromosomes with a dye or involve testing for a specific function. Giemsa, reverse, centromere, and quinacrine banding are the most used dye-based chromosomal banding techniques. Positive bands are those that exhibit strong staining, while negative bands exhibit weak staining. Different bands stain at various intensities, therefore the staining patterns are not black and white. R-positive (R-) bands are often commonly referred to as G-positive (G-) bands. Constitutive heterochromatin can be seen in positive C-bands. G-bands and Q-bands are thought to be interchangeable (Bickmore, 2001).

The most popular methods for chromosomal identification (karyotyping), chromosome abnormalities, material translocations from one chromosome to another, and deletions, inversions, or amplifications of chromosome segments include G- and R-banding. This has had a significant influence on human genetics and medicine, and by combining cytogenetics with fluorescence in situ hybridization (FISH), the potency of this strategy has increased tremendously in its applications.

Applications

Cytology is becoming increasing useful in the detection of human genetic diseases or disorders (Mehrotra *et al.*, 2012). Chromosomal abnormalities are the basis for a substantial proportion of human morbidity and mortality, most at infant. Hence, cytology and Cytogenetics continues to contribute significantly to our knowledge of clinical genetics, chromosomal fine structure and function, and prenatal diagnosis of genetic diseases. Genetic diseases can be categorised as shown in *Figure 2*.

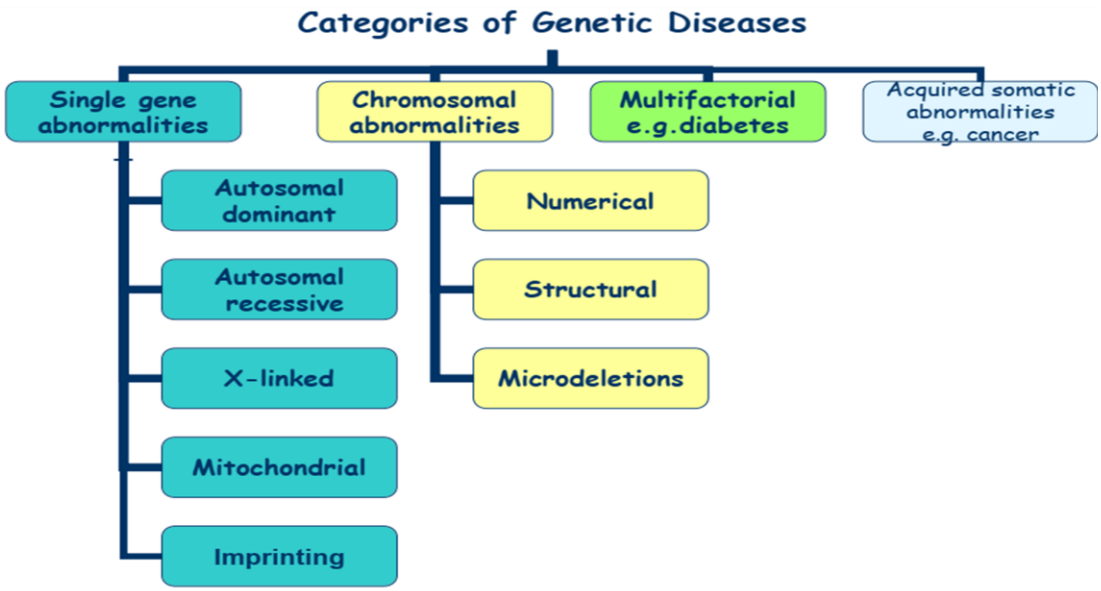

Figure 2. Classification of Genetic diseases (Hamany, 2011)

a. Monogenic Genetic Diseases

Monogenic disorders are a type of genetic disorder in which only one or specific gene is mutated. Examples include cystic fibrosis, sickle cell anaemia, Fragile X syndrome, muscular dystrophy, Familial hypercholesterolemia (FH)

b. Complex Genetic Diseases

Complex genetic diseases or multifactorial inheritance disorders is another form of human genetic disorders which are caused due to small inherited variations in genes and are often triggered together with environmental factors causing different type of diseases. Examples include heart disease.

c. Chromosomal Aberrations

Chromosomal disorders are another type of genetic disorder which are caused due to an error at the chromosomal level. Due to the addition or subtraction of an entire gene from the chromosome or because of structural changes in the chromosomes. Down syndrome, for example, is caused by an extra copy of chromosome 21 (called trisomy 21), although no individual gene on the chromosome is abnormal. Prader-Willi syndrome, on the other hand, is caused by the absence or non-expression of a group of genes on chromosome 15. A specific form of blood cancer (chronic myeloid leukaemia, CML) may be caused by a chromosomal translocation, in which portions of two chromosomes (chromosomes 9 and 22) are exchanged. No chromosomal material is gained or lost, but a new, abnormal gene is formed that leads to the formation of cancer.

Howell (2022) categorized chromosomal disorders into two basic types:
(a) Structural errors and (b) Numerical errors

Structural errors or aberrations are due to the change in the structure of a chromosome. Which can be altered in several ways (More and Best, 2001).

a. **Deletions**: A portion of the chromosome is missing or deleted.
b. **Duplications**: A portion of the chromosome is duplicated, resulting in extra genetic material.
c. **Translocations**: A portion of one chromosome is transferred to another chromosome. There are two main types of translocations. In a reciprocal translocation, segments from two different chromosomes have been exchanged. In a Robertsonian translocation, an entire chromosome has attached to another at the centromere.
d. **Inversions**: A portion of the chromosome has broken off, turned upside down, and reattached. As a result, the genetic material is inverted.
e. **Rings**: A portion of a chromosome has broken off and formed a circle or ring. This can happen with or without the loss of genetic material

Numerical errors or abnormalities can be a gain or loss in one or more chromosomes or chromosome sets (Robinson and McFadden, 2002). This may result from non-disjunction during mitosis or meiosis. The various types include;

a. *Monosomy* (2n-1) is when a single chromosome is lost leading to a disorder like Turner Syndrome (45, X).
b. *Nullisomy* (2n-2) is the loss of a pair of chromosomes and in most cases, the individual does not survive.
c. *Trisomy* (2n+1) is when there is a gain in an extra chromosome to the normal set of a chromosome which can be found in Down syndrome (Trisomy-21), Klinefelter syndrome (47, XXY).
d. Others include double monosomy (2n -1-1), tetrasomy (2n+2) and double tetrasomy (2n+2+2) as shown in Figure 3.

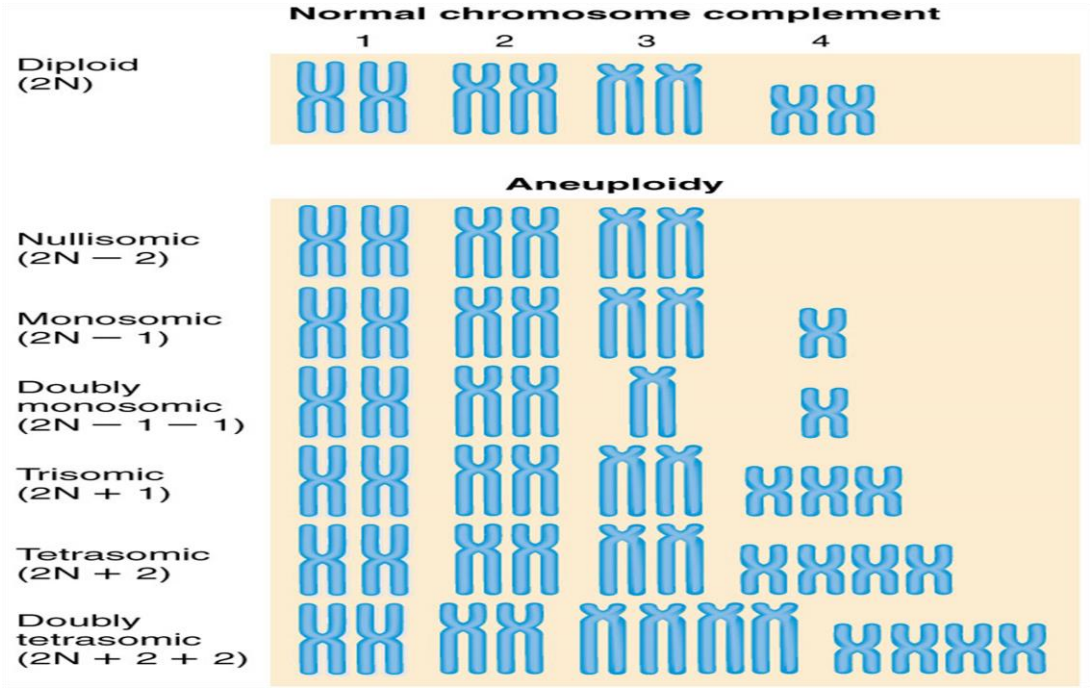

Figure 3. Various numerical abnormalities

Applications in Cancer Research

The detection of somatic genetic alterations in neoplastic cells is one crucial application area for cytogenetic methods in cancer care. This is particularly pertinent for haematological malignancies, but cytogenetics is becoming more prevalent in solid tumours as well. Cytogenetic studies in cancer can be utilised to aid in diagnosis, provide prognostic information, or assist in determining the best course of therapy (Lau 2016).

Genetic changes that take place in a single somatic cell leads to cancer. A sequence of genetic and epigenetic modifications that affect gene activity and alter the cellular phenotype through a selection process are accumulated in all of the cells produced by the first neoplastic clone. The tumour is regarded as benign after neoplastic cells have multiplied into a distinctive cellular mass. Only when a tumour exhibits malignancy-related traits, such as the capacity to infect nearby tissues through blood or lymphatic vessels and cause additional tumours or metastases, is it deemed to be malignant.

Large chromosomal changes may facilitate the observed genetic modifications in malignant cells that are linked to the development or growth of a tumour and may thus be cytogenetically evident. The chromosomal variations in a tumour might be utilised for tumour categorization, diagnosis, and prognosis, according to cytogenetic data. It can be nearly hard to distinguish between various tumour types when the histological characteristics of one tumour type coincide with those of another (Oliveira-Junior *et al.,* 2014).

Certain chromosomal events in some kinds of leukaemia, especially the acute variety, allow for the classification of those types into various subtypes. Additionally, several studies have shown the significance of gene fusions brought on by chromosomal translocations in the development of cancer. Parts of two genes are juxtaposed in these translocations, resulting in chimeric gene products that play distinct functions in cell proliferation and alter the expression of the genes involved. Leukaemia, lymphomas, and sarcomas have all been linked to these chromosomal changes; one such instance is the translocation between chromosomes 12 and

15 seen in congenital fibrosarcoma, which results in the creation of a marker chromosome from the fusion of the oncogenes ETV6 and NTRK3 (Figure 1).

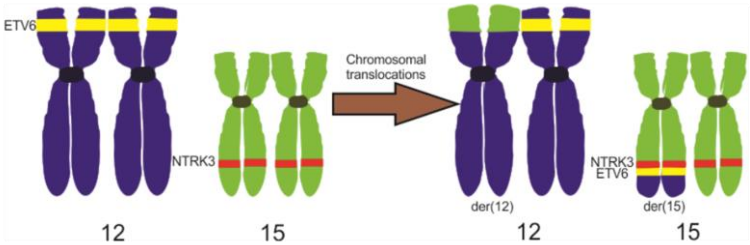

Figure 1. Schematic representation of the translocation between chromosomes 12 and 15 (Gersen and Keagle, 2005).

According to Oliveira-Junior *et al.* (2014), a normal cell first develops polyploidy as a result of a flawed replication or checkpoint control mechanism brought on by physiological, genetic, or environmental factors. Endoreduplication can thereby produce additional copies of chromosomes, a process typically seen in tumour cells (Lime *et al.*, 2004; Davoli and de Lange, 2012). Because polyploid cells are unable to go through appropriate chromosomal segregation and have increased genomic instability, polyploidy itself appears to greatly accelerate the loss of chromosomes.

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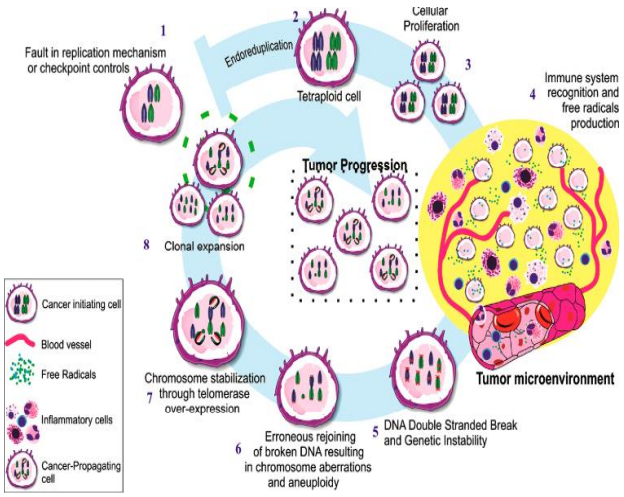

Figure 1. A proposed model for the karyotype evolution of a cancer cell. A normal cell undergoes endoreduplication to transform into a polyploid one when the replication process or check-point controls are flawed. The immune system recognises the cells produced after several rounds of mitosis and attempts to eradicate the aberrant cells by creating cytotoxic mediators such free radicals. Due to the impact of these reactive substances on DNA, double strand breaks and genetic instability result. The incorrect re-joining of fragmented DNA occurs

as a result of attempts to stabilise the double-strand breaks, which results in aneuploidy. When the chromosomes are maintained by telomerase over-expression, a rare cell with a beneficial near-tetraploid karyotype may have a higher proliferative capacity. Through clonal expansion, these specialised proliferating cells advance tumour growth (Oliveira-Junior *et al*., 2014).

Global Statistics of Human Genetic Disease Prevalence

Statistically, of all infants, 2-3% have at least one major congenital abnormality, at least 50% of which are caused exclusively or partially by genetic factors. Chromosomal abnormalities occur in about 0.5% of infants. Monogenic disorder occurs in about 1% of infants. A chromosome abnormality is present in 40-50% of all recognized first-trimester pregnancy loss. Approximately 1 in 6 of all pregnancies results in spontaneous miscarriage, thus around 5-7% of all recognized conceptions are chromosomally abnormal. Most chromosomal disorders occur at the conception level when the egg and sperm are conceived which is why these kinds of abnormalities occur at every cell level. And it can be transferred to the next generation if they survive but, in most cases, it results in spontaneous abortion. Genetic disorder accounts for 50% of all childhood blindness, 50% of all childhood deafness and 50% of all cases of severe learning difficulty. Approximately 1% of all malignancy is caused by monogenic disorder inheritance and between 5% and 10% of common cancers such as breast, colon and ovary have a strong hereditary component.

Management of Human Genetic Diseases

The management of genetic disease can be divided into counselling, diagnosis, and treatment. In brief, the fundamental purpose of genetic counselling is to help the individual or family understand their risks and options and to empower them to make informed decisions. Abarca-Barriga *et al*. (2021) however stated concerning diagnosis and medical treatments, it is of utmost importance that the management of all these conditions is multi and interdisciplinary and carried out by qualified professionals within laboratories and institutions properly certified for these purposes.

Recommendations/Suggestions

a. Government

1. In realising SDG-3 which is good health and well-being, it is imperative for the Government to encourage cytogenetic screening in medical diagnosis for early diagnosis of these disorders in order to make adequate management provisions for the affected. Also, there should an awareness or sensitizing campaign of the need for such screening as early as possible
2. The government should provide enabling environment for affected individuals to be nurtured and not seen as societal liability. This could be achieved by providing education subsidies and special need schooling to affected families at local government areas.
3. Employment opportunities should be made available for the affect to serve as encouragement to others in the same circumstance. This could be achieved through a non-discriminant policy that begins by determining the monthly labour participation rate, also involve the private sectors. Additionally, the government should set a minimum living wage for the state or country, and it should be paid by both private and public sector jobs.

b. Organisations (such as GSN, Universities, Corporate bodies. Researchers, NGOs, etc.)

4. Research outputs from universities, and research institutes should not end up on the shelves. They should be made to translate into usable and useful products for the populace.

5. Corporate bodies should increase their funding in human genetic/ medical research, for those that have been so, and others that have not been doing so should key into it.
6. Science-based societies e.g., Genetics Society of Nigeria (GSN) should admonish members to engage more in implementable and practicable research rather than academic research most times, and to an extent, encourage members with some form of funding as well as give adequate recognition to translatable and usable research outputs.
7. Humanitarian and development actors must base programmes and interventions on a thorough understanding of the context, and strengthen inclusive, locally-led initiatives.
8. Donors, UN agencies, nongovernmental organizations (NGOs), and local actors must commit to flexible, need-based, cross-sectoral, and multiyear planning and financing.
9. Non-Governmental Organizations should work hand in hand with research institutes, universities, researchers, etc, with a view of giving research outputs from these sources adequate and enough publicity for the awareness of the end-users.
10. Nigerian researchers should move towards the future of cytology practice, or SMART (Single Cell, Multiplex, AI-Driving, and Real Time) cytology should apply an integrated approach with the combination of traditional morphology armed with AI/ML (Artificial Intelligence/Machine Learning) tools, and molecular profiling

PARTING COMMENTS

The health care infrastructure in the country has a shortage of basic services to be provided for genetic disorder patients. With some policy resolutions and facility strengthening, it is possible to provide advanced services for a genetic disorder even at the local government health system level. Hence, concerted efforts must be made by all stakeholders

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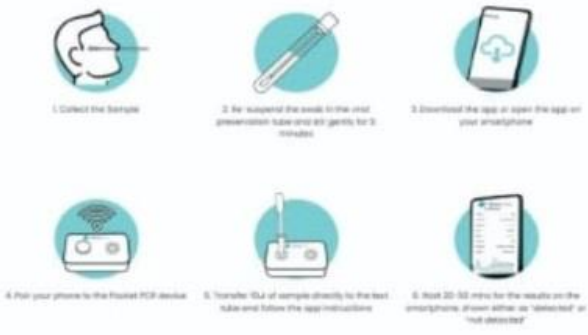

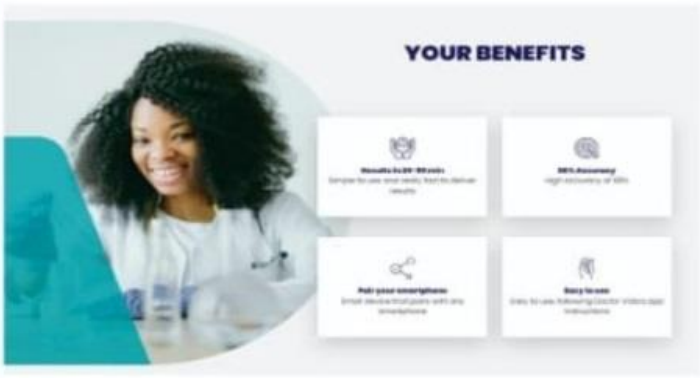

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SCIENTIFIC PAPERS

ADDENDUM

A DESCRIPTION OF LINKAGE DISEQUILIBRIUM AND POPULATION STRUCTURE OF 211 CULTIVATED SOYBEAN ACCESSIONS

Adeboye, K. A.[1*], Bhat, J. A.[2], Ganie, S. A.[3], Oyetunde, O. A.[4], Idehen, E. O.[5], Awopegba, T. M.[1], Fayose, C. A.[1], Varshney, R. K.[6,7] and Yu, D.[2]

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ABSTRACT

The pattern of linkage disequilibrium (LD) and population structure among germplasm resources has implications for further utilization in breeding. This study described the population structure and linkage disequilibrium among 211 diverse soybean accessions using single nucleotide polymorphism (SNP) markers from the NJAU 355K SoySNP Array. After stringent quality control procedures (genotyping rate = 0.99; missing genotype = 0.01; minor allele frequency (MAF) = 0.01; Hardy-Weinberg exact test (HWE) = 0.00001; pairwise genotypic coefficient = 0.5), a total of 5,611 highly polymorphic markers were retained for linkage disequilibrium and Population Structure Analysis. Our results revealed continuous distribution of the 211 cultivated soybean accessions based on 5,611 SNP markers without any distinct structure. Furthermore, the LD decay curve reached half-decay at 927.3 kbp, the genome-wide critical distance to detect linkage and quantitative trait loci (QTL). The 211 cultivated soybean accessions represent valuable resources for genome-wide association studies of important agronomic traits.

Keyword: Hardy-Weinberg Exact test (HWE); genotyping rate; GWAS; pairwise genotypic coefficient; SNP

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INTRODUCTION

Linkage disequilibrium (LD) is the nonrandom association of alleles at different loci that reflects their proximity and the corresponding probability of recombination (Collins, 2007). It is a sensitive indicator of the population genetic forces that structure the genome – genome diversity (Chao *et al.*, 2010). LD and population structure have implications for breeding and genetic studies. Information on LD and Population structure can aid selection of promising parental breeding material. It is also crucial to understanding and discovering genetic mechanisms underlying traits; this knowledge helps determine the best approaches to minimize false association, enabling the incorporation of ideal superior traits/genes into new cultivars.

Therefore, it is necessary to estimate the pattern of LD and the population structure of germplasm before further use in breeding/genetic studies. The present study described linkage disequilibrium and population structure of 211 diverse soybean accessions using single nucleotide polymorphism markers.

MATERIALS AND METHODS

A panel of 211 soybean accessions was selected from diverse soybean cultivation ecological regions of the Peoples' Republic of China. Single-nucleotide polymorphism (SNP) markers were obtained from the NJAU 355K SoySNP Array (Wang *et al.*, 2016). Quality control analysis was implemented in PLINK v1.07 (Purcell *et al.*, 2007) using the following criteria: missing genotype = 0.01; minimum minor allele frequency (MAF) = 0.01; Hardy-Weinberg exact test (HWE) = 0.00001; pairwise genotypic coefficient = 0.5. Population structure was assessed based on soybean ecological regions in China using the principal component analysis. Optimal numbers of PCA were estimated using the Bayesian information criterion (BIC) (Schwarz, 1978). For the Linkage disequilibrium

(LD) analysis, pairwise squared allele-frequency correlations (*r2*) between SNP markers were calculated in 100 sliding windows using TASSEL v5.2.73 (Bradbury *et al.*, 2007). Expected values of *r2* under drift equilibrium were calculated according to (Hill and Weir, 1988) and plotted against physical distance (Kbp). The LD decay curve line was fitted on the scatterplot using the smoothing spline regression line at the genome level following the procedure of (Remington *et al.*, 2001) in *the* R environment.

RESULTS AND DISCUSSION

After a stringent quality control analysis with a 99% genotyping rate, a total of 5,611 highly polymorphic markers were retained for further analysis. The markers were reasonably distributed across the 20 soybean chromosomes covering 5935.6 cM (Table 1). Previously *Wang et al.*, (2016) obtained a total of 207,608 SNPs for 264 cultivated soybean genotypes, which include the 211 genotypes used in this study and others. In other studies (Bhat *et al.*, 2022a; Bhat *et al.*, 2022b) involving the same 211 soybean genotypes, different numbers of SNPs were obtained due to differences in the quality control metrics such as the minimum minor allele frequency and Hardy-Weinberg exact test.

Chromosome 13 has the highest number of markers, while chromosome 1 has the lowest number of markers. According to Chao *et al.*, 2009, Eltaher *et al.*, 2018 and Adeboye *et al.*, 2020, fewer polymorphic markers on a chromosome may be an indication that the contribution of the chromosome to the overall genetic diversity of the population is low. There was a total of 2,370,000 gametes in the genome (Table 2). Out of this, only about 1.5% were missing. The heterozygosity index of markers is an indication of the diversity level of the population and molecular markers (Adeboye *et al.*, 2020). The average heterozygosity across the soybean genome is 0.11, while the average minor allele frequency was 0.07. This result indicates the suitability of the markers for estimating the genetic structure and diversity of the studied germplasm. The distribution of the minor allele frequency and heterozygosity across the soybean genotypes is presented in Figure 1.

The graphical representation of the population structure and linkage disequilibrium characteristics of the studied soybean genotypes is presented in Figure 2. The population structure was analyzed based on soybean ecological regions in China (Figure 2a). It revealed a continuous distribution without any distinct structure as previously reported by Bhat *et al.,* (2022a). The average linkage disequilibrium (r^2) value for the genome was 0.04, while the LD decay curve started at 0.46 and reached half-decay at 0.23 (Figure 2b). The decay curve intersected with the half-decay at 927.3 kbp, which represents the genome-wide critical distance to detect linkage; markers associated with the same traits within this distance could be considered single quantitative trait loci.

The LD metrics obtained in this study is similar to those obtained by Bhat *et al.*, (2022a). However, the half-decay distance in the present study is larger. This may be attributed to the use of fewer molecular markers. Wang *et al.*, (2016) also reported half-decay distance of 130 kbp using a larger number of molecular markers. The heatmaps and dendrograms of the kinship matrix, based on 5,611 polymorphic SNPs for the studied genotypes, indicated that there was no clear clustering among the genotypes (Figure 3). This further corroborates the population structure analysis.

Conclusion

Based on the estimates of linkage disequilibrium and population structure, substantial genetic diversity is prevalent among the studied soybean cultivars. Breeders developing cultivars with improved characteristics see this interesting. The obtained knowledge about SNP informativeness and the LD estimation are worthwhile for selecting markers for considering the composition of a population in association mapping studies of traits of interest.

The 211 cultivated soybean accessions represent valuable resources for genome-wide association studies or understanding of essential agronomic traits, including yield characters/architecture and stress mechanisms in soybean.

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Table 1. Marker distribution of 211 diverse soybean accessions across the soybean genome

Chromosome	Chromosome coverage (bp)	Number of Markers	Chromosome Length (cM)
1	266002-55580484	198	272.5113
2	30208-51547432	292	314.3745
3	82297-47715831	363	388.4074
4	59908-49081720	264	188.9234
5	79354-41895382	226	152.3192
6	322237-50560368	280	307.4721
7	170685-44531877	277	335.4604
8	302781-46790842	308	346.0902
9	34563-46056722	251	363.1088
10	162363-50962539	243	208.962
11	120426-39164024	247	260.7535
12	364675-40099583	255	144.0734
13	70853-44291240	415	484.0143
14	90752-49700697	279	199.0733
15	75457-50920933	274	314.7433
16	129371-37390602	320	308.2315
17	140120-41656503	228	365.663
18	19295-62270319	400	535.3019
19	61505-50570288	238	229.4636
20	174624-46765314	253	216.6693
Whole Genome		5611	5935.616

Table 2. Soybean genome summary statistics of the 211 cultivars based on 5,611 markers from NJAU 355K SoySNP Array

Stat Type	Value
Number of Taxa	211
Number of Sites	5611
Sites x Taxa	1.18E+06
Number Not Missing	1.17E+06
Proportion Not Missing	0.9846
Number Missing	18227
Proportion Missing	0.0154
Number Gametes	2.37E+06
Gametes Not Missing	2.33E+06
Proportion Gametes Not Missing	0.9846
Gametes Missing	36454
Proportion Gametes Missing	0.0154
Number Heterozygous	134228
Proportion Heterozygous	0.11338
Average Minor Allele Frequency	0.07237

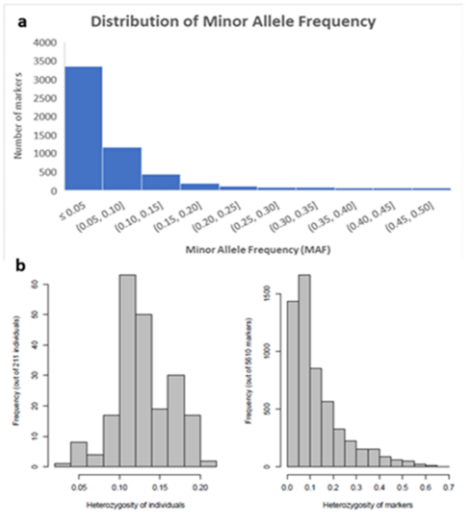

Figure 1. (a) Minor allele frequency and (b) heterozygosity of markers across the 211 Soybean cultivars

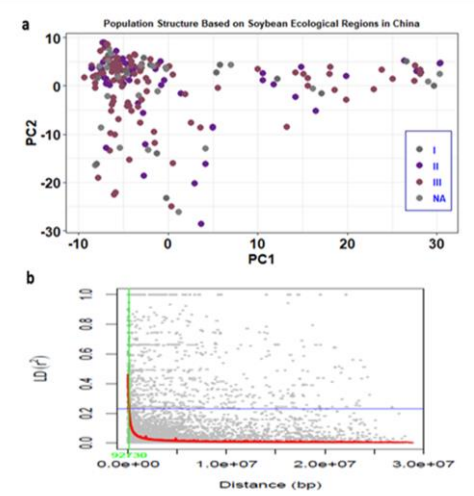

Figure 2. (a) Linkage disequilibrium curve and (b) Population structure of the 211 Soybean cultivars

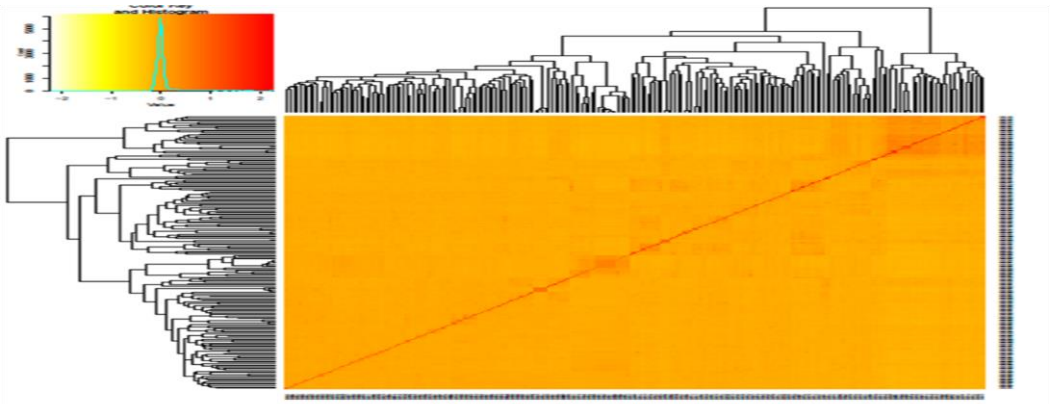

Figure 3. Heatmaps and dendrograms of the kinship matrix, based on the 5,611 polymorphic SNP markers for the studied genotypes, indicating that there is no clear clustering among the genotypes

CONSISTENCY OF PERFORMANCE OF SOME GENOTYPES OF COFFEE IN NIGERIA COFFEE GERMPLASM

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ABSTRACT
Climate change impacted productivity of coffee significantly and fluctuation in the weather made its performance unpredictable. Consistence of performance is a major requirement in sustainable coffee production. Nineteen coffee varieties conserved in-situ in four replications at Cocoa Research Institute of Nigeria were selected, harvested, wet processed and evaluated in Ibadan South west Nigeria during 2012, 2013 and 2014 seasons. Data were fitted to Additive Main effect and Multiplicative Interaction (AMMI), as well as Genotype plus genotype x environment GGE biplot stability models. AMMI model revealed significant genotype and genotype x environment interaction were significant. The model identified genotype C36 the most desirable variety, combined high seed yield with stability. GGE biplot identified D57, C36 and T1049 as high yielding and stable. Year 2012 was the most discriminatory of the three years.

Keywords: coffee, consistency, environment, genotype, genotype x environment

INTRODUCTION
Coffea is a woody perennial dicotyledonous plant which is indigenous to Africa and is a major genus of the Rubiaceae family widely distributed in the tropics (Thomas, 1940). The genus *Coffea* L. is reported to have 105 species (Medina-Filho *et al*., 2007), which are prevalent in Africa and Madagascar (Prakash *et al*., 2005). Coffee was first introduced to Nigeria in 1921-1931 by former Department of Agriculture although from the export figure it was known that the crop has been cultivated for much longer period. In Nigeria, cultivation on a large scale started as far back as the 1940s but gain momentum in the early to mid-1950s. By 1989, approximately 250,000 farmers cultivated coffee in Nigeria, thus providing livelihood for about 1 million people spread in fourteen states of Nigeria. Nigeria produced about 95,000 metric tonnes of coffee. Except for the parts of Mambilla and Jos Plateau and some parts of Obudu in Cross River State of Nigeria where *C. arabica* is cultivated, majority of the coffee planted in Nigeria is *C. canephora* (Adepoju *et.al*, 2017). At present, there is a great decline in Nigerian coffee production. One of the major factors responsible for this climate change resulting to poor yield (Omolaja, 2009; Ayoola *et al*., 2015).

Changes in rainfall pattern and continuous rise in temperature trigger extreme weather conditions like flooding, drought, and heat waves (Feulner 2017) which affect available water for crop growth, thereby encouraging insurgence of pests and diseases, and subsequently reduced crop yields and income of small hold farmers in Africa (Waldman and Richardson 2018). These problems are predominant in sub-Saharan countries of Africa and pronounced particularly in West Africa where there is dependence on rain fed agriculture and high population growth is at exponential rate and little effort is made towards mitigation of climate change (Waldman and Richardson 2018). According to Goncalves *et al.* (2008), Genotype–year interaction in perennial crops indicates how genotype responds differentially to changing in annual weather condition.

The objectives of this study were to assess the lowland coffee genotype-year interaction in Ibadan under unpredictable weather condition fluctuation and to determine temporally stable genotypes for three annual yield evaluations.

MATERIALS AND METHODS
The experiment was carried out at Cocoa Research Institute of Nigeria (CRIN) at Ibadan, Nigeria Observations were made or superimposed on existing coffee plantation of coffee germplasm on nineteen coffee varieties planted in a Randomized Complete Block Design with four replicates at a spacing 3 x3 m during 2012, 2013 and 2014 were utilized for this study.

The berries harvested were processed using wet processing method (Mburu, 1999). The following characters were also observed: berry length (mm), berry width (mm), berry thickness (mm), seed length (mm), seed thickness (mm), seed width (mm), weight of berries per tree (g), 100 berries weight (g), weight of seeds per tree (g) and 100-seeds weight (g) using IPGRI coffee descriptor.

Statistical analyses

The data collected were subjected to Analysis of Variance (ANOVA) across the three years using PROC GLM in SAS according to the procedure of Gomez and Gomez (1974). The observations were also subjected to stability models of AMMI (Zobel *et al*., 1988) and GGE biplot (Yan 2001).

RESULTS AND DISCUSSION

The AMMI biplot in Figure 1 showed that genotypes D57, C108, C36, T1049 and C111 produced above average seed yield. All other genotypes were below average in seed yield because they were located at left hand side of the vertical line. Genotype C36 was the most stable as it had IPCA score almost equal to zero. D57 and T1049 were relatively stable for seed yield. C111 had the highest yield but highly unstable. Genotypes 36, D57 and T1049 were the most desirable in respect of seed yield as they combined high yield with stability. In AMMI, the desirable cultivar should combine high yield with consistent performance across a range of environments. Although C111 had the highest yield, it was unstable. This was in agreement with the report of Kamdi (2001), that high yielding genotypes were usually unstable. So, for coffee genotypes in three years of study at Ibadan, C36 was the best genotype because it was both consistent and high yielding followed by genotypes D57 and T1049.

The polygon view of the GGE biplot is a visualization pattern which reveals which genotype was superior in a specific mega-environment, i.e. "which-won-where". The polygon for yield per plant is a pentagon with four sectors (Figure 2). The three environments were located in the same sector, where C108, C111 and T1049 were the vertex varieties indicating their superiority in the three years.

In the polygon view, according to Yan (2001) and Yan *et al.* (2000; 2010), the vertex cultivars in each sector represents the highest yielding cultivar in the locations that fall within that particular sector. This implies that genotypes that occur in a particular environment in the biplot show specific adaptation to that environment. Based on this information, genotypes C108, C111 and T1049 were selected as high yielding genotypes. An ideal location should be highly differentiating for the tested genotypes and at the same time representative of the target location (Yan and Kang, 2003).

The environment-focus scaling in GGE biplot is used to test how discriminatory and representative each environment was. Discriminatory ability is based on the vector length of each environment, the longer the more discriminatory. Hence, E1 (2012) was the most discriminatory environment for seed yield (Figure 3). However, the three years are positively correlated because of acute angles among the environment vectors but E3 was the most representative. In this study, year 2012 was the most discriminatory for the genotypes and in respect of the yield however, no year was most representative due to positive correlations among the tested years. Figure 4 shows the average yield (across the test environments) and stability of each genotype approximated by the projection of their position on the AEC abscissa (average environmental axis- x axis), with an arrow pointing to a greater value (ideal genotype) based on the mean performance of the genotypes across the environments. The double-arrowed line separates the genotypes with below-average yield from those with above average yield. Therefore, genotypes with the above-average yield were D57 (G9), C108 (G5), C36 (G7), T1049 (G15), and C111 (G6). The stability of the genotypes is measured by their projection on the double-arrowed line (average environment coordinate- y axis). The longer the projection of a vector of cultivar on the double-arrow line the less stable it is (Yan *et al*., 2010). Genotype C36 had no projection on the AEC abscissa and therefore most stable; D57 and T1049 had short projections which made them to be relatively stable, C108 and C111 had long projections and therefore most unstable despite their high mean performance.

The result of this GGE analysis is best understood by identifying the performance of different genotypes in an average environment. In this case, the most desirable was C111 while other desirable genotypes with above average seed yield were T1049 to D57 and C108.

Conclusion

AMMI model showed those genotypes with better performance in term of yield, in addition to identifying consistent genotypes. From GGE biplot, relationship among the genotypes and environments visualization was possible, stable/consistent and high yielding genotypes were also identified. This study had successfully provided information on consistency of coffee genotypes in Genotype x Year interaction in the face of unpredictable climatic condition. Of all lowland coffee genotypes studied, genotypes D57, C108, C36 T1049 and C111 were identified as genotype with above average performance. Among these genotypes, C36 and T1049 could be recommended to farmers because of its performance consistency even in the face of unpredictable climate.

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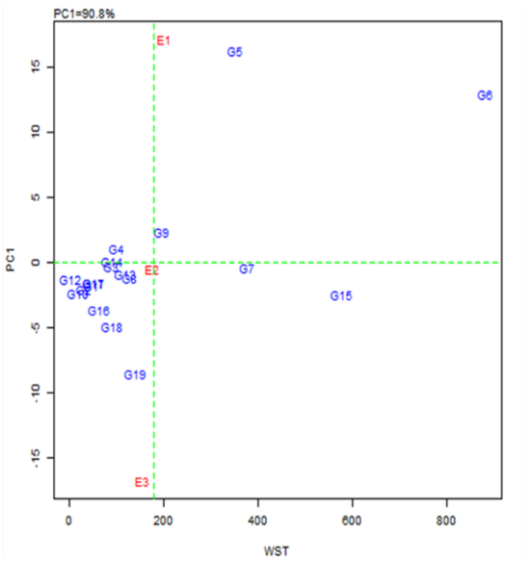

Figure 1. AMMI 1 biplot for weight of seed per tree of nineteen coffee genotypes showing means of genotypes plotted against their PC1 scores

G1=A110, G2=A81, G3=C105, G4=C107, G5=C108, G6=C111, G7=C36, G8=C96, G9=D57, G10=E1, G11=E106, G12=H139, G13=M10, G14=M53, G15=T1049, G16=T204, G17=T24, G18=T921, G19=W109

E1=2012, E2=2013, E3=2014

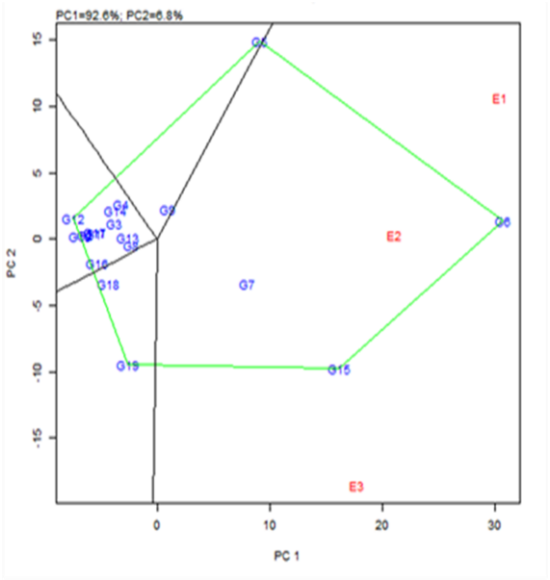

Figure 2. The polygon view of GGE biplot showing genotype that yielded best in a particular year

G1=A110, G2=A81, G3=C105, G4=C107, G5=C108, G6=C111, G7=C36, G8=C96, G9=D57, G10=E1, G11=E10s6, G12=H139, G13=M10, G14=M53, G15=T1049, G16=T204, G17=T24, G18=T921, G19=W109

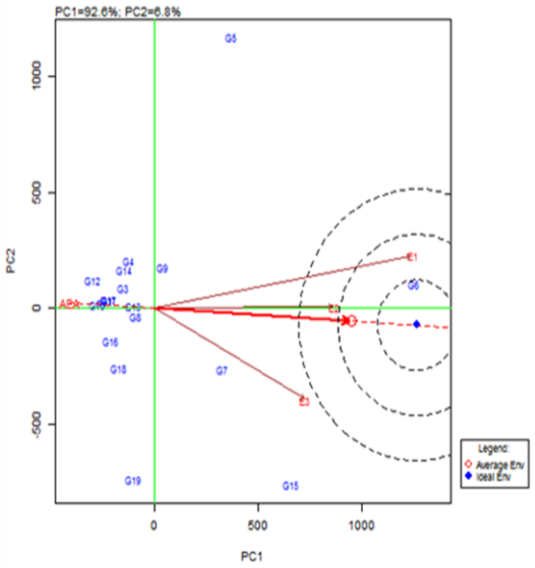

Figure 3. GGE biplot of the discriminating power versus representativeness of test years in coffee for weight of seed per tree

G1=A110, G2=A81, G3=C105, G4=C107, G5=C108, G6=C111, G7=C36, G8=C96, G9=D57, G10=E1, G11=E106, G12=H139

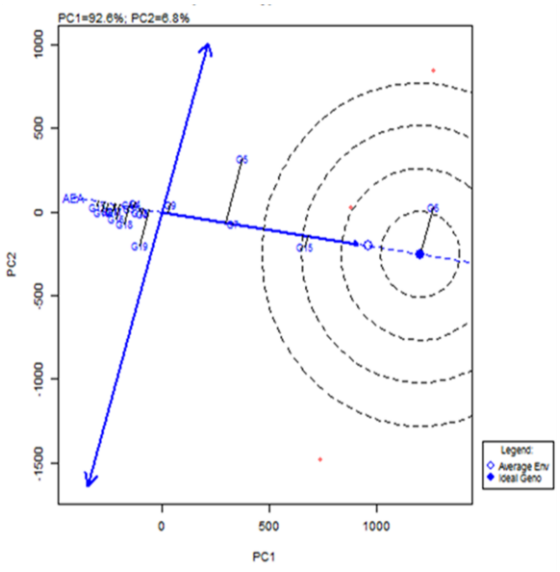

Figure 4. The mean performance versus stability of nineteen coffee genotypes across the test year

G1=A110, G2=A81, G3=C105, G4=C107, G5=C108, G6=C111, G7=C36, G8=C96, G9=D57, G10=E1, G11=E106, G12=H139, G13=M10, G14=M53, G15=T1049, G16=T204, G17=T24, G18=T921, G19=W109

GROWTH AND YIELD RESPONSE OF SOME MEDIUM MATURING SOYBEAN (*Glycine max* (L.) MERILL) GENOTYPES IN KEFFI, NASARAWA STATE

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ABSTRACT
Soybean meals and oils are essential for human and animal health. The objective of the study was to ascertain the correlation between the oil content and yield parameters of five varieties of medium-maturing soybeans. The research was conducted at the Nasarawa State University, Keffi, Botanical Garden Farm, during the 2015 rainy season. The experiment was laid out in a Randomized complete block design with three replications. Growth and yield collated data were analysed. Traits varied significantly ($p < 0.05$) between varieties. Oil content positively correlated with the number of pods r = 0.410, total seed weight per plot r = 0.3406, 100 seed weight r = 1, number of seeds per pod r =0.9162*, and Grain yield r = 0.215*. The variety TGx1989–45F had the highest seed weight per plot (3733 per 1000 g) while Variety TGx1989–42F had the highest mean for oil content (17.0 ml).

Keywords: correlation, medium maturing, oil content, soybean, yield

INTRODUCTION
Soybean (*Glycine max* (L.) Merrill) is one of the most economically significant crops in the world due to its versatile use and the great value of its seeds (Jarecki *et al*., 2020). It is often referred to as a 'miracle crop' due to its highly nutritious content as it contains high-quality proteins (40%), and high oil content (18%), making it a prime source of vegetable oil in the international market (Rajni *et al*., 2020). It is the best source of plant protein which can substitute animal-protein sources which are usually inadequate in supply for poor households (Seyi, 2014).

Understanding the relationships between various morphological characteristics and seed yield is crucial to finding the proper selection criteria. When characters are correlated, selection for one character may lead to either positive or negative responses in the other characters. Suitable varieties for a region can be selected if the correlation and heritability of the characters are known, as it can be challenging for farmers and breeders to choose specific varieties for planting for either seed yield, oil content, or both. A correlation study is a powerful tool for finding reliable associations among morphological characters for aiding selection (Amsalu *et al*., 2014). This study was therefore conducted to evaluate the correlation between oil content and yield parameters of soybean (*Glycine max* (L.) Merill) in Keffi, Nasarawa State, Nigeria.

MATERIALS AND METHODS
The field experiment was carried out during the rainy season of 2015 at the Botanical Garden of the Department of Biological Sciences, Plant Science and Biotechnology unit farm of Nasarawa State University, Keffi. Nasarawa state is located 8º32'N 8°18'E in the Guinea Savannah Zone of Nigeria and annual rainfall figures range from 1100 mm to about 1600 mm. Five medium maturing varieties with maturity dates ranging between 115 – 130 days (TGx1990-106FM, TGx1990-106FM, TGx1989–45F, TGx1989–42F, TGx1990–78F) were used for the study. All of these varieties were sourced from the International Institute of Tropical Agriculture, Ibadan (IITA). The experiment was laid out in a randomized complete block design (Gerald, 2012). The varieties were planted in three blocks and the treatments were the five different varieties. It was arranged such that each block had a different arrangement of treatments. This was to ensure no bias and to check the performance of varieties on different blocks (Gerald, 2012). Data were collected before and after harvest.

Statistical analysis
Data were analyzed using a general linear model of Statistical Analysis system software version 9.3 (SAS9 3, July 2011) for analysis of variance at $p = 0.05$. Correlation coefficients (r) were analyzed using Pearson Correlation.

RESULTS AND DISCUSSION

Analysis of Variance was conducted for yield traits. The mean squares of ten characters in the five varieties evaluated in eight weeks are A Pearson correlation was conducted between the oil content and some yield parameters (Number of seeds per plot (NSP), 100 seed weight (HSW), total seed weight per plot (TSW), Number of pods (NP), and grain yield) for the five medium maturing varieties. The results were presented in Table 2. The correlation between oil content, number of seeds per pod, and grain yield was positive and highly significant. Indicating an increase in the number of seeds per pod will lead increase in grain yield and oil content. This is obtainable if all conditions for proper growth and environment are met (Salimi, 2012).

A significant positive correlation was observed between the number of seeds per pod with the number of pods and grain yield, a significant correlation was also observed between 100 SW and the number of pods and yield. This indicated that an increase in any one of these characters will principally increase the grain yield of soybeans this agreed with the findings of Moradi and Salimi (2012), who observed significant variations in all the yield parameters studied and showed a significantly positive correlation.

There was a highly significant positive correlation between Grain yield with oil content, total seed weight (TSW), and the number of pods it was also positively significant with the Number of seeds per pod (NSP) and 100seed weight (HSW) indicating interrelationships between yield and its components in soybean genotypes this agrees with findings by Ali *et al.,* (2006) who reported that seed yield per plant was positively and significantly associated with all parameters studied. They suggested that pods per plant, seeds per pod, and 100 seed weight were the three key factors affecting yield, with pods per plant having the maximum significant direct effect on yield per plant.

Conclusion

From the study on the correlation between oil content and yield traits for some medium-maturing varieties of soybeans, a significant positive correlation between desirable traits is favorable because of the simultaneous improvement of both characteristics, while a negative correlation will hinder the simultaneous expression of both. Total seed weight per plot correlated positively with 100 seed weight and the number of pods. In comparison, there was no correlation between total seed weight per plot, presented in Table 1. All the characters varied significantly except for the number of leaves and plant height, indicating considerable genetic variability exists among the selected genotypes.
number of seeds per pod, and oil content. Grain yield correlated positively with the number of seeds per pod, number of pods, 100 seed weight, total seed weight per plot, and oil content. Depending on the farmer's need, some economic compromise has to be made in selecting varieties. Therefore, knowledge of the relationship between yield and its components obtainable through correlation and regression analysis helps a great deal in formulating selection. The correlation coefficient (r) measures the degree (intensity) and nature (direction) of association between characters (Moradi & Salimi, 2012). Results obtained from the study show significant variability in the seed yield and oil content of the five medium-maturing soybean varieties. This clearly indicated that seed yield improvements are possible by selecting suitable varieties for the location. Variety TG × 1989 – 45F had the highest grain yield, while TG × 1989 – 42F produced the highest oil content; both are recommended for adoption by farmers interested in grain yield and oil content, respectively.

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Table 1. Mean squares for characters of medium maturing soybean varieties

Source of variation	Replicate (df = 2)	Genotype (df = 4)	Error (df = 8)
DF	2	4	
Number of leaves	5756.28	3355.76	
Stem diameter (cm)	7052.73	2612.61**	
Leaf area	36.55	45.66*	
Plant height (cm)	17046.1	574.76	
Number of pods	330.53	12866.13**	
100-seed weight per plot (g)	5.24	14.84**	
Total seed weight per plot (g)	0.04	0.44**	
Number of seeds per pod	0.53	5.33**	
Grain yield (g)	450.64	100344.88**	
Oil Content	0.08	488.02**	

* 0.05 significant difference, ** 0.01 highly significant difference,

Table 2. Correlation between oil content and some yield parameters of medium maturing varieties

Character	Oil Content	No of seed per pod	100-seed weight	Total seed weight per plot	Numbe of pods	Grain yield
Oil content	1					
Number of seeds per pod	0.59**	1				
100-seed weight	0.65**	0.43	1			
Total seed weight per plot	0.02	0.57	0.19	1		
Numbe of pods	0.26	0.61	0.43*	0.57**	1	
Grain yield	0.19**	0.84*	0.63*	0.51**	0.34**	1

* 0.05 significant difference, ** 0.01 highly significant difference

GRAIN YIELD TRAITS AND NUTRITIONAL VALUES AMONG OFADA RICE MUTANTS AND SOME NERICA RICE VARIETIES

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ABSTRACT

Estimation for genetic variability among seven selected Ofada rice mutants and some NERICA varieties was carried out at screen house of Olabisi Onabanjo University, College of Agricultural sciences, Ayetoro Campus, Ogun State, Nigeria. The study was conducted using complete randomized design in three replications. Result of analysis of variance revealed significant ($p < 0.01$) variation among the studied traits except for grain length and grain width. The magnitude of difference between phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) was relatively low or none for all the studied nutritional values revealing little or no influence of environmental factors while high PCV and GCV values observed from grain weight per plant, grain width, fat, amylose, gel consistency indicating possibility of improvement of the characters through simple selection.

Keywords: heritability, Ofada, NERICA, variability

INTRODUCTION

Rice is the world's leading food grain crop that supplying more than half of the daily calories and proteins for more than half of the world's population (Zhang *et al.*, 2020).

The nutritional properties of rice are of great importance to rice consumers mainly because of the significant contribution of dietary energy, protein and fat supply especially in countries where rice is regarded as a staple food (Rohman *et al.*, 2014). Therefore, high yielding traits in rice is not enough to recommend such variety for cultivation and consumption; varieties of rice for cultivation and consumption must also possess some desirable traits in terms of grain qualities and nutritional values.

Crop improvement programme is largely dependent on the nature and magnitude of available genetic variability, heritability and transfer of desired traits into new genotypes. Also, knowledge of genetic parameters are useful biometric tools for measuring genetic variability (Aditya and Bhartiya, 2013). Hence, this study was carried out to estimate genetic variability, heritability and genetic advances among promising Ofada mutants and selected NERICA rice varieties to provide information that could help in improvement of grain yield and nutritional values.

MATERIALS AND METHODS

The experiment was carried out of the screen house of Teaching and Research Farms of College of Agricultural Sciences, Olabisi Onabanjo University, Yewa Campus, Ayetoro. Twelve rice genotypes including seven Ofada mutants (OG13602-100, OG13605-200, OG13606-250, OG13608-300, OG13609-300, OG13611-350, OW13621-300) derived from FUNAABOR 1 and FUNAABOR 2 Ofada rice, FUNAABOR 1 parent and four NERICA varieties (NERICA 1, NERICA 2, NERICA 3 and NERICA 8) were used as the plant materials. The experiment was carried out in a Completely Randomized Design with three replications. The plants were watered adequately and other intercultural operations were done when necessary.

Agronomic data were collected at maturity stage of rice growth on panicle length, grain weight/panicle, spikelet number per panicle and grain weight per plant. Whole grains that are free from damages were selected for physical, physicochemical and nutritional value analysis. One hundred grains were selected randomly and weighed separately with the use of sensitive weighing balance. Grain weights were measured in gram while grain length and grain width were measure in 'mm' with the use of Vernier caliper.

Physicochemical properties and values were analysed according to the official methods of analysis as described by the Association of Official Analytical Chemist (A.O.A.C., 18th Edition, 2005). The treatment means for all the characters were subjected to analysis of variance technique. The variance components include:

Phenotypic and Genotypic coefficient of variation (PCV and GCV), broad sense heritability (h^2b) was calculated and the Genetic advance (GA) was also estimated by the formula given by Johnson *et al.* (1955).

RESULT AND DISCUSSION

Analysis of variance (Table 1 and 2) showed significant difference among the genotypes for all the studied traits except for grain length and grain width indicating appreciable variability that can be exploited for the next breeding program. Estimates of mean, PCV, GCV, broad sense heritability and GA for grain traits and grain nutritional values are shown in Table 3. The magnitude difference between PCV and GCV was relatively low for fat (38.26, 37.22), fiber (12.36, 12, 35), moisture (14.29, 14.24), carbohydrate (1.51, 1.49), amylose (25.31, 25.29) and gel consistency (25.85, 25.84) and none for protein (18.01, 18.01) and amylopectin (3.95, 3.95) revealing low environmental influence and predominance of genetic factors controlling these traits. GCV was high for grain weight per/plant (39.04), crude fat (37.23), gel consistency (25.84), amylose (25.29), spikelet number per panicle (18.10) and crude protein (18.01). This indicates wide variation among studied genotypes for these traits. Similarly, high values of GCV were recorded for grain yield per plant and protein content in the study carried out by Chand *et al.* (2005). High PCV and GCV estimates also were recorded for grain weight per plant (49.45, 39.04), crude fat (37.23, 38.26), amylose content (25.31, 25.29) and gel consistency (25.85, 25.84). This shows that simple selection can be used for further improvement of these traits. Moderate values of PCV and GCV were also observed for panicle length (16.98, 13.64), crude protein (18.01, 18.01), crude fibre (12.35, 12.35) and % moisture (14.29, 14.27). However, other studied traits revealed low PCV and GCV estimates.

High heritability estimates (>50%) were recorded for all studied traits except for grain weight per panicle (36.58) and spikelet number per panicle (47.3%) indicating the least environmental effects on expression of the studied nutritional values among the genotypes. High heritability (broad sense) coupled with moderate genetic advance was revealed for gel-consistency (99.94%, 17.07%) may be due to dominance epistatic effects and least effect of additive genes according to Chand *et al.* (2005). Low heritability with moderate genetic advance (47.3%, 30.23%) was recorded for spikelet number per panicle. Also, moderate heritability coupled with low genetic advance was observed for panicle length (64.5, 5.62) and grain weight per plant (62.3, 9.41) and this may be due to the genes having non-additive effects. Similar result was reported by Yadav et.al, 2017.

Conclusion

The results from this study revealed that the genotypes considered harbor an appreciable variability for the grain and grain nutritional values that can be exploited for selection, hybridization and further selection for improvement of grain yield and nutritional value. Considering all points related to genetic variability discussed above, traits such as grain weight per plant, can be improved through direct simple selection.

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Table 1. Mean square for grain traits among Ofada mutants and NERICA varieties

Source	Df	Panicle length	Grain weight/ panicle	Spikelet number/ panicle	Grain weight/ plant	Grain length	Grain width
Genotype	11	40.94**	0.64*	1871.36**	120.761**	0.02	0.01
Replicate	2	27.28	2.18	2652.08	16.80	0.01	0.01
Error	22	6.35	0.24	506.45	20.26	0.01	0.01
R^2		0.78	0.69	0.70	0.75	0.40	0.38

Table 2. Mean square for physicochemical and nutritional values among Ofada mutants and NERICA varieties

Source of variation	Df	Crude protein	Crude fat	Crude fibre	% Moisture	Carbohydrate	Amylose	Amylopectin	Gel consistency
Genotype	7	3.553**	1.637**	0.155*	7.079**	3.958**	35.546**	34.936**	206.090**
Replicate	1	0.036	0.000	0.003	0.003	0.000	0.002	0.009	0.456
Error	7	0.000	0.030	0.000	0.005	0.033	0.020	0.000	0.038
R^2		0.100	0.982	0.999	0.999	0.992	0.999	0.999	0.999

** significant at $p < 0.01$

Table 3. Estimate of mean, phenotypic coefficient of variation, genotypic coefficient of variation, heritability and Genetic advance for grain traits, and nutritional values among Ofada rice mutants and NERICA varieties

Characters	Mean	PCV	GCV	H^2b (%)	GA (%)
Panicle length	24.90	16.98	13.64	64.50	5.62
Grain weight/ panicle	3.39	17.94	10.83	36.50	0.46
Spikelet number / panicle	117.83	26.31	18.10	47.30	30.23
Grain weight per/ plant	114.83	49.45	39.04	62.30	9.41
Grain length	0.53	21.97	6.49	8.70	0.02
Grain width	0.17	76.08	11.23	2.60	0.01
Crude protein	6.04	18.01	18.01	99.99	2.24
Crude fat	1.97	38.26	37.22	94.67	1.47
Crude fibre	1.84	12.36	12.35	99.96	0.47
% Moisture	10.76	14.29	14.27	99.81	3.16
% Carbohydrate	76.73	1.51	1.49	97.52	2.33
Amylose (%)	13.61	25.31	25.29	99.83	7.08
Amylopectin (%)	86.36	3.95	3.95	99.99	7.03
Gel consistency (mm)	32.07	25.85	25.84	99.94	17.07

DIVERGENCE IN NEWLY COLLECTED *Corchorus olitorius* ACCESSIONS: A BREEDING CONCEPT

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ABSTRACT
Jute mallow (*Corchorus olitorius* L.) is a valuable leafy vegetable with numerous nutritional advantages. Identifying promising adapted accessions in a breeding programme is necessary for improving desirable traits and selecting parental lines. Variations in agronomic performance were observed in 40 *Corchorus olitorius* accessions laid out in an 8 x 5 α-lattice design with three replicates across two years at National Center for Genetic Resources and Biotechnology in Ibadan, Nigeria. Qualitative and quantitative data were collected and analyzed. For all measured traits, the results show highly significant ($p < 0.001$) mean squares among accessions. Accessions NGB00215, NGB00224, NGB00207, NGB00231 and NGB00210 were ranked as the top five superior accessions useful for the production of leaves, which is the edible harvestable part of the plant, as well as having high seed yield, required for propagation. The clustering analysis grouped sets of accessions that were related by certain criteria. As a result of genetic divergence and gene complementarity, inter-cluster hybridization may benefit from heterosis.

Keywords: **a**ccessions; *Corchorus olitorius*, leaf area, seed yield, selection, variation

INTRODUCTION
Jute mallow (*Corchorus olitorious* L.), a member of the genus *Corchorus* was previously classified with the family Tiliaceae, then Malvaceae and now Sparrmaniaceae (Heywood *et al.*, 2007). The leaves contain a lot of vitamins C and A, as well as β-carotene, folic acid, iron, calcium, and phenolic antioxidative compounds. For large segments of the urban and rural populations, it represents low-cost but high-quality nutrition.

Increased population, climate change, and reduced cultivable land due to urbanization have all posed significant challenges to global food security (Shukla *et al.*, 2019). As a result, more emphasis is being placed on the conservation and utilization of plant genetic resources for sustainable food production and improved nutrition. Understanding phenotypic divergence among diverse genetic materials will aid in effective management and their incorporation into breeding programmes. Additionally, the assessment of variations in mean performance among accessions is critical for meaningful selection. Breeders must concentrate their efforts on selecting superior adapted accessions and incorporating them into breeding programmes to improve desirable traits. (Mukul and Akter, 2021).

Agro-morphological traits and molecular makers have been utilized to assess diversity in *Corchorus* species collections (Adeyemo *et al.*, 2021). The National Center for Genetic Resources and Biotechnology (NACGRAB), Ibadan, Nigeria, houses a large collection of *C. olitorius* germplasm of unknown origin, some of which is grown locally by farmers. For the purpose of germplasm characterization and identification of outstanding accessions that may be useful as parental lines in the development of improved varieties, this study aims to explore the phenotypic diversity in 40 *C. olitorius* accessions maintained at NACGRAB, Ibadan, Nigeria.

MATERIALS AND METHODS
Forty accessions of *Corchorus olitorius* L. were obtained from the seed genebank and evaluated at the experimental field of NACGRAB Ibadan, Nigeria. Twenty-eight days seedlings nursed in the screen house were transplanted in a field experiment laid out in 8 x 5 α-lattice design with three replicates. The experimental field was ploughed and harrowed with a tractor and each experimental plot was a single row of 5 m × 0.5 m. Fertilizer was applied as required at one week after transplanting and subsequently. Hand weeding was carried out as required to maintain weed free plots.

Data collection
Data was taken on both quantitative and qualitative morphological traits to evaluate the level of variation among the accessions. Quantitative traits measured includes: Plant

height (PH), Leaf length and Leaf width. Leaf area (LA) was estimated according to Peksen, (2007) as; LA = 0.919 + 0.682 LW where, LA is leaf area, L is leaf length and W is leaf width. The numbers of primary branches (PB), total number of matured pods per plant (NPP), Total number of matured seeds in a pod (SP), and weight of 1,000 dry seeds (WTHS), while the qualitative traits recorded were leaf colour and leaf shape.

Data Analysis

Analysis of variance (ANOVA) and descriptive statistics were calculated using SAS. Fishers protected least significant difference test (LSD) was used to compare means at 0.05 probability level. The accessions were ranked for outstanding performance according to Mulamba and Mock (1978) Rank Summation Index (RSI). The clustering of the accessions was displayed as a dendrogram which grouped the accessions based on phenotypic similarity using R statistical software.

RESULTS

Leaf colour and shape showed distinct divergence (Table 1). Twenty-four accessions had dark green leaves, nine accessions had light green colour and seven had glossy dark green leaf colour. Four diverse type of leaf shape was also observed among the accession. Fifteen of the accessions had elliptical leaf shape, lanceolate leaf shape was observed in twelve out of forty accessions while seven accessions had ovate leaf shape and six accessions had palmate leaf shape. Considering the agronomic traits measured, plant height ranged from 76.1 - 117.4 cm with a mean of 92.3 cm (Table 2). Number of primary branches varied from 7.3 to 13.9 with a mean of 9.9, while leaf area varied from 8.1 to 41.7 cm^2 with a mean of 16.9 cm^2. Significant variation was also recorded for seed traits. Number of pods per plant ranged from 34 to 140 with a mean value of 62.7. The mean value for thousand seed weight was 1.5 g, ranging from 1.2-2.2 g. Number of seed per pod varied from 82 to 162 with a mean of 121. The clustering analysis grouped the 40 *C. olitorius* accessions into three distinct groups (Figure 1). Nine accessions were in cluster I, cluster II consisted of 16 accessions and cluster III comprised of 15 accessions.

DISCUSSION

Variability assessment is critical in crop improvement programmes. The qualitative and quantitative traits measured revealed a considerable level of variation among the accessions evaluated. The differences in leaf colour and shape were significant enough to distinguish the accession. These variations highlight the potential of the accessions and their use in breeding programmes (Jatothu *et al*., 2018).

The tallest accession was NGB00232 which also doubled as the third accessions with the highest weight for 1000 seeds. The two accessions with the highest comparable number of branches were NGB00236 and NGB00235. The later also had significantly higher weight for 1000 seeds. In the selection of accessions with high leaf yield which is the harvestable part of the plant, the leaf area estimate is highly important (Ngomuo *et al*., 2017). Accessions NGB00215, NGB00224 and NGB00207 were ranked among the top five and had leaf areas of 25.2, 30.1 and 41.7 cm^2, respectively well above the mean leaf area (16.9 cm^2) of the 40 accessions. The highest number of pods per plant was recorded in accession NGB00229 which was also significantly taller than other accessions. Accession NGB00210 had the highest weight for 1000 seeds and was comparable to the top five accessions in height. The significant variations among accessions for all traits measured suggest the possibility of meaningful selection for *Corchorus* improvement (Bhor *et al*., 2020). The hierarchical cluster revealed three distinct groups, emphasizing variability sufficiently to justify selection. Accessions in the same cluster have a closer relationship than those in other clusters (Kar *et al*., 2009). Interestingly, four accessions among the superior top five clustered together and these accessions could be selected for varietal development. For parental line selection, accessions with the highest mean value for each trait in different clusters may be considered (Sawarkar *et al*., 2015). It is expected that hybridization between accessions from different clusters will result in the desired segregants.

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Table 1. Description of the 40 Corchorus accessions used in this study

S/N	Accession	Leaf colour	Leaf shape	S/N	Accession	Leaf colour	Leaf shape
1	NGB00189	Light green	Eliptical	21	NGB00218	Dark green	Ovate
2	NGB00192	Dark green	Eliptical	22	NGB00221	Dark green	Eliptical
3	NGB00193	Dark green	Ovate	23	NGB00222	Dark green	Eliptical
4	NGB00195	Dark green	Palmate	24	NGB00224	Glossy dark green	Lanceolate
5	NGB00196	Dark green	Eliptical	25	NGB00225	Dark green	Eliptical
6	NGB00197	Glossy dark green	Eliptical	26	NGB00226	Dark green	Palmate
7	NGB00198	Dark green	Eliptical	27	NGB00228	Light green	Eliptical
8	NGB00199	Light green	Palmate	28	NGB00229	Dark green	Eliptical
9	NGB00200	Glossy dark green	Lanceolate	29	NGB00230	Glossy dark green	Lanceolate
10	NGB00202	Dark green	Lanceolate	30	NGB00231	Dark green	Lanceolate
11	NGB00204	Light green	Eliptical	31	NGB00232	Dark green	Palmate
12	NGB00205	Dark green	Lanceolate	32	NGB00233	Dark green	Eliptical
13	NGB00207	Dark green	Eliptical	33	NGB00235	Light green	Lanceolate
14	NGB00208	Dark green	Palmate	34	NGB00236	Light green	Eliptical
15	NGB00209	Glossy dark green	Lanceolate	35	NGB00237	Dark green	Ovate
16	NGB00210	Dark green	Palmate	36	NGB00277	Glossy dark green	Lanceolate
17	NGB00212	Light green	Ovate	37	NGB00651	Dark green	Lanceolate
18	NGB00213	Dark green	Eliptical	38	NGB00652	Glossy dark green	Ovate
19	NGB00215	Dark green	Lanceolate	39	NGB00653	Dark green	Lanceolate
20	NGB00217	Light green	Ovate	40	NGB01261	Light green	Ovate

Table 2: Mean performance of the evaluated Corchorus accessions based on rank summation index

Accession	Rank sum	PH (cm)	PB	LA (cm2)	NPP	WTHS (g)	SP
NGB00215	27	107.9	11.9	25.2	73.6	1.7	136.4
NGB00224	67	106.2	9.9	30.1	67.6	1.7	114.9
NGB00207	68	87.6	9.4	41.7	76.6	1.7	143.3
NGB00231	80	99.1	11.9	12.8	82	1.6	119.6
NGB00210	86	100	10.5	12.9	101.8	2.2	104.3
NGB00192	90	87.2	11	18	70.8	1.5	162.2
NGB00205	90	103.8	8.5	17.3	62	1.6	152.7
NGB00229	91	110.8	9.4	14.9	140.5	1.5	121.7
NGB00232	94	117.4	8.5	23.7	34.4	1.8	134.6
NGB00221	95	101.8	8.7	20.4	46.5	1.6	159.2
NGB00236	95	96.1	13.9	17.9	55.9	1.5	119.9
NGB00235	96	94.5	13.1	11.8	69.9	1.7	109.6
NGB00195	101	95.8	8.8	20.3	49.9	1.6	134.9
NGB00225	105	99.4	8.9	13.2	69.9	1.5	135.2
NGB00230	105	93.3	10.7	21.5	44.4	1.6	125.3
NGB00277	106	102.8	8	15.7	52.4	1.9	126.9
NGB00226	110	99.2	8.9	20.4	55.9	1.6	110.7
NGB01261	111	95.2	10.3	16.4	74.2	1.4	110.4
NGB00197	112	94.6	8.5	14.2	60.8	1.7	129.8
NGB00202	117	83.2	8.9	17.2	59.6	1.6	143.5
NGB00237	117	92.4	11.6	19.8	38.9	1.6	112.1
NGB00651	126	90.8	11.7	10.9	68	1.4	123.1
NGB00189	133	89.1	11.3	15.5	57.7	1.4	114.5
NGB00212	138	89.1	7.3	12.8	58.5	1.6	128.8
NGB00209	141	80.1	11.3	13	67.2	1.2	124.8
NGB00213	142	88.6	11.8	11.5	56.7	1.4	119.3
NGB00222	145	87.7	11	11.7	69.2	1.2	118.8
NGB00204	146	82.1	9.4	15.5	62.4	1.6	98.4
NGB00233	146	88.7	10.1	10	48.8	1.6	118.1
NGB00198	151	84.4	9.2	15.1	61.6	1.5	107.6
NGB00196	152	82.1	9.8	12.9	60.3	1.4	120.6
NGB00200	152	85	7.8	8.4	119.5	1.4	127.2
NGB00228	155	85	11.4	11.3	40	1.5	115.6
NGB00653	164	92.7	9	15.3	54.6	1.3	101.8
NGB00652	166	79.6	9.9	28.4	34.5	1.3	102.3
NGB00193	167	76.1	9.1	24.8	38.2	1.5	91.5
NGB00199	179	87.8	9.4	9.9	47.2	1.5	82.2
NGB00218	179	92.3	8.6	12.3	58.1	1.3	101.4
NGB00208	183	78.2	8.8	16.7	45.3	1.4	101.6
NGB00217	192	86	8.2	8.1	70.9	1.3	82.2
G M		92.3	9.9	16.9	62.7	1.5	121
Range		41.3	6.6	33.6	106.2	1	80
SD		9.3	1.5	6.6	21	0.2	18.3
SE (±)		1.5	0.2	1	3.3	0	2.8
LSD (0.05)		9.5	2.7	1.5	16.4	0.3	14.4
CV (%)		9	23.7	12.8	22.9	14.1	12.3

PH = plant height; PB = number of branches; LA = leaf area; NPP = number of pods per plant; WTHS = weight of 1000 seeds; SP = seeds per pod. GM= grand mean, SD= standard deviation, SE= standard error

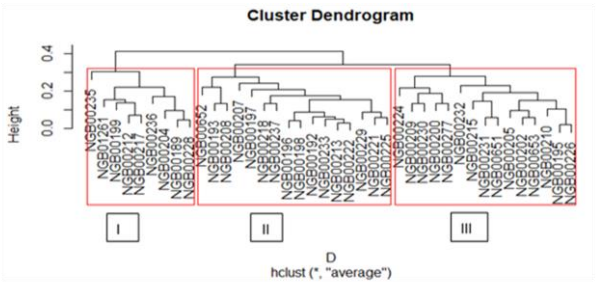

Figure 1. Dendrogram of the 40 Corchorus accessions following Ward's cluster analysis based on the Euclidean distance

EVALUATION OF GAMMA IRRADIATED MUTANTS OF SESAME (*Sesamum indicum* L.) FOR YIELD AND YIELD PARAMETERS

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ABSTRACT: Mutation breeding is applied in many crop improvement programs as it can rapidly create the variability of inherited traits in crops. This study was designed to evaluate the yield potential of some mutant (M_4) lines of sesame. Eleven M_4 mutant lines alongside three checks were raised to maturity in a randomized complete block design (RCBD) in Minna and trial fields of National Cereals research institute, Badeggi. The results revealed M_5 mutant lines showed significant changes in some of the parameters measured. Site1 (Minna) showed improved yield traits than Site2 (Badeggi). ML11A11 exhibited the lowest days to 50% flower (47.00; 41.33). ML1A9 site1 showed the highest 1000 seed weight (3.02g), ML3A7 in site1 (2.41 g). The capsule per leaf axil in C1A12 Site2 obtained the highest (2.67). ML4A6 Site1 showed highest number of capsule (123.67). The highest yield per hectare was recorded mutant ML8A2 Site1 (779.63 kg/hectare); ML6A4 Site1 (681.86 kg/hectare); (672.59 kg/hectare). The results especially for yield, revealed the possibility of new varieties of sesame from the mutant lines, thus presenting gamma irradiation as a very effective mutagen for improvement of the crop.

Keywords: breeding, mutation, parental stock,

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INTRODUCTION

Sesame (*Sesamum indicum* L.) belongs to the family Pedaliaceae and is known under various names such as til, gingelly, sim-sim, gergelim (Mohamed *et al*., 2022). Muhammad *et al.* (2018), opined that sesame is locally called in Nigeria by different names; 'Ridi' in Hausa, 'Esso' in Nupe, 'Eeku' in Yoruba and 'Ekuku' in Igbo. Sesame is one of the oldest aromatic, medicinal, and oilseed crops in the world and is native to tropical and subtropical regions (Kavak and Boydak, 2006; Tufail *et al.,* 2020). Due to its increasing export value, its production area has expanded to arid and semi-arid regions in Africa, Asia and South America (Anilakumar *et al.,* 2010; Weldemichael *et al.,* 2021).

Food and Agriculture Organization (FAOSTAT) (2022), reported that sesame is grown on a global area of about 12.82 million hectares (ha), and Sudan, India, and Myanmar lead in terms of the harvested area, with 5,173,521, 1,520000 and 1,500,000 ha, respectively. According to FAOSTAT (2022), more than 6.5 million tons (t) of sesame seeds were produced globally in 2020. In Nigeria, Sesame seeds are mainly grown in the northern part of Nigeria. It is grown in States such as Benue, Kano, Jigawa, Katsina, Kogi, Nassarawa, Gombe, Kebbi, Plateau, Bauchi, Taraba, Kaduna, Kwara, Borno and Yobe States (Yakubu and Yusuf, 2020). The world volume of exports and imports is about 560,000 metric tons yearly with an annual growth rate of 2.6- 4% of this gross value is taken up by Nigeria and it is the second largest producer of Sesame seed in Africa and also ranked 7th in the world (Yakubu and Yusuf, 2020). The global demand and trade of sesame seeds have increased rapidly over the past two decades (Dossa *et al.,* 2017). Although the global sesame cultivation area is expanding, especially in Africa, productivity and yield are still very low, resulting in a huge gap between seed supply and demand (Sarkar *et al.,* 2016). In order to address these challenges, there is need to develop new improved varieties through technologies like induced mutation. Gamma ray is one of the most effective physical mutagens and most mutant varieties developed using a physical mutagen registered at the Mutant Variety Database (Joint FAO/IAEA) resulted from exposure to gamma rays (Hase *et al*., 2020).

There is no doubt the ever-increasing human population is directly tied to food security. It has created pressure to increase crop production including sesame in many countries, leading to expansion of land area dedicated to farming. This is unsustainable but the only sustainable

approach is cultivation of improved varieties with significant yield advantage over existing one. Therefore, aim of this study was to evaluate some mutant lines of sesame for yield and yield parameters in order to identify the lines with higher yield potentials.

MATERIALS AND METHODS

The study was conducted in two stations. Station 1 was located at Minna; Station 2 was located at National Cereal Research Institute, Badeggi. A total of 14 entries (11 mutants and 3 checks) were raised in a plot size of 3 x 3 M_2 in three replicates. In each plot, the planting space was 20 x 20 cm. An average of 3 seeds per hole was observed. The experiment was conducted between the months of August, 2021 and December, 2021 planting season. Data recorded were based on the methods stated in the standard descriptors of sesame by IPGRI and NBPGR (2004). They include; Days to 50% flowering, number of capsules per leaf axil, number of capsules per plant, yield per plot and one thousand (1000) seed weight.

Data analyses

The data were subjected to Randomized Complete Block Design combined analysis of variance (ANOVA) at P=0.05 using Statistical Tool for Agricultural Research (STAR) by International Rice Research Institute (IRRI) 2013 - 2020 All rights reserved.

RESULTS AND DISCUSSION

The results showed significant ($p < 0.05$) difference among the genotypes for each trait, hence, indicating evident variability among the mutant lines for the characters studied. There was significant variation in the days to 50% flower of the mutants in both sites. ML1A9 (50.33 ± 1.67), ML2A8 (49.00±1.00) and ML3A7 (50.67±0.66) in site1 recorded the highest number of days to 50% flowers than all mutants in both sites (Table 1). There was no significant difference in the 1000 seed weight of the mutants both sites. However, ML1A9 (3.02g; 2.98g) recorded the highest 1000 seed weight. The mutant lines showed consistent number of capsules per axil in both sites. ML1A9 and ML4A6 in site1 obtained (1.67), while ML2A8 (2.67), C1A12 (2.67), ML4A6 (3.00) in site2 recorded the highest number of capsules per axil. ML4A6 (123.67), ML10A10 (112.33) in site1 and C1A12 site2 (86.00) recorded the highest number of capsules per plant. ML8A2 (779.63 kg ha-1), ML6A4 (681.11kg ha-1), ML11A11 (672.58 kg ha-1) in site1 while ML1A9 (664.81 kg ha-1), ML8A2 (650.74 kg ha-1) and ML10A10 (641.11) in site2 recorded the highest yield.

The significant variations recorded in plant yields could be due to exposure to higher doses of gamma rays. This study revealed the days to 50% flower range of (41.00 - 50.33). A similar result was obtained from the study of Suha and Paul (2017) who reported the ranges for days to 50% flowering from 43.03 to 56.77 days in sesame. The delay in flowering might be attributed disturbances in biochemical pathway which aid in synthesis of flower inducing substances as reported by Veni *et al.* (2016). The range of 1000 seed weight (2.42-3.02) observed in this study is not too far from those (2.87 -3.15 g) reported by Pavani *et al.* (2020). Similarly, Zebib *et al.* (2015) mentioned mass of 1000 seeds (2.7 to 3.1 g) for different sesame cultivars. The number of capsules per plant range (25.67-123.67) is lower than Aristya *et al.* (2018), who reported (274.57) in sesame irradiated at 400 Gy. However, Saha *et al.* (2017) reported (31.45) at 300 Gy nine sesame mutants. *Shamsiah et al.* (2022), reported high number of fruits (8/plant) in *Capsicum annuum* irradiated with 80 Gy and 40 Gy. The evident rise observed in the number of capsules per plant of some mutants could be associated to the stimulatory effects of gamma rays on capsule or pod formation and differences in the genetic makeup of these genotypes (Sabiel *et al.,* 2015).
The yield per hectare recorded range (389.63-779.63 kg ha-1) is slightly higher than Saha and Paul (2017), who reported (324.2 kg ha-1) in M1 generation of sesame at 450 Gy. Koitilio *et al.* (2018), reported range (409 - 1838 kg ha-1) in sesame

Conclusion

Sufficient genetic variation exists among the mutant lines for seed yield and other yield traits. Gamma irradiation induced mutation with a high genetic level on sesame yield components. The variations expressed in the mutant lines provide a huge scope for the selection of promising genotypes. The mutant lines show a high potential for varietal release.

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Table 1. Yield parameters of M_4 generation of irradiated sesame lines

Mutants	Pedigree	Days to 50%F		1000-seed weight	
		Site1	Site 2	Site1	Site 2
ML1A9	04E450G1-3	50.33 ± 1.67ab	41.33 ± 0.58a	3.02 ± 0.02a	2.98 ± 0.01a
ML2A8	04E450G2-3	49.00 ± 1.00ab	43.00 ± 0.33a	2.86 ± 0.02abc	2.81 ± 0.02abcd
ML3A7	04E450G3-3	50.67 ± 0.66ab	43.00 ± 0.00a	2.41 ± 0.03e	2.42 ± 0.04e
C1A12	0	47.00 ± 0.00b	42.3 3± 0.33a	2.59 ± 0.05bcde	2.57 ± 0.01bcde
ML4A6	01M350G2-22	47.00 ± 0.00b	41.00 ± 0.00a	2.66 ± 0.12bcde	2.67 ± 0.16abcde
ML5A5	01M350G1-21	48.00 ± 1.00b	42.67 ± 1.67a	2.56 ± 0.01cde	2.54 ± 0.05bcde
ML6A4	01M550G2-2	49.00 ± 1.45ab	41.00 ± 0.00a	2.61 ± 0.10bcde	2.64 ± 0.06abcde
ML7A3	01M350G1-2	47.00 ± 0.00b	41.67 ± 0.67a	2.52 ± 0.04de	2.49 ± 0.09cde
C2A13	0	53.67 ± 3.67a	41.67 ± 0.67a	2.78 ± 0.05abcd	2.81 ± 0.05abcd
ML8A2	03L550G1-2	47.00 ± 0.00b	43.33 ± 0.67a	2.85 ± 0.03abc	2.81 ± 0.04abcd
ML9A1	03L450G2-2	47.00 ± 0.00b	43.33 ± 0.88a	2.61 ± 0.11bcde	2.60 ± 0.11bcde
ML10A10	03L250G1-1	47.00 ± 0.00b	42.67 ± 0.33a	2.52 ± 0.02de	2.49 ± 0.06de
ML11A11	03L2501-11	47.00 ± 0.00b	41.33 ± 0.89a	2.87 ± 0.06abc	2.86 ± 0.08ab
C3A14	0	49.66 ± 1.45ab	43.00 ± 1.00a	2.91 ± 0.041ab	2.86 ± 0.04abc

Values along the same column with different superscript are significantly different at $p < 0.05$

Table 2: Yield parameters of M_4 generation of irradiated sesame lines

Mutants	Pedigree	Number Capsule per Axil		Number of capsules	
		Site1	Site 2	Site 1	Site 2
ML1A9	04E450G1-3	1.67 ± 0.33a	1.33 ± 0.33b	77.67 ± 2.60b	51.67 ± 8.11bcd
ML2A8	04E450G2-3	1.00 ± 0.00a	2.67 ± 0.00a	61.33 ± 2.60bc	38.00 ± 1.33cde
ML3A7	04E450G3-3	1.00 ± 0.00a	1.00 ± 0.00b	72.00 ± 8.50b	34.33 ± 2.19de
C1A12	0	1.33 ± 0.33a	2.67 ± 0.33a	32.00 ± 0.58d	86.00 ± 1.00a
ML4A6	01M350G2-22	1.67 ± 0.33a	3.00 ± 0.00a	123.67 ± 3.18a	60.33 ± 9.82bc
ML5A5	01M350G1-21	1.00 ± 0.00a	1.00 ± 0.00b	39.67 ± 5.21cd	25.67 ± 0.33e
ML6A4	01M550G2-2	1.00 ± 0.00a	1.33 ± 0.33b	75.00 ± 3.61b	39.33 ± 2.96cde
ML7A3	01M350G1-2	1.00 ± 0.00a	1.33 ± 0.33b	44.00 ± 3.79cd	42.00 ± 2.65cde
C2A13	0	1.00 ± 0.00a	1.00 ± 0.00b	45.67 ± 13.86cd	41.67 ± 2.33cde
ML8A2	03L550G1-2	1.00 ± 0.00a	1.00 ± 0.00b	79.00 ± 2.08b	51.33 ± 3.38bcd
ML9A1	03L450G2-2	1.00 ± 0.00a	1.00 ± 0.00b	46.00 ± 1.53cd	32.67 ± 1.45de
ML10A10	03L250G1-1	1.00 ± 0.00a	1.00 ± 0.00b	112.33 ± 3.84a	60.00 ± 1.73bc
ML11A11	03L2501-11	1.00 ± 0.00a	2.67 ± 0.33a	57.67 ± 2.03bc	44.33 ± 2.03bcde
C3A14	0	1.00 ± 0.00a	1.00 ± 0.00a	61.00 ± 3.79bc	65.33 ± 2.03ab

Table 2 cont.

Mutants	Pedigree	Gross yield (kg ha^{-1})	
		Site 1	Site 2
ML1A9	04E450G1-3	588.14	664.81
ML2A8	04E450G2-3	538.52	478.52
ML3A7	04E450G3-3	495.56	630.00
C1A12	0	383.70	412.97
ML4A6	01M350G2-22	305.92	578.52
ML5A5	01M350G1-21	471.11	389.63
ML6A4	01M550G2-2	681.11	542.97
ML7A3	01M350G1-2	534.44	425.19
C2A13	0	623.33	558.52
ML8A2	03L550G1-2	779.63	650.74
ML9A1	03L450G2-2	636.67	420.00
ML10A10	03L250G1-1	574.44	641.11
ML11A11	03L2501-11	672.58	501.11
C3A14	0	612.97	404.08

Values along the same column with different superscript are significantly different at $p < 0.05$

GENETICS OF ALUMINUM TOLERANCE IN COWPEA ACCESSIONS SCREENED IN POTS UNDER THE FIELD CONDITIONS

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ABSTRACT

Aluminum toxicity is a major factor limiting crop productivity on acid soils, thus posing a challenge to food production. This study assessed the level of genetic diversity for aluminum tolerance in cowpea and the intercharacter association of important traits for the effective selection of tolerant genotypes. Ten accessions of the crop were screened in pots filled with topsoil employing a 10 x 4 factorial experiment in a completely randomized design. The aluminum treatments imposed were 0, 50, 100, and 200 µM $AlCl_3$. Results revealed significant differences among accessions for all traits studied. Aluminum treatment imposed significant differences on all traits except seeds/plant and seed yield while the interaction was significant for all traits except emergence percentage and plant height. Heritability was high (≥ 60%) for all traits except pods/plant (57.98%), and genetic advance as a percent of the mean was high (≥ 20%) for all traits except days to flowering (11.08%) and plant height (15.87%). Biplot revealed that high seed yield under aluminum stress was directly associated with high seeds/plant, a higher number of roots/plant, and high root weight/plant while higher seeds/pod was a consequence of deeper root length, late flowering, higher root weight, and higher number of roots.

Key words: acidity, growth, heritability, toxicity, variability, yield

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INTRODUCTION

Excessive acidification of soils is a consequence of uninterrupted rigorous agriculture as well as the alteration of environmental conditions propelled by global climate change (Shetty *et al.*, 2021). Aluminum (Al) toxicity is a major factor limiting crop productivity on acid soils, thus limiting food production. When its concentration in soil surpasses 3 mg kg^{-1} of soil at a pH of 5.5, its toxicity is manifested (Casierra-Posada *et al.*, 2021). Al inhibits root elongation in Al-sensitive plants as a consequence of its quick inhibition of cell division and cell expansion of root meristems (Phukunkamkaew *et al.*, 2021) and can also obstruct the uptake of minerals as well as water (Kochian, 1995). This can lead to serious drought stress and nutrient deficiency (Tang *et al.*, 2002).

Presently, 40% of the world's arable lands in many subtropical and tropical areas of the world (Phukunkamkaew *et al.*, 2021), and more than 50% of the world's potentially arable lands are acidic (Siecinska and Nosalewicz, 2016). In Nigeria, up to 18% of the total land area is acidic (Ajayi, 2021). The largest amount of cowpea (*Vigna unguiculata* L. Walp) is produced in Nigeria which stands at 36% of the world's total (FAO, 2022). Nigeria belongs to the tropical belt where agriculture is largely practiced on acidic soils as semi-subsistence farming (Akinrinde *et al.*, 2006). Several agronomic strategies including the application of lime and organic matter are employed by farmers for the management of acid soils to sustain yield. However, the impracticality of these soil improvement strategies in many regions lies in their high cost of deployment (Siecinska and Nosalewicz, 2016). Hence, as a cost-effective strategy, it is imperative to examine the source of aluminum tolerance present in the adapted crop species such as cowpea in Nigeria and other tropical regions of the world.

Several studies on Al tolerance in cowpea exist based on several agronomic and yield traits (Akinrinde *et al.*, 2006; Ajayi, 2021). However, information regarding the level of genetic diversity and character association in cowpea under aluminum stress is limited. To develop Al-tolerant genotypes of cowpea, a better understanding of the presence and magnitude of the genetic diversity for Al tolerance in a gene pool is important. Heritability of traits and their genetic gains are critical to successful breeding programs since the strengths of such estimates provide the extent to which improvement can be made while the association of important traits is useful for multiple selections of yield contributing traits (Ajayi *et al.*, 2014). In cognizance of the above, the present study assessed the level of genetic diversity for aluminum tolerance in cowpea and the

intercharacter association of important traits for the effective selection of Al-tolerant genotypes.

MATERIALS AND METHODS

The ten accessions involved had been previously screened under aluminum stress based on germination parameters (Ajayi, 2021) and are presented in Table 1. The location of the present study was the Plant Science and Biotechnology Experimental Field, Adekunle Ajasin University, Nigeria, and the period was between July and October 2016. The accessions were supplied by the International Institute of Tropical Agriculture (IITA), Nigeria.

This experiment was performed following a modified procedure from Ezeh et al. (2007). Six hundred bottom-perforated plastic pots (5L capacity) were filled each with topsoil collected near the experimental field (five pots per accession per treatment per replicate). The experimental field soil surface was covered with polythene before the arrangement of the plastic pots during the course of the experiment. Seeds were planted (after pre-planting soil analysis by spectrometry) in the pots each containing 3.5 kg of topsoil treated twice (at 1-week intervals) with 500 ml of 0, 50, 100, and 200 µM $AlCl_3$ in a completely randomized design with 3 replicates. Each accession was sown in pots at the rate of three seeds per pot with five pots per treatment per replicate and thinned to one plant per pot 10 days after emergence. Treatment application continued once per week until week 5 after planting (WAP).

Data collection

The emergence percentage was determined 10 days after planting (DAP). Plant height and the number of leaves were determined at 5 WAP. The number of days to first flowering was determined as plants flowered. Parameters such as the number of pods per plant, the number of seeds per pod, seed yield per plant, the number and length of main roots, and dry root weight were determined at maturity. The root parameters were determined by cutting the stem from the roots of the plants and carefully removing the soil from the roots by immersing the whole pot in a big bowl of water. After this, counting of the main roots was done and the length of the tap root was measured. The root dry weight was recorded after oven drying at 80°C to constant weights for 24 hrs.

Statistical analyses

Data were subjected to analysis of variance (ANOVA) using the GLM procedure of SPSS (version 20). Accessions were ranked based on their level of tolerance to aluminum stress using the tolerance index (TI) calculated as $(X \times Y)/(\bar{X})^2$, where X was the mean performance of accession for a trait under the control treatment, and Y the average mean performance of accession for a trait under aluminum treatments, and $\bar{X}$ was the grand mean of all accessions for that trait under the control treatment. Accessions with mean TI greater than the grand mean of TI were deemed to be more tolerant while the ones with lower values were more susceptible. Estimates of genetic parameters were performed according to Ojo and Ayuba (2016) with modifications as follows: Error variance (V_E) = σ_E^2 = Mean square error (MS_E). Genotype × treatment variance (V_{GT}) = $\sigma_{GT}^2 = (MS_{GT} - MS_E)/r$. Genotypic variance ($V_G$) = $\sigma_G^2 = (MS_G - MS_E)/rT$. Phenotypic variance ($V_P$) $= V_G + V_{GT}/T + V_E/rT$. Genotypic coefficient of variation (GCV) $= \frac{\sqrt{V_G}}{\bar{X}} \times 100$. Phenotypic coefficient of variation (PCV) $= \frac{\sqrt{V_P}}{\bar{X}} \times 100$. Broad-sense heritability (H^2) = $V_G/(V_G + (V_{GT}/T) + (V_E/rT))$. Genetic advance (GA) $= \frac{VG}{\sqrt{VP}} \times k$; k = 2.06 (selection differential). Genetic advance as percent of the mean (GAM) = $\frac{GA}{\bar{X}} \times 100$; where T, $\bar{X}$, and r are the number of treatments, grand mean of trait, and replicates, respectively. Genetic parameters were categorized as cited in Ajayi et al. (2014). Data were subjected to biplot analysis with paleontological statistics (PAST) version 4.01 for the estimates of genotype x character association.

RESULTS AND DISCUSSION

The significant effect of accession revealed in the present study for all measured traits indicated the presence of a sufficient level of variations among the accessions under aluminium stress as reported by Ojo and Ayuba (2016). The significant effect of aluminium treatment for most traits indicated that the treatment was effective on the measured traits except for seeds per plant and seed yield per plant. The highly significant effect of accession × treatment on measured traits indicated that the response of accessions varied under different treatments (Villagarcia et al., 2001; Akinrinde and Neumann, 2006), except for emergence percentage and the number of days to first flowering (ANOVA Table not presented). In this regard, identification of accessions with high stability and superior yield across different levels of

aluminium stress would be important to maximizing yield and also useful for cowpea breeding programs for aluminium tolerance. Generally, aluminium treatment influenced all measured traits among the accessions; while inhibitory responses occurred in some traits, the effect was stimulatory in others. In traits such as emergence percentage, root length, and dry weight of roots, treatment of up to 50 – 200 μM, 100 – 200 μM, and 50 – 100 μM, respectively caused a significant reduction in the traits (Table 2). However, amongst traits with stimulatory effects due to aluminium stress, only the number of leaves per plant was significantly stimulated in plants treated to 100 - 200 μM. In the present study, responses to aluminium stress were accession dependent as described by Ezeh *et al.* (2007) and Kushwaha et al. (2017) in cowpea.

Previous studies have reported information on the level of aluminum tolerance in cowpea and many other crop species. However, information regarding the genetic variability and character association of the crop under aluminum stress is scarce (Ojo and Ayuba, 2016). In the present study, the combination of high GCV and PCV obtained for traits such as the number of pods per plant, seeds per pod, seeds per plant, seed yield per plant, number of roots, root length, and dry weight of roots indicated that the accessions had a broad genetic base for these characters under aluminum stress. However, low PCV and GCV shown in plant height and days to first flowering suggested that these characteristics would be less responsive to improvement through selection (Table 3). These results agree with Ojo and Ayuba (2016) for yield, plant height, and root parameters as reported by Ojo *et al.* (2016). Little differences between GCV and PCV for most characters indicated a strong genetic effect on these characters. Moderate heritability in pods per plant and high heritability for other characters with moderate to high GAM indicated additive gene effects superiority (Singh et al., 2022), and that the traits are effectively transmitted to the progeny, hence, selection for these traits will be effective for aluminum stress tolerance in cowpea for the tropical regions. These results are in agreement with the findings of Bianchi-Hall *et al.* (1998), Ogunbayo *et al.* (2014), and Ojo and Ayuba (2016) in soybean.

Tolerance indices (Table 4) based on all parameters were able to group accessions into different classes of tolerance: AC03, AC04, AC05, AC06, AC08, and AC09 were the highly tolerant accessions with above-average values for all the aluminium tolerance indices. AC02 was moderately tolerant while AC01, AC10, and AC07 were the highly susceptible accessions. Notable differences existed among accessions for each of the tolerance indices as reported by Massot et al. (1992), Alamgir and Akhter (2009), and Roy and Bhadra (2014). Several aluminum tolerance indices have been found effective in the discrimination of different genotypes of crop species among which one of the best is the aluminum tolerance index based on root parameters (Hede *et al.*, 2002; Lisitsyn, and Amunova, 2015; Phukunkamkaew *et al.*, 2021).

Bi-plot analysis (Fig. 1) separated accessions according to their levels of tolerance. The first two PCs were used for the identification of important traits and their correlations. The GT biplot in the present study captured 75.90% of the variations due to genotype and genotype × trait interactions. The length of the trait vector projected from the origin shows the traits' ability to discriminate among accessions. Hence, important traits such as the number of seeds per pod, seed per plant, seed yield per plant, number of pods per plant, number of leaves, and all the root parameters were identified as influential traits for aluminum tolerance because they possessed longer vectors which gave them extraordinary discrimination powers. Conversely, traits such as plant height and emergence percentage were deemed as not important because of their short projection of vectors under aluminum stress.

The correlation between two traits is defined by the cosine of the angle between them (Atnaf *et al.*, 2017). Due to the acute angles observed among these traits' vectors, seed yield per plant was directly associated with higher seeds per plant, a higher number of roots, and a high dry weight of roots, and weakly correlated with seeds per pod, days to first flowering, and root length. This is an indication that the number of roots, seeds per plant, and dry weight of roots, as well as root length, seeds per pod, and higher number of days to flowering in cowpea plants, can be used to select high-yielding and tolerant plants under aluminum stress. A higher number of seeds per pod was directly related to deeper root length and late flowering under aluminum stress. This indicated that a deeper root system can be used to select tolerant, late-maturing genotypes with a higher number of seeds per pod under aluminum stress. However, a higher number of pods per plant was slightly associated with a higher number of leaves. Number of leaves was

negatively correlated with seed yield and all the root parameters under aluminum stress due to the observed obtuse angle between them, indicating that selection for a lower number of leaves under aluminum stress can improve seed yield. Similar findings have been reported by Ojo and Ayuba (2016) using correlation analysis. In this study, the tendency of traits in discriminating accessions in the right and the left-hand direction of the biplots depended on whether they had strong positive associations or negative associations as reported by Atnaf *et al.* (2017).

Conclusion

The present study has established that there is sufficient variability and heritability of growth, root, and yield parameters of cowpea accessions screened in pots under aluminum stress. The observed genetic variability among accessions could be exploited for developing tolerant lines through hybridization. The tolerance indices technique based on multiple quantitative traits is effective at identifying aluminum tolerant accessions.

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Table 1. Selected cowpea accessions

Accession ID	Tolerance for germination parameters	Code	Accession ID	Tolerance for germination parameters	Code
TVu-199	Highly susceptible	AC01	TVu-241	Highly tolerant	AC06
TVu-207	Moderately susceptible	AC02	IT98K-205-8	Moderately susceptible	AC07
TVu-218	Moderately tolerant	AC03	IT98K-555-1	Moderately tolerant	AC08
TVu-235	Moderately tolerant	AC04	TVu-4886	Moderately susceptible	AC09
TVu-236	Moderately tolerant	AC05	TVu-9256	Highly tolerant	AC10

Table 2. Effect of aluminum treatment on growth and yield traits of accessions of cowpea under aluminum stress

Treatment	EM (%)	PH (cm)	NL	DFF	PDP	SPP	SDPL	SDYPL (g)	NRT	RTL (cm)	DWR (g)
Control	89.33b	13.06a	6.45a	54.11a	11.30a	7.65a	82.39a	10.74a	12.03a	16.66b	0.74b
50 µm	67.33a	12.59a	6.98ab	51.95a	10.30a	8.51a	84.03a	11.37a	11.81a	15.70b	0.60a
100 µm	62.67a	12.39a	7.26b	52.58a	10.67a	8.17a	91.05a	10.94a	12.54a	13.80a	0.55a
200 µm	60.00a	12.49a	7.42b	53.33a	11.10a	8.02a	88.06a	11.82a	11.96a	13.77a	0.77b
±SE	4.27	0.31	0.22	0.82	0.45	0.39	5.79	0.8	0.29	0.36	0.03

Means followed by the same alphabets within a column are not significantly different from one another at $p \leq 0.05$ using DMRT; SE: Standard error. EM: Emergence percentage; PH: Plant height; NL: Number of leaves per plant; DFF: Number of days to first flowering; PDP: Number of pods per plant; SPP: Number of seeds per pod; SDPL: Number of seeds per plant; SDYPL: Seed yield per plant; NRT: Number of roots per plant; RTL: Root length per plant; DWR: Dry weight of roots.

Table 3. Estimates of genetic parameters of growth and yield traits of accessions of cowpea under aluminum stress

Trait	GM	σ_G^2	σ_P^2	σ_E^2	σ_{GT}^2	GCV (%)	PCV (%)	H^2 (%)	GAM (%)
EM	69.83	138.06	163.98	546.67	-78.56	16.83	18.33	84.19	31.79
PH	12.63	1.09	1.25	2.92	-0.35	8.27	8.85	87.20	15.87
NL	7.03	1.78	1.95	1.41	0.21	18.98	19.86	91.28	37.52
DFF	52.99	9.09	10.16	19.93	-2.38	5.69	6.02	89.47	11.08
PDP	10.85	6.01	7.21	6.10	10.09	22.62	24.77	57.98	29.53
SPP	8.08	4.18	5.10	4.44	2.21	25.30	27.94	81.96	47.15
SDPL	86.38	632.04	1014.91	1005.75	119.24	29.10	36.88	62.28	47.31
SDYPL	11.22	8.31	11.88	19.03	7.91	25.72	30.75	69.95	44.26
NRT	12.09	5.76	7.21	2.49	4.95	19.85	22.21	79.89	36.48
RTL	14.98	9.16	12.02	3.93	10.16	20.20	23.14	76.14	36.30
DWR	0.67	0.04	0.05	0.03	0.03	29.85	33.37	80.00	55.90

GM: Grand mean; σ_G^2: Genotypic variance; σ_P^2: Phenotypic variance; σ_E^2: Error variance; σ_{GT}^2: Genotype × treatment variance; EM: Emergence percentage; PH: Plant height; NL: Number of leaves per plant; DFF: Number of days to first flowering; PDP: Number of pods per plant; SPP: Number of seeds per pod; SDPL: Number of seeds per plant; SDYPL: Seed yield per plant; NRT: Number of roots per plant; RTL: Root length per plant; DWR: Dry weight of roots. GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; H^2: broad sense heritability; GAM: Genetic advance as a percent of the mean. EM: Emergence percentage; PH: Plant height; NL: Number of leaves per plant; DFF: Number of days to first flowering; PDP: Number of pods per plant; SPP: Number of seeds per pod; SDPL: Number of seeds per plant; SDYPL: Seed yield per plant; NRT: Number of roots per plant; RTL: Root length per plant; DWR: Dry weight of roots.

Table 4. Aluminum tolerance indices and (ranks) based on growth and yield traits of accessions of cowpea under aluminum stress

Accession	EMI	PHI	NLI	DFFI	PDPI	SPPI	SDPLI	SDYPLI	NRTI
AC01	0.86 (4)	1.35 (1)	1.47 (4)	0.89 (4)	0.99 (5)	0.49 (8)	0.54 (9)	0.65 (9)	0.61 (8)
AC02	0.59 (9)	1.15 (2)	1.60 (2)	0.85 (1)	1.16 (3)	0.66 (5)	0.87 (6)	1.05 (4)	0.40 (9)
AC03	0.69 (6)	0.85 (6)	0.61 (9)	0.97 (5)	1.13 (4)	2.17 (1)	2.69 (1)	2.09 (1)	1.46 (1)
AC04	0.95 (2)	1.01 (5)	0.75 (8)	1.06 (7)	0.98 (6)	1.41 (3)	1.55 (2)	1.54 (2)	1.42 (2)
AC05	0.89 (3)	1.07 (3)	0.77 (7)	1.19 (9)	0.49 (9)	1.71 (2)	1.07 (4)	0.87 (6)	1.29 (3)
AC06	0.82 (5)	0.80 (7)	0.59 (10)	1.16 (8)	0.69 (7)	1.41 (3)	1.09 (3)	1.22 (3)	1.08 (5)
AC07	0.22 (10)	0.76 (9)	0.99 (6)	1.02 (6)	0.45 (10)	1.41 (3)	0.66 (8)	0.65 (9)	1.03 (6)
AC08	0.97 (1)	0.78 (8)	1.59 (3)	0.87 (2)	1.28 (2)	0.52 (6)	0.72 (7)	0.83 (7)	1.14 (4)
AC09	0.62 (7)	1.03 (4)	2.12 (1)	0.87 (2)	1.84 (1)	0.51 (7)	1.03 (5)	1.04 (5)	1.08 (5)
AC10	0.61 (8)	0.85 (6)	1.12 (5)	0.88 (3)	0.63 (8)	1.07 (4)	0.72 (7)	0.72 (8)	0.85 (7)
GM	0.72	0.97	1.16	0.98	0.97	1.13	1.09	1.07	1.04

GM: Grand mean; EMI: Emergence percentage index; PHI: Plant height index; NLI: Number of leaves per plant index; DFFI: Number of days to first flowering index; PDPI: Number of pods per plant index; SPPI: Number of seeds per pod index; SDPLI: Number of seeds per plant index; SDYPLI: Seed yield per plant index; NRTI: Number of roots per plant index, RTLI: Root length per plant index; DWRI: Dry weight of roots index. *RS*: Rank sum; $\bar{R}$: Mean ranks; σR: Standard deviation of ranks.

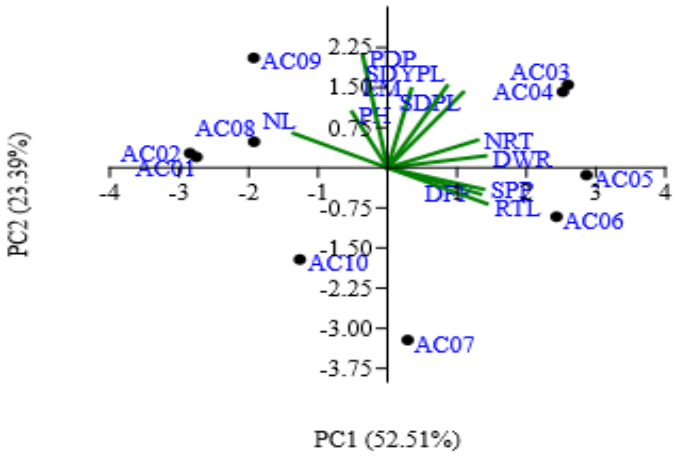

Fig. 1. Bi-plots of accessions of cowpea under aluminum stress.

GENETIC VARIABILITY AND CHARACTER ASSOCIATION STUDIES IN HYBRID MAIZE VARIETIES IN AKURE

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ABSTRACT

Maize improvement requires availability of genetic variability and knowledge of correlation. Thus, a field experiment was conducted in the early and late cropping seasons of 2020 at The Federal University of Technology Akure, to determine genetic variability and character association of some hybrid maize varieties for grain yield and related traits. Line x tester mating design was used to develop 36 hybrids consisting of 15 hybrids for the early maturing and 21 hybrids for the late maturing. Result revealed that PCV recorded was higher than the corresponding GCV for all traits. Genetic advancement (GAM) was also high in the two seasons for traits evaluated. Thus, the high heritability estimates accompanied by GAM and moderate GCV for these characters may be more promising because of the high degree of additive effect. Field weight and cob length could be used as selection criteria because they showed positive phenotypic and genotypic correlation with grain yield. Characters such as plant height, number of ears at harvest, and field weight can be selected as criteria for maize yield improvement.

Keywords: maize, hybrid, rainforest, heritability, correlation

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INTRODUCTION

Maize (*Zea mays* L.) belongs to the family *Gramineae* (*Poaceae*) is one of the most important cereal crops in the world following wheat and rice (Jaliya *et al.,* 2011). It is widely used for food, feed, fuel and fiber in many parts of the world. In Sub-Saharan Africa, maize is consumed by 50 percent of the population and is the preferred food for one-third of all malnourished children and 900 million poor people worldwide. By 2025, maize will be the developing world's largest crop and between now and 2050 the demand for it in the developing world is expected to double (FAO, 2018; Popescu, 2018).

For drought occurring during or shortly before flowering in crops, the estimated yield loss may be in the range of 21 to 50% (Olaoye *et al.,* 2009). According to FAO (2010) and Derera *et al.,* (2018), additional irrigation could possibly improve maize production in drought prone areas but in general, most rain fed farmers are resource poor, smallholders, and have a limited capacity to adopt high-input technologies (Bänziger and Diallo, 2001). A better approach to help these resource poor subsistence farmers is by using varieties that tolerate or escape the periodic droughts which befall the region. Since the timing of mid-season drought is unpredictable, early maize cultivars that can tolerate the effects of reduced moisture supply during flowering could reduce farmers' risk in drought-affected ecologies (Hussain *et al.,* 2011) and compete less for moisture, light, and nutrients than late maturing ones when used as an intercrop (CIMMYT, 2000).

Evaluation of extra early, early and late/intermediate maturing groups have formed part of their varietal trials in the marginal environments of the region under the auspices of International Institute of Tropical Agriculture (IITA) Ibadan, Nigeria (Olaoye and Omueti, 2006; Oluwaranti *et al.,* 2008). Several studies have been conducted to identify maize populations and varieties that may be recommended for better performance in the late season of the rainforest ecology (Badu-Apraku, *et al.,* 2010; Oluwaranti, *et al.,* 2015; Eze *et al.,* 2020). In all trials, early and extra-early varieties were not as high yielding as the late maturing varieties. It became necessary, therefore, to identify early or late maturing varieties that are specifically adapted to the conditions of the rainforest ecology and the traits that characterize them. This study aims to evaluate the growth and yield responses of the 36 hybrid maize for early and late season growth in the rainforest ecology and the traits that characterize them.

MATERIALS AND METHODS

The experimentation was carried out during the rainy and dry cropping seasons of 2020 at the Teaching and Research Farm of The Federal University of Technology, Akure, Ondo State, Nigeria. Located at an altitude of 332 m above sea level, 7°16'N and 5°12'E in rain forest south-

western region of Nigeria. A total of 36 maize hybrids generated from inbred lines of two different maturity groups (early and late) were used for the study. The inbred lines were collected from the International Institute of Tropical Agriculture (IITA) Ibadan, Oyo State Nigeria.

From Table 1, the 36 maize hybrids consisted 15 hybrids gotten from the crossing of five inbred lines (which serve as females and coded as G6, G17, G18, G20 and G30) with three testers (serving as males and coded as G25, G26 and G33); and 21 other hybrids gotten from the crossing of seven inbred lines (which serve as females and coded as G19, G23, G25, G27, G29, G33 and G35) with the three testers (serving as males). coded as G6, G9 and G30

The first five female lines were early maturity lines and the other 7 were late maturity lines. Line x tester mating design was followed for making 36 F_1 progenies consisting of 15 hybrids for the early maturing and 21 hybrids for the late maturing. The experiment was laid out in a randomized complete block design with three replications. Each hybrid was planted on single row of 5 m long at the spacing of 25 cm (intra-row) and 75 cm (inter-row). Two (2) seeds were planted per hole. Planting was carried out in two different seasons (rainy and dry seasons). Both pre-harvest and post-harvest data were collected. Data collected on yield and other important agronomic traits were taken on plot and individual plant basis. For data on individual plant basis, three plants of each plot for each genotype were used. Data were collected on the following parameters: days to silking, days to tasseling, anthesis-silking interval, plant height, ear height, plant harvested, ears harvested, grain yield, field weight, ear aspect, ear rot, moisture content, cob girth and 100 grains weight.

Genetic advance as percentage of the mean (GAM) was computed according to the formula given by Robinson *et al.*, 1949

$$GAM = \frac{GA \times 100}{\bar{x}}$$

Where $\bar{x}$ = Mean

$$\text{Phenotypic coefficient of var. (PCV)} = \frac{\delta^2 p}{\bar{x}} \times 100$$

$$\text{Genotype coefficient of var. (GCV)} = \frac{\sqrt{\delta^2 g}}{\bar{x}} \times 100$$

Where:

$\delta^2 p$ = Phenotypic variance

$\delta^2 g$ = Genotypic variance

$\bar{x}$ = grand mean of character being evaluated

PCV and GCV were determined by rating them as high (> 20%), medium (11-20%) and low (0 - 10%) as indicated in Siva-Subramamian and Melon (1973). Analysis of covariance was carried out on pairs of variables which exhibited significance ($p \leq 0.05$), using the PBTools version 1.3 statistical software.

RESULTS AND DISCUSSION

Analysis of variance of some characters of 36 early and late maturing hybrid maize genotypes are represented in Table 2. It was however observed that varieties varied significantly at $P < 0.01$ and $P < 0.05$ for all traits in each of the seasons and across seasons. This suggests the presence of significant amount of genetic variability among the hybrids and provides opportunity for improvement through selection. This result is in agreement with the findings of Ram Reddy *et al.* (2013) and Manjunatha *et al.* (2018). Significant differences were observed among genotypes in the early growing season for some traits, namely: plant height, days to 50% tasseling, ear harvest, field weight, cob girth and 100 grain weight. (Sanjay *et al.*, 2017) Similar trends occurred in the late growing season Manjunatha *et al.,* (2018). Field weight was positive and significant correlation with ear harvest (0.23), cob girth (0.19) and grain yield (0.24). These findings are in accordance with the reports of Oyekola and Fayeun (2019) for field weight

Conclusion

The 36 tomato genotypes are genetically different based on parameters like plant height, field weight, ear harvest, 100 Grain Weight, days to 50% tasseling and Cob girth. Thus, they are important selection criteria for maize yield improvement.

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Table 1. List of maize genotypes and codes

S/N	Code	Genotypes	Sources	Group
1	G6	TZISTR1181	IITA	Late
2	G9	TZISTR1244	IITA	Late
3	G17	TZISTR1225	IITA	Late
4	G18	TZISTR1010	IITA	Early
5	G19	TZISTR1301	IITA	Early
6	G20	TZISTR1304	IITA	Early
7	G23	TZISTR1312	IITA	Early
8	G25	TZISTR1323	IITA	Early
9	G26	TZISTR1324	IITA	Early
10	G27	TZISTR1327	IITA	Early
11	G29	TZISTR1329	IITA	Early
12	G30	TZISTR1330	IITA	Late
13	G33	9540	IITA	Early
14	G35	1393	IITA	Early

Table 2. Mean square from analysis of variance of characters of 36 early and late maturing hybrid maize genotypes

Source of variance	Replicate	Genotype	Error
PH (cm)	10.15	107.84**	14.46
D50%T	0.84	12.83**	3.71
CG (cm)	1.79	15.74**	3.02
EH	0.67	1.88**	0.36
FW (kg/ ha)	0.002	0.035**	0.002
100 GW (g)	14.65	38.42**	9.05

** = Significant at $p \leq 0.05$ and $p \leq 0.01$ probability levels respectively SV: Source of Variance.
PH- plant height, FW- Field weight, EH- Ear harvest, 100 GW- 100 Grain Weight, Days to 50% tasseling, CG- Cob girth

Table 3. Phenotypic correlation coefficients of thirteen agronomic traits evaluated in thirty-six hybrid maize varieties

Characters	Season	EH	100 GW(kg)	CG	GY (ton/ha)
Field weight	Early	0.23*	-0.02	0.19*	0.24**
	Late	0.12	0.01	0.28**	0.26**
Ears harvest	Early		0.01	0.10	0.15
	Late		-0.24*	0.24	0.10
100-grain weight	Early			0.05	0.04
	Late			-0.03	-0.08
Cob girth	Early				0.01
	Late				0.15

** = Significant at $p \leq 0.05$ and $p \leq 0.01$ probability levels respectively

AGRONOMIC AND YIELD PERFORMANCE OF F_6 PROGENIES OF GARDEN EGG (*Solanum aethiopicum*)

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ABSTRACT: Garden egg is one of the most important fruit vegetable crops in Africa. The field trial was conducted at NIHORT, Ibadan Nigeria in the year 2020 to determine the performance of selected F_6 progenies from two crosses. The F_1s were advanced to F_6 generations between 2013 and 2020. Nine F_5 progenies were laid out in Randomized Complete Block Design (RCBD) with three replications as F_6 generation. Quantitative data collected were subjected to ANOVA while means were separated using R-statistics. There were significant variations for all the characters observed except for number of branches, days to first flowering and first fruit set. Highest number of leaves per plant was recorded in G4 while the lowest was observed in G9. G2 had the highest number of fruits and fruits weight per plant while the lowest were recorded in G4. Therefore, G1, G2, G3, G5, G6, G7 and G8 were selected and advanced to On-station trial for possible release.

Keywords: character, data, fruits, generations, progenies, selected

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INTRODUCTION

African eggplant also referred to as Garden egg or Scarlet eggplant (*Solanum aethiopicum*) is a vegetable fruit crop which belongs to the *Solanaceae* family. It is cultivated across African continent most especially in West and East Africa (Eze *et al.*, 2012). It is a leaf and fruit vegetable with its fruits consumed raw or cooked. Garden egg is grown in Nigeria for its nutritional, medicinal and economic qualities derived from its leaves and fruits (Onunka *et al.*, 2011). Its leaves have been confirmed to reduce blood sugar level when consumed by diabetic patients (Okafor *et al.*, 2016). However, little attention has been given to its cultivation when compared to other *Solanaceae* family like tomato. Due to its nutritional and economic benefits, development of improved varieties with high yield and good nutritional qualities is highly recommended. The objective of the study was therefore, to determine the performance of F_6 progenies selected from two crosses with relation to yield and yield related characters.

MATERIALS AND METHODS

The experiment was carried out on Vegetable Research field of National Horticultural Research Institute (NIHORT), Ibadan during the cropping season of the year 2020. Nine F_5 progenies were laid out in RCBD with three replications. The F_5 seeds were used to establish the F_6 generation of Garden egg improved lines. These were selected from advancement of F_1 seeds of two crosses (NHS10-71 X NHS10-22 and NHS10-71 X NHS10-28) which were advanced to F_6 generation through selfing and selections made by breeders and agronomists from the year 2013 to 2020.

Data collection

The quantitative data collected includes: plant height (cm), number of leaves per plant, stem girth (mm), number of branches per plant, days to first flowering, days to first fruit set, number of fruits per plant, fruits weight per plant and unit fruit weight.

Data analysis

The data collected were subjected to analysis of variance while means were separated using R-statistics version 4.1.0.

RESULTS AND DISCUSSION

There were significant variations for all the characters observed except for number of branches per plant, days to first flowering and first fruit set (Table 1). This is an indication that there was sufficient genetic diversity for yield improvement of Garden egg lines. This agrees with the report of Kubie, 2013) who worked on "Evaluation of genetic diversity in Garden egg germplasm in Ghana. The tallest plant was observed in G3 (79.85 cm) while the shortest genotype was G8 (47.25 cm). Genotype 4 had the highest number of leaves per plant (271 leaves) while the least was observed in G9 (101 leaves).

Number of branches per plant was not significantly different from one another but ranged from 14.13 – 25 branches. The highest number of branches per plant was recorded in G2 while the least was found in G1. The earliest genotype to flower and fruit was G9 (86 and 92 days respectively) while the latest was G5 (Figure 1).

Figure 1 also displays the yield of the F_6 progenies with the highest number of fruits per plant (289) and fruits weight per plant (6.5kg) recorded in G2. This was followed by G3 with 142 fruits and 4.19kg per plant respectively. However, the lowest yield was recorded in G4 (3.5 fruits and 0.4kg fruits weight per plant). The highest unit fruit weight was recorded in G1 (57.17g) while the least was recorded in G3 (37.98g). This is in conformity with the work of Mawuli *et al*., 2022 on "Genetic variability for yield parameters in garden egg (*Solanum spp*)" They recorded variations in plant height, stem girth, canopy spread, number of branches, number of leaves, days to 50% flowering, fruit number per plant and fruit yield among others.

Conclusion

Significant variations were observed among the yield and yield related parameters in this study. Therefore, G1, G2,G3, G5, G6, G7 and G8 were selected and advanced to F_7 generation for On-station trials and future release.

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Table 1. Analysis of variance for seven characters observed in nine genotypes of Garden egg

Source	Gen. (df = 8)	Rep. (df = 1)	Res. (df = 17)	CV
PH(cm)	3971.1**	17.8	16.7	6.46
NLVSP	12695**	851	918	18.89
NBRP	30.75	54.25	15.81	20.51
DSFL	103.83	0.22	44.58	7.06
DSFR	155.5*	8	56	7.34
NFRTP	23949**	207	749	29.25
FWTP(kg)	12.9**	0.08	0.72	30.77

Df= degree of freedom; PH= plant height; NLVSP= number of leaves per plant; NBRP= number of branches per plant; DFL= days to flowering; DFR= days to fruiting; NFRP= number of fruits per plant; FWTP= fruit weight per plant

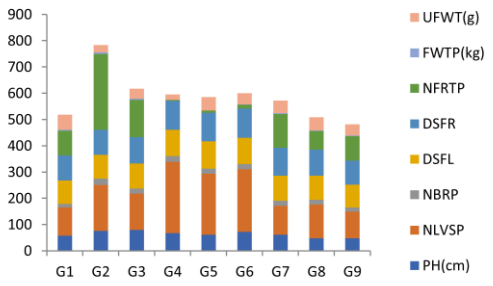

Figure 1. Mean Performance for seven characters observed in nine genotypes of Garden egg

PH= plant height (cm); NLVSP= number of leaves per plant; NBRP= number of branches per plant; DFL= days to flowering; DFR= days to fruiting; NFRP= number of fruits per plant; FWTP= fruit weight per plant (kg) and Unit fruit weight (g)

AGRONOMIC RESPONSE OF TOMATO VARIETY TO COLCHICINE ($C_{22}H_{25}NO_6$) TREATMENT IN DIVERSE GROWING SEASON

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ABSTRACT

The Response of tomato variety (UC-82B) to colchicine treatment for improved growth and yield related traits was investigated with the aim of inducing variability that could be exploited in the improvement of some quality traits in Tomato in dry and wet seasons. The seed of the tomato variety (UC-82B*)* was treated with three different concentrations of colchicine (1.0 mM, 1.5 mM, 2.0 mM and 0.0 mM as control). The result indicated that, the interaction makes the tomato variety to respond more to the mutagenic treatments during the rainy season than the dry season. It showed that, seedlings height, height at maturity and pericarp thickness of the controls have the highest response during the dry season. However, all the mutants treated with 1.0 mM concentration showed highest response in all the selected traits during rainy season except fruit diameter. Similarly, all the 1.5 mM treated mutants showed highest response during rainy season except in leaf area where highest response was found in dry season. Similar result was found in 2.0 mM treated mutants.

Key words: colchicine, UC82, rainy season, dry season, mutation**.**

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INTRODUCTION

Tomato is one of the most highly praised vegetables consumed widely and it is a major source of vitamins and minerals. It is one of the most popular salad vegetables and is taken with great relish. Tomatoes and tomato products are rich in health-related food components as they are good source of carotenoids (lycopene and carotene), ascorbic acid (vitamin C, vitamin A, vitamin E, folate, flavonoids, minerals, proteins) and dietary fibre (Beecher, 2001 and Davis, *et al.*, 2003). Regular consumption of tomatoes has been correlated with a reduce risk of various types of cancer and heart disease. These positive effects are believed to be attributable to the anti-oxidant particularly the carotenoid, flavonoids, ascorbic acid and phenolic compounds Giovanelli, *et al.*, 2006.

In Nigeria, especially in the Southern region, tomato production is highly seasonal and mostly weather dependent, which as lead to surfeit during the favorable season and scarcity during the unfavorable season. This scenario has caused unfriendly consumer price of this commodities during the off season. The demands for high quality, moderate sized, red colored tomato with high firm fruit, acceptable appearance and good taste is increasing, while grower prefer high yielding, higher weight, indeterminate growth habit and resistance to pest and diseases. The solution to these is to find suitable varieties for growing that will meet the consumer's wants under a controlled environment. Growth, yield and fruit quality performance of tomatoes varieties under controlled environment conditions.

Colchicine is a chemical mutagen and has been one of the most powerful mutagens in crop plants. The mutagen is mediated through the production of an organic metabolite of azide compound. This metabolite enters into the nucleus, interacts with DNA and creates point mutation in the genome (Kozgar et *al.,* 2011; Mustafa, 2011). It has also proved its worth as chemical lmutagens to induce genetic variability. Thus, this chemical mutagen has become important tool to enhance agronomic traits of crop plants. Khan, 2006. Presently imported varieties and hybrid tomatoes are introduced into the market; greenhouse vegetable growers use this variety without full knowledge of the performance of these varieties under controlled environment. The main aim of this study was to investigate the response of tomato variety (UC-82B) to colchicine with the aim of inducing variability that could be exploited in the improvement of some quality traits in Tomato.

MATERIALS AND METHODS

Study Site

The research was conducted in the Green House of the Botanical Garden of the Department of Biological Sciences, Ahmadu Bello University

Zaria (2014). (Lat 11° 12´N, Long. 7 ° 37´E, Alt. 550 - 700 m above sea level).

Sources of the seeds

Seed of the cultivated tomato (UC-82B) was collected from the Institute for Agricultural Research (I.A.R), Ahmadu Bello University Zaria, Nigeria.

Treatment and experimental design

The treatments used in the research are mutation using various concentrations of colchicine, The seeds of the tomato variety were treated with four different concentrations of Sodium Azide (1.0 mM, 1.5 mM, 2.0 mM and 0.0 mM as control) respectively. The tomato variety used was UC-82B. It flourishes and grows successfully during the dry season. The treated plants were grown in 45 polythene bags arranged in a completely randomized design with three repetitions in each season as described using McVoy (2005) protocol.

Data analysis

All the data collected were analyzed using Analysis of Variance, and the means were separated using Duncan's Multiple Range Test (DMRT).

RESULTS

The result of the response of the tomato variety to the colchicine concentrations in dry and wet season is presented in the table above. The result indicated that, the interaction makes all the three varieties of tomato to respond more to the mutagenic treatments during the rainy season than the dry season. The interaction showed that, seedlings height, height at maturity and pericarp thickness of the controls have the highest response during the dry season. However, all the mutants treated with 1.0 mM concentration showed highest response in all the selected traits during rainy season except fruit diameter. Similarly, all the 1.5 mM treated mutants showed highest response during rainy season except in leaf area where highest response was found in dry season. Similar result was found in 2.0 mM treated mutants.

DISCUSSION

The distinct differences observed in most of the quantitative and qualitative traits among the colchicine induced mutants of tomato evaluated showed significant improvements in the selected traits. Although there were few traits with no significant differences in responses to the applied treatments; the ability of the mutants to germinate faster after one and two weeks of planting in respect to the controls showed that the mutagenic treatments induced increase enzymatic activities, which could be responsible for the early germination. This finding is in agreement with the findings of Mensah *et al.* (2007) who reported decreased in germination with increase in the dose of chemical mutagens. In the present investigation, germination, plant heights and leaf number and area decreased with increasing concentration of colchicine. This finding conformed to the earlier report by Ahloowalia and Maluszynski (2001) that, the viable mutants observed are mainly dependable measure of genetic effect in mutagen. The increased in the number of leaves, fruit number and plant heights due to colchicine treatments is also in conformity with the work of Adamu and Aliyu (2007) who reported increased in growth and yield parameters of tomato due to colchicine treatments. Reductions in germination percentages and diameter of the fruit due to the effects of mutagens on various crop plants have earlier been documented by Mensah and Akomeah (1997) and Mensah *et al.* (2005).

The increased in the leaf area and seedling height among the mutants signifies the ability of the mutagen (colchicine) to initiate more foliar buds. This finding agrees with the work of Maluszynski *et al.* (2001) who independently reported an increase in leaf number and leaf area among *Zea mays* mutants.

More so, the improvement in the growth and yield components of tomato due to colchicine treatments stressed the effect of mutation on the growth and yield of plants. This is in conformity to the work of Adamu *et al.* (2002) when groundnut was treated with gamma rays and Sheeba *et al.* (2005) when gamma rays and EMS were used to treat *Sesanum indicum* L. where seed germination, seedling, survival, plant height and pollen fertility were reduced significantly with an increase in dosage levels of both mutagens. However, in contrast, Sasi *et al.* (2005) showed that all plant mutant types registered lower yields compared to their parents in the study of the effects of diethylsulphate and EMS on Okra (*Abelmoschus esculentum* (L.) var. MDU-1).

The increased in fruit quality, such as pericarp thickness due to induced mutagenesis by colchicine signifies the vital role played by the mutagen in improving the quality traits of tomato. The increased in dry weights of the tomato varieties due to sodium azide treatments is in contrast to the findings of Ikhajiagbe *et al.*

(2012). Significant improvements were found among the mutant tomatoes in both the dry and wet seasons.

Conclusion

It was concluded that, there is significant difference in the effect of colchicine concentration on the growth and yield components of the tomato variety under study. It was found that 1.0 mM concentration of colchicine has the highest effect on the characters.

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Table 1. Effects for interaction of concentration, variety and seasons on some selected tomato traits

Concentration (mM)	Variety	Season	Germination % (2 WAP)	Seedlings Height (cm)	Survival Rate (%)	Height at Maturity (cm)	Number of Leaves
0.0	UC	Dry	40.51a	22.83a	44.29a	37.73a	15.11a
	UC	Rainy	40.66a	19.44a	23.70a	30.81a	12.44a
1.0	UC	Dry	83.11a	33.07b	83.11a	55.50a	20.33a
	UC	Rainy	73.70b	34.97a	62.66b	50.35b	17.55b
1.5	UC	Dry	75.77a	29.07b	73.66a	47.31a	18.77a
	UC	Rainy	64.37b	29.78a	49.92b	41.54b	16.33b
2.0	UC	Dry	64.48a	27.54a	58.88a	43.46a	17.77a
	UC	Rainy	53.40b	25.66b	38.81b	38.32b	14.33b

Means within the columns with the same letter(s) are not significantly different ($p \leq 0.05$)

Table 1. Contd.

Concentration (mM)	Variety	Season	Leaf Area (cm^2)	Number of Fruits	Pericarp Thickness (mm)	Fruit Diameter (cm)	Root DW (g)
0.0	UC	Dry	9.83a	2.77a	0.40a	0.39a	1.66a
	UC	Rainy	11.50a	1.77a	0.30a	0.42a	2.60a
1.0	UC	Dry	31.83a	9.33a	0.28b	0.15a	3.04a
	UC	Rainy	30.66b	4.77b	0.50a	0.14b	2.90b
1.5	UC	Dry	25.94a	6.22a	0.25b	0.28b	2.77a
	UC	Rainy	23.33b	3.22b	0.28a	0.30a	2.58b
2.0	UC	Dry	17.72a	4.55a	0.21b	0.36b	2.47a
	UC	Rainy	14.83b	2.44b	0.32a	0.45a	2.26b

Means within the columns with the same letter(s) are not significantly different ($p \leq 0.05$)

AGRONOMIC PERFORMANCE OF NEW TOMATO (*SOLANUM LYCOPERSICUM* L.) BREEDING LINES UNDER OPEN FIELD RAINFED CONDITION IN SOUTH WEST NIGERIA

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ABSTRACT
Twenty-six early generation (F_4) tomato breeding lines were evaluated with six check varieties under open field rainfed conditions at NIHORT, Ibadan Nigeria. Field appraisal of agronomic and yield characteristics of the breeding lines were undertaken to improve selection of promising lines adapted to the high humid environments of Nigeria. Highest estimate of variability was recorded for average fruit weight while fruit width had the minimum variability. Average number of fruits (86%) and fruit length (81%) were the most heritable trait and could be easily favoured through selection. Breeding lines 40-4 x AVTO1219-52-1 and 40-4 x AVTO1219 -48-1 were the top performers for yield (2327 g and 2257 g respectively). Average fruit weight exhibited high significant positive association with average number of fruits per plot while average fruit length had high positive significant association with fruit width. This shows the feasibility of indirect selection for high number of fruits in this population.

Keywords: agronomic, breeding lines, tomato, variability, yield

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INTRODUCTION
Tomatoes (*Solanum lycopersicum* L.) is one of the most important vegetables commercially produced in Nigeria and also harvested in home gardens (unpublished data). It is mostly produced during the late seasons in the northern states of Nigeria with minimal production from the southern states. Tomato contains minerals, vitamins, polyphenol, and lycopene, which have health benefits for human beings (Islam *et al.*, 2022). Tomato yield in Nigeria is below world averages (Agele *et al.*, 2002; Oladitan and Akinseye, 2014). To increase productivity, it is necessary to develop superior varieties mainly for open filed rainfed production that is prevalent among farmers in Nigeria. Planning and execution of a breeding program for improvement of quantitative attributes such as yield depends to a great extent upon the magnitude of genetic variability and the extent to which desirable characters are heritable (Islam *et al.*, 2022). Heritability estimates the influence of environment in expression of characters and the extent to which improvement is possible after selection (Tembe, 2018)). However, correlation studies between fruit weight and its components and their relative contribution to yield are of value in planning if promising high yielding genotypes with other desired farmers preferred traits are to be favoured in a breeding program. This study reports the yield potential of new promising tomato breeding lines under open field rainfed cultivation for selection and advancement.

MATERIALS AND METHODS
The trial was carried out at the National Horticultural Research Institute (NIHORT), Ibadan, Nigeria, located in the humid forest savannah transition zone (210 masl, 7°30'N, 3°54'E). It experiences a bimodal annual rainfall pattern of about 120–128 rainy days amounting to 1,200–1,400 mm. Pan evaporation is between 1,550 and 1,600 mm. The wet season is from March through October and the dry season from November through February with annual maximum temperature ranging between 27°C and 34°C and annual minimum temperature of 20–23°C (Ogungbenro and Morakinyo, 2014,).
Experimental materials comprised of 32 new tomato breeding lines (F_4) developed by crossing selected parents comprising of popular tomato landraces/cultivars in Nigeria and exotic advanced breeding lines from AVRDC. These

landraces (parents) were collections from farmers' field across different tomato growing regions in Nigeria and have undergone over 4 generations of selfing and selections and are maintained in the Institute's tomato genetic improvement programme.

For the field experiment, seeds were sown in perforated plastic trays containing sterilized loamy sand in a screen house (soil was sterilized by steaming). Developing plants were watered using 75 cl of water for each tray 3 times a week until 30 days after sowing. The field was arranged in an alpha lattice design (10 stands per plot) with plant spacing of 0.5 m within row and 0.6 m between rows with 2 replications. Fertilizer was applied 3 weeks after planting at 140 kg·ha^{-1} of N and 25 kg·ha^{-1} of P. The N was from urea and the P from single superphosphate. Manual weeding was carried out at 3 and 8 weeks after transplanting, while staking and trellising of plants was done at one week prior to the onset of flowering.

Data were obtained on TFW= Total fruit weight, TNOF= Total number of fruits per plot, FL= average fruit length, FW= average fruit weight, DTF= Days to 50% flowering. Analysis of variance and heritability estimates (broad sense) were with PB Tools (ver. 1.1.0, http://bbi.irri.org/products); while phenotypic correlation was developed with STAR statistical software. Heritability was estimated as the ratio of total genotypic variance to phenotypic variance according to Falconer (1981). Heritability percentage was categorized as low (0–30%), moderate (31 – 60%) and high ≥60% (Johnsonetal.,1955). Correlation coefficients "r" were considered very weak (0-0.19), weak (0.20-0.39), moderate (0.40-0.59), strong (.60-.0.79), very strong (0.80-1.00) according to Evans (1996).

RESULTS

The mean, range, and heritability estimates of traits are presented in Table 1. High significant difference was observed for all the traits ($P \leq 0.01$). The highest mean and maximum range was recorded for total fruit weight while minimum range was observed for days to 50% flowering. Moderate heritability estimate in the broad sense was recorded for TFW 64%, FW (66%) and DTF (68%) while TNOF and FL had high heritability estimates of 86 and 81 % respectively. The mean of evaluated F_4 lines and checks for each considered trait are presented in Table 2. Breeding line 40-4 x AVTO1219-52-1 was the top performing genotypes for yield (2327.19g) in this trial while AVTO1219 X 39-9E-59 was the earliest to reach 50% flowering (47 days). Two commercial tomato hybrid checks Padma F_1 (44.05 cm) and Cobra 26 (37.42cm) exhibited the highest fruit length and fruit width respectively (Table 2). Very high positive significant association was recorded between total fruit weight and total number of fruits. Moderate positive high significant association was observed between fruit length and fruit width (Table 3).

DISCUSSION

Understanding the variability among genotypes enhances selection and advancement of promising individuals in a breeding programme. The high significant variation observed for all the traits in this populations shows the feasibility of their improvement through selection. This supports the work of Bationo-Kando *et al.* 2015 who reported high significant variation among traits considered in tomato. Top performing breeding lines for earliness (AVTO1219 x 39-9E-59), higher number of fruits per plot and yield (40-4 x AVTO1219-52-1) are promising candidates that could be advanced for used as parents for creating new gene combinations for early maturing high yielding tomato varieties in Nigeria.

Heritability estimates are important for selection based on phenotypic expression since it determines the transfer of genes across generation. Heritability determines how much of the
phenotypic variability has a genetic origin, its response to the influence of environment, and therefore helps breeders to select on genetic basis (Falconer 1981). Moderate to high estimates of heritability observed for total fruit weight, fruit width, fruit length, days to 50% flowering is an indication that selection based on phenotypic observable traits will be efficient towards improvement of these traits. This is in line with earlier reports by Reddy *et al.* 2013 on high heritability for considered traits of tomato.

Correlation between traits is important because it helps the breeder to select important genotypes with desired characters from the breeding population. Selection for most complex traits such as yield and its component traits are influenced by interaction of genotype and environment and its selection efficiency can be improved by indirect selection of correlated traits

based on correlation coefficient in a breeding programme. The significant positive association observed between yield and total number of fruits in this populations shows that selection in favour of breeding lines with high number of fruits will favour genotypes with high yield potential. Furthermore, selection in favour of long fruits will lead to selection in favour of big fruits. This is in accordance with Islam *et al.* (2010) who reported positive significant association between total fruit weight and number of fruits in tomato but in contrast to Saleem *et al.* (2013) that reported significant negative association between fruit length and fruit width among tomato genotypes.

Conclusion

Moderate to high heritability estimates for yield and yield related traits observed from this study shows the feasibility of identifying top performing genotypes for considered traits from this population. Top performing breeding lines for earliness (AVTO1219 X 39-9E-59) and yield (40-4 x AVTO1219-52-1) were identified as promising candidates that could be advanced for further evaluation.

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Table 1. Descriptive statistics and heritability of traits among F_4 Tomato breeding lines

Traits	Min	Max	Mean	StdDev	Heritability
TFW	1042.51	2327.19	1615.59**	303.24	0.64
TNOF	27.04	136.06	64.72**	24.8	0.86
FL	16.24	44.05	30.31**	5.19	0.81
FW	19.09	37.42	30.73**	3.86	0.66
DTF	47.55	62.68	55.37**	3.98	0.68

TFW= Total fruit weight, TNOF= Total number of fruits per plot , FL= average fruit length, FW= average fruit weight, DTF= Days to 50% flowering

Table 2. Means of 32 tomato genotypes for evaluated traits

Genotypes	TFW	TNOF	FL	FW	DTF
40-4 x AVTO1219-52-1	2327.19	136.06	30.5	30.53	54.08
40-4 x AVTO1219-48-1	2257.23	120.55	27.26	28.83	52.71
40-4 x AVTO1219-45-2	1995.32	83.06	31.18	34.43	53.05
AVTO1219 X 39-9E-8	1966.57	77.46	29.51	30.67	53.05
54-7 X AVTO1219-4-3	1945.17	86.08	31.48	29.23	50.3
54-7 X AVTO1219-4-9	1943.57	84.78	29.98	37.29	57.87
AVTO1219 X 39-9E-64	1857.65	88.23	33.26	30.72	53.74
G7 x AVTO0102-6-14	1831.78	27.04	31.56	31.54	58.9
AVTO1219 X 39-9E-5	1817.08	71.86	34.33	34.79	59.24
UC82	1698.58	49.88	42.06	35.49	59.59
G11 x AVTO0102-6-105	1677.18	51.17	25.6	27.92	50.3
006B x G7-2	1672.39	83.92	20.28	22.88	60.27
006B x G7-16-1	1652.91	74.44	28.03	28.18	60.62
39 x 3 x AVTO1219-7-100	1650.67	59.36	30.16	32.31	50.3
COBRA 26	1643.64	56.77	34.34	37.42	58.21
40-4 x AVTO1219-23-1	1626.71	70.13	29.26	30.81	54.08
006B x G7-1-7	1620.01	84.35	34	28.71	54.08
40-4 x AVTO1219-50-1	1605.63	60.65	27.77	32.97	54.08
AVTO1219 X 39-9E-44	1563.15	60.22	32.58	36.8	61.31
40-4 x AVTO1219-55-2	1545.9	55.91	33.34	34.03	52.02
54-7 X AVTO1219-4-42	1533.13	79.61	25.13	27.29	52.71
AVTO1219 X 39-9E-36	1522.58	66.68	25.43	30.37	53.39
PLATINUM	1403.44	48.16	33.67	30.07	54.08
AVTO1219 X 39-9E-59	1359.68	56.77	28.74	30.6	47.55
AVTO1219 X 39-9E-32	1359.05	60.65	30.71	30.23	56.83
IBADAN LOCAL	1326.78	27.47	26.3	28.77	50.99
G23 x AVTO1314-61-1	1318.16	44.71	33.47	33.71	53.39
40-4 x AVTO1219-45-1	1268.97	63.67	30.46	27.07	52.71
G7 x AVTO0102-6-20	1237.99	31.35	29.04	30.95	57.87
PADMA	1233.84	30.06	44.05	28.72	62.68
G7 x AVTO0102-6-18	1194.55	46.43	30.02	31.07	62.34
TROPIMECH	1042.51	33.5	16.24	19.09	59.37

TFW= Total fruit weight , TNOF= Total number of fruits per plot , FL= average fruit length, FW= average fruit weight, DTF= Days to 50% flowering

Table 3. Phenotypic correlation of traits for F_4 tomato breeding lines

	TFW	TNOF	FL	FW	DTF
TFW	1	0.7906**	0.0858	0.2979	-0.2022
TNOF		1	-0.1085	0.0233	-0.239
FL			1	0.6174**	0.196
FW				1	0.0475

TFW= Total fruit weight , TNOF= Total number of fruits per plot , FL= average fruit length, FW= average fruit weight, DTF= Days to 50% flowering

EFFECT OF CHITOSAN SEED COATING ON FUNGAL INCIDENCE OF STORED RICE (*Oryza sativa*)

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ABSTRACT
Rice (*Oryza sativa* L.) seed storage is constrained with deterioration caused by fungal pathogens. The use of synthetic fungicide is known to cause health problems and environmental pollution, hence the need for biofungicide as safety protectant. Therefore, this study evaluated the percentage fungal incidence of (Faro 44. 52 and 61) rice varieties before and after coating with 1% high molecular weight chitosan and stored for a period of six months. The results analyzed using ANOVA after storage period showed four fungal species belonging to two genera were isolated (*Aspergillus* sp and *Fusariun* sp). Significant reduction was recorded in percentage fungal incidence from initial of 35% to 12% in Faro 44 while, there was no fungal incidence observed in Faro 52 and 61 at the end of storage period with initial of 29% and 32% respectively. It was therefore concluded that chitosan may be used to prevent deterioration of rice by fungi during storage.

Keywords: chitosan, coating, fungal, rice, storage

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INTRODUCTION
Rice (*Oryzae sativa* L.) is a major food crop grown primarily in tropical and subtropical climates. After sugarcane and maize, it is the agricultural commodity with the third highest global production (FAO, 2014). Fungal pathogens are the major biological constraints, infecting rice crops from the field to storage, (Islam and Ahmed, 2017). These fungal pathogens deteriorate seed quality, cause germination failure and reduce yield (Ahmed et al., 2013). Over time, the use of synthetic fungicides has been the primary method of controlling seed-borne fungal pathogens (Gilberto et al., 2017). However, there is serious concerns on health risks posed by the exposure of farmers working with these fungicides as well as environmental pollution. Therefore, there is need for the use of alternative curatives such as bio fungicides (chitosan) which are environmentaly safe. This study was carried out to evaluate the effect of chitosan on post-harvest deterioration of stored rice varieties during storage.

MATERIALS AND METHODS
Collection of samples
Fifteen (15) samples of released rice seeds were obtained from Farmers across Lavun Local Government Area of Niger State, Nigeria. The samples were taken to the FUTMINNA Plant Biology Department laboratory for analysis. High molecular weight chitosan (MW 760 kDa; ≥ 85%) and Potato Dextrose Agar were purchased from sigma Aldrich, USA.

Preparation of Media
Potato Dextrose Agar (PDA)
Thirty-nine (39) gram of PDA (Himedia) was suspended in 1000 ml distilled water and heated to dissolve the powder completely, the medium was sterilized by autoclaving at 121°C for 15 minutes

Determination of fungal Incidence
Twenty-five (25) rice seeds of each sample were surface sterilized in 15 ml of 1 % sodium hypochlorite, sterile water and inoculated on PDA in a Petri dish. The plates were in triplicates and incubated at 28 ± 2°C for 5 days (Madushani *et al.,* 2012). The percentage fungal incidence was calculated using the formular

$\% = \frac{F}{N} \times 100$, Where F is total number of fungal count in samples and N is total number of the rice seeds inoculated

Invivo Antifungal activity of chitosan on stored rice seeds

Two Kilogram (2 kg) each of rice samples were sun dried and moisture content (MC) determined at interval of 6 hours until the MC was 10%. One percent (1%) of chitosan was used to spray the rice seeds, allow to dry, bagged and stored at room temperature for period of six (6) month. The percentage incidence of the associated fungi with the samples were determined after the period of storage.

Data analysis

All data generated were subjected to analysis of variance (ANOVA) and New Duncan Multiple range test was used to separate the means.

RESULTS AND DISCUSSION

Four fungi species belonging to two genrea were isolated from the stored rice seed samples (Table 1). *Fusarium monilforme* has the highe incidence (56%) followed by *Aspergillus flavus* (18%) while *A. fumigatus* was the least (12%). The highe incidence of Fusarium monilforme was because the fungi was able to survive on healthy rice grains under low temperatures for long periods. The result in in line with Phan *et al.,* 2021 who reported 36% as the highest among the isolated fungal pathogens

The results of the percentage fungal incidence in three released rice varieties (Faro 44, 52 and 61) from farmers store showed that Faro 44 has the highest initial fungal incidence of 35% follwed by Faro 61 and 52 with incidence of 32% and 29% respectively. However, the percentage fungal incidence reduced after coating and six month period of storage to 12% in Faro 44 and no incidence was recorded in Faro 52 and 61 respectively (Table 2). The initial high percentage incidence of fungal in the rice samples from farmers store may be due to poor postharvest management such as high moisture content of the paddy as well as poor storage environment. Ppersistent moisture condensation is sufficient for fungal growth and multiplication. This was similar to earlier report of 68% by Bertuzzi *et al.,* (2019) at room temperature. The reduction in fungal incidence after coating and period of storage may be attributed to the fact that chitosan is a defense enzyme inducer.

Conclusion

Based on the reduction or total eradication of fungal incidence in chitosan coated rice, it was therefore concluded that chitosan may be used to prevent deterioration of rice by fungi during storage

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Table 1. Percentage incidence of isolated fungi

Isolated Fungi	% Incidence
Fusarium moniliforme	56
Aspergillus flavus	18
Aspergillus fumigatus	12
Aspergillus niger	14

Table 2. Incidence of fungal in rice varieties before and after coating with 1% HMWC

Varieties	Fungal Incidence before Coating		Fungal Incidence After Coating with 1.0% HMWC	
	Mean±SE	% FI	Mean±SE	% F I
Faro 44	6.75±0.95^{jk}	27	1.33±0.88	5.3
Faro 44	6.00±0.58^{j}	24	0.00±0.00	0
Faro 44	5.00±0.71^{jk}	20	1.67±0.67	6.7
Faro 44	7.25±1.38^{kl}	29	0.00±0.00	0
Faro 44	6.75±1.38^{jk}	27	0.00±0.00	0
Faro 44	8.75±0.75^{mn}	35	3.00±0.88	12
Faro 44	4.25±0.25^{ij}	17	0.33±0.33	1.3
Faro 44	7.00±0.91^{kl}	28	0.67±0.67	2.7
Faro 52	5.50±1.85^{jk}	22	0.00±0.00	0
Faro 52	0.50±0.50^{ab}	2	0.00±0.00	0
Faro 52	4.50±1.84^{ij}	18	0.00±0.00	0
Faro 52	5.00±0.41^{jk}	20	0.00±0.00	0
Faro 52	7.25±0.75^{kl}	29	0.00±0.00	0
Faro 61	4.00±0.41^{i}	16	0.00±0.33	0
Faro 61	8.00±0.71^{mn}	32	0.00±0.00	0

Fungal Incidence (FI)

EVALUATION OF F_5 COWPEA HYBRID FOR SEED YIELD AND REACTION TO BROWN BLOTCH (*Colletotrichum capsici*) IN HUMID FOREST AGRO-ECOLOGY

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ABSTRACT

Colletotrichum capsici is a major disease problem of cowpea in humid agroecology. The magnitude of variation and heritability for pod and seed yield, incidence and severity of brown blotch were investigated. Cowpea F_5 generations viz. L-83-B, L-11-B, L-22-B, L-72-C, L-61-B, L-6-B, L-59, L-76-C and L-43-A and two checks were planted for evaluation in a randomized complete block design with four replications. Seed yield, incidence and severity of brown blotch were assessed. The area under disease progress curve was used for resistance class determination. Disease and yield data were analyzed using the area under disease progress curve and PROC GLM procedure of SAS. Significant response for traits suggests variability and selection. High heritability for disease severity suggests preponderance of both additive and non-additive genes. Inheritance of brown blotch showed transgressive segregation in L-11-B, L-83-B, L-25, L-59, L-43-A and L-22-B. Two breeding lines 'L-25' and 'L-83-B' promising for grain yield and resistance to brown blotch are recommended for commercialization in the study location.

Keywords: Cowpea, F_5 population, Single seed descent, additive gene, Brown blotch disease

INTRODUCTION

Cowpea (*Vigna unguiculata* [L.] Walp) grains are nutritious and a cheap contributor as protein to the livelihoods in the tropics (Quin, 1997). Worldwide cowpea production is estimated at 6.5 MMT annually with 80% of production occurring in West Africa (Boukar et al. 2016). Cowpea brown blotch (*Colletotrichum capsici*) is a seed borne disease in humid forest of South-western Nigeria (Adebitan, 1996) enhanced by heavy rainfall and high humidity. The symptoms of cowpea brown blotch are seedling damping-off, stem girdling, flower abortion, immature pod mummifying, reduced seed yield, poor taste and low market value (Allen *et al*., 1998). Therefore, the need to identify source of resistance, alongside high grain yield adaptable to the humid forest agro-ecology becomes imperative. Several attempts have been made to control the disease, these includes use of resistant varieties (Singh, 1994), seed treatment with fungicides (Emechebe, 1994), spacing and cropping pattern (Adebitan *et al*., 1996), phosphorus fertilization (Owolade *et al*., 2008), and bio-control agent (Channya, 2011). Emechebe (1994) had reported 8 races of *C. capsici,* four races were reported in rain forest zones. The cultivars IT99K-573-2-1 and 503/46-13 showed highly specific resistance to two (Ccap-PO and Ccap-SA) and one (Ccap-PO) of the three pathotypes (Adebitan *et al*., 1992). Large scale production cowpea in rain forest agro-ecological zone is promising provided high seed yielding varieties that are resistant to brown blotch are available for cultivation. The objectives of this research were to evaluate variability and heritability for pod and seed yield traits, incidence and severity of brown blotch.

MATERIALS AND METHODS

Location, experimental design, planting and crop husbandry

The field experiment was carried out at the Teaching and Research Farm, Federal University Oye Ekiti (07º 48.137´ N, 005º 29.526´E and 547 m above sea level) between August and November, 2021. The climate of Ikole is considered as tropical. Ten cowpea F_5 generations (L-83-B, Check-2, L-11-B, L-22-B, L-72-C, Check-1, L-61-B, L-6-B, L-59, L-76-C, L-43-A, and L-25) and two check (one resistant and one susceptible) were developed through single seed decent method. The procedure for development of the population, laboratory and field screening from F_1 to F_4 were carried out at the cowpea breeding unit, Institute of Agricultural Research and Training, Moor Plantation Ibadan, Nigeria. The F_5 generation were stable with varying level of reaction to brown blotch in cowpea and seed yield. The experimental area (456 m^2) was prepared manually prepared, a randomized complete block design with four replications was adopted for field evaluation. A four-row plot of 3 by 1.8 meter and 0.8 meter between plots, and ridges

were made 1 m apart. Each variety was allotted to each plot and replicated four times. Each replicate comprised of 12 plots and were separated from the other by 1 meter distance. Three seeds of each variety were planted per hole at a spacing of 0.60 meter between plants and 0.60 meter between rows. A week after planting (WAP) supplying was done for missing stands, while thinning was carried out 2 WAP to maintain two plants/hill. Insecticidal spray of Lambra Cyhalothrin plus Dimethoate (300 g/l) was applied three times during the growth cycle.

Data collection and Disease assessment

Number of pods plant was estimated by counting the number of pod/plant on 10 randomly picked plants/plot at mid podding stage. Pods were harvested/plot at maturity and air dried (12% moisture content), threshed and weighed on weighing balance for seed yield/plot (kg). Thereafter, one hundred seeds were randomly picked/plot and weighed on sensitive electronic weighing balance for determination of 100-seed weight (g). Disease severity was assessed as percentage of leaf area exhibiting virus symptoms according to the rating scale of Arif and Hassan, (2002). The disease severity data were subjected to area under disease progress curve (AUDPC) described by (Shaner and Finney, 1977). Data collected were analyzed using PROC GLM procedure of Statistical Analysis System (SAS, 2012). The means were separated using the Tukey Honesty Significance Difference (HSD). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated according to the formula described by Singh and Choudhary (1985). Values between 0 and 10% for low, 10–20% for intermediate and greater than (> 20%) for high. The Genotypic and phenotypic co-efficient of variations were estimated according to Singh and Choudhary (1985). Broad sense heritability was done following the formula by Johnson *et al.* (1955). In accordance with Khan *et al.* (2020), the heritability was categorized as between 0 and 30% for low, 30–60% for intermediate and greater than 60% as high.

RESULTS

Mean squares for vegetative traits among the cowpea F_5 generations

The cowpea lines showed significant mean squares ($p < 0.05$) for number of pods per plant, seed yield/plant and 100 seed weight (Table 1). On the other hand, days to 50% flowering, days to 50% maturity and seed yield/plot showed insignificant ($p > 0.05$) mean squares. The estimates of the phenotypic coefficient of variation are larger in magnitude than their corresponding genotypic coefficient of variation. The brown blotch incidence and severity showed significant mean squares ($p < 0.05$). The estimates of the phenotypic coefficient of variation are greater in magnitude than their corresponding genotypic coefficient of variation. The genotypic coefficient of variation (%) was a low (11.76) for brown blotch incidence and high (21.74) for brown blotch severity. The broad sense heritability estimate was low for brown blotch incidence (30.17) and high for brown blotch severity (65.22) (Table 1). The weight of 100 seeds was 19 g in L-25 and 13.75 g in L-72-C. The number of pods per plant varied from 22 pods in L-59 to 55 in L-76-C (Table 2). A breeding line L-6-B recorded the highest seed yield/plot (761.50 g), while the Check 2 recorded 385.50 g. Also, brown blotch severity varies from 2.0 in L-6-B, L-11-B, L-83-B, L-25, L-59, L-43-A and L-22B to 4.0 in Check 1 with coalescent spot on leaves, stem and pods and presence of ascervuli, but surviving plant. The AUDPC value was low (504) in L-22-B and 553 in LB- 59 compared to the check variety (1344.0) (Figures 1 and 2).

DISCUSSION

Differential response was found among the F_5 population for seed metric traits, brown blotch incidence and severity. The number of pods per plant and 100 seed weight showed substantial variation among the F_5 population. Two lines 'L-25' and 'L-59' with high 100 seed weights are promising compared with check. Insignificant mean squares found for number of pod per peduncle, seed yield per plot and seed yield per plant among the population demonstrated high seed yielding ability of the F_5 population. Also, the F_5 lines showed increased homozygosity for these traits due to continuing selfing through single descent method (Rahul *et al.*, 2018).

The brown blotch incidence and severity were statistically significant. This indicates differential response by the F_5 population to the pathogen (*C. capcisi*). The symptoms were maximum in Check 1, but all the plants survive till harvesting time. However, check 2 showed resistance while Check 1 was susceptible. As shown in Table 2, the incidence of brown blotch was low in the Check 2, followed by L-22-B and L-83-B while the severity peaked in Check 1. The brown blotch severity scale of 2.0 recorded in L-11-B, L-83-B,

L-25, L-59, L-43-A and L-22-B suggest transgressive segregation. The development and deployment of cowpea varieties that are high seed yielding and resistant to brown blotch disease is important for sustainable production in the rain forest agro ecology. The AUDPC for brown blotch (Figures 1, 2 and 3) showed the progress of the pathogen and is consistent with the severity and incidence scores. The breeding line 'L-25' (Figure 2) and 'L-83-B' (Figure 3) had mean values for pods/plant, weight of 100 seeds, and low brown blotch incidence and high plot yield are promising for commercialization in the rain forest agro ecology and specifically Ekiti state, Nigeria. However, four entries viz. L-83-B. L-72-C, L-59 and L-43-A had mean values greater than check 2. A little difference between PCV and GCV estimates for number of pods per plant and Brown blotch severity indicates less environmental sensitivity. Therefore, selection based on phenotype will be worthwhile for improvement. The foregoing is similar to previous report of Jakkeral *et al.* (2014) in groundnut. Broad sense heritability estimates were high for brown blotch severity (65.22%) and number of pods per plant (77.92%). High heritability estimates for number of pods/plant and brown blotch severity is consistent with high degree of correspondence and transmission of high pod number and brown blotch severity from generation to another. Also, the possibility of both additive and non-additive genes controlling inheritance of these traits. On the other hand, low heritability for brown blotch incidence and number of seeds/plant may be ascribed to non-additive gene (epistatic gene action) for these traits.

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Table 1: Mean squares for seed yield traits and disease incidence among F_5 cowpea generation evaluated

Source of variation	Df	Number of pod per plant	100 seed weight (gm)	Brown blotch incidence	Brown blotch severity
Lines	11	4250.00***	116.23**	273.92**	14.73**
Replication	3	53.15	19.06	165.75**	0.06
Error	33	843.39	121.19	296.25	5.19
Grand mean		43.23	15.90	16.96	2.25
σ^{2P}		115.77	5.4	12.96	0.46
σ^{2G}		90.21	1.73	3.98	0.30
σ^{2E}		25.56	3.67	8.98	0.16
PCV (%)		24.89	14.62	21.23	26.91
GCV (%)		21.97	8.27	11.76	21.74
Broad sense heritability (Hb %)		77.92	32.04	30.17	65.22

*significant at P < 0.05 level, **significant at P < 0.01 level, *** significant at P < 0.001 level.

Table 2. Mean separation for seed yield traits among cowpea F_5 generation evaluated for agronomic, seed yield and reaction to brown blotch disease

Lines code	Number of pod/plant	Seed yield per/plot (gm)	Seed Yield per plant (gm)	Brown blotch incidence	Brown blotch severity	Days to 50 % flowering	Days tc 50% mature pod	100 seed weight (gm)
Check 1	35d	705.30a	36.18a	20a	4a	48a	71a	15.25ab
L-61-B	50ab	711.50a	34.18a	19a	3bc	50a	72a	15.25ab
L-6-B	49abc	761.50a	33.36a	19ab	3bc	50a	72a	16.50ab
L-11-B	34d	625.50a	30.71a	19ab	2c	50a	71a	15.25ab
L-83-B	46abcd	684.00a	42.83a	15ab	2c	51a	71a	14.50ab
L-25	55a	684.00a	44.34a	17ab	2b	48a	70a	19.00a
L-72-C	43bcd	614.50a	31.66a	19ab	3bc	49a	72a	13.75b
L-59	22e	675.30a	40.42a	16ab	2b	48a	71a	18.75a
L-76-C	55b	710.50a	34.40a	19ab	3b	50a	70a	14.25ab
L-43-A	49abc	616.80a	40.02a	16ab	2b	49a	70a	15.75ab
L-22-B	37cd	522.50a	33.86a	14ab	2c	48a	70a	16.50ab
Check 2	44abcd	385.50a	38.25a	12b	3bc	49a	70a	16.00ab

[a] Values in columns followed by the same letter are not significantly different α (p = 0.05 by Tukey HSD

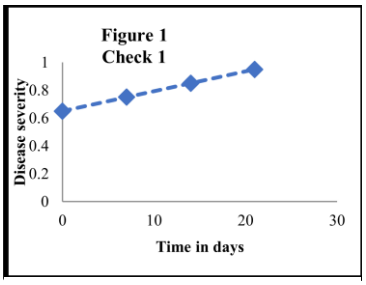

Figure 1. Disease progress curve showing the disease severity over observation period (time in days) for the Check

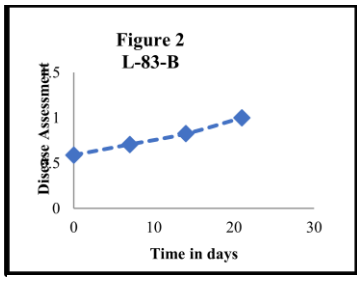

Figure 2. Disease progress curve showing the disease severity over observation period (time in days) for the L-

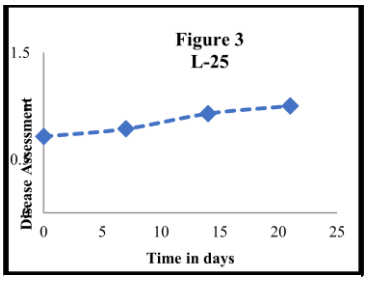

Figure 3. Disease progress curve showing the disease severity over observation period (time in days) for L-25

CHARACTER CORRELATION AND PRINCIPAL COMPONENT ANALYSES IN MAIZE (*Zea mays* L)

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ABSTRACT
A study was carried out at the Federal University of Agriculture Abeokuta (FUNAAB), Nigeria in 2017 to determine the character association among agronomic traits in maize and identify the traits accounting for variability among the tested genotypes. Mean, range and coefficient of variation were obtained for the studied trait and data also subjected to correlation and principal component analyses. Days to 50% silking and grain yield had the lowest and highest coefficient of variation, respectively. Correlation between traits showed significant ($p \leq 0.01$) and positive association of grain yield with plant height (0.65), ear diameter (0.78), ear length (0.68) and ear weight (0.98). Days to 50% silking had significant ($p \leq 0.01$) negative correlation with grain yield (-0.69), ear diameter (-0.68), ear weight (-0.67) and seed length (-0.61). It was also negatively correlated ($p \leq 0.05$) with ear length and seed width. Other characters also had positive and negative correlations *inter se*. Principal component analysis identified ear diameter, ear weight, days to 50% silking and plant height as traits with the highest contribution to the variation observed among the maize genotypes. Additional information on the influence of varied growth conditions on these relationships and the inheritance pattern of the traits are required.

Keywords: association, genotype, grain yield, maize

INTRODUCTION
Maize (*Zea mays* L.) is the most important cereal in sub-Saharan Africa (SSA), mainly used for human consumption and in livestock industry with a small percentage used in agro-allied industries ((DT Maize, 2014). Maize grows well in Nigeria, with its cultivation spanning the rain forest ecologies of the south to the savannah regions of the north. Despite an increased area of land which has been dedicated to cultivate maize since the mid - 2000s, production per hectare is rather low in West Africa when compared to global averages and thereby compelling nations to invest several millions of naira on maize importation (Badu-Apraku *et al*., 2013). Several biotic and abiotic factors including drought, stem borer attack, e.t.c. are responsible for the reported low yields (Banziger *et al*., 2000; Oloyede-Kamiyo *et al*., 2012). It then becomes imperative to explore the existing variability among local and exotic maize germplasm to enhance the chances of breeding desirable genotypes to meet local demands. An understanding of the character relations among important agronomic traits would reliably guide the breeders on traits to be targeted in the construction of efficient selection index for the development of superior genotypes (Denton and Nwangburuka, 2011; Olayiwola and Ariyo, 2015). Ajala *et al.* (2018) reported that grain yield had significant correlations with plant height, days to 50% silking, ear aspect and ears per plant under contrasting conditions. Begum *et al.* (2016) found that days to 50% silking had significant correlations with ear length, ear diameter and plant height. Kravić *et al.* (2016) opined that these associations could be explored for faster gain in maize breeding programs.

In the quest to understand the pattern of genetic variability within plant populations, breeders have employed Principal Component Analysis (PCA), a statistical tool that breaks total variation into components and thus identify traits that are responsible for the observed variation (Mounika *et al*., 2018). Kravic *et al.* (2016) observed that number of kernels per row, leaf width and grain yield chiefly accounted for differences among the forty-seven maize inbreds used in their study. Mounika *et al.* (2018) subject trait data of twenty-three maize genotypes to PCA and found that days to 50% silking, days to maturity, plant height, ear length, grain yield per plant and number of kernels per row were mostly responsible for the observed differences. As a consequence of development of different genotypes from various source populations, the possibility of different gene associations and

complexes in different genotypes cannot be ruled out. The aim of our study was to determine character association among agronomic traits in a collection of maize inbred lines and to identify the traits accounting for variability among the genotypes.

MATERIALS AND METHODS

The experiment was carried out at the Directorate of University Farms (DUFARMS) of Federal University of Agriculture, Abeokuta (FUNAAB), located on latitude 7°15'N and longitude 3°23'E in the transitory rain forest vegetation zone of southwestern Nigeria in 2017. Eight maize inbred lines derived from different source populations were obtained from DUFARMS based on documented performance. The experiment was laid out in randomized complete block design and was replicated three times. Each genotype was sown on 3 m long two-row plot at 0.75 m between rows and 0.25 m on the rows. The genotypes were sown at two seeds per hill but were thinned to one per hill two weeks after sowing. All standard best practices required for optimum performance were followed as necessary.

Data were collected on days to 50% silking, plant height (cm), ear diameter (cm), ear length (cm), ear weight (g), seed length, seed thickness (mm), seed width (mm), 1000-seed weight (g) and grain yield per plot (g). The data collected were averaged over replications to get the means and the standard error was obtained as the square root of mean variance. The range for each character was determined and the coefficient of variation (CV) was calculated. Furthermore, the data obtained was subjected to correlation and principal component analyses using SAS software version 9.1 (SAS Institute, 2000)

RESULTS AND DISCUSSION

The range of values, mean, standard error and coefficient of variation (CV) of the measured traits are shown in Table 1. Grain yield ranged from 102 g/plot to 576 g/plot with a mean value of 344.46 g/plot. The trait had the highest coefficient of variation of 49.76 while days to 50% silking had the lowest coefficient of variation (3.76) but ranged from 62.77 to 68.73 days with a mean of 66.49 days. The range of values and the coefficient of variation for the characters measured underscored the magnitude of variability within the population and offer opportunity for genetic enhancement. This is very apt for ear weight and grain yield, which incidentally are the major consideration in maize cultivation (Fajemisin, 2014).

The correlation coefficients among the measured characters are presented in Table 2. Grain yield had a positive and highest significant ($p \leq 0.01$) correlation with ear weight (0.98) followed by ear diameter (0.78), ear length (0.68), plant height (0.65), 1000-seed weight (0.54) and seed length (0.49) in that order. The trait had negative but highly significant ($p \leq 0.01$) correlation with days to 50% silking (-0.69). That grain yield was positively correlated with plant height, ear diameter, ear length, ear weight, 1000-seed weight and seed length, suggested that the traits could be targeted for the improvement of grain yield by indirect selection especially as the traits also had significant correlations *inter se* (Ajala *et al.*, 2018). This would particularly be beneficial to maize breeding because grain yield is usually associated with low heritability, hence difficult to improve *via* direct selection but benefits from the interplay among several agronomic traits (Begum *et al.*, 2016). However, it might be important to thread with caution when improving grain yield indirectly by selecting for plant height. Tall plants are likely to lodge or break after grain filling and could lead to commercial losses. There would be need to either peg the desired height or break the linkage between plant height and grain yield through recombination. Days to 50% silking also had a negative and significant correlation with ear diameter, ear length, ear weight and seed length. Notably, ear weight had a positive and significant correlation with all traits except with days to 50% silking where the correlation was negative (-0.67). The negative correlation between days to silking and grain yield offers hope for development of high yield and early maturing maize genotypes. A compromise in the selection scheme would increase the chance of availability of favorable alleles in this direction. Ear diameter had a significant and positive correlation with ear length, ear weight, 1000-seed weight and seed length. Ear length had a significant and positive correlation with ear weight and 1000-seed weight. 1000-seed weight had a positive significant correlation with seed length which also had negative and positive significant correlations with seed thickness and seed width, respectively.

The result of the principal component analysis (PCA) showed the pattern of character variation among the evaluated genotypes (Table 3) and identified the traits that contributed most to the variation within the population (Nwangburuka *et*

al., 2011; Osarawu *et al.*, 2013). The first four principal components (PC) accounted for 82% of the total variation in the study. The first PC which accounted for 53% of the total variation was loaded with ear diameter and ear weight suggesting that the traits could be targeted in maize improvement. PCs 2, 3 and 4 accounted 14%, 9% and 6%, respectively. Seed width, days to silking and plant height had the top loadings in PC 2 and could be valuable target for the improvement of populations that could be obtained from the evaluated inbred lines. Seed width and seed length had the highest loadings in axes 3 and 4, respectively. However, these two PCs combined explained less than 20% of the total variation captured by the four PCs, indicating that the two associated traits may not yield faster progress if they were targeted in the improvement of the maize genotypes.

Conclusion

The study revealed that there were some amounts of variability among the studied genotypes and this could be explored to improve grain yield by indirect selection through ear diameter, ear weight, days to silking and plant height. Furthermore, the potential of developing early maturing and high yielding genotypes manifested in the inverse relationship between the traits. However, additional information on the influence of varied growth conditions on the character relationships would be invaluable to success of maize breeding program. Similarly, an understanding of the inheritance pattern of the characters would be desirable.

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Table 1. Range, mean, standard error and coefficient of variation of the evaluated characters

Traits	Range	Mean	SE	CV
Grain yield(g/plot)	102 - 576	344.46	195	49.76
Days to 50% silking	62.77 - 68.73	66.49	2.25	3.76
Plant height (cm)	127.5 - 176.67	155.56	16.92	13.77
Ear diameter (cm)	11.8 - 13.27	12.44	1.11	10.1
Ear length (cm)	15.2 - 17.25	15.91	1.49	12.24
Ear weight (g)	190 - 869.33	513	259.8	45.53
1000-seed weight (g)	160 - 260	229.2	2.38	15.46
Seed length (mm)	9.15 - 10.31	9.68	0.39	5.42
Seed thickness (mm)	4.42 - 4.94	4.61	0.16	5.3
Seed width (mm)	8.28 - 9.05	8.57	0.21	4.43

Coefficient of variation (CV), Standard error (SE)

Table 2. Simple correlations among nine agronomic traits in maize

Traits	Days to silking	Plant height	Ear diameter	Ear length	Ear weight	1000-seed weight	Seed length	Seed thickness	Seed width
Grain yield	-0.69**	0.65**	0.78**	0.68**	0.98**	0.54**	0.49*	-0.3	0.15
Days to silking		-0.24	-0.68**	-0.42*	-0.67**	-0.34	-0.61**	0.39	-0.43*
Plant height			0.66**	0.65**	0.66**	0.77**	0.28	-0.34	-0.08
Ear diameter				0.84**	0.80**	0.65**	0.66**	-0.38	0.14
Ear length					0.70**	0.48*	0.34	-0.27	-0.13
Ear weight						0.57**	0.50*	-0.34	0.15
1000-seed weight							0.41*	-0.27	0.27
Seed length								-0.64**	0.41*
Seed thickness									-0.18

*, **: significant at $p \leq 0.05$ and $p \leq 0.01$, respectively

Table 3. Character loading, eigen value, proportion of variance explained and cumulative variance obtained from principal component analysis

Traits	PC 1	PC 2	PC 3	PC 4
Grain yield	0.27	-0.07	0.03	-0.31
Days to silking	-0.22	0.38	0.07	0.06
Plant height	0.24	0.26	0.21	-0.03
Ear diameter	0.29	-0.02	-0.11	0.14
Ear length	0.26	0.17	-0.2	0.06
Ear weight	0.28	-0.06	0.05	-0.27
1000-seed weight	0.22	0.04	0.27	0.09
Seed length	0.19	-0.26	0.03	0.42
Seed thickness	-0.13	0.15	-0.05	-0.39
Seed width	0.04	-0.42	0.39	0.07
Eigenvalue	10.62	2.73	1.75	1.3
Cum variance	0.53	0.67	0.75	0.82
Total variance (%)	53	14	9	6

ASSESSING THE SUITABILITY OF STRIGA RESISTANCE IN WILD MILLET *MONODII* FOR HYBRID DEVELOPMENT USING COMBINING ABILITY

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ABSTRACT
Five pearl millet genotypes were crossed to four testers (wild millet) in a line × tester mating design in 2021/2022 dry season. The resulting 20 crosses, 9 parents and a check were evaluated in two trials during the 2022 rainy season. The general and specific combining ability variances were determined among the entries. Days to 50% flowering, plant height, number of panicles/plot, grain yield, Striga count and downy mildew incidence were the characters evaluated. Significant differences were observed in the combining ability analysis of variance in all the characters. Results revealed that additive and non-additive genetic effects were important in controlling most of the agronomic characters with more preponderance of non-additive effects. The PS202 and Ex-Monguno and the cultivars SOSAT-C88 and PEO5684 have been identified as good general combiners for grain yield at harvest and downy mildew incidence with appreciable resistance to *S. hermonthica*. The hybrid SOSAT-C88 x Ex-Monguno, PEO5684 x Ex-Monguno, Zango x PS202 and LCIC9702 x PS202 have been identified as specific combiners for days to 50% flowering, plant height, grain yield, *Striga* count and downy mildew incidence. Therefore, there is great potential for producing economically profitable hybrid pearl millet. PS202 and Ex-Gubio could be utilized in breeding programmes to improve pearl millet with the required characteristics. However, LCIC9702 is a genotype with greater performance in most agronomic characters and could be used in commercial cultivation. The preponderance of non-additive genetic effects, observed among the characters in the parents, crosses, and the check studied, would be a great asset in a breeding programme and require further testing.

Keywords: Pearl millet, Wild millet, Line x Tester, Combining ability, Genetic effects

INTRODUCTION
Pearl millet (*Pennisetum glaucum* L. R. Br.) is a staple food and source of feed, fodder and fuel (Gupta *et al*., 2022). Pearl millet improvement programme in Africa and Asia are concerned with high grain yields because of the high genotypic variability that exists among the landraces both from the secondary and tertiary germplasm (Singh and Nara, 2023). One of the most important constraints to pearl millet production is *Striga* infestation (Rouamba *et al.,* 2022). Estimated yield losses have been put to 10-95% depending on the varietal reaction, ecology and cultural practices (Wilson *et al.,* 2004). Conventional herbicides are prohibitive in cost and ineffective since the damage is done before *Striga* emerges from the soil, and also a source of pollution of the environment, disturbance of ecological balance, and toxicity to humans and their high cost increases the cost of production. Using nitrogenous fertilizers, irrigation and herbicides is beyond the means of poor resource farmers. Hand hoeing or hand pulling *Striga* is time-consuming, very tedious and ineffective. However, one of the most promising approaches to controlling *Striga* is using resistant crop varieties which reduces labour demand, since weeding to control *Striga* seeds will not be necessary (Wilson *et al.,* 2004). However knowledge about the breeding materials with respect to their general or specific combining ability variances and effects of parents and hybrids needed to be exploited to design practical strategy.

MATERIALS AND METHODS
Nursery experiment was conducted for the initial breeding population in a line by tester mating design. The resulting $20F_1$, 9 parents and a check were evaluated under *Striga* hot spots and infestation increased as per Badu-Akpraku *et al.*

(2012) at Maiduguri (11°6' N; 13°17' E, 354 msl) and Benisheikh (11°48'N; 12°29'E, 200-500 msl), 2022 rainy season. The design was randomized complete block design and replicated 3 times at each location. Data were collected on, Days to 50% flowering, Plant height (cm), Number of panicles/plot, *Striga* count, and Grain yield (kg/ha).

Statistical analyses

Data were analysed using R Statistical software using descriptive statistics and analysis of variance at p=0.05.

RESULTS AND DISCUSSION

Days to 50% flowering and the number of panicles/plant were controlled by additive gene actions (Table 1). The significant mean squares for GCA and SCA for most of the traits studied showed the importance of additive and non-additive genes in the inheritance of these traits. The combined result was slightly different from the individual locations in which most of the characters were controlled by non-additive gene action except *Striga* count and downy mildew incidence which were controlled by additive gene actions. It is then apparent that the non-additive genetic effect was more important than the additive genetic effect as most ratios were less than unity. These results agree with Roumba *et al.* (2022) and Alimatu *et al.* (2022) who worked on millet and maize respectively. These results showed that parental lines would be utilized to develop millet hybrids.

The proportional contribution to total variance indicated that line x tester interaction (SCA) was higher than lines and testers in almost all the analysis at the combine combined locations. The tester PS202 exhibited superior GCA effects for most characters studied (Table 2). Similarly, Ex-Monguno showed a better GCA effect for *Striga* count, and grain yield showed that this parent in a cross combination could produce heterotic segregates for these characters. The hybrids SOSAT-C88 x Ex-Monguno, PEO 5684 x Ex-Monguno, Zango x PS202 and LCIC 9702 x PS202 are good hybrids when breeding for striga resistance and grain yield. Furthermore, the hybrids Zango × PS202, LCIC 9702 × PS202, SOSAT-C88 × Ex-Monguno, and Zango × Ex-Gubio are good specific combiners for earliness and high grain yield (Table 3). These hybrids probably have potential as parents of hybrid varieties, as well as for inclusion in breeding programmes, since they may contribute superior alleles in new populations for high grain yield (Bello *et al.*, 2005) and other biotic stresses in pearl millet production, especially in the Sahel and Sudan savannah zone.

Conclusion

Genetic variability existed among the pearl millet population evaluated. PS202, Ex-Gubio, and Zango were genotypes that performed better in most agronomic characters studied. Though PS202 and Ex-Gubio showed great performance, they are not commercially acceptable mainly due to their tiny seeds and stem. However, Zango is a good genotype farmers can rely on for commercial cultivation. Furthermore, this study has identified SOSAT-C88 x Ex-Monguno, PEO5684 x Ex-Baga, LCIC9702 x PS202, SOSAT-C88 x PS202, LCIC9702 x Ex-Monguno, Ex-Borno x Ex-Monguno, Ex-Borno x Baga, LCIC9702 x Ex-Gubio and Ex-Borno x Ex-Gubio as desirable segregates to be used for the development of agronomically acceptable pearl millet.

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Table 1: Analysis of variance for combining ability, genetic variance and proportional contribution to total variance among the measured traits at Maiduguri and Benisheikh, 2022

Source of variation	DF	DFF	PLH	NPP	GYD	SCH	DMI
Replication	5	0.89	9584.2**	935.75*	146560.89	577.43	104.09
Line (GCA)	4	7.03	4490.63	778.90	533527.05	1600.9	543.58
Tester (GCA)	3	358.86**	7687.16	14363.81**	814986.80	7839.4	1475.71
Line x Tester (SCA)	12	15.56	3757.2**	713.11**	414752.9**	2398.0**	536.35**
Error	145	7.49	1179.32	194.67	75597.26	370.52	87.68
Cov. H. S. Lines		-0.56	48.90	4.39	7918.27	-53.14	0.48
Cov. H.S. Testers		28.61	327.50	1137.56	33352.82	453.45	78.28
Cov. F. S.		37.82	1349.92	1612.09	167712.91	1162.1	248.92
δ^2 GCA		33.12	440.43	1346.86	48104.64	10813.3	2392.76
δ^2 SCA		43.05	13748.68	2764.99	1808830.39	476.17	92.89
Ratio GCA/SCA		0.77	0.03	0.49	0.027	22.71	25.76
Lines		9.12	16.68	5.69	22.33	10.91	16.68
Testers		40.73	33.96	78.69	25.59	40.07	33.96
Lines x Testers		14.46	52.36	15.63	52.08	49.02	49.37
GCA (Line x Tester)		49.85	50.64	84.38	47.92	50.98	50.64
GCA/SCA		0.99	1.03	5.40	0.92	1.04	1.03

*, and *** indicate 0.05 and 0.001 level of significance and DF- Degree of freedom, DFF= Days to 50% flowering, PLH= Plant height, NPP= Number panicles per plant, GYD= Grain yield, SCH= Striga count, DMI= Downey mildew incidence

GENETIC ANALYSIS OF SOME QUANTITATIVE TRAITS IN SIX GENERATIONS OF PRO-VITAMIN A MAIZE (*Zea mays* L.)

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ABSTRACT
Five parental lines SUWAN-1-SR (P_1) and DMR-ESR (P_2) males; ILE-1-OB (P_3), DMR-SR-W (P_4) and ART98/SW6-OB (P_5) females were used to produce F_1, F_2, BC_1 and BC_2. All the 6 generations were evaluated at the Federal University of Agriculture, Abeokuta in 2019 to determine gene actions and to identify promising hybrids for improving Pro-Vitamin A maize. The experiment was laid out in a randomized complete block in three replicates. Data collected were subjected to analysis of variance, test of significance and combining ability analyses. The parents and their crosses were significantly different. High grain yield (5.87 t/ha) was produced in the cross between P_3 (4.05 t/ha) and P_5 (3.34 t/ha). The variance of GCA was higher than SCA for the characters except plant height, leaf area, field weight and ear height, indicating the pre-dominance effect of additive gene over the dominant gene in controlling the expression of these characters. The 6-parameter model of the Generation Mean Analysis revealed significant effects of additive gene and interaction of additive × dominance gene on grain yield. This suggested the influence of favorable alleles for grain yield improvement.

Keywords: additive, dominance, GCA, SCA, Variability and Pro-Vitamin A maize

INTRODUCTION
Maize (*Zea mays* L.) ranks third most important cereal crop after rice and wheat. The maize grain is a major feed for man and livestock diets where it is used as a source of energy (Heuzé *et al.,* 2017). With pro vitamin A maize, several million people particularly in the developing countries, derive their protein and calorie requirements from maize. Choice of parents in a breeding programme is important. (Khodambashi *et al.*, 2012). Quantitative characters in crop plants are often controlled by many genes; therefore, the inheritance of these characters mostly depends on the gene action and their interaction as well as environmental effects.

The additive genetic variance, VA, is of particular importance because it defines the level of narrow sense heritability (h2), which in turn determines the fraction of the total variance of a quantitative trait that is transmissible from generation to generation (Lush, 1943). Generation mean analysis belongs to the quantitative biometric methods and it is a useful technique for estimating main gene effects (additive and dominance) and their interactions (additive × additive, additive × dominance and dominance × dominance) responsible for the inheritance of quantitative traits. The estimation of these genetic effects can help the plant breeder to decide the breeding procedures appropriate for the improvement of quantitative traits. The objectives of this study were 1) to estimate gene action and 2) to study the gene interaction effect that control quantitative traits in PVA maize.

MATERIALS AND METHODS
The experiment was carried out at the Teaching and Research Farms, Federal University of Agriculture, Abeokuta (7°15'N and Longitude 3°25'E), Ogun State during the cropping season of 2018 and 2019 with five Parental lines of maize (SUWAN-1-SR, DMR-ESR, ILE-1-OB, DMR-SR, ART98/SW6-OB). Crosses were made to generate the F_1 and Back-cross generations, F_{1s} was selfed to produce the F_2 generations after which all the 6 generations including parents were laid in randomized complete block design with three replications for evaluation. Each row was 4 m long. Two seeds were planted per hole to make a population of 20 plant stands per line for each of the generations. The Inter-row and intra-row spacing was 60 cm × 40 cm, respectively. A pest was controlled with the use of Cypermethrin at 1.5 liters per hectare at vegetative, flowering stages and also, weeding was done manually at appropriate time.

Data collected as seen in Table 1 were subjected to Analysis of Variance (ANOVA) to test significant differences among the characters evaluated using SAS Version (9.4). Means

separation was done using Duncan's Multiple Range Test at 5% probability level.

RESULTS AND DISCUSSION

Analysis of variance for quantitative traits in fifteen genotypes of maize is presented in (Table 1). Genotypic effect was highly significant for all the characters evaluated in this study. Thus, the magnitude of variability existing among the genotypes aid selection of good parents for good hybrid combinations (Bhanu *et al.,* 2017).

Mean performance of parents and the F_1s progenies for characters evaluated in maize is presented in (Table 2). There was significant difference among the parental lines and the crosses for days to 50% tasseling. P_2 had the highest value (53.70) days to 50% tasseling while P_1 had (47.70) days to 50% tasseling. Hybrids derived from cross P_2 x P_3 had the highest values of days to 50% tasseling of 52.53 days and this make it to tassel late while hybrid derived from P_3 x P_4 with the value of (47.07) days to 50% tasseling performed best in this regard. Mean values of days to silking for parental lines ranged from (52.57) days for P_1 to (59.32) days for P_2 while crosses recorded values ranged from (51.80) days for P_3 x P_4 to (60.07) days for P_2 x P_5. Thus, hybrid P_3 x P_4 with 51.80 days to silking exhibited earliness to silking. These hybrid combinations revealed possibilities of obtaining good parent for hybrid combinations.

Mean squares of general combining ability (GCA) and specific combining ability (SCA) for some quantitative traits in Pro-vitamin A maize are presented in Table 3. Genotypic effect was significant at $p < 0.01$ for all the characters studied for both GCA and SCA (except leaf width and leaf area). General combining ability effects of five maize genotypes evaluated for some quantitative traits are presented in Table 4. The estimates of GCA effects varied significantly among the five parents. Days to tasseling varied from (-1.10) for P_1 (SUWAN-1-SR) to (1.21) for P_2 (DMR-ESR). However, P_2 (DMR-ESR) and P5 (ART/SW6-OB) registered significant positive GCA effect 1.21 and 0.55, respectively for days to tasseling while P_1 (SUWAN-1-SR) and P_4 (DMR-SR-W) had negative significant GCA effects. The results of the present study revealed that P_3 is the best general combiner for grain yield and most other key agronomic characters, which implies that it is able to transmit its favorable alleles to its progenies. Also, P_2 has desirable GCA effect for grain yield, 1000-seed weight, ear height, and some other important agronomic characters. Only P_3 x P_5, P_2 x P_5 and P_1 x P_2 had desirable specific combining ability effects for grain yield. Late 50% tasselling was recorded in hybrids derived from crosses P_2 x P_3 while P_3 x P_4 performed best for days to 50% tasseling. Thus early maturity. Similar result was published by Fasahat *et al*., 2016.

Conclusion

There was appreciable variability among the Pro-Vitamin A maize study. The GCA and SCA were significant for all the characters measured except leaf width and leaf area. There was pre-dominance effect of additive gene over the dominant gene in controlling the expression of all the characters studied. The 6-parameter model of the Generation Mean Analysis revealed significant effects of additive gene and interaction of additive × dominance gene on grain yield. Hybrid P_3 x P_4 is outstanding, any combination with P_3 and P_4 as parent was high yielding

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Table 1: Mean squares for general and specific combining ability for some quantitative traits in maize

Source of variation	Block (df = 2)	Genotype (df = 14)	GCA (df = 4)	SCA (df = 10)	Error (df = 28)
Days to tasseling	1.77	10.56**	22.53**	5.77**	1.86
Days to silking	2.35	17.91**	22.53**	5.77**	1.67
Plant height (cm)	71.29*	1012.89**	3000.83**	217.71**	17.60
Leaf length (cm)	0.20**	1.33**	3.72**	0.37**	0.04
Leaf width (cm)	0.00	0.02**	0.04**	-	-
Leaf area (cm^2)	0.49	2.85**	8.33**	0.66	0.43
Stem girth (mm)	0.34	9.31**	25.35**	2.90**	0.40
Number of ears/plant	0.00	0.05**	0.09**	0.04**	0.01
Cob length (cm)	3.86*	7.44**	7.20**	7.53**	1.07
Number of seeds/row	12.02	14.39**	29.38**	8.40**	1.84
Number of rows/cob	0.10	0.95**	1.95**	0.55**	0.11
Field weight (g)	11.97	1564.63**	4615.62**	344.24**	63.15
Ear height (cm)	25.77	753.96**	2252.90**	154.43**	11.82
1000-seed weight (g)	95.06	4527.28**	12915.66**	1171.92**	176.87
Seed weight (g)	80.19*	860.31**	1956.67**	421.77**	23.56

GCA – General combining ability, SCA – Specific combining ability

Table 2. Mean performance for growth and ear characters evaluated in 5 maize parental lines and their F_1 hybrids

Hybrid	Days to tasseling	Days to silking	Plant height	Leaf length	Leaf width	Leaf area	Stem girth	Number of ears/
P_1 x P_2	48.07ef	53.13ef	175.40cd	8.18de	0.94a	7.66bcd	15.15c	1.47a
P_1 x P_3	51.33abc	55.67cd	190.27b	9.04c	0.90ab	8.12abc	16.46b	1.20bc
P_1 x P_4	48.80c-f	54.00def	162.93e	7.99e	0.79b-e	6.29e	15.33c	1.00e
P_1 x P_5	50.67b-d	55.07cde	154.73f	8.23de	0.83a-e	6.86de	14.89cd	1.00e
P_2 x P_3	52.53ab	58.60ab	207.42a	9.43b	0.86a-d	8.10a-d	13.95def	1.20bc
P_2 x P_4	50.40b-e	56.93bc	197.81b	9.72ab	0.89abc	8.70ab	13.40ef	1.07cde
P_2 x P_5	51.87ab	60.07a	194.20b	8.95c	0.87a-d	7.78bcd	13.79def	1.07cde
P_3 x P_4	47.07f	51.80f	180.63c	8.99c	0.78cde	7.01cde	16.66b	1.13b-e
P_3 x P_5	51.20a-d	56.20cd	196.29b	9.61ab	0.75de	7.25cde	18.07a	1.27b
P_4 x P_5	50.53b-e	55.73cd	168.09de	8.45d	0.76de	6.40e	14.63cd	1.00e
P_1	47.70f	52.57f	165.43e	8.03e	0.86a-d	6.95cde	14.19cde	1.05de
P_2	53.70a	59.32a	196.93b	9.81a	0.93a	9.16a	13.27ef	1.18bcd
P_3	51.23a-d	56.25cd	205.92a	9.71ab	0.89ab	8.75ab	18.94a	1.22b
P_4	48.65def	53.23ef	168.18de	8.34de	0.73e	6.12e	12.95f	1.02e
P_5	50.68b-d	55.38cde	153.48f	8.51d	0.75de	6.42e	14.29cde	1.00e

P_1 = SUWAN- ISR P_2= DMR-ESR-Y P_3= ILE-10B-W P_4= DMR-SR-W P_5= ART/SW6-OB-W

Table 2. Contd.

Hybrid	Cob length	Number of seeds	Number of rows/cob	Field weight	Ear height	1000-seed weight	Grain yield
P_1 x P_2	18.72ef	31.40a	14.27a	104.73d-g	86.49b	313.93a	95.34bcd
P_1 x P_3	14.52	26.33cd	13.07b	100.47fg	100.87a	283.13b-e	98.33bc
P_1 x P_4	14.6	23.40e	12.13def	114.47c-f	68.00e	211.07fg	72.53fg
P_1 x P_5	14.79	28.87abc	12.73b-d	79.47h	56.00f	233.07f	65.11gh
P_2 x P_3	14.41	30.00ab	12.80bc	104.00efg	106.11a	283.13b-e	86.60de
P_2 x P_4	14.15	28.27bc	12.73b-d	119.07bcd	78.37c	278.33cde	89.93cd
P_2 x P_5	14.02	28.60bc	12.73b-d	91.53gh	77.93cd	265.33e	90.12cd
P_3 x P_4	14.67	28.20bc	12.47b-f	156.50a	75.35cd	273.00de	99.33b
P_3 x P_5	15.51	29.20ab	12.67b-e	123.33bc	87.16b	295.47a-d	120.87a
P_4 x P_5	14.63	28.87abc	12.07ef	115.74cde	68.76e	216.47fg	78.98ef
P_1	13.46	25.22de	12.47b-f	86.15h	72.10de	262.90e	78.82ef
P_2	14.3	28.92abc	13.05b	103.23efg	84.95b	305.28ab	94.92bcd
P_3	18.53	30.17ab	12.62b-e	145.69a	105.02a	302.05abc	117.75a
P_4	13.49	24.70de	11.85f	130.92b	66.48e	194.03g	75.00f
P_5	14.45	28.32bc	12.28c-f	77.24h	56.70f	212.85fg	63.34h

P_1 = SUWAN- ISR P_2= DMR-ESR-Y P_3= ILE-10B-W P_4= DMR-SR-W P_5= ART/SW6-OB-W

Table 3. General combining ability effects of five maize genotypes evaluated for some quantitative traits

Character	SUWAN-1-SR	DMR-ESR	ILE-1-OB	DMR-SR-W	ART/98/SW6-OB
Days to tasseling	-1.07**	1.21**	0.40	-1.10**	0.55*
Days to silking	-1.51**	1.97**	0.17	-1.24**	0.61*
Plant height	-10.41**	11.66**	14.19**	-5.89**	-9.55**
Leaf length	-0.53**	0.39**	0.47**	-0.20**	-0.13**
Leaf width	0.02	0.06**	0.01	-0.05**	-0.04**
Leaf area	-0.26	0.85**	0.48**	-0.57**	-0.50**
Stem girth	-0.03	-1.08**	1.80**	-0.64**	-0.06
Number of ears	0.00	0.06**	0.07**	-0.07**	-0.06**
Cob length	-0.02	0.03	0.92**	-0.67**	-0.26
Number of seeds	-1.11**	1.13**	0.84**	-1.44**	0.57*
Number of rows	0.17*	0.38**	0.04	-0.41**	-0.17*
Field weight	-12.80**	-5.03**	16.38**	15.23**	-13.78**
Grain weight	-5.98**	3.01**	15.69**	-5.72**	-7.00**
1000-Seed weight	-0.72	25.61**	23.83**	-29.30**	-19.43**
Ear height	-2.94**	6.10**	14.78**	-7.53**	-10.41**

*-Significant at 5% probability levels; **-Significant at 1% probability levels

Table 4. Specific combining ability effects of Pro-vitamin A maize crosses evaluated for some quantitative traits

Character	$P_1 \times P_2$	$P_1 \times P_3$	$P_1 \times P_4$	$P_1 \times P_5$	$P_2 \times P_3$	$P_2 \times P_4$	$P_2 \times P_5$	$P_3 \times P_4$	$P_3 \times P_5$	$P_4 \times P_5$
Days to tasseling	-2.37**	1.71*	0.67	0.44	0.62	-0.01	0.78	-2.54**	0.08	1.33
Days to silking	-2.92**	1.41*	1.15	0.37	0.86	0.60	1.67*	-2.73**	0.14	0.87
Plant height	-7.03**	5.30*	-1.94	-1.41	0.39	10.86**	3.34	-8.85**	6.81**	1.14
Leaf length	-0.55**	0.23*	-0.15	0.25*	-0.29**	0.66**	0.01	-0.15	0.31**	-0.22*
Leaf width	0.02	0.03	-0.02	-0.01	-0.04	0.05	-0.00	-0.02	-0.01	0.00
Leaf area	-0.37	0.46	-0.32	0.21	-0.67	0.99**	0.02	-0.34	0.19	-0.15
Stem girth	1.19**	-0.38	0.93**	-0.91**	-1.84**	0.05	0.23	0.42	1.52**	-0.57
Number of ears	0.28**	0.00	-0.05	-0.15**	-0.05	-0.04	-0.12**	0.01	0.08*	0.05
Cob length	3.76**	-1.33*	0.34	-1.32*	-1.49**	-1.16	-1.40*	-0.54	1.63**	0.49
Number of seeds	3.35**	-1.43*	-2.09**	0.77	-0.00	0.54	-2.51**	0.76	0.21	1.24
Number of row	1.06**	0.20	-0.28	-0.45*	-0.28	0.10	-0.51**	0.18	0.20	-0.00
Field weight	12.39**	-13.28**	1.87	-2.55	-17.52**	-1.29	3.30	14.72**	13.32**	-5.59
Grain weight	9.85**	0.15	-4.24	-8.07**	-20.56**	4.18	6.10*	0.89	21.62**	1.20
1000-Seed	27.04**	-1.98	-20.92**	-6.46	-28.31**	20.02**	-10.80	16.46*	21.45**	-6.19
Ear height	3.97*	9.68**	-0.89	-11.39**	5.89**	0.45	-3.71*	-11.26**	-0.44	9.52**

*-Significant at 5% probability levels; **-Significant at 1% probability levels, P_1 = SUWAN- ISR P_2= DMR-ESR-Y P_3= ILE-10B-W P_4= DMR-SR-W P_5= ART/SW6-OB-W

EVALUATION OF GAMMA-RAY INDUCED MUTANT LINES OF SESAME (*Sesamum indicum* L.) FOR PHYSICOCHEMICAL PARAMETERS OF THE SEED-OIL

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ABSTRACT

The physicochemical properties of sesame oil determine its application and also form the criteria for genetic improvement of the crop. Most of the released sesame varieties in Nigeria do not consider oil properties of the seed and where it is only oil quantity is used. This study was conducted to evaluate the physicochemical parameters of gamma-ray induced mutant M_5 lines of sesame seed oil. The physicochemical parameters determined include the refractive index, free fatty acid, ester, glycerine, viscosity, iodine, peroxide, saponification, unsaponification and acid values. The results revealed M_5 mutant lines displayed significant disparity in some of the parameters measured. The highest values in viscosity (10.00, 10.00), Saponification (219.49), Acid (3.14), ester (217.55) were from NCRIBEN-03L, 03L-250-G_{1-1}; 01M-350-G_{1-2}, 01M-350-G_{2-2-2} and 01M-350-G_{1-2} (217.55) respectively, while the least values for the respective parameters were from 03L-450-G_{2-2} (4.00); 04E-550-G_{1-3} (172.43); 04E-550-G_{2-3} (0.4) and 04E-550-G_{1-3} (171.92). The study deduced that gamma-ray irradiation could be used as a tool for the improvement of seed oils. Oils from mutants (NCRIBEN-03L, 03L-250-G_{1-1}; 01M-350-G_{1-2}, 01M-350-G_{2-2-2} and 01M-350-G_{1-2}) have the potential to be used for cosmetic industry and Mutants (03L-450-$G_{2-2;}$ 04E-550-G_{2-3}) for domestic and confectionery applications.

Keywords: cold-press, extraction, hexane solvent, oil seed

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INTRODUCTION

Sesame (*Sesamum indicum* L.) belongs to the family Pedaliaceae and is widespread in tropical and subtropical regions of Asia, Africa and South America. In Nigeria, sesame is locally called by different names; 'Ridi' in Hausa, 'Esso' in Nupe, 'Eeku' in Yoruba and 'Ekuku' in Igbo (Muhammad, 2018). Sesame seeds contain nearly 44% – 57% oil, 18% – 25% protein and 13% - 14% carbohydrates (Borchani *et al.,* 2010). According to Hegde (2012), sesame seed contains 37%–63% oil depending on the variety, growing season and cultivar. The most prominent feature of Sesame oil is its resistance towards oxidation rancidity during long exposure to air (Islam *et al.,* 2016). Islam *et al.* (2016); Mujtaba *et al.* (2020), reported that Sesame is the most valued and oldest oilseed crop due to its high-quality seed oil. Sesame is utilized for the treatment of anaemia, amenorrhea, respiratory infections, cholera, scorpion bites, dysmenorrhea, tinnitus, diarrhoea, dizziness, memory enhancement and bleeding piles (Khan *et al.,* 2014; Kapoor, 2017). Hegde (2012), opined sesame oil is used to treat coughs, burns, migraines, snake bites, tuberculosis, hair loss, eye diseases and demulcent in addition to being used as an antitussive. Low quality sesame oil is also used to produce soap, paints and lubricants (Anilakumar *et al.,* 2010).

Sesame is considered as a major source for solving the problem of deficiency of micronutrients deficiencies in modern day nutrition (Aglave, 2018). Most of the released sesame varieties in Nigeria do not consider oil properties of the seed and where it is only oil quantity is used. The aim of this study is to evaluate the physicochemical parameter of gamma induced mutant M_5 lines of sesame.

MATERIALS AND METHODS

The Gamma-irradiated mutant genotypes of Sesame used for the experiment were obtained from the stored gamma-irradiated mutant lines of M_5 generation in the department of Plant Biology Federal University of Technology Minna Niger state, Nigeria. A total of 14 entries (11 mutants and 3 checks) were raised in a Randomized complete block design (RCBD) with three replicates. Each plot size of 3x3M^2 was used, with planting space of 20 x 20 cm. After the

harvest, the sesame oil was extracted using cold-press and hexane solvent as described by Kate *et al.* (2014) with little modifications. The physicochemical properties as the refractive index, Acid value, Free fatty acid, Iodine value, Peroxide value, Saponification value, Unsaponification value, Ester, Glycerine, Viscosity was determined by reported methods described by Olaleye *et al.* (2018) and (United State pharmacopeial convention, 2015).

Statistical analyses

The data was subjected to Randomized Complete Block Design analysis of variance (ANOVA) at P=0.05 using Statistical Tool for Agricultural Research (STAR) by International Rice Research Institute (IRRI) 2013 - 2020.

RESULTS AND DISCUSSION

The results from this study revealed significant changes ($p < 0.05$) in the physicochemical parameters of the oil. However, there was no significant difference in the refractive index and unsaponification value (Table 1). Similarly, no significant change was recorded in the iodine value except in check-3 NCRIBEN-03L (15.62) had the highest value. The highest acid value (3.14), free fatty acid
(1.57) (Table 2).

The refractive index obtained (1.46-1.49) could be corroborated with Olaleye *et al.* (2018), who reported (1.47) in sesame samples. Aniołowska *et al.* (2016), opined that the high refractive index of oil is due to the presence of long-chain fatty acids. The refractive index is in agreement with the acceptable range (1.465-1.469) International Codex standard (2005). The acid value (0.40-3.14) recorded is slightly higher than the findings of Zahran *et al.* (2020), who obtained ranged (0.28 - 0.37) in sesame. Ogbonna and Ukaan, (2013) recorded the range of iodine value of (76.14-130.07). The acid value for 04E-550-$G_{1-3.}$ (0.51) 04E-550-G_{2-3} (0.40) is within the permissible level (0.6 mgKOH/g) for all edible oils recommended by FAO/WHO. However, other mutants were above the recommended value. The saponification values (172.43-219.49) recorded is similar to findings of Olaleye *et al.* (2018), who reported (212.45-214.53) in sesame. Warra, (2011) reported 189 saponification value for sesame seed oil. Saeed and Shola (2015), obtained slightly higher saponification (229.545 mgKOH/g) for sesame oil. The current findings are slightly above the range (186-195 mg KOH/g) of the Codex Standard (2005). According to Tunde-Akintunde *et al.* (2012), the high saponification value suggests the use of the oil in production of liquid soap, shampoos and lather shaving creams. The peroxide value range (0.55 – 3.10) observed in this study is consistent with Zahran *et al.* (2020) who reported (1.01- 2.87 meg/kg) in sesame. The peroxide value in the different treatments was less than the acceptable level (5 meq/kg) for oils according to the FAO/WHO (2009). The iodine value (11.48-15.62) is lower than the values (100-103 g) reported by Warra, (2011), Olaleye *et al.* (2018) (83.73- 92.38 g) in sesame. The iodine value is within FAO/WHO recommended iodine value (50–55/gram). The free fatty acid observed in this study (0.20- 1.57) lower than that previously reported in M_4 lines of these mutants but falls within the acceptable limits (Codex, 2001). Free fatty acid is a vital parameter that confirms the stability of oil. High level of free fatty acid indicates poor quality of oil as it gives a bad taste (Dayrit *et al.*, 2007). The presence of unsaponifiable matter directly affected the oxidative stability of vegetable oils (Abou-Gharbia et al., 2000). The observed unsaponification value (1.31 -1.67) is in line with the findings of Zahran *et al.* (2020) reported 0.92- 1.65 for five sesame genotypes. The Viscosity value recorded (4-10) was higher than the report of Mazaheri *et al.* (2019) who obtained (5.50–7.95) for black seed oil.

Conclusion

The variations in some physicochemical parameter of sesame oil of the mutants, implied gamma ray is capable of inducing changes in the physicochemical properties of sesame oil. The variations have also placed oils from some mutants to more suitable in sector than the other.

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Table 1. Physicochemical parameters of the seed-oil

Mutants	SV	USV	Ester	Glycerin
04E-550-G1-3	172.43 ± 0.21a	1.31 ± 0.00a	171.92 ± 0.21a	9.39 ± 0.01a
04E-550-G2-3	183.72 ± 0.28b	1.39 ± 0.00b	183.32 ± 0.29d	9.69 ± 0.31ab
04E-550-G3-3	188.63 ± 0.70c	1.43 ± 0.00c	187.84 ± 0.68e	10.13 ± 0.09abcd
NCRIBEN-04E	183.58 ± 0.14b	1.39 ± 0.00b	182.13 ± 0.13cd	9.88 ± 0.08abc
01M-350-G1-2	219.49 ± 0.70g	1.67 ± 0.01g	217.55 ± 0.70i	11.58 ± 0.34e
01M-350-G1-2-1	188.77 ± 0.56c	1.43 ± 0.00c	187.95 ± 0.56e	10.47 ± 0.23abcd
01M-350-G2-2	208.97 ± 1.40f	1.58 ± 0.01f	207.10 ± 1.41h	10.85 ± 0.55cde
01M-350-G2-2-2	199.01 ± 0.14e	1.51 ± 0.00e	195.87 ± 0.14g	10.51 ± 0.21bcd
NCRIBEN-01M	180.43 ± 0.21b	1.37 ± 0.00b	179.05 ± 0.20bc	10.12 ± 0.35abcd
03L-250-G1-1	176.01 ± 3.50a	1.33 ± 0.02a	175.15 ± 3.50ab	10.20 ± 0.44abcd
03L-250-G1-1-1	196.56 ± 0.21de	1.49 ±0.00de	194.78 ± 0.20fg	10.30 ± 0.35abcd
03L-450-G1-2	212.47 ± 2.10f	1.62 ± 0.02f	209.69 ± 2.09h	11.60 ± 0.25e
03L-450-G2-2	194.24 ± 2.10d	1.47 ± 0.02d	191.11 ± 2.10ef	11.06 ± 0.51de
NCRIBEN-03L	193.26 ± 0.28d	1.46 ± 0.00d	191.94 ± 0.28efg	10.50 ± 0.00bcd

Values are mean ± standard error of the mean. Values along the same column with different superscripts are significantly different at $p < 0.05$. SV: Saponification value, USV: Unsaponification value

Table 2: physicochemical parameters of the seed-oil

Mutants	RI	AV	FFA	IV
04E-550-G_{1-3}	1.46 ± 0.01^{a}	0.51 ± 0.01^{b}	0.26 ± 0.00^{b}	12.54 ± 0.69^{a}
04E-550-G_{2-3}	1.47 ± 0.01^{a}	0.40 ± 0.02^{a}	0.20 ± 0.03^{a}	12.65 ± 0.58^{a}
04E-550-G_{3-3}	1.47 ± 0.02^{a}	0.79 ± 0.00^{c}	0.40 ± 0.03^{c}	12.72 ± 0.50^{a}
NCRIBEN-04E	1.46 ± 0.01^{a}	1.45 ± 0.00^{h}	0.73 ± 0.01^{h}	12.50 ± 0.73^{a}
01M-350-G_{1-2}	1.46 ± 0.01^{a}	1.94 ± 0.00^{k}	0.97 ± 0.02^{k}	12.46 ± 0.77^{a}
01M-350-G_{1-2}^{1}	1.46 ± 0.00^{a}	0.82 ± 0.00^{d}	0.41 ± 0.00^{d}	12.54 ± 0.68^{a}
01M-350-G_{2-2}	1.46 ± 0.01^{a}	1.87 ± 0.01^{j}	0.94 ± 0.02^{j}	12.52 ± 0.71^{a}
01M-350-G_{2-2}^{2}	1.49 ± 0.00^{a}	3.14 ± 0.00^{m}	1.57 ± 0.01^{m}	12.47 ± 0.76^{a}
NCRIBEN-01M	1.46 ± 0.00^{a}	1.38 ± 0.01^{g}	0.69 ± 0.00^{g}	13.22 ±1.27^{ab}
03L-250-G_{1-1}	1.46 ± 0.00^{a}	0.86 ± 0.02^{e}	0.43 ± 0.00^{e}	12.15 ± 1.08^{a}
03L-250-G_{1-1}^{1}	1.46 ± 0.01^{a}	1.78 ± 0.02^{i}	0.89 ± 0.02^{i}	12.55 ± 0.68^{a}
03L-450-G_{1-2}	1.47 ± 0.00^{a}	2.79 ± 0.01^{l}	1.39 ± 0.00^{l}	12.46 ± 0.77^{a}
03L-450-G_{2-2}	1.47 ± 0.02^{a}	3.13 ± 0.01^{m}	1.57 ± 0.10^{m}	11.48 ± 0.01^{a}
NCRIBEN-03L	1.46 ± 0.00^{a}	1.32 ± 0.00^{f}	0.66 ± 0.02^{f}	15.62 ± 1.38^{b}

Values are mean ± standard error of the mean. Values along the same column with different superscripts are significantly different at $p < 0.05$. RI: refractive index, AV: Acid value, FFA: Free fatty acid, IV: Iodine value, PV: Peroxide value.

Table 3: physicochemical parameters of the seed-oil

Mutants	PV	Viscosity
04E-550-G_{1-3}	1.60 ± 0.10^{c}	9.00 ± 0.00^{d}
04E-550-G_{2-3}	3.10 ± 0.10^{f}	6.00 ± 0.00^{b}
04E-550-G_{3-3}	1.95 ± 0.05^{d}	5.00 ± 0.00^{a}
NCRIBEN-04E	1.35 ± 0.05^{b}	9.00 ± 0.01^{d}
01M-350-G_{1-2}	0.75 ± 0.15^{a}	9.00 ± 0.00^{d}
01M-350-G_{1-2}^{1}	1.45 ± 0.05^{bce}	5.00 ± 0.00^{a}
01M-350-G_{2-2}	2.25 ± 0.05^{e}	5.00 ± 0.00^{a}
01M-350-G_{2-2}^{2}	0.68 ± 0.08^{a}	6.00 ± 0.03^{b}
NCRIBEN-01M	1.45 ± 0.05^{bc}	8.00 ± 0.00^{c}
03L-250-G_{1-1}	1.65 ± 0.05^{c}	10.00 ± 0.00^{d}
03L-250-G_{1-1}^{1}	1.95 ± 0.05^{d}	9.00 ± 0.00^{d}
03L-450-G_{1-2}	2.36 ± 0.03^{e}	8.00 ± 0.00^{c}
03L-450-G_{2-2}	1.50 ±0.10^{bc}	4.00 ± 0.01^{a}
NCRIBEN-03L	0.55 ± 0.05^{a}	10.00 ± 0.00^{d}

Values are mean ± standard error of the mean. Values along the same column with different superscripts are significantly different at P < 0.05 PV: Peroxide value

SEASONAL VARIATION IS COMPLICIT TO DROUGHT TOLERANCE IN COWPEA LANDRACES

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ABSTRACT
Drought is a constraint that affect cowpea production globally. It is unpredictable and occur at any growth stage of cowpea or simultaneously with other environmental stresses. Changing climatic global trend that kept narrowing cowpea growing season necessitated the study to elucidate foresight data of the tolerance of cowpea landraces to seasonal variation in the bid to harness available germplasm. Thus, drought tolerance of Four hundred and twenty-two (422) cowpea genotypes obtained from farmers' collection (308) and International Institute of Tropical Agriculture (114) were evaluated by adopting the wooden box technology. The mean square values for all evaluated traits were significant ($p \leq 0.05$). Leaf senescence progressed rapidly in Cool temperatures (6°C - 18°C). Recovery rate after water was reintroduced was also higher during cold temperature. However, percentage recovery and stem greenness of drought stressed plants was positively associated with hot temperatures (22°C - 36°C). Percentage recovery was genotype dependent and influenced by temperature regimes. Therefore, as current climatic changes push cowpea production into hotter planting season, the resilience shown by the landraces in northern Nigeria are positive. Hence optimum yield is obtainable with current climatic conditions.

Keywords: cowpea, drought tolerance, landrace, seasonal variation

INTRODUCTION
Cowpea is a grain legume that is widely adapted to a variety of climatic and soil types. It is highly adapted to West Africa especially in warm climates (Ajayi *et al.*, 2018). Identification of tolerance relies majorly on crop adaptability to morphology and physiology. The morphological indicators of growth and development; leaf wilting/chlorosis, stem necrosis and plant greenness are correlated, failure in their development lead to significant plant death in cowpea genotypes. When such phenomenon occurs, it is not uncommon that recovery will be low after resumption of water supply (Ravelombola *et al.*, 2018; Cui *et al.*, 2020). Leaf senescence is a determinant of the type of drought tolerance in cowpea depending on its ability to delay senescence in trifoliate and unifoliate leaves (Ravelombola *et al.*, 2018).

Drought is one of the major agricultural disasters globally. Cowpea is rain dependent especially at the seedling stage. For such crop, cessation of rainfall at an early stage could be detrimental to further development (Ravelombola *et al.*, 2018). Drought can occur at any time during the planting season and significantly affects the yield of cowpea (Qin *et al.*, 2018). In Asia and Africa, the production losses due to drought exceed the total losses caused by other environmental stresses (Cui *et al.*, 2020). Among the leguminous crops, cowpea has relatively high adaptation to drought. However, considerable variation has been found in drought tolerance among cowpea (Qin *et al.*, 2018; Cui *et al.*, 2020). In some regions of West Africa, cowpea can experience multiple stresses at the same time such as drought and heat or drought and cold stresses (Ajayi *et al.*, 2018).

Breeding of crops resilient to drought condition could help in alleviating the effect of the stress (Qin *et al.*, 2018). Information on cowpea drought tolerance at the seedling stage would be substantial in efforts toward developing drought-tolerant cultivars. Phenotyping cowpea for drought tolerance is especially challenging due to complexity of the trait, lack of effective phenotyping and screening approach (Ravelombola *et al.*, 2018). Several researchers have conducted drought screening of cowpea in the field. The field results were shown to be affected by heterogeneity of temperature and water transmission in the soils (Alidu, 2018).

Therefore, phenotyping for drought tolerance at the seedling stage could be a promising alternative when conducted under controlled condition (Hall, 2012). In addition, cowpea cultivars with proven drought tolerance at the seedling stage are limited, this challenges cowpea breeders to explore new sources of variation for sustainable improvement programmed that will meet up the increasing threats to crop production.

Therefore, this study was conducted during cold and hot season to explore the effect of seasonal variation to drought tolerance of cowpea landraces at seedling stage.

MATERIALS AND METHODS

Three hundred and seven (307) cowpea landraces were collected from local farmers and were identified by their local names and characteristics. One hundred and thirteen (113) cowpea lines were also collected from the core collection of the International Institute of Tropical Agriculture (IITA), Ibadan Nigeria, the cowpea lines comprised of one (1) drought tolerant check (Danila) and one (1) drought susceptible check (TVu-7778). These total of 422 cowpea accessions were used for the study. Two separate experiments were conducted at the screen house, Department of Botany, Ahmadu Bello University, Zaria in a wooden box set up. The first experiment was conducted from 22nd October, 2020 to 7th December, 2020 when the daily temperature ranged from 6 - 18°C, (cold stress referred to as experiment 1). The second experiment was conducted from 22nd March, 2021 to 8th May, 2021 when the daily temperature ranged from 22°C - 36°C (heat stress referred to experiment II).

Sand and farm top soil were sieved and mixed thoroughly at a ratio of 3:1, the soil mixture was placed in wooden boxes of 100 x 50 cm dimensions. The boxes were then irrigated and allowed to drain. Seeds were treated with fungicide Apron star. One healthy and treated seed was then planted per each hole. The seeds were planted in rows such that each box comprises 20 entries with eighty individual plants. The experiment was arranged in randomized complete block design with two replications. The boxes were slightly irrigated daily until germination (IITA, Kano; Cui *et al.*, 2020). Irrigation was withheld at approximately 14 days after planting when majority of seedlings have at least one trifoliate. Soil temporal moisture content was monitored (Santos *et al.*, 2020).

Data on number of plants per plot, trifoliate number and plant height was collected at 5-day interval. Leaf Senescence was scored visually using a scale of 1-5. Stem greenness was recorded when the susceptible genotype was completely dead (0= not green, 1=green). Irrigation was resumed when seedlings of drought sensitive check (TVu-7778) and most tested lines reached permanent wilting point. Recovery was then assessed. Recovery rate corresponded to the number of plants that fully recovered after 1 week of re-watering (Ajayi *et al.*, 2018). The same methodology was employed in both experiment I and II. Data obtained were subjected to Analysis of Variance (ANOVA) to determine significant difference at $p \leq 0.05$. Correlation was determined among the parameters.

RESULTS AND DISCUSSION

Analysis of variance on the data obtained revealed significant difference ($p < 0.05$) in both experiments. The mean square values of the traits recorded in experiment I were lower than in experiment II, except in PH, LS and RR; which is vice versa (Table 1). In Table 2, the correlations of morphological traits in response to seedling drought during cold season experiment are presented. Significant correlation ($p \leq 0.05$) in the morphological traits was obtained. Number of plants positively correlated with plant height, number of trifoliate, leaf senescence and stem greenness at 0.05 level of significance. Both positive and negative correlations were obtained among the traits. In table 3, the correlations of morphological traits in response to seedling drought during hot season experiment are presented. Significant correlation ($p \leq 0.05$) in the morphological traits was obtained. Number of morphological traits that correlated were fewer than in the cold season experiment (experiment 1). In the same trend with experiment I, number of plants positively correlated with plant height, number of trifoliate, leaf senescence and stem greenness at 0.05 level of significance. Percentage recovery ranged from 25.0% to 100.0% in both experiments. However, the number of genotypes with high percentage recovery were 28 and 37 in experiment I and II respectively. Also, the landraces; Dan Tsaye, Dan Ringim and Shiswa showed 100.0% recovery in experiment I. Landraces Npak (small), Waken Rumfa Brown and Dan Misrah Katsina showed 100.0% recovery in experiment II.

Several indicators such as environment, varieties, growth stages and seasons are used for

comprehensive evaluation of cowpea drought tolerance. In this study, the effect of seedling drought on cowpea due to seasonal changes has been studied. Alidu (2018) reported that variation in cowpea response to drought depends on genotype, drought intensity and the growth stage. A large variation in the traits evaluated for seedling drought was found between the two seasons and among the cowpea genotypes. Most genotypes were susceptible to drought stress. This is attributable to the inability of the susceptible plants to either maintain stem greenness or tolerate leaf senescence, a phenomenon that led to significant senescence in the cowpea genotypes, these genotypes failed to recover after the water was re-introduced. The findings are similar to the report of Ravelombola *et al.* (2018). Mechanism of drought tolerance at leaf level stage has been extensively studied. Genotypes with the ability to tolerate drought at both unifoliate and trifoliate stages are type I drought tolerant while type II drought tolerant are capable of surviving trifoliate chlorosis (Qin *et al.*, 2018). Some researchers opined that a possible genetic network is associated with drought tolerance in cowpea. They explained that transport of nutrients is more active in drought tolerant varieties, further analysis in legumes revealed candidate genes such as auxin efflux carrier protein in chickpea suggested to confer drought tolerance (Li *et al.*, 2018; Qin *et al.*, 2018). Inheritance of drought susceptibility in cowpea at vegetative stage is also under the control of a single recessive gene (Nkomo *et al.*, 2021).

Plant greenness score and recovery rate have been previously shown to be accurate parameters for assessing drought tolerance at seedling stage in cowpea (Ravelombola *et al.*, 2018). The present study is corroborated by the findings of Santos *et al.* (2020) who reported lower value of stem greenness in cowpea genotypes subjected to drought compared to the control. They asserted that stem greenness is an important indicator of drought tolerance in cowpea genotypes at a seedling stage. Positive correlations among morphological and recovery parameters suggests that seedlings with more trifoliate number during drought stress will recover faster through regrowth and stem greenness. The findings in the current study are in line with the report of Ajayi *et al.* (2018) who reported strong positive correlation of PH, SG and RR.

Conclusions and Recommendation

Drought at seedling stage has an adverse effect on cowpea growth and morphology. Seasonal variations impacted tolerance to drought stress in cowpea. Temperature range for optimum cowpea productivity is (22ºC -36ºC). The landraces exhibited differential response in percentage recovery to the temperature regimes which was significantly pronounced in hot temperature. Similarly, recovery rate after drought imposition favorably skewed towards cold temperatures. It is recommended that physiological mechanism that enabled significant recovery rate at colder temperatures during drought imposition could be evaluated.

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Table 1. Mean Square for the traits of cowpea at seedling drought during cold and hot season experiment

Trait	SDCS	SDHS
PN	147.94*	474.86*
PH	7657.34*	7587.46*
TN	17.93*	18.21*
LS	497.91*	434.70*
SG	5734.56*	7406.52*
RR	628.84*	170.51*

* Significant at 0.05 level, SDCS- Seedling drought during cold, SDHS- Seedling drought during heat, PN- Number of plants, PH- Plant height, TN- Number of trifoliate, LS- Leaf senescence, SG- Stem greenness, RR- Percentage recovery

Table 2. Correlation of morphological traits in seedling drought under cold season experiment

Trait	PN	PH	TN	LS	SG
PH	0.52**	1.00			
TN	0.40**	0.50**	1.00		
LS	0.61**	0.46**	0.49**	1.00	
SG	0.32**	0.30**	0.47**	0.28**	1.00
RR	0.050	0.071*	0.102**	-0.01*	0.16**

**. Correlation is significant at the 0.01 level
* Correlation is significant at the 0.05 level

Table 3. Correlation of morphological traits in seedling drought under hot season experiment

Trait	PN	PH	TN	LS	SG
PH	0.48**	1.00			
TN	0.60**	0.54**	1.00		
LS	0.40**	0.26**	0.34**	1.00	
SG	0.13**	0.06	0.10**	0.009	1.00
RR	0.03	0.03	0.05	-0.03**	0.19**

**. Correlation is significant at the 0.01 level

GENETIC VARIABILITY AMONG FIFTEEN ACCESSIONS OF SESAME (*Sesamum indicum* L.)

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ABSTRACT: The degree of success in any breeding program is dependent, to a large extent, on the genetic variation existing among the crop germplasm. Fifteen accessions of sesame (*Sesamun indicum* L.) were evaluated for agronomic traits and seed fatty acids in a replicated field experiment at the Research Farm of the Federal University of Agriculture, Abeokuta. Principal component (PC) and FASTCLUS analyses were used to explore the variation pattern among the accessions. Significant ($p < 0.01$) variation was revealed among the accessions for the traits except days to 50% flowering. The biplot between PC 1 and 2 explained 62% of the genetic variation among the accessions. High oleic acid content was related to three accessions while tall plant stature and high grain yield were associated with two accessions. Plant height, grain yield and number of capsules/plant accounted mostly for six homogenous groups among the accessions. Promising genetic rearrangement can be exploited among the accessions to improve and develop new cultivars through hybridization.

Keyword: capsule, genetic diversity, oleic acid, stearic acid

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INTRODUCTION

Sesame (*Sesamum indicum* L.) is an ancient oil-seed crop ranked 9th among the top 13 oil crops (Chellamuthu *et al.*, 2020). The oil content (about 60% of the seed) contains palmitic, stearic (saturated fatty acid), oleic and linoleic acids (unsaturated fatty acids), with small quantities of vaccenic, linolenic, arachidic, behenic and eicosenoic acids (Were *et al.* 2006; Dar *et al.* 2015). The fatty acid composition determines the nutritional and industrial use of sesame oil (Panthee *et al.* 2006; Canakci *et al.*, 1999; Xue *et al.*, 2022). The market demand for sesame oil has led to an increasing interest in both its cultivation and production. Nigeria is the third largest producer of sesame seed in Africa after Sudan and Tanzania, producing 510,000 tons in 2019 (FAO, 2019). It is commonly grown in the Northern part of the country. However, dearth of high seed yielding, nutritional and adaptable cultivars have limited the productivity of the crop. Therefore, there is a need to improve existing cultivars and develop new ones. Genetic diversity is critical to success in any breeding program. It contributes to selection of superior parental materials for the development of high yielding and quality cultivars. This study was carried out to characterize fifteen accessions of sesame and determine the extent of genetic diversity among the accessions.

MATERIALS AND METHODS

Fifteen accessions of sesame collected from the Germplasm Unit of the National Centre for Genetic Resources and Biotechnology (NACGRAB), Ibadan were evaluated at the Research Farm of the Federal University of Agriculture (FUNAAB), Abeokuta (Lat. 7°15′N, Long. 3°25′E and Alt. 159 masl) Southwestern Nigeria in 2021. The trial was laid out in a randomized complete block design in three replicates. Each accession was sown to a 2-row plot, 3 x 1 m. Seeds were sown at 0.50 m between rows and 0.10 m within row. Seedlings were thinned to one plant per stand at 3 weeks after sowing.

Data collection and analysis

Data were collected on ten randomly selected plants per plot for days to 50% flowering, plant height (cm), number of capsules/plant, number of seeds/capsule, 1000-seed weight (g) and seed yield (g). The seeds oleic and stearic acid contents were also determined (AOCS, 1990). The data collected were subjected to analysis of variance and means were separated with Duncan's multiple range test at 5% probability. Principal component and FASTCLUS analyses were employed to determine genetic diversity among the sesame accessions (SAS, 2022).

RESULTS AND DISCUSSION

Significant ($p < 0.01$) variation was observed among the 15 accessions of sesame for the fatty

acids and agronomic characters except days to 50% flowering (Table 1). This indicated that, at least, two accessions will be different for each character and this will provide the choice to select parental genotypes with superior performance, relative to the characters. Seed yield of NGB04125, NGB04133, NGB04134, NGB04137 and NGB04140 were above the average seed yield of the fifteen accessions with NGB04137 (66.94 g), NGB04134 (58.59 g) and NGB04133 (57.31 g) having the highest value (Table not presented). Of these accessions, NGB04125, NGB04133 and NGB04134, ranked among the accessions with high number of seeds/capsule (43 - 49).

Genetic diversity among the fifteen accessions based on the biplot between the first and second principal component axes is presented in Figure 1. The biplot explained 62.41% of the total genetic variation among the sesame accessions. The accessions were distributed within four quadrants. High oleic acid content was related to NGB04116 (1), NGB04140 (14) and NGB04126 (7) in quadrant I. NGB04119 (2), NGB04136 (12), NGB04122 (4) and NGB04128 (8) were closely related in quadrant II characterized by high content of stearic acids and number of capsules/plant. Other accessions distributed in quadrant II are NGB04121 (3) and NGB04124 (5). Accessions NGB04137 (13) and NGB04134 (10) were associated in quadrant III and distributed as tall stature and high seed yielding accessions. Late maturing accessions with high number of seeds/capsule were described in quadrant IV. The accessions in the quadrant include NGB04135 (11), NGB04125 (6), NGB04142 (15) and NGB04133 (9).

The sesame accessions were separated into six homogenous groups based on FASTCLUS procedure of SAS (Table 3). Plant height, grain yield and number of capsules/plant accounted mostly for the genetic diversity among the clusters. High grain yielding and seed quality groups were clusters III (NGB04133, NGB04134) and V (NGB04137). Accessions in clusters I and III are characterized by high number of seeds/capsule. High capsule-bearing groups were clusters V and VI. Accessions with potential for high fatty acid content were defined in clusters I and VI. Tall statured accessions were grouped in V and VI. It was observed that no group or accessions had the desirable traits combined in a single accession.

Conclusion

Success of any breeding program depends on the variations in the genetic resource. Such variation would make up a valuable source for selection of parents for further hybridization and development of improved cultivars. The greater the genetic variability the better the chances of success to be achieved through selection. In the current study, heterosis could be enhanced by making crosses between accession showing morphological measure of distance for the desired character while promising genetic rearrangement can also be exploited to improve and develop new cultivars.

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Table 1. Mean squares of characters measured in 15 genotypes of sesame

Source of variation	Block (df = 2)	Genotype (df = 14)	Error (df = 28)
Days to 50% flowering	4.62	5.69	3.88
Plant height (cm)	1064.03**	148.31**	50.07
Number of capsules/plant	6.48	200.96**	42.40
Number of seeds/capsule	7.75	123.17**	42.98
1000-Seed weight (g)	0.73**	0.81**	0.13
Grain yieldd (g)	74.36	585.74**	32.74
Oleic acid	0.003**	4.01**	0.00
Stearic acid	0.000	0.06**	0.00

* significant at 5% level of significance,
** significant at 1% level of significance

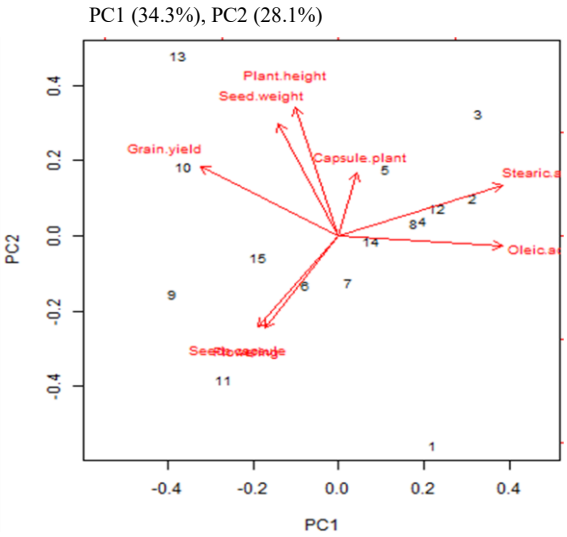

Figure 1. Genetic diversity among 15 accessions of sesame based on the biplot between principal component (PC) axes 1 and 2

1	NGB04116	**6**	NGB04125	**11**	NGB04135
2	NGB04119	**7**	NGB04126	**12**	NGB04136
3	NGB04121	**8**	NGB04128	**13**	NGB04137
4	NGB04122	**9**	NGB04133	**14**	NGB04140
5	NGB04124	**10**	NGB04134	**15**	NGB04142

Table 3. Character pattern of six clusters in ten accessions of sesame

Character	I	II	III	IV	V	VI	R^2
	NGB04116	NGB04119, NGB04126, NGB04128, NGB04136, NGB04140, NGB04142	NGB04133, NGB04134	NGB04122, NGB04135	NGB04137	NGB04121, NGB04124, NGB04125	
Days to 50% flowering	41.33 (0.00) [þ]	40.67 (0.70)	40.34 (2.35)	41.50 (2.12)	41.67 (0.00)	39.89 (2.14)	0.18
Plant height (cm)	112.00 (0.00)	124.91 (2.26)	126.09 (2.43)	125.69 (3.84)	144.47 (0.00)	131.89 (2.54)	0.91
Number of capsules/plant	30.78 (0.00)	32.45 (5.06)	31.25 (7.88)	41.65 (1.09)	47.24 (0.00)	47.45 (4.66)	0.75
Number of seeds/capsule	43.87 (0.00)	33.84 (2.96)	43.86 (0.74)	42.79 (9.31)	33.33 (0.00)	40.65 (8.67)	0.51
1000-seed weight (g)	1.43 (0.00)	2.76 (0.14)	3.02 (1.15)	2.42 (0.07)	3.23 (0.00)	2.59 (0.15)	0.61
Grain yield (g)	24.07 (0.00)	31.59 (5.73)	57.95 (0.91)	23.69 (0.30)	66.94 (0.00)	33.07 (5.47)	0.92
Oleic acid	41.60 (0.00)	40.87 (1.04)	38.92 (0.01)	39.94 (1.38)	39.07 (0.00)	41.25 (0.09)	0.61
Stearic acid	43.67 (0.00)	42.96 (1.55)	40.21 (0.05)	41.29 (1.53)	41.08 (0.00)	43.28 (0.33)	0.57

Standard deviation (þ)
Coefficient of variation (R^2)

RESPONSES TO THREE DIFFERENT CONCENTRATIONS OF SODIUM AZIDE (NaN_3) ON GROWTH AND YIELD OF SOME SELECTED TRAITS IN EGGPLANT (*Solanum melongena* L.)

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ABSTRACT
The effect of Sodium Azide induced mutation on the growth and yield of two varieties of Eggplant was investigated with the aim of inducing variability that could be exploited in the improvement of some quality traits in Eggplants. Three different treatments of sodium azide were applied on to the two Egg plant varieties. The seeds of the two varieties of eggplant: *White Eggplant* and *Green Apple* varieties were treated with three different concentrations of Sodium Azide (0.1 mM, 1.0 mM, 2.0 mM and 0.0 mM as control). The result showed significant improvement in almost all the selected traits with decrease in the mutagen concentration for the two varieties except in the fruit diameter where an increase in the mutagen concentration was observed. It was observed that, 0.1 mM concentration of Sodium Azide was significant in inducing variability that could be exploited in the improvement of highly economic crops like Eggplant.

Key words: sodium Azide, green apple eggplant, germination percentage, survival rate, white eggplant

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INTRODUCTION
The prime strategy in mutation breeding has been upgrade to the well adapted plant varieties by altering one or more major traits which limit their productivity or enhance their quality. The increasing demand of egg plants has gone along with rapid growth of population. This is due to the increasing awareness toward the benefit of vegetables in fulfilling the nutrient of the family (Jumini and Marliah. 2009). Gandhi and Sundari (2012) reported that eggplant can also be utilized as medicine to reduce cholesterol in blood and it is suitable as diet to regulate hypertension, owing to high nutrient content of the eggplant.

Eggplant production for the last 3 years has decreased. In 2013, the national production of eggplant reduced to 509,380 ton from 519,481 in 2011 (Directorate General of Horticulture, 2014). One of the main causes of such reduction is the decreasing fertility of the soil and organic matter in the soil (Ullah *et al.*, 2008). According to Waseem *et al.* (2013), the use of organic fertilizer in long term has reduced physical, chemical, and biological traits, as well as organic matters in the soil, and up course, they will affect efficiency of nutrients absorption. Excessive application of inorganic fertilizers would contaminate environment and food yield that may harm human health (Jagatheeswari, 2013). Therefore, some efforts are required to fulfill a part of nutrients and improve the physical, chemical and biological traits through the application of organic fertilizers. The demand of nutrients for the eggplant could not be fulfilled completely through the application of organic fertilizers. Sutanto (2002) reported that the application of organic fertilizer might reduce the production, whereas the use of chemical fertilizers without organic fertilizers could damage the environment. Effort to increase vegetables production will keep relying on the use of outer input, including organic and chemical fertilizers.

Sodium azide (NaN_3) is a chemical mutagen and has been one of the most powerful mutagens in crop plants. The mutagenicity is mediated through the production of an organic metabolites of azide compound. These metabolites enter into the nucleus, interact with DNA and creates point mutation in the genome. Several factors such as properties of mutagens, duration of treatment, pH, pre and post treatment, temperature and oxygen concentrations influence the effect of mutagens. The dose of the mutagen applied is an important consideration in any mutagenesis program. Generally, it was observed that the higher concentrations of the mutagen the greater the biological damage. (Khan *et al.*, 2009). Sodium azide is perhaps the least dangerous, yet most efficient mutagen that induces high M_1 sterility. Although, in some cases it has been reported that treatments with sodium azide, the physiological effect of azide are weak, are induced and it delays germination growth. However, azide-treated seed show complete apparently normal growth in M_1 except for M_1

sterility and a high frequency of M_1 chlorophyll chimaeras. More knowledge about the effect of time, pH value, temperature, seed soaking and various concentrations are required to enhance the mutagenic effectiveness and efficiency of Sodium azide and especially the metabolites, (Khan *et al*., 2009). Apart from the phenotypic traits, the mutagenic effect can be assessed more precisely using molecular markers. However, little information is available for using mutagens in the improvement of certain plants of economic interest in Nigeria. The main objective of this research is to determine the mutagenic effect of Sodium azide on some selected traits of two varieties of eggplant (*Solanum melongena* L.).

MATERIALS AND METHODS

Study Site

The research was conducted in the Botanical Garden of the Department of Biological Sciences, Usman Danfodio University, Sokoto (Lat. 14° 12'N, Long. 7° 37'E, Alt. 550 - 700 m above sea level).

Sources of the Seeds

Seeds of two varieties of cultivated Eggplant (White and Green apple varieties) were collected from the Institute for Agricultural Research (I.A.R), Ahmadu Bello University Zaria, Nigeria.

Treatment and Experimental Design

The seeds of the two Eggplant varieties were treated with three different concentrations of Sodium azide (0.1 mM, 1.0 mM, 2.0 mM and 0.0 mM as control) via pre-soaking for four hours as described by Asmahan (1993). The controls were pre-soaked in distill water. The treated plants were washed in running water for one hour and allowed to dry at room temperature for 24 hours. The seeds were then sown in polythene bags arranged in a completely randomized design (CRD) in three repetitions and grown during the 2013 rainy season. Data were obtained on Germination percentages, number of fruits/plant, diameter of the fruits, survival rate and plant height.

Data analysis

All the data obtained were analyzed using Analysis of Variance. The means were separated using Duncan's Multiple Range Test at 5% probability.

RESULTS

The result of the combination of variety and Sodium azide concentrations on some selected traits of Eggplant is presented on the table below. The result showed significant improvement in almost all the selected traits with decrease in the mutagen concentration for all the two varieties except in the fruit diameter where an increase in the mutagen concentration was observed.

DISCUSSION

The distinct differences observed in most of the quantitative and qualitative traits among the Sodium azide induced mutants of eggplant evaluated showed significant improvements in the selected traits. Although there were few traits with no significant differences in responses to the applied treatments. Similar result was also reported by Nura *et al*., (2013) on the effect of chemical mutagen in improving the number of fruits and size of sesame leaves. The above result in general agrees with other researchers who found that yield and quantitative characteristics of the egg plants fruits were not affected by Sodium azide concentration, contrary to (Bletsos *et al*., 2003; Ramano and Paratore, 2001). The differences in quality, yield and earliness could be attributed to the different growth characteristics of cultivars and their different affinity to mutation and compatibility with the rootstock. Thus. (Suzuki and Morishita, 2002; Sebahattin *et al*., 2009) showed that *Solanum torvum* is a vigorous rootstock, and a mutagen concentration of a vigorous cultivars with an equally vigorous root stock reduce the amount of fertilizer required for the same yield. The earliness could also be associated with the high vigor of the rootstock. Gisbert *et al*. (2011) reported that the earliness was observed mainly in the interspecific hybridization between *S. melongena* and *S. aethiopicum* or *S. incanum*. The increased in fruit quality on fruit number due to induced mutagenesis by Sodium azide signifies the vital role played by the mutagen in improving the quality traits of eggplant.

Conclusion

It was concluded that, there were significant differences in the effects of various concentrations of Sodium azide on the selected studied traits of eggplant. The effect of mutagen (Sodium azide) was significant in inducing variability which could be exploited in the improvement of highly economic crops like eggplant. Lower concentration of Sodium azide (0.1 mM) was found to be more effective in improving the agronomic traits of eggplant.

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Effects of the Interaction of Variety and Sodium Azide Concentrations on some Selected Traits of Egg plant

Variety	Concentration (mM)	Germination % (1 WAP)	Germination % (2 WAP)	Survival rate (%)	Plant height at maturity (cm)	Number of fruits	Fruit diameter (cm)
White egg plant	0.0	28.35d	42.36d	31.29d	30.94d	2.16d	0.28d
	0.1	74.87a	83.11a	69.94a	51.87a	7.11a	0.20b
	1.0	57.20b	72.05b	56.33b	41.52b	4.33b	0.21a
	2.0	39.55c	59.59c	44.33c	37.17c	3.00c	0.18c
Green egg plant	0.0	27.42d	40.59d	33.99d	34.27d	2.27d	0.41d
	0.1	77.57a	78.40a	72.88a	52.92a	7.05a	0.14c
	1.0	57.18b	70.07b	61.79b	44.42b	4.72b	0.29b
	2.0	46.01c	58.94c	48.85c	40.89c	3.50c	0.40a
	Mean	52.77	61.77	48.38	40.96	3.85	0.25

PRELIMINARY EVALUATION OF EARLY MATURING COWPEA (*Vigna unguiculata* L. WALP.) GENOTYPES IN BADEGGI, NIGERIA

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ABSTRACT
Cowpea plant is a climate resilient crop that is able to survive water and drought stress condition, making it a good crop for fighting hunger in this age. However, the continuous rising temperatures, erratic rainfall pattern with its increasing attendant hunger; drought escape and earliness in cowpea maturity time will portend a great solution to the problems of drought and hunger. The study was aimed at evaluating early maturing cowpea landraces and varieties with wild acceptance among farmers for high yield. This study was carried out at National Centre for Genetic Resources and Biotechnology (NACGRAB) Research Fields at Badeggi, Nigeria. Eleven early maturing cowpea genotypes mostly landraces cultivated by farmers in Niger State were evaluated for morphological and agronomic parameters. The experiment was laid out in a randomized complete block design and replicated three times, Results of the study showed significant difference among the genotypes in yield and yield related parameters but not for physiological parameter such as days to flowering and maturity. The white local 1 had significantly and highest number of seeds per plant (503.6) and seed yield per plant (96.13 g). This variety also has good seed size compared to others in this study. This variety is recommended for farmers in this part of the divide.

Keywords: climate resilient, drought, early maturing, cowpea

INTRODUCTION
Amongst the most valuable cultivated legumes, Cowpea (*Vigna unguiculata* L. Walp) has displayed several agronomic, environmental and economic advantages, contributing to additional improvement in the diets and incomes of peasant farming across Africa, Asia and South America (Gonçalves *et al.,* 2016). Cowpea is economically valued for its vital nutritional contents, such as low fat, high fiber, and high protein content, its grain comprises a high proportion of protein (19 to 35%) which is rich in two essential amino acids, lysine and tryptophan (Osipitan *et al.* 2021). Cowpea plays a vital role among the livelihoods of millions of smaller holder farmers who depend on it as a source of economic livelihood and nutritional well-being (Horn *et. al.* 2022). Besides its nutritional components, the crop has multiple advantages to farmers, including its ability to grow and produce high yields on poor, sandy soils unsuitable for the production of other crops, high rates of symbiotic nitrogen fixation, and lower fertilizer requirements (Timko and Singh, 2008).

Cowpea belongs to the family Fabaceae and sub-family Faboideae (Horn and Shimelis, 2020). It is a self-pollinating crop with low and narrow genetic diversity, making it susceptible to various environmental factors. The World production of the crop is estimated at over 8.9 million MT per year on about 14.4 million hectares (FAOSTAT 2020). In West Africa, the major cowpea producing region is the sub-Saharan Africa (SSA) with Nigeria, the highest major producer followed by Niger covering 80% of the total regional production through the past 14 years (Boukar *et al.,* 2018). The leaves, green pods, and grains of this crop are consumed as a dietary source of protein among many households in African countries (Horn *et al.,* 2016).

Owing to several biotic and abiotic factors including insect pests, diseases, parasitic weeds, drought, heat, poor soil fertility and agronomic practices (Boukar *et al.* 2018) the average yield of the crop on farmers' field falls lower than 600 kg ha^{-1} which is below the genetic potential of 1500 to 2500 kg ha^{-1}(Mohammed *et al.,* 2021). Over the past 50 years, investments in crop genetic improvement by national and international agricultural research institutions have led to the development and release of a number of productivities enhancing improved crop varieties

in many countries in SSA (Walker and Alwang, 2015). Crop genetic diversity is important as it offers an opportunity to plant breeders for developing new and improved cultivars with desirable characteristics which embraces both farmers' and breeders' preferred traits (Horn and Shimelis, 2020).

A significant adaptation in agroecological zone of the arid and semiarid tropics is Early maturity that is with short growing seasons in addition to ability to escape terminal drought as well as pests and diseases that normally occurs later in the cropping season and unfavorable temperatures during flowering and podding stages (Owusu *et al.*, 2018). Climate variability has made the onset and termination of rains unpredictable resulting in a shift to the cultivation of early maturing varieties by farmers (Armah *et al.,* 2010). These early maturing varieties are considered climate smart cultivars, in cowpea, the genotypes could mature between 55 and 60 days and usually ideal for cultivation (Abadassi, 2015).

MATERIALS AND METHODS

Genotypes and design

Eleven early maturing cowpea genotypes mostly landraces cultivated by farmers in Niger state were evaluated at Badeggi, Nigeria. These were evaluated for morphological and agronomic parameters. The experiment was laid out in a randomized complete block design and replicated three times. Each genotype planted on 4 m three row plots at a distance of 25 cm between plants and 75 cm between rows.

Data

Data was collected from five randomly pre-tagged plants in the middle row. Parameters measured include: growth type, pod pigmentation, stem pigmentation, peduncle pigmentation, flower colour, colour of mature pod, seed coat colour, eye colour and pod shape, germination percent, days to first flowering, days to 50% flowering, plant height (cm), No of branches, peduncle length (cm), pods/ peduncle, peduncle/plant, pod /plant, seed /pod, pod length (cm), seed /plant, 100 seed weight (g) and seed yield/ plant (g).

Statistical analysis

Analysis of variance was used to test for significant differences among computed means for each parameter measured. And where significant difference was detected, means where partitioned by Students Newman Keuler (SNK) test using Statistical Tools for Agricultural Research (STAR).

RESULTS AND DISCUSSION

Results from Table 1 showed there were no significant differences among the genotype for percentage germination, days to first and 50% flowering, number of branches and pods per peduncle. This means that the differences in the values are too minimal to be partitioned by the analysis. This implied that the genotypes under evaluation may originate from the same parents as continuous variation. There was however, high significant (P = 0.01) differences among the genotypes for the following parameters: plant height (cm), peduncle length (cm), peduncles per plant, pods per plant and seeds per pod. There were also significant (P = 0.01) differences among the studied genotypes for seeds per plant, 100 seed weight and seed yield per plant. These differences may arise due to heterogenous inheritance of traits from parents.

Plant height ranged from 44.33 cm to 310.12 cm for TVU 3346 and Early white respectively. Number of branches had a range between 2.27 to 6.33. Peduncle-length ranged from 9.35 cm short for Bob Marley to 26.75 cm long for IT97K – 556 – 4. Pods per peduncle ranged from 1.50 (IT97K - 556 – 4) to 3.17 (White Local 1). Peduncle per plant ranged between 6.17 and 36.83 for IT97K – 76 and White Local respectively Table 2. It is worthy of note that White local in addition to significantly highest number of pods per peduncle, had the highest number of peduncles per plant and pods per plant (86.0). the variations observed may be due to genetic make-up of the genotypes and ecological adaptations.

Results in Table 3 shows pods per plant ranged between 12.33 (IT97K – 76) and 86.00 (White Local 1) while pod length ranged from 11.58 cm in Bob Marley to 19.38 in IT97K 556-4.
Seed per pod ranged from 9.33 g lowest in Bob Marley to 13.33g highest in IT97K – 76. Seed per plant ranged from 95 (TVU 3346) to 503 g (White Local 1). This could not be far from the fact that the more the number of pods the more the quantity of seeds obtained from plants. Seed size estimated as 100seeds weight ranged from 1.70 g for TVU 3346) to 39.00 g for White Local 2 (Table 4). Seed yield per plant was lowest for TVU 3346 (9.68 g) and highest for White Local (196.13 g).

There was high significant difference between Genotype and Seed per plant, 100 seed weight and seed yield per plant relates to the fact that the

quantity of seed produced per plant is directly proportional to 100 seed weight and total seed yield of the plant. The longer the peduncle length the more amenable it becomes for mechanization.

This could mean that the number of peduncles is inversely proportional to the number of pods. It is worthy of note that White local had the highest number of peduncles per plant and pods per peduncle.

Conclusion

The eleven genotypes evaluated has proven earliness trait which will help in circumventing the problem of erratic rainfall experienced within the study area over time.

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Table 1. General Analysis of Variance of various Agronomic traits of 11 Early Maturing Cowpea Genotypes at Badeggi, Nigeria in 2018

Source of Variation	DF	Germ %	Days to 1st flowering	Days to 50% flowering	Plant height (cm)	No of branches	Peduncle Length (cm)	Pods/ Peduncle
Replication	2	44.21	49.58	1.30	163.87	1.67	576.59	0.099
Genotype	10	17.76ns	15.55ns	9.72ns	14048.38**	4.47ns	1842.31**	0.58ns
Error	20	29.01	7.54	13.10	1491.67	2.19	501.79	0.32

ns = not significant; *, **, = significant difference at 5% and 1% probability levels respectively

Table 1 Contd.

Source of variation	df	Peduncle /plant	Seed /Plant	100 seed weight (g)	Seed yield/ plant (g)	Pod /plant	Seed /pod	Pod length (cm)
Replication	2	9.12	998.73	0.96	1.88	7.73	1.11	1.44
Genotype	10	257.65**	37280.11**	241.98**	2540.41**	1267.17**	5.39**	15.77**
Error	20	23.79	916.34	1.16	3.26	175.17	0.95	0.92

ns = not significant; *, **, = significant difference at 5% and 1% probability levels respectively, SNK.

Table 2. Agronomic traits of 11 early maturing cowpea genotypes evaluated in 2018 rainfed season at Badeggi, Nigeria

Genotype	Germ % count	Germ.%	Days to 1st flowering	Days to 50% flowering	Plant height (cm)	No of branch	Peduncle Length (cm)	Pods/ Peduncle	Peduncle/ plant
Bob Marley	15.67	78.33	39	44	94.67bc	3.00	9.35d	2.17	8.50cde
Brown Local	13.67	68.33	35	44	134.12bc	5.17	14.30bcd	1.67	20.00bcd
Early White	12.00	60.00	37	46	310.12a	3.83	11.30cd	2.33	18.50bcde
IAR-48	14.00	70.00	36	44	170.75b	5.83	26.03a	2.33	17.00bcde
IT97k-499-10	10.67	53.33	36	45	149.23bc	6.33	26.35a	2.33	25.17b
IT97K-556-4	12.67	63.33	36	40	131.50bc	4.83	26.75a	1.50	25.83b
IT97K-76	18.67	93.33	40	41	123.13bc	4.67	21.83abc	2.00	6.17e
Light Brown	10.00	50.00	37	44	144.17bc	5.33	21.00abc	2.17	21.00bc
TVU 3346	14.67	73.33	33	45	44.33c	2.27	12.90bcd	2.00	7.67de
White Local 1	14.33	71.67	38	43	111.50bc	4.83	23.15ab	3.17	36.83a
White Local 2	12.00	60.00	40	44	73.03bc	3.67	20.00abc	2.50	11.67cde
SE±									

Means with the same letter along the column are not significantly different at P ≤ 0.05 probability SNK.

Table 3. Yield and yield related traits of 11 early maturing cowpea genotypes evaluated in 2018 rainfed season at Badeggi, Nigeria

Genotype	Pod /plant	Pod length (cm)	Seed/pod	Seed/Plant	100 seed weight (g)	Seed yield/plant (g)
Bob Marley	19.83^{c}	11.58^{d}.	9.33^{d}	262.00^{cd}	17.67^{e}	42.57^{d}
Brown Local	33.00^{bc}	14.62^{bc}	10.83^{a-d}	286.17^{c}	20.10^{d}	27.17^{f}
Early White	42.33^{bc}	14.58^{bc}	9.50^{d}	294.50^{c}	20.87^{d}	82.30^{b}
IAR-48	40.17^{bc}	16.28^{b}	11.50^{a-d}	213.17^{d}	14.53^{f}	34.20^{e}
IT97k-499-10	59.00^{b}	18.55^{a}	10.50^{bcd}	375.50^{b}	17.25^{e}	83.97^{b}
IT97K-556-4	40.17^{bc}	19.38^{a}	12.17^{abc}	366.83^{b}	23.80^{c}	65.77^{c}
IT97K-76	12.33^{c}	13.23^{c}	13.33^{a}	144.17^{e}	18.04^{e}	34.91^{e}
Light Brown	42.67^{bc}	16.52^{b}	12.33^{abc}	289.00^{c}	17.93^{e}	33.60^{e}
TVU 3346	15.00^{c}	14.42^{bc}	9.83^{cd}	95.00^{e}	1.70^{g}	9.68^{h}
White Local 1	85.00^{a}	16.53^{b}	12.67^{ab}	503.00^{a}	26.70^{b}	96.13^{a}
White local 2	31.00^{bc}	14.00^{bc}	11.50^{a-d}	269.33^{cd}	39.00^{a}	18.59^{g}
SE±						

Means with the same letter along the column are not significantly different at P = 0.05 probability SNK.

PRELIMINARY EVALUATING OF THE F_1 PROGENIES OF TALL COCONUT ACCESSIONS FROM SELECTED GENEPOOL

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ABSTRACT
Evaluation of elite coconut accessions and their performances will assist in identifying heterotic groups for the production of hybrid coconut seedlings. This study evaluated 158 palms from 18 accessions of tall varieties. Seednuts were raised in the nursery and thereafter planted in randomized complete block design (RCBD) with ten accessions per plot in three replicates. Vegetative traits of the seedlings were taken six months after planting. Petiole length (PL; cm), Leaf width (LW; cm), Number of split leaves (SL), Number of leaves (NL), Plant Height (PH; cm), Girth (G; cm) and the Fruit Weight (FWT; kg). ANOVA indicated high variability at $p<0.01$ level of probability for all the traits evaluated among the accessions. High variability is common in tall coconut varieties because of the high potential for cross pollination. Seedlings derived from bigger fruits with high fruit weight had slower growth rate, and slower rate of leaf production compared with those from smaller fruit. The study inferred that at the young stage of development in the field, seedlings raised from accessions with high fruit weight had slower growth rate

Keywords: fruit weight, growth rate, variability, seedling

INTRODUCTION
Coconut, *Cocos nucifera* Jacq L. is a monospecific crop i.e. it is the only crop grouped in its genus "*Cocos*". It belongs to the family *Arecaceae* and order *Arecales* (Harris, 1978). The coconut palm is often referred to as the "tree of Life", "tree of Heaven" because of its versatility in uses and the numerous needs it meets. It is an invaluable crop with diverse uses. It has the capacity to meet all the basic need of life; food, shelter and security Ahanon *et. al.,* (2016). It is successfully grown in the tropic and sub-tropic areas, hence referred to as 'king of the tropical palms. In Nigeria, coconut is produced in the Southern part with majority of it coming from the South West and Lagos State being the major coconut hub in the country where Nigeria gets it major supply from in terms of production as well as importation from neighbouring West African countries before it is distributed to other parts of the country (Factfish, 2016). However, despite production being concentrated to the South, it is widely consumed and used all over the country as food or raw material for industries.

The main economic part of the crop which is the fruit can be fashioned into over a hundred different uses. In fact, some literatures highlighted that its uses can be as much as having different uses for the palm every day of the year (Ahuja *et al.,* 2014; Odufale *et al.*, 2021). In recent time, for more than a century before the popularity of palm oil, it was the primary source of vegetable oil in many temperate countries where it is produced. The remarkable diversity of the products, derived from coconut include: coconut juice, edible kernel, oil, shell, fiber, peaty cortex, plank; building material from the frond and trunk; sap (toddy) coconut wine drink and provide sugar, and fuel from the bunch stalks, all of these provide the rationale for the title "The Tree of Life" (Adkins, 2010). Coconut breeding is a time and space consuming activity. This is as a result of its biology and long gestation period. The major emphasis in coconut breeding is targeted towards increased yield of the fruit or nut as it is often referred to, resistance to diseases especially deadly disease such as the lethal yellowing disease of coconut (LYD). In recent times, traits such as taste and abundance of water in the nut is being considered, Badouin 2002, Odufale *et al.,* 2021.

Considering the biology and characteristics of the coconut palm, there are intrinsically two basic types of coconut; the tall and dwarf variety (Odufale *et al.,* 2021). The two varieties can be differentiated by their vegetative configuration as well as their fruit conformations. The dwarf variety is characterized by small fruit and nut size while the tall coconut variety have bigger fruit size. There is wide variation in the fruit of the tall

which is basically as a result of its wide diversity (Harris 2012, Odufale 2021and 2022). The tall group or varieties are heterogeneous in nature due to them being highly prone to cross-pollination (allogamous) and the dwarf group or varieties which are more homogeneous due to their higher affinity for self-pollination (autogamy). The production of hybrid coconut has influenced increase in coconut production across the coconut planting countries of Indonesia, Malaysia, India, Sri-Lanka among others. India has about 200ha of land planted out with hybrid coconut seedlings (Harris 1978; Bourdeix *et al*., 2001; Perera *et al.,* 2014; FAO, 2017; Lédo *et al*., 2018). Sometimes, it is possible and fascinating to see combination of tall by tall coconut hybrid. However, it is a more common occurrence to see dwarf by tall hybrid in coconut improvement programmes. This has been proven to have better productivity than the tall by tall counterpart because of the higher prolific nature of the dwarf coconut type. Hence, it is usually made the female tree in such crosses. In coconut hybrid production involving the tall and dwarf coconut types, the dwarf is usually made the female tree because of its high prolificity and short stem. The short and slender stem of the dwarf tree makes it easier to climb for emasculation and or pollination in case of mass production, hand pollination or both. However, the tall variety is preferred to the dwarf because of the much bigger fruit, kernel, husk and coconut meat (Dissanayaka *et al*., 2008; Perera *et al*., 2008; Perera *et al* 2014).

Evaluation of these elite coconut accessions and their performances will go a long way in making selections and identifying different groups for the possible production of hybrid coconut seedlings that will mitigate this gap in the demand and supply of coconut in Nigeria.

MATERIALS AND METHODS

The experiment was carried out at the NIFOR Coconut Substation Badagry, Lagos State Nigeria. A total of 158 palms from 18 accessions and six genepool population were evaluated in this study. All the accessions were of the tall varieties. Accessions with high nut yield were marked and selected from each genepool. Twenty accessions that met the benchmark of minimum of eighty nut yield per annum were randomly selected from the pool. Out of the twenty, seedlings could not be raised for two of them and hence, they were dropped from the study leaving a total of eighteen accessions. Seednuts from the selected accessions were harvested and sown in the nursery in 2001. The experiment was established in 2022 by planting out the seedlings in a randomized complete block design (RCBD) with ten accessions per plot laid out in three replicates.

Data Collection

Yield data of the germplasm fields were taken for two consecutive years; 2021 and 2022. Five nuts were selected randomly from each of the accessions and weighted on an electronic scale and the average was regarded as the fruit weight for each of the accessions. After field establishment, vegetative traits of the sown seedlings were taken on the field six month after planting. The traits were: Petiole length (PL) measured in cm, Leaf width (LW) measured in cm, Number of split leaves (SL), Number of leaves (NL), Plant Height (PH) measured in cm, Girth of the stem (G) measured in cm and the Fruit Weight (FWT) measured in kg. The weighing was done two weeks after harvesting when the seednuts were cured. The data collected were subjected to analysis of variance and Correlation analysis using SAS software.

RESULTS AND DISCUSSION

Analysis of variance

Result of the Analysis of variance indicated high significant variation at $p < 0.01$ level of probability for all the traits evaluated; petiole length (PL), leaf width (LW), number of split leaves (NSL), number of leaves (NL), plant height (PH) and fruit weight (FWT) except the girth which was significant at $p < 0.05$ level of probability.

Correlation analysis

The number of leaves produced by the coconut accessions at the early stage of planting in the field had positive significant correlation with the split leaves (0.18; $p < 0.05$), girth formed at the base of the plant (0.23; $p < 0.01$) and negative significant correlation with the fruit weight (-0.17; $p < 0.05$). The height of the young palms had positive correlation with the length of the petiole (0.80; $p < 0.01$), leaf width (0.31; $p < 0.01$), split leaves (0.32; $p < 0.01$), (0.40; $p < 0.01$) and negative correlation with fruit weight (-0.20; $p < 0.05$). The earliness to splitting of the leaves was affected mostly by the width of the leaves (0.66; $p < 0.01$), girth of the stem (0.56; $p < 0.01$), height of the palm (0.32; $p < 0.01$) length of the petiole (0.25; $p < 0.01$). The fruit weight had no influence whatsoever on the leaf width, split leaves and girth of the stem but had negative

correlation with petiole length (-0.17; $p < 0.05$), number of leaves initiated (-0.17; $p < 0.05$) and palm height (-0.20; $p < 0.05$)

DISCUSSION

Tall coconut varieties are allogamous in nature hence, high variability is a common occurrence because of the high potential for cross pollination. This is because there is no overlap in the male and female phase of same inflorescence (Perera *et al.,* 2014). This might have been responsible for the high of variability observed by the Analysis of Variance for the vegetative traits. The high value of the coefficient of determination (R^2) of the fruit weight impacted preponderously on the outcome of the growth rate of the seedlings in the nursery and in the short period spent on the field. This was responsible for the high differentials observed in the vegetative traits among the accessions. The tall palms are easily distinguished by their thick and wide girth. The high significant correlation between the girth and the quintet of petiole length, leaf width, number of split leaves, number of leaves produced and the height of the palm indicated that vigourous palms established quickly on the field and their photosynthetic part increases at par. Fruit weight had significant effect on the growth of the emerging seedling even after being planted on the field.

Seedlings derived from bigger fruits with high fruit weight had slower growth rate at the initial growing stage. This is in congruent with the findings of Eufemia and Rebecco, 1980; Fernando *et al.,* 1993. Fernando *et al.,* 1993 reported in their study which involved dwarf and tall coconut varieties that at the initial growth phase, the dwarf varieties had faster growth rate than the tall varieties. This is obviously because of their smaller fruit size and fruit weight. Results from this study showed that fruit weight had significant negative correlation with petiole length and rate of leaf production. This emphasized the result of Odufale *et al.,* 2021, 2022 which stated that accessions with high fruit weight had shorter petiole and slow rate of frond or leaf production.

Conclusion

It can be inferred from this study that at the young stage of development of the seedlings in the field, planting materials sourced from accessions with high fruit weight had slower growth rate than the planting materials obtained from accessions with smaller fruit weight.

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Table 1. Yields of 18 coconut accessions selected from six genepools obtained at the NIFOR coconut substation, Badagry Lagos State.

	Accession Number	AFW (kg)	PFW (kg)	AY (ton-ha)	PMY (ton-ha)	PNY	PNY
1	A1	0.98	0.99	3.69	12.22	87	60.54
2	A2	1.12	0.99	15.34	12.22	92	60.54
3	A3	NA	0.99	NA	12.22	82	60.54
4	A4	0.82	0.99	11.99	12.22	81	60.54
5	B1	1.15	1.11	58.88	17.56	151	64.91
6	B2	1.09	1.11	28.58	17.56	129	64.91
7	B3	0.79	1.11	22.03	17.56	136	64.91
8	B4	1.17	1.11	19.78	17.56	83	64.91
9	C1	0.83	0.86	12.91	12.08	86	77.9
10	C2	0.68	0.86	16.06	12.08	132	77.9
11	C3	0.81	0.86	19.73	12.08	136	77.9
12	C4	0.75	0.86	16.25	12.08	121	77.9
13	C5	0.71	0.86	14.31	12.08	112	77.9
14	D1	0.72	0.8	16.74	10.06	114	60.83
15	D2	0.56	0.8	7.43	10.06	85	60.83
16	E1	0.73	0.78	4.93	9.15	93	55.79
17	E2	0.84	0.78	21.13	9.15	123	55.79
18	F1	1	0.94	6.55	8.36	82	42.17

NA = Not Available, AFW = Accession Fruit Weight, PFW = Population Fruit Weight, AY = Accession Yield, PMY = Population Mean Yield, ANY = Accession Nut Yield, PNY = Population Nut Yield

Table 2. Mean squares derived from Anova for vegetative phase of 18 coconut accessions selected from six genepools obtained at the NIFOR coconut substation, Badagry Lagos State

Source of variation	df	PL	LW	SL	NL	PH	G	FWT
Accessions	17	1489.78**	738.29**	8.58**	2.59**	4633.32**	7.78*	0.30**
Rep	9	669.17*	139.31ns	2.09 NS	1.08 NS	1234.65ns	4.13ns	0.01ns
Error	130	343.9	189.51	1.73	0.8	1054.99	4.08	0.01
R2		0.43	0.36	0.42	0.35	0.41	0.25	0.85
CV		33.68	47.1	93.84	17.96	21.88	18.15	9.38

ns, *, ** = Not significant, significant at $p< 0.05$ and $p< 0.01$ level of probability respectively, PL = Petiole length, LW = Leaf width, SL = Number of split leaves, NL = Number of leaves, PH = Plant Height, G = Girth, FWT = Fruit Weight

Table 3. Correlation analysis of vegetative phase of 18 coconut accessions selected from six genepools obtained at the NIFOR coconut substation, Badagry Lagos State

Trait	PL	LW	SL	NL	PH	G	FWT
PL	1	0.19*	0.25**	-0.07ns	0.80**	0.35**	-0.17*
LW		1	0.66**	-0.01ns	0.31**	0.54**	0.05ns
SL			1	0.18*	0.32**	0.56**	-0.10ns
NL				1	0.07ns	0.23**	-0.17*
PH					1	0.40**	-0.20*
G						1	-0.08ns
FWT							1

ns, *, ** = Not significant, significant at $p < 0.05$ and $p< 0.01$ level of probability respectively, PL = Petiole length, LW = Leaf width, SL = Number of split leaves, NL = Number of leaves, PH = Plant Height, G = Girth, FWT = Fruit Weight

SELECTION OF PARENT LINES FOR IMPROVEMENT AMONG SOME SOYBEAN (*Glycine max* L. Merril) GENOTYPES

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ABSTRACT

Plant breeders need to assess genetic diversity among available germplasm of important crops in order to optimize crop potential, identify and select superior genotypes to be used in crop improvement. Eleven quantitative characters were observed on 13 Soybean genotypes at the Teaching and Research Farm of Federal University of Agriculture, Abeokuta using the randomized complete block design with three replicates. Principal Component Analysis (PCA), Single Linkage Cluster Analysis (SLCA) and FASTCLUS technique were employed to determine genetic divergence and identify superior genotypes for improvement. The first three principal components accounted for 69.94% of total variation observed. The genotypes were sorted into four distinct groups by both the SLCA and FASTCLUS. Leaf and branch population, plant height, days to flowering and net plot yield contributed the largest proportion of variation among the genotypes. At 47% similarity level, TGx1989-19F x TGx1987-10F-5-3-1-2-2-I and SC-SIGNA were distinguished from the rest of the population and could therefore be used as suitable parents for improvement of Soybean genotypes.

Key words: genetic diversity, improvement, similarity, superior genotype

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INTRODUCTION

Soybean (*Glycine max (*L.) Merril) is a self-pollinating, herbaceous annual plant of the family *Fabaceae* grown for its edible seeds in the tropical, subtropical and temperate regions. Soybean is the most important legume crop in the world being a great source of both protein and oil. Singh (2017) and IITA (2021) reported that the crop contains more than 30% carbohydrates, 36% proteins, 20% oil and excellent amount of dietary fiber, vitamins, and minerals. In recent years, soybean is also becoming a source of biodiesel. Soybean root fixes nitrogen through symbiosis with a rhizobacterium; *Bradyrhizobia japonicum*, improving soil health (Pagano and Miransari, 2016).

Soybean imports into Nigeria continue to rise as the country's demand for the oilseed expands for both food and feed usage (USDA, 2021; Donley, 2021). Plant Breeders therefore have to bridge the limitation of soybean production such as low yield, insect and disease susceptibility, and adaptability to varying weather conditions (drought and high temperature, etc.) to meet up with the increasing demand for the crop, even at the global level. Hence, the need for Plant Breeders to assess genetic diversity among available germplasm of important crops in order to optimize crop potential, identify and select superior genotypes to be used in crop improvement (Begna, 2021). Selection being one of the core techniques employed in classical and modern plant breeding to improve and/or develop crops with desirable traits. This study therefore aimed to determine the genetic divergence among thirteen (13) genotypes of Soybean based on agro-morphological characters and also identify superior soybean genotypes which could be used as parents in soybean improvement programmes.

MATERIALS AND METHODS

This study, which was laid out in a Randomized Complete Block Design with three replications was carried out at the Teaching and Research Farm of the Federal University of Agriculture, Abeokuta between August, 2021 and January, 2022. The thirteen Soybean genotypes used were obtained from the germplasm of International Institute Tropical Agriculture (IITA), Ibadan, Nigeria. Seeds of the 13 genotypes were sown in four row plots of 3 m long and 50 cm apart after being mixed with NoduMax to facilitate nodulation. NPK 15:15:15 and Triple Superphosphate fertilizer were applied simultaneously with the seed sowing operation. Within row spacing was 5 cm and seeding rate was two seeds per stand. Two weeks after emergence, thinning operation was carried out to maintain optimum population. Hand weeding was done twice at 5 and 9 weeks after sowing.

Data were collected on eleven agro-morphological characters from five randomly selected plants in each plot; plant height (cm), number of leaves, number of branches, stem girth(cm), leaf area (cm^2) days to flowering, days

to maturity, lowest pod height (cm), 100 seed weight (g), pod length (cm), and net plot yield (g). The data were subjected to Principal Component Analysis, Single Linkage Cluster Analysis and FASTCLUS technique using procedure of the SAS/PC version 9.

RESULTS AND DISCUSSION

The first three of the twelve principal component axes accounted for 69.94% of the total variation that existed among the thirteen genotypes (Table 1). The first principal component axis (PC1) accounted for the highest percentage variation of 32.03%. The relative discriminating power of the axes was determined by the Eigen values; the highest was obtained in principal component axis 1 (4.16) while axes 2 and 3 had 2.83 and 2.10, respectively. Major characters loaded on the first principal component axis 1 included number of leaves, number of branches, and net plot yield. PC2 was associated with characters such as plant height, number of leaves, number of branches and days to flowering while PC3 had stem girth, leaf area, stem girth, days to flowering and pod length loaded on it. This indicated that these characters could be used to distinguish among the soybean genotypes. This observation is in line with the findings of Ayo-Vaughan *et al.* (2013), who working on Kenaf stated that characters with factor coefficient of 3.0 and above are reliable enough to discriminate among the genotypes. Ghiday and Sentayehu, (2015) also identified plant height and number of branches, among other traits, as being important in multivariate studies of Soybean genotypes.

The characteristic means of the four cluster groups in the 13 soybean genotypes generated by the FASTCLUS technique are presented in Table 2. Cluster I had six genotypes, clusters II and III had one genotype each while cluster IV had five genotypes. Members of cluster I recorded the highest number of leaves, number of branches, pod length and the least value for stem girth. The only genotype in cluster II recorded the highest value for stem girth, lowest pod height and net plot yield. It was also observed to be earliest flowering. Also, the only genotype in cluster III recorded the tallest plant height, latest days to maturity and highest value for 100 seed weight while members of cluster IV were the latest to flowering and recorded the lowest number of leaves.

The dendrogram derived from the Single Linkage Cluster Analysis showing the relationship among the 13 soybean genotypes revealed a range of diversity among the 13 genotypes (Figure 1). It is important to note that the genotypes also formed four clusters and the clustering agreed with that of the FASTCLUS technique. All 13 genotypes were very distinct from each other at 100% similarity level while at 16% they had all formed a single cluster. At 82% level, the first set of similarities was observed between genotypes 11 and 12. At 47% coefficient of similarity, four distinct clusters had been formed with genotype 2 being the most distinct from the population. The overall genetic similarity ranged from 0.16 – 0.82, indicative of wide variability among the genotypes. This implies that there is prospect for selection among the soybean genotypes used for this study. In addition, when parents from diverse genetic background are included in hybridization programme, they are likely to produce progenies with high heterotic values and transgressive segregations are likely to be observed in the segregating generation of crosses.

Conclusion

This study concluded that the first three component axes explained 69.94% of the total variation among the population studied with lowest pod height and 100 seed weight not contributing substantially to the variation observed among the genotypes. High level of genetic diversity was observed with TGx1989-19F xTGx1987-10F-5-3-1-2-2-1 (G2) being the most distinct. In addition, G2, the only member of Cluster II was characterized with earliness, largest leaf area and highest net plot yield while SC-SIGNA, the lone member of Cluster III was late maturing and lowest yielding. Therefore, TGx1989-19F xTGx1987-10F-5-3-1-2-2-1 could be used as a parent in improving the earliness and yield characteristics of SC-SIGNA.

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Table 1. Factor scores of major characters, Eigen-values and percentage total variation accounted for by the first four principal component axes of the ordination of the 13 soybean genotypes

Characters	PC1	PC2	PC3
Plant height (cm)	0.191	**0.432**	0.049
Number of leaves	**0.335**	**-0.342**	0.139
Number of branches	**0.323**	**-0.363**	0.093
Stem girth (cm)	-0.258	0.203	**0.354**
Leaf Area (cm^2)	0.167	0.049	**0.569**
Days to flowering	-0.055	**-0.352**	**-0.389**
Days to maturity	0.222	0.412	0.059
Lowest pod height (cm)	-0.053	0.129	0.016
100-seed weight (g)	0.280	0.202	0.143
Pod length (cm)	0.288	0.253	**-0.432**
Net plot yield (g)	**-0.413**	0.144	-0.093
Eigen-value	4.160	2.830	2.100
Variation accounted for (%)	32.030	21.750	16.170
Cumulative percentage variation (%)	32.030	53.770	69.940

Table 2. Major characteristics of four clusters of 13 genotypes of soybean showing their means and standard deviations in parenthesis

Characters	I	II	III	IV
	G1, G5, G7, G10, G11, G12	G2	G3	G4, G6, G8, G9, G13
Plant height	46.29 (5.47)	41.93 (0.00)	48.00 (0.00)	41.25 (7.88)
Number of leaves	83.40 (9.09)	25.00 (0.00)	31.33 (0.00)	39.80 (22.85)
Number of branches	29.73 (4.78)	10.67 (0.00)	12.33 (0.00)	15.07 (6.37)
Stem girth	3.19 (0.23)	4.53 (0.00)	4.50 (0.00)	3.37 (0.13)
Leaf area	67.13 (15.51)	67.38 (0.00)	66.90 (0.00)	52.66 (9.45)
Days to flowering	55.93 (6.31)	53.00 (0.00)	54.33 (0.00)	57.46 (4.68)
Days to maturity	105.47 (3.31)	101.67 (0.00)	111.00 (0.00)	103.27 (2.8)
Lowest pod height	9.13 (3.58)	10.17 (0.00)	7.75 (0.00)	8.77 (2.75)
100 seed weight	13.95 (0.95)	12.37 (0.00)	15.00 (0.00)	13.35 (0.87)
Pod length	3.83 (0.17)	3.27 (0.00)	3.67 (0.00)	3.77 (0.19)
Net plot yield	189.15 (17.69)	393.30 (0.00)	125.20 (0.00)	273.37 (29.66)

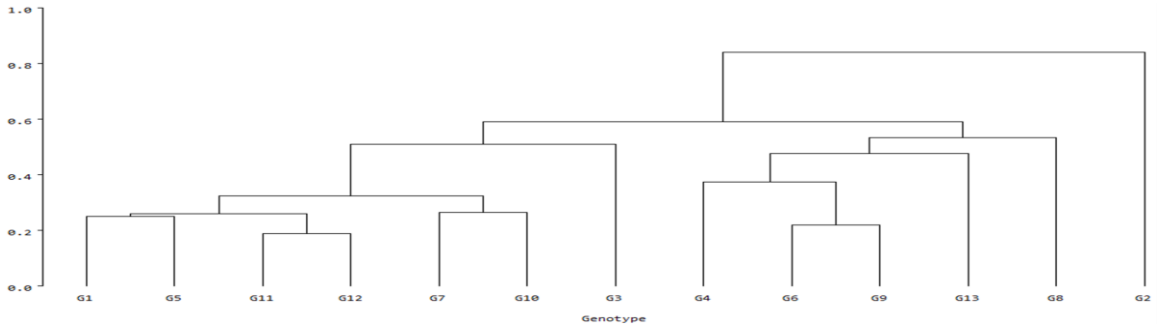

Figure 1. Dendrogram from Single Linkage Cluster Analysis (SLCA) of the 13 genotypes
1 - TGx1989-11F xTGx1987-10F-1-1-3-1-3-I, 2 - TGx1989-19F xTGx1987-10F-5-3-1-2-2-I`, 3 - SC-SIGNA, 4 - TGx2029-39F, 5–SONGDA, 6 - TGx1951-3F, 7 - TGx2029-22F, 8 - (TGx1987-10F/TGx1740-2F)-#F5-1011-6, 9 - TGX1987-10F xTGX1989-19F-10, 10 - TGX1988-5F xTGX1989-19F-17 11 - TGX1988-5F xTGX1989-19F-912 - TGx2029-42F 13 - TGx2029-5F

EFFECTS OF TITANIUM DIOXIDE NANOPARTICLE (TiO_2) ON GROWTH OF MICROPROPAGATED SWEET POTATO (*Ipomoea batatas*) UNDER WATER-DEFICIT STRESS

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ABSTRACT
Sweet potato (*Ipomoea batatas*) ranks fifth as the most valuable food crop in the tropics in terms of annual production. However, abiotic factors affect its yield and production. A modified Murashige and Skoog medium with varying concentrations of Titanium dioxide (TiO_2) (50, 70, 80, 100 and 150 mg L^{-1}) nanoparticles was assessed on the growth of potato explants under water-deficit stress induced by addition of 40 g L^{-1} D-sorbitol. Water stress significantly reduced the number of roots, but addition of 50 mg L^{-1} and 100 mg L^{-1} TiO_2 increased it to 3.80 ± 0.41 and 3.10 ± 0.42 roots respectively. Root length (21.07 ± 0.91 cm) was highest in Treatment 5 (150 mg l^{-1} TiO_2). Shoot length was highest in the control treatment but it produced thinner and shorter roots, compared to the TiO_2 nanoparticles treated plantlets which had much thicker and longer roots, for better water absorption. Plantlets were successfully acclimatized and the luxuriant growth of Treatment 4 plants visible. Application of TiO_2 nanoparticles at 100 to 150 mg l^{-1} enhanced growth of sweet potato plantlets under water-deficit. TiO_2 nanoparticles could be utilized for sweet potato production in arid regions.

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Keywords: micropropagation, nanoparticles, sweet potato, water-deficit stress,

INTRODUCTION
Potato (*Ipomoea batatas*) belongs to the Solanaceae family, and it is one of the essential tuber crops grown globally, with about a million tons produced (Yamada *et al.* 2009). It is an essential economic crop in most countries. It ranks fifth as the most important food crop in the tropics in terms of annual production, and seventh in the world food production after wheat, rice, maize, potato, barley, and cassava (FAOSTAT 2016). Drought and heat stresses are the most important environmental factors limiting sweet potato production especially in sub-Saharan Africa. It affects the quality of the tubers and its yield. Efforts to improve potato production under drought and heat stress using conventional breeding methods is cumbersome as the traits are polygenic with low inheritance (Muthoni and Shimelis 2020). However, the use of modern breeding methods and nanotechnology could lead to production of sweet potato resilient crops or mitigate the effects of abiotic stresses on its yield. Nanotechnology deals with the production, manipulation, and deployment of particles otherwise known as nanomaterials, with sizes between 1-100 nm having one or more dimensions (Ojuederie *et al.*, 2022). TiO_2 nanoparticles can have various profound effects on the crop's physiological, biochemical, and morphological characteristics (Mishra *et al.*, 2014). We investigated the effect of TiO_2 nanoparticles on micropropagation of sweet potato (*Ipomoea batatas*) under water-deficit stress, and determined the most suitable medium for growth of sweet potato micro propagated plantlets in media amended with TiO_2 nanoparticles.

MATERIALS AND METHODS
Sweet potato tubers were purchased at Bodija market, Ibadan, Oyo state. The samples collected were transported to the Biotechnology Laboratory, Kings University, Odeomu, where they were kept at room temperature for 3 weeks till shoots and leaves sprouted from the tubers. The culture media used for this study is presented in Table 1. The pH of the media was adjusted to 5.7 ± 0.1 before been autoclaved at 121° C for 15 min at 15 psi. The TiO_2 nanoparticle used in this study was synthesized at the Department of Chemistry, University of Zululand, South Africa. This was achieved according to the method of

Mhlanga and Ray (2014). To evaluate the crystal structure, phase, and crystallinity of TiO_2 nanoparticles, Powder X-ray diffraction (p-XRD) analysis was carried out by using a Bruker AXS D8 Advance diffractometer equipped with nickel-filtered Cu-Kα radiation (λ = 1.5418 Å) at 40 kV and 40 mA. The optical absorbance measurements were performed at the UV-Vis spectral range on a Varian Cary 50 UV/Vis spectrophotometer using ethanol as a dispersing solvent. Estimation of the crystallite size of the synthesized TiO_2 nanoparticles was carried out by employing Debye Scherrer's formula (Equation 1), where d, 0.89 λ, β and θ represent the crystalline size of the nanoparticles, constant crystalline shape factor, wavelength of the X-ray source, the full angular width at half maximum (FWHM) of XRD peaks, and the Bragg's diffraction angle, respectively.

$$d = \frac{0.89\lambda}{\beta \cos\theta} \quad (1)$$

The explants were cut into nodal cuttings and surface sterilized with 70% ethanol for 5 mins in a sterile beaker. The 70% ethanol was decanted, and explants sterilized with 10% sodium hypochlorite solution with a drop of Tween 20, for 5 mins. The solution was decanted, and the explants rinsed at least thrice with sterile distilled water. The cultured explants were transferred to the growth room in the biotechnology laboratory at Kings University and incubated at 26 ± 2°C at 12 hr. photoperiod for 5 weeks. The growth response of the sweet potato nodal cuttings was monitored weekly. At the 5th week, the root and shoot lengths were measured. Regenerated plantlets were successfully acclimatized using a mixture of 90 g loamy soil and 10 g vermiculite for 4 weeks during which further growth and morphology was observed.

Statistical analyses

Data were analysed with the Statistical Analysis System (SAS 9.3) software using descriptive statistics and analysis of variance at $p \leq 0.05$.

RESULTS AND DISCUSSION

The p-XRD pattern of the synthesized TiO_2 nanoparticles displayed in Fig. 1a shows diffraction peaks at 2θ = 25.54°, 38.07°, 48.31°, 54.19° 55.27°, 62.89°, 68.86°, 70.60° and 75.34° which can suitably be indexed to the Miller indices (hkl) values: (1 0 1), (0 0 4), (2 0 0), (1 0 5), (2 1 1), (2 0 4), (1 1 6), (2 2 0), and (2 1 5), respectively. These peaks along with their hkl values correspond to the tetragonal crystalline anatase phase of TiO_2 (ICCD #. 01-073-1764). The successful fabrication of phase pure TiO_2 nanoparticles indicated the absence of impurities of the peaks. The sharp peaks indicated the crystalline nature of the nanoparticles. The calculated crystallite size of TiO_2 nanoparticles was found to be 14.8 nm. The p-XRD patterns obtained in this study agree well with the previously reported spectra for TiO_2 nanoparticles (Sharma *et al.* 2020). The spectrum indicates a prominent absorption peak at 280 nm (Fig. 1b) which is in the range of 200 to 600 nm, confirming the successful synthesis of TiO_2 nanoparticles (Ramakrishnan *et al.* 2018). Treatment T5 produced plantlets with the highest root length, which was not significantly different from the Treatment T4, implying that TiO_2 nanoparticles played a major role in increasing root length in sweet potatoes under water-deficit stress (Fig. 2). Application of TiO_2 via roots or leaves at low concentrations enhances crop performance by stimulating the activity of antioxidant enzymes, augmenting chlorophyll content and photosynthesis, promoting nutrient utilization, biotic and abiotic stress tolerances and improving crop yield and quality (Chaudhary and Singh 2020). The Shoot length was significantly highest in the control Treatment 0 but reduced in Treatment 1 and Treatment 2 (Fig. 2).

Addition of TiO_2 nanoparticles to the growth media had varying effects on the morphology of sweet potato plantlets at different concentrations. The highest number of roots (5.02 ± 0.37) was recorded in the control treatment devoid of water stress (Fig. 3). Water stress significantly reduced the number of roots. However, addition of 50 mg L^{-1} and 100 mg L^{-1} TiO_2 increased the number of roots to 3.80 ± 0.41 (Treatment 1) and 3.10 ± 0.42 roots (Treatment 4) respectively. Considering the number of shoots, Treatment 0 (control) had the highest number of shoots followed by Treatment 4 (Fig. 3). Number of leaves was significantly highest in Treatment 3 (4.33 ± 0.34) which was not significantly different from the number of leaves produced by Treatment 5. The control treatment produced thinner and shorter roots, compared to the TiO_2 nanoparticles treated sweet potato plantlets which had much thicker and longer roots, for better water absorption (Fig. 4), Treatment 4 plants were successfully acclimatized with luxuriant leaves (Fig. 5) TiO_2 nanoparticles are not seen as plant nutrients but are important in plant protection and at lower doses; it is effective due to its photocatalytic property or as a UV protector. It therefore

promotes chlorophyll formation, stimulate Ribulose 1, 5-bisphosphate carboxylase activity, and increases photosynthesis, thus, increasing plant growth and development (Chaudhary and Singh 2020).

Conclusion

Titanium dioxide nanoparticles mitigated water-deficit stress in sweet potato plantlets by improving the root architecture of the plant, which were longer and Thicker. Treatment 4 (100 mg l^{-1} TiO_2) plants had leaves with larger surface area for more efficient photosynthesis compared to the control. TiO_2 nanoparticles could be utilized in agriculture especially for sweet potato production in arid regions regularly plagued by drought as this will greatly improve productivity and enhance food security.

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Table 1. Media composition of the various treatments used in this study

Trts	T0	T1	T2	T3	T4	T5
MS(Gl^{-1})	4.43	4.43	4.43	4.43	4.43	4.43
Dsorbitol (gL^{-1})	40	40	40	40	40	40
Myo Inositol (mgL^{-1})	100	100	100	100	100	100
Sucrose (gL^{-1})	30	30	30	30	30	30
Agar (gL_{-1})	7	7	7	7	7	7
NAA (mg l^{-1})	0.001	0.001	0.001	0.001	0.001	0.001
BAP (mg l^{-1})	0.6	0.6	0.6	0.6	0.6	0.6
TiO_2 (mg l^{-1})	0	50	70	80	100	150

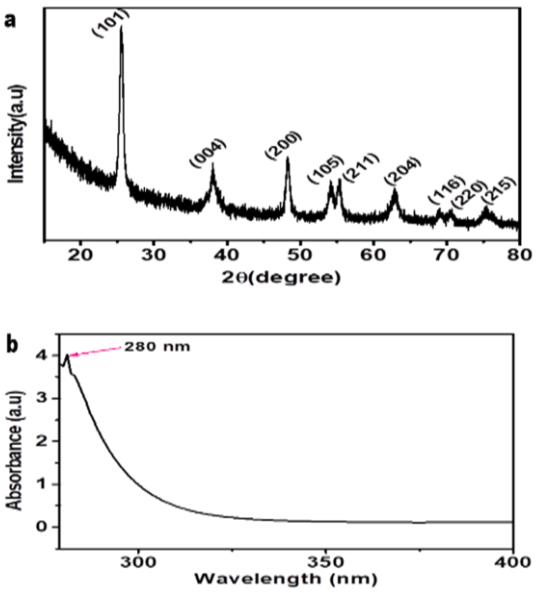

Figure 1 (a) The p-XRD spectrum of Titanium dioxide (TiO_2) Nanoparticles revealed that the TiO 2 NPs used were all in the anatase phase **(b)** UV-vis absorption spectrum of the nanostructured anatase TiO_2

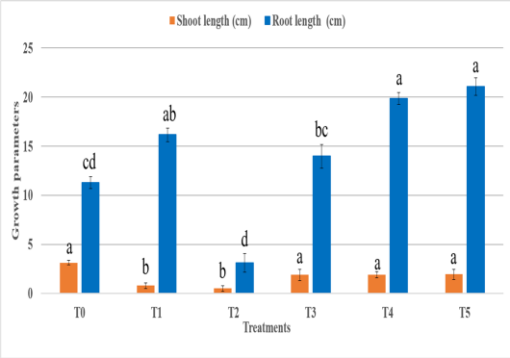

Figure 2. Effect of Titanium dioxide (TiO_2) nanoparticles on the shoot and root lengths of sweet potato (T0-Control, TI- (50 mg l^{-1} TiO_2) T2-(70 mg l^{-1} TiO_2) T3-(80 mg l^{-1} TiO_2) T4-(100 mg l^{-1} TiO_2) T5-(150 mg l^{-1} TiO_2). Data are presented as Means ± Standard deviation. Means followed by the same letters are not significantly different from each other using Duncan Multiple Range Test ($p < 0.05$)

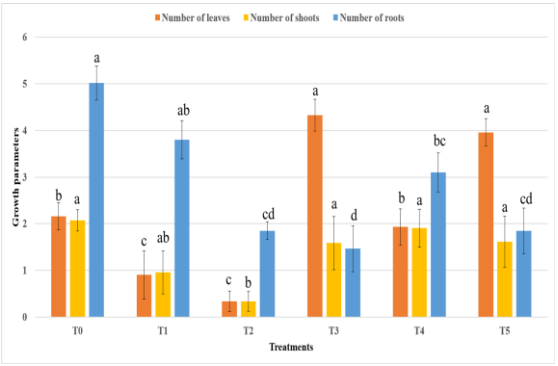

Figure 3. Effect of TiO2 nanoparticles on growth parameters of sweet potato. (T0-Control, TI- (50 mg l-1 TiO2), T2-(70 mg l-1 TiO2), T3-(80 mg l-1 TiO2), T4-(100 mg l-1 TiO2), T5-(150 mg l-1 TiO2) Data are presented as Means ± Standard deviation. Means followed by the same letters are not significantly different from each other according to Duncan Multiples Range Test ($p < 0.05$)

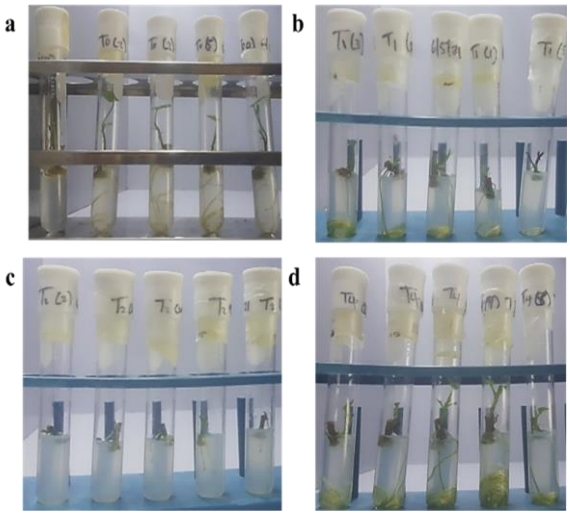

Figure 4. Morphogenic response of plantlets (a) Treatment 0- 0 mg L^{-1} TiO_2 (control) (b) Treatment 1- 50 mg l^{-1} TiO_2 (c) Treatment 2- 70 mg L^{-1} TiO_2 (d) Treatment 4- 100 mg L^{-1} TiO_2 under

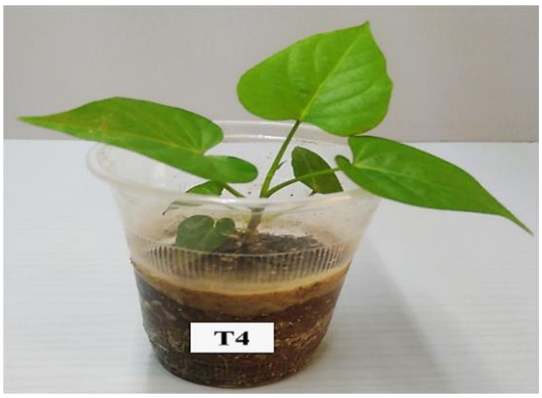

Figure 5. Treatment 4 (100 mg l^{-1} TiO_2) treated sweet potato plant five weeks after acclimatization

PHENOTYPIC VARIABILITY OF 26 TOMATO (*Solanum lycopersicon* MILL.) GENOTYPES USING QUANTITATIVE TRAITS

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ABSTRACT
Tomato is a choice crop in disease prevention because it is rich in essential nutrients. An important crop like this needs continuous improvement through introgression of desirable genes and evaluation of the level of genetic diversity that exists among their progenies. Therefore, this study was carried out to determine genetic diversity among twenty-six genotypes comprising progenies and their parents. Data collected on growth and yield characters were subjected to Principal Component Analysis (PCA) and Single Linkage Cluster Analysis (SLCA). Results showed that the genotypes were different from one another. The first eight PCA axes captured 97.36% of the total variance. leaf width, leaf length, thickness of fruit wall, days to flowering, days to 50% flowering, days to maturity, number of fruits harvested were identified as most important characters in discriminating the genotypes. Genotypes from the seven diverse clusters obtained based on their level of similarity by the SLCA could serve as parents in heterotic breeding.

Keywords: genetic diversity, PCA, *Solanum lycopersicon,* SLCA

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INTRODUCTION
Tomato (*Solanum lycopersicum* Mill.) is a member of the *Solanaceae* family and the second-most significant vegetable crop after potatoes (FAOSTAT, 2019). It is cultivated in several countries in the world since it can adapt to wide range of soil and climatic conditions. The average amount of tomatoes produced per hectare worldwide is 376 tons. 11.8 percent of the world's tomatoes are produced in Africa (FAOSTAT, 2019). The Food and Agricultural Organization (FAO) reports that Nigeria produced 4.1 million tons of tomato fruits in 2017, making it the most produced berry fruit in the country (FAOSTAT, 2020). Tomato has a low calorie content and is a great source of fiber, minerals, phenols, vitamins A, C, and E and antioxidants (mainly lycopene and β-carotene), making it a great "functional food" that satisfies essential nutritional needs (Saleem *et al*., 2013; Giovannetti *et al.,* 2012). It is advantageous for the preservation of health and the prevention of sickness and treatment of ailments like diabetes, high blood pressure and cancer (Usman and Bakari, 2013; Ghaffari *et al.,* 2015).

In crop breeding programmes, genetic diversity assessment is crucial because it aids in the selection of diverse parental combinations that will produce segregating offspring with the greatest genetic variability (Barrett and Kidwell, 1998). Crop genetic diversity is measured using multivariate statistical techniques such as PCA and SLCA. So many researchers frequently employ multiple techniques to study genetic diversity in crops due to the complementary effects of the techniques on the analysis and the opportunity for comparison between the techniques to determine which one captures the majority of the variation and provides a clearer and more informative display of the positions of the genotypes (Odiyi *et al*., 2014). An important crop like tomato needs continuous improvement through introgression of desirable genes and evaluation of the level of genetic diversity that exists among their progenies. Therefore, this study aims to determine genetic diversity among twenty-six genotypes comprising progenies and their parents and to identify useful agronomical traits that are most important in discriminating the genotypes.

MATERIALS AND METHODS
The experimental site was located at the Teaching and Research Farm of the Federal University of Technology, Akure (FUTA), Ondo State, Nigeria (7°16'N, 05°12'E). Thirteen (13) tomato genotypes (parent materials) were sourced from different locations. The parent materials, source of collection, acronyms and crosses generated are presented in Table 1. Cross pollination of the tomato plants was done as highlighted by Chetelat and Peacock (2013).

Thirteen (13) crosses were generated. The crosses were planted and evaluated alongside the parent materials, making 26 genotypes in all. The experimental design used was completely randomized design. The bags containing 20 kg of sterilized top soil were arranged in three (3) replications in the screen house. Four (4) bags were allotted for each of the twenty-six genotypes in the three replications at two seedlings per bag. Agronomic data were collected on number of days to 50% flowering, number of days to maturity, number of fruits per plant, leaf length, leaf width, plant height at flowering, plant height at harvest, thickness of fruit wall, fruit size, fruit weight, fruit length and fruit width. The plant and fruit descriptors used for this study and their method of assessment are in accordance with the methods described by International Plant Genetic Resource Institute (IPGRI, 1996). Principal component and single linkage cluster analyses were performed using the PAST package.

RESULTS AND DISCUSSION

The scores of the major characters describing the first eight principal component axes are presented in Table 2. The first eight principal component axes jointly accounted for 97.36% of the total variation among the genotypes studied. PC1 was positively loaded with leaf width (0.39), leaf length (0.37), thickness of fruit wall (0.27), days to flowering (0.42), days to 50% flowering (0.38), days to maturity (0.33) and negatively loaded with number of fruits harvested (-0.37). PC2 was also positively loaded with leaf length (0.35**)**, thickness of fruit wall (0.27**)**, fruit length (0.44**)**, plant height at flowering (0.35**)** and negatively loaded with fruit width (-0.32) and days to maturity (-0.34). This means that these traits contributed significantly to the variability among the genotypes. In PC2, a negative correlation was observed between growth related traits (days to flowering, days to 50% flowering and days to maturity) and fruit related traits (fruit length, fruit weight and number of fruits harvested). This inverse correlation could be due to the fact that tomato plants with early maturity are not necessarily good fruit yielders. This is also similar to the findings of Mohammed *et al.*, 2019 and Liu *et al.*, 2021.

The single linkage cluster analysis grouped the 26 genotypes based on their level of similarity for some characters. The ordination of the genotypes on axes 1 and 2 (Fig. 1) shows that DIV, UC82B, BSK, EARSPG, RM VF, PADM, IKR 1 x RM VF and IGED x PADM were most distant from all other genotypes as characters associated with PC1 and PC2 described them; thus, selection for heterotic breeding can be made among these genotypes. DIV had the highest positive interaction with PC1 (figure 2). This implies that it performs best in terms of leaf width, leaf length, thickness of fruit wall, days to flowering, days to 50% flowering and days to maturity.

The genotypes were grouped into seven clusters, each containing tomato genotypes sharing common attributes and being similar to one another. This grouping of the genotypes by SLCA did not follow a particular pattern. The PCA and SLCA when used together proved to be effective methods in grouping the tomato genotypes and that may facilitate effective management and utilization of the crop in future breeding programmes (Fayeun and Odiyi, 2012; Odiyi, 2014).

Conclusion

PCA and SLCA were appropriate for the classification of diversity among the tomato genotypes. Leaf width, leaf length, thickness of fruit wall, days to flowering, days to 50% flowering, days to maturity, and number of fruits harvested were identified as most important characters in discriminating the genotypes.

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Table 1. Tomato parent materials, source of collection, acronym and crosses generated

S/N	Genotype	Source of Collection	Acronym	S/N	Crosses
1	Alausa	Ondo	ALS	14	ALS×PLA
2	Ibadan local	Ibadan	IBL	15	IBL×DIV
3	Akoko	Akoko	AKK	16	AKK×RM VF
4	Beske	Akure	BSK	17	BSK×IGED
5	Ikaram 1	Ikaram	IKR 1	18	IKR 1×IGED
6	Ikaram 2	Ikaram	IKR 2	19	IKR 2×PLA
7	Igedegede	Igedegede-Akoko	IGED	20	IGED×PADM
8	UC82B	NIHORT	UC82B	21	IKR 1 × UC82B
9	Early Spring	NIHORT	EARSPG	22	EARSPG×AKK
10	Roma VF	NIHORT	RM VF	23	IKR 1×RM VF
11	Padma	Commercial seed store	PADM	24	DIV×IBL
12	Platinum	Commercial seed store	PLA	25	IBL×BSK
13	Diva F1	Commercial seed store	DIV	26	DIV×ALS

Table 2. Eigen vector for agronomic characters of the first four principal components.

	PC 1	PC 2	PC 3	PC 4	PC 5
Leaf Width	0.39	0.26	0.18	-0.19	0.29
Fruit Width	0.05	-0.32	0.56	0.09	-0.26
Leaf Length	0.37	0.35	0.16	-0.21	0.21
Thickness of fruit wall	0.27	0.27	0.08	-0.04	-0.42
Number of fruits harvested	-0.37	0.21	0.21	0.16	0.26
Fruit Length	0.14	0.44	0.08	0.52	0.16
Plant Height at harvest	0.02	-0.2	0.38	-0.57	0.32
Days to Flowering	0.42	-0.24	-0.17	0.07	0.21
Days to 50% flowering	0.38	-0.21	-0.21	0.25	0.23
Plant Height at flowering	0.13	0.35	-0.08	-0.29	-0.51
Fruit Weight	0.19	-0.12	0.55	0.36	-0.17
Days to Maturity	0.33	-0.34	-0.19	0	-0.22
Eigenvalue	3.96	2.19	1.93	1.24	1.01
Proportion of variance (%)	32.98	18.23	16.05	10.35	8.4
Cumulative variance (%)	32.98	51.21	67.26	77.62	86.01

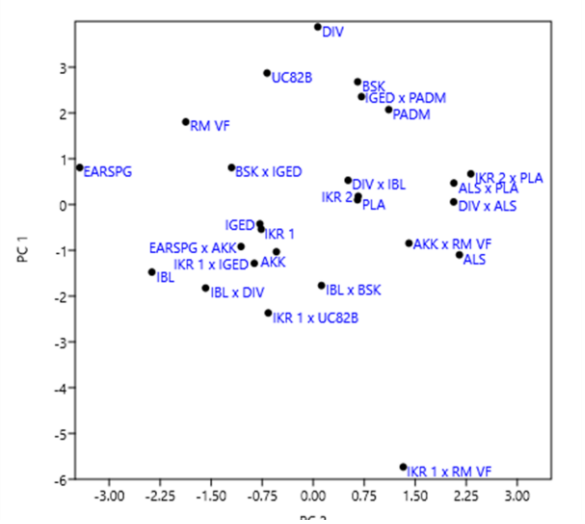

Figure 2. Configuration of twenty-six tomato genotypes under axes 1 and 2

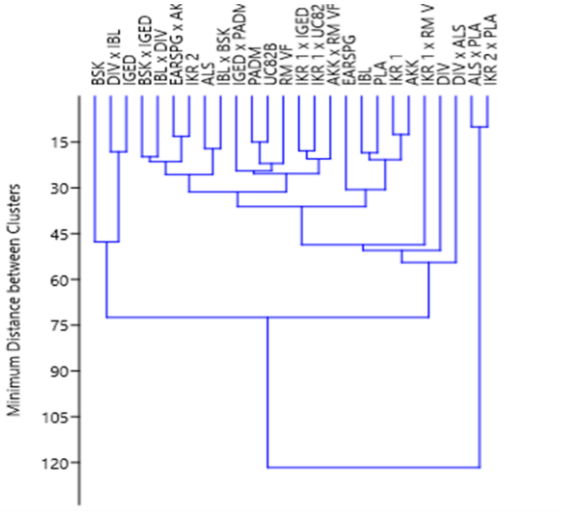

Figure 1. Dendrogram resulting from single linkage cluster analysis of twenty-six tomato genotypes of Tomato

Table 3: Distribution of the 26 tomato genotypes into clusters by single linkage cluster analysis

I (1)	II(2)	III (18)	IV (1)	V (1)	VI (1)	VII (2)
BSK	DIV×IBL IGED	BSK×IGED, IBL×DIV EARSPG×AKK IKR 2, ALS, IBL×BSK IGED×PADM PADM, UC82B RM VF IKR 1 ×IGED IKR 1×UC82B AKK×RM VF EARSPG IBL PLA, IKR 1 AKK	IKR 1×RM VF	DIV	DIV×ALS	ALS×PLA IKR2×PLA

CHARACTERIZATION AND PRELIMINARY EVALUATION OF AMARANTH SELECTION PROGENIES AFTER TWO CYCLES OF SELECTION

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ABSTRACT
One hundred and two (102) amaranth genotypes were evaluated in the 2021/2022 dry season under irrigated conditions. The materials were selections (S_2) derived from accessions conserved in the genebank of National Horticultural Research Institute (NIHORT), Ibadan which had expressed significant phenotypic variability. Plants were raised in the nursery and transplanted to field plots at 4 weeks. Characterization and evaluation data were recorded on 21 quantitative and qualitative traits. Significant differences were observed among the genotypes for all quantitative traits studied. Genotype 108-1-2 was the tallest (184.2 cm), followed by 108-1-6 (156 cm). Genotype 108-1-2 also recorded the widest mean stem diameter (34.5 mm) and had the second longest leaves (26.5 cm). The shortest genotype was 102-2-1 (68.6 cm). Genotype 151-1-5 recorded the highest mean number of branches (41). Genotype 109-2-3 recorded the largest leaves with 37 cm mean leaf length and 27.6 cm mean width. The materials are being advanced and evaluated for potential as new leafy or grain amaranth genotypes, and are maintained in the NIHORT Genebank for conservation, breeding and related research.

Keywords: genetic improvement, genebank, germplasm conservation, NIHORT, pure line selection

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INTRODUCTION
Amaranths are a major group of crops consumed widely in tropical diets as vegetable or pseudo-cereal, and constitute one of the most taxonomically diverse crops in regions where it is grown (RTI and van Stolen, 1981). The genus *Amaranthus* comprises over 70 species (Ebert *et al.*, 2011), about seventeen of which are useful as vegetable amaranths with edible leaves, while three are grain types (*A. caudatus, A. cruentus* and *A. hypochondriacus*). The highly nutritious vegetable types are rich in protein, calcium, iron, vitamins A, C and K, riboflavin (B_2), niacin (B_3), vitamin B_6, and folate (B_9) (Calderon de la Barca *et al.*, 2010; Ebert *et al.*, 2011; Akin-Idowu *et al.*, 2013).

As part of homegrown amaranth genetic improvement for production systems in Nigeria, we advanced and evaluated 102 selection progenies (S_2) of amaranth during the 2021/2022 dry season under irrigated field conditions at the National Horticultural Research Institute, Ibadan, Oyo State, Nigeria. The evaluated genotypes were derived from amaranth accessions of both leafy vegetable and grain types conserved in the NIHORT Genebank that expressed significant phenotypic variability for different traits as observed during germplasm regeneration.

MATERIALS AND METHODS
Seeds of the genotypes were retrieved from the NIHORT Genebank and sown in seedling trays filled with heat-sterilized loamy topsoil. Plants were raised under nursery conditions for 4 weeks, and then transplanted to experimental plots. Transplanted plants were spaced 0.5 m apart between and within rows on 1.5 m x 1.5 m plots, with an inter-plot spacing of 1 m. No raised beds were used. The field was irrigated to field capacity by pressurized overhead sprinklers every three days. Evaluation data were recorded on seven (7) quantitative and twelve (14) qualitative traits and subjected to statistical analyses to observe morphological differences between the genotypes.

RESULTS AND DISCUSSION
Significant differences were observed among the genotypes for all the quantitative characters

studied. Table 1 summarizes the performance of 20 of the 102 genotypes selected on the basis of plant height (10 of the tallest and 10 of the shortest). Genotype 108-1-2 was the tallest genotype (184.2 cm), followed by 108-1-6 (156 cm). Both genotypes, together with 3 others that featured among the tallest evaluated are derived from the same original population NHAM0108, a grain-type accession that expressed morphological variation. Genotype 108-1-2 also recorded the widest mean stem diameter (34.5 mm) and had the second longest leaves (26.5 cm). The shortest genotypes were 102-2-1 and 109-2-4, both with mean plant height of 68.6 cm. Genotypes 151-1-5 recorded the highest mean number of branches (41), followed by 108-1-6 (23). Genotype 109-2-3 recorded the broadest leaves with 37 cm mean leaf length and mean width of 27.6 cm.

The diversity of qualitative morphological plant and seed traits is shown in Table 2. It was generally observed that most of the genotypes were morphologically homogenous for qualitative characters such as pigmentation of stems and leaves after two cycles of selection, while few still expressed varying degrees of variation for some characters. Seed coat color was generally observed to be associated with the purported use-type of the parent accession, with the grain types mostly expressing cream and golden seeds while the leafy vegetable types mostly expressed darker seed coat colors such as black and brown. The presence of spines was observed on only one genotype which was selected from a wild genebank accession.

The study has provided a basis for the identification of promising potential new amaranth genotypes for various end-user preferences. The selections are currently being advanced and evaluated for potential as new leafy or grain amaranth genotypes. Over 7 kg in total of seed was generated for the different amaranth selections, and will be maintained in the NIHORT Genebank for conservation, breeding and related research.

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Table 1. Diversity of selected quantitative vegetative characters of the tallest and shortest amaranth genotypes evaluated

Genotype ᵅ	Parent population ᵝ	Plant height, cm	Stem diameter, mm	Leaf length, cm	Leaf width, cm	No. of branches
108-1-2	NHAM0108	184.2 (5.3)	23.9 (1.2)	24.6 (0.4)	11.6 (0.9)	9.6 (2.7)
108-1-6	NHAM0108	156.0 (0.0)	34.5 (0.0)	26.5 (0.0)	11.0 (0.0)	23.0 (0.0)
112-1-3	NHAM0112	153.8 (5.2)	18.7 (2.2)	21.3 (1.4)	10.3 (0.6)	13.2 (1.9)
112-1-9	NHAM0112	146.8 (6.5)	18.1 (1.9)	23.2 (1.4)	12.5 (1.6)	10.0 (1.8)
108-3-1	NHAM0108	146.4 (7.2)	28.5 (4.8)	23.9 (0.9)	12.6 (1.0)	7.8 (1.3)
108-2-2	NHAM0108	144.6 (9.3)	27.4 (2.7)	25.3 (1.9)	11.1 (1.1)	13.8 (2.3)
114-1-2	NHAM0114	143.2 (9.7)	16.1 (1.6)	19.2 (0.9)	9.0 (0.5)	11.8 (3.0)
108-3-4	NHAM0108	142.8 (11.5)	17.9 (2.2)	20.4 (1.0)	8.5 (0.5)	8.6 (1.5)
100-1-2	NHAM0100	141.0 (6.0)	18.6 (0.9)	22.0 (1.6)	8.6 (0.5)	17.0 (0.9)
585-1-2	NHAM0585	140.2 (11.8)	19.2 (3.2)	17.0 (2.4)	8.9 (0.7)	12.6 (1.9)
587-1-1	NHAM0587	82.0 (9.0)	10.9 (1.9)	9.6 (1.2)	3.8 (0.4)	8.8 (1.7)
111-1-6	NHAM0111	81.6 (11.6)	15.3 (1.5)	11.6 (1.0)	5.3 (0.6)	13.4 (3.3)
757-1	NHAM0757	81.4 (10.7)	20.5 (1.9)	7.9 (1.6)	5.1 (0.4)	11.0 (0.7)
110-1-4	NHAM0110	79.6 (7.8)	17.5 (1.8)	15.6 (1.2)	8.6 (2.3)	10.6 (1.9)
587-2-1	NHAM0587	78.2 (6.6)	13.1 (1.1)	10.5 (0.7)	4.9 (0.3)	5.6 (0.7)
113-1-5	NHAM0113	77.0 (7.1)	10.9 (1.5)	12.8 (1.7)	5.4 (0.7)	7.6 (1.7)
113-1-3	NHAM0113	72.6 (5.6)	10.3 (0.3)	12.7 (1.2)	5.8 (0.6)	11.4 (1.1)
110-1-1	NHAM0110	71.2 (4.6)	16.4 (2.3)	14.8 (0.8)	6.7 (0.4)	9.6 (1.0)
109-2-4	NHAM0109	68.6 (5.4)	12.5 (2.1)	13.2 (1.1)	7.6 (0.9)	3.8 (0.8)
102-2-1	NHAM0102	68.6 (6.0)	10.1 (1.0)	9.1 (0.7)	4.5 (0.4)	6.8 (1.0)
LSD (5%)		23.6	5.9	6.5	6.7	7.6

ᵅ S_2 progeny code. ᵝ Parent population accession ID, † Values shown are means of 5 replicates (standard errors of mean in parenthesis).

Table 2. Diversity of qualitative vegetative and seed characteristics of the tallest and shortest amaranth genotypes evaluated

Genotype ᵅ	Stem pigmentation	Leaf pigmentation	Presence of spines	Seed shape	Seed coat color
108-1-2	GPB	Normal green	Absent	Spherical	Cream
108-1-6	GPB	Normal green	Absent	Spherical	Cream
112-1-3	Green	Normal green	Absent	Spherical	Brown
112-1-9	GPB	Normal green	Absent	Ovoid	Dark brown
108-3-1	GPB	Normal green	Absent	Spherical	Cream
108-2-2	GPB	Normal green	Absent	Spherical	Dark brown
114-1-2	Variable: G, GPB	Normal green	Absent	Ovoid	Brown
108-3-4	GPB	MVP	Absent	Spherical	Cream
100-1-2	Green	Normal green	Absent	Ovoid	Dark brown
585-1-2	Variable: G, GPB	Variable: NG, DG, MVP	Absent	Spherical	Cream
587-1-1	GPB	Dark green	Absent	Spherical	Golden
111-1-6	GPB	Variable: DG, MVP	Absent	Spherical	Black
757-1	Variable: P, PDB	Dark green	Present	Spherical	Black
110-1-4	Green	Normal green	Absent	Spherical	Dark brown
587-2-1	Green	Normal green	Absent	Ellipsoid	Golden
113-1-5	Green	Normal green	Absent	Ovoid	Dark brown
113-1-3	Green	Normal green	Absent	Spherical	Dark brown
110-1-1	Green	Normal green	Absent	Spherical	Dark brown
109-2-4	GPS	Dark green	Absent	Ellipsoid	Dark brown
102-2-1	Green	Normal green	Absent	Spherical	Black

ᵅ S_2 Progeny code, G: Green; GPB: Green with pigmented base; GPS: Green with pigmented stripes; P: Pigmented; PDB: Pigmented with darker base; NG: Normal green; DG: Dark green; MVP: Margin and veins pigmented

HERITABILITY AND PLANT CHARACTER ASSOCIATION ON YIELD AND ITS COMPONENTS IN EGGPLANT (*Solanum melongena* L.)

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ABSTRACT: Breeding for high yield based on direct selection is a combination of yield component attributes and this is determined by the extent of genetic variability, the strength of association, and heritability status on measured agronomic traits. In this study, three accessions of eggplants; Black beauty, F_1 Djamba, and Bello obtained from NIHORT, Ibadan, Oyo State Nigeria were grown in an open field arranged in a randomized complete block design with three replications. Seeds were sown in rows at a distance of 60 cm x 60 cm between and within rows at a planting depth of 2 - 3 cm. Cultural practices such as weeding, insect pest control, and fertilizer application were carried out. Data were collected on the following agronomic traits: plant height; the number of branches per plant; the number of days to flowering; the number of fruits per plant; fruit weight; fruit diameter and number of days to maturity. Our results showed that fruit weight (99.97%), and number of days to flowering (99.89%), had the highest heritability estimate and low heritability was observed in the number of branches (40.00%). Genetic advance (GA) was found to be the highest in fruit weight (226.64) and the least was recorded in the number of branches per plant (0.61). A significant correlation with a positive coefficient was recorded between plant height and the number of fruits per plant (0.937) thus, negatively correlated with fruit weight (-0.982), number of days to flowering (-0.941) and number of days to first fruit set (-0.927). However, high genetic variability and heritability estimates obtained for most of the traits indicated the prevalence of additive gene effect governing their expression. Therefore, direct selection based on the combination of traits would help in elucidating good genotypes with high yield potentials in further crop improvement programs.

Keywords: additive gene, crop improvement, genetic advance, plant character, selection

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INTRODUCTION

Crop improvement is dependent not only on the magnitude of the phenotypic variability but also on the extent to which the desirable characters are heritable. The heritable variability and more particularly its genetic component, is clearly the most important aspect of the genetic constitution of the breeding material, which has a close bearing on its response to selection (Chattopadhyay *et al.,* 2011). Heritability denotes the proportion of phenotypic variation repeatable and is due to genes and thus helps the breeders to select the elite variety for a character (Koundinya *et al.* 2013).

A measure of heritability and genetic advance give an idea about the expected gain in next generation. Thus, high yield can be achieved by selection of those characters that have high heritability coupled with genetic advance (Koundinya *et al.,* 2017). The value of heritability estimates is enhanced when used together with the selection differential or genetic advance (Ibrahim and Hussein, 2006). Information on the amount and direction of association between yield and yield related characteristics is important for rapid progress in selection and genetic improvement of a crop (Binodh *et al.,* 2008). This will indicate the interrelationship between two or more plant characters and yield, providing suitable means for indirect selection for yield.

Hence, there is a need for studying the association of various component characters with yield to formulate effective selection criteria (Koundinya *et al.,* 2017). Again, selection of one trait invariably affects a number of associated traits which evokes the necessity in findings out the inter-relationships of various yield components both among themselves and with yield (Chattopadhyay *et al.,* 2011). The study is aimed at evaluating the heritability and plant character association on yield and its components in Eggplant (*Solanum melongena* L.).

MATERIALS AND METHODS

This study was carried out at the Teaching and Research Farm, Adekunle Ajasin University, Akungba-Akoko, Ondo State, Nigeria. The study

materials comprised of three varieties of garden eggs namely: Black Beauty, F_1 Djamba and Bello obtained from NIHORT, Ibadan, Oyo State, Nigeria. The experimental plot was cleared, ploughed and harrowed with tractor mounted implement. Plot layout was done with pegs and each experimental unit was demarcated in a plot size of 3 m x 3 m. The land area used was 121 m^2. The experimental design used in the study was randomized complete block design in three replicates. Seeds were sown in rows at the distance of 60 x 60 cm between and within row at about 4 inches depth. The seeds were thoroughly covered with soil. Hoeing was done after 10 - 13 days after germination to allow proper aeration followed by weeding to avoid crop-weed competition for emergence of vigorous seedlings. The plants were sprayed with Cypermethrin to control insect pest. In order to maintain the desired plant population, after one week gap filling was done at points where no emergence of seedling was observed. A compound fertilizer N: P: K (15-15-15) was applied after 4 weeks of planting and before fruiting.

Data collected

Data were collected on the following agronomic and yield parameters which includes; Days to first flowering, Plant height, Number of branches and fruits per plant, Fruit weight (g) and fruit diameter,

Statistical analyses

Data obtained were subjected to analysis of variance (ANOVA) using Statistical Package for Social Sciences (SPSS) version 20. The means were separated using Duncan Multiple Range Test. Correlation coefficient analysis of the parameters was carried out to determine the degree of association among the traits measured. Genetic variability parameters, such as phenotypic and genotypic component of variances were computed according to Osekita and Ajayi 2013).

Heritability (h^2) estimates (Broad sense) and genetic advance were computed according to Burton and De Vane (1953) and Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Mean Squares and Coefficient of variation

The mean squares and coefficient of variation among quantitative traits in egg plant is presented in Table 1. All the treatments showed highly significant differences from the result of the analysis of variance. The coefficient of variation ranged from 0.33 in both number of days to maturity and fruit diameter to 20.96 in fruit weight. Based on this, the genetic component of variation is very important since only this is transmitted to the next generation and therefore responds to selection (Pramila *et al.,* 2015).

Estimate of genetic parameters

Estimate of genetic parameters on eight quantitative traits in eggplant were presented in Table 2. Genotypic (GCV) and Phenotypic (PCV) Coefficient of variation were found to be highest in fruit weight (83.35, 83.44), followed by number of fruits per plant (60.77, 60.93), and while number of branches recorded the least (7.82, 12.36). High phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were found to be highest in fruit weight. This result corroborates with the report by Pramila *et al.* (2015). In general, the values of phenotypic coefficients of variation (PCV) are slightly higher than that of genotypic coefficients of variation (GCV). But the magnitude of the difference between PCV and GCV is a little lower, as an indication of less environmental influence on the expression of these attributes. This study was in accordance with the findings of Golani *et al.* (2007). Similar results were reported by Sharma and Swaroop (2000) for number of plant yield. However, most agronomic character estimates obtained for GCV and PCV in this study were high. Thus, suggesting sufficient genetic variability to facilitate improvement through selection of these agronomic traits (Danquah and Ofori, 2012).

Heritability

Relatively very high heritability in broad sense ($ħ^2$) were obtained for all the parameters observed with fruit weight recording the highest (99.97%) and the least was found in number of branches (40.00%). Genetic advance (GA) was found to be highest in fruit weight (226.64), and lowest in number of branches (0.61). Genetic advance as percent of mean were found to be highest in fruit weight (171.50) and the least was recorded in number of branches (10.17). The three parameters showed the same trend in their responses towards selection. Whenever a character is of a range between medium and large heritability, a selection due to specific performance can allow rapid progress (Bello and Aminu, 2017). However, high heritability value alone is not enough to ensure a high genetic gain (Ibrahim and Hussein, 2006). High heritability accompanied by high genetic advance (GA) observed for weight of fruit in this study indicates

negligible environment effect and this trait will be more amenable to improvement through mass progeny selection, aiming at exploiting the additive variance. High heritability and genetic advance were observed for number of fruits per plot and plant height suggesting that selection based on phenotypic performance of these traits is possible. High genetic advance observed in fruit weight and number of fruits per plot in this study corroborates the finding of Pramila *et al.* (2015). The high genetic advance observed in number of fruits per plot and fruit weight showed predominance of additive gene action.

Correlation analysis

Correlations among agronomic traits are shown in Table 3. Plant height was significantly and negatively associated with fruit weight (-0.982), number of days to flowering (-0.941) and number of days to first fruit set (-0.927). In addition, plant height was significantly and positively correlated with number of fruits per plant (0.937). Number of branches was significantly and negatively associated with fruit weight (-0.713) and number of days to flowering (-0.680). Also, number of fruits per plant showed negative correlation and significant with fruit weight (-0.955), number of days to flowering (-0.882), number of fruits per plant (-0.857), number of days to fruit ripening (-0.881) and fruit diameter (-0.961). However, fruit weight was positively correlated and significant with number of days to flowering (0.977), number of days to first fruit set (0.966) and fruit diameter (0.969). Also, number of days to first fruit set showed positive correlation and significant with number of days to plant maturity (0.998). Similarly, number of days to plant maturity was significantly and positively associated with fruit diameters (0.968). Inter correlations between various components of yield were essential as improvement in one character would simultaneously improve the performance of other character if both characters were positively correlated (Koundinya *et al.,* 2017). Plant height was significantly and positively correlated with number of fruits per plot. This result was in line with the findings reported by Danquah and Ofori (2012). The result suggests that selection for shorter plants would not produce more fruits compared to taller plants. However, longer fruit length which attract premium price in the market, selection for this agronomic trait could increase the gestation period (Danquah and Ofori, 2012). Similarly, plant height was significantly and negatively associated with fruit weight, number of days to flowering and number of days to first fruit set. It was quite evident that fruit weight gets reduced with increase in the number of fruits per plant. Earlier flowering or early conversion to reproductive stage reduces the plant vegetative growth which resulted in the negative association between days to flowering and plant height as reported by (Koundinya *et al.,* 2017).

Reliability analysis

Covariance matrix for eight quantitative traits in egg plants for reliability analysis were presented in Table 5: Plant height is expected to not less than 58.99 cm tall, number of branches per plant (0.5), number of fruits per plot 384.75 fruits at the peak of harvest, fruit weight of about 9120.47 g per plot, a flowering duration of 227.25 days, the maximum number of days to first fruit set of the late flowering types (141.00) in days, about 163.25 days to the longest matured plant to senescence and with moderate fruit diameters of 4.66 cm.

Conclusion

Based on the results obtained it was concluded that high genetic variability and heritability estimates obtained for most of the characters indicated the prevalence of additive genetic effects (fixable) governing their expression. Therefore, direct selection based on the combinations of traits would help in harnessing for selecting good genotypes with high yield per plant in improvement programmes.

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Table 1. Mean Squares and coefficient of variation among quantitative traits in egg plant

Source of variation	df	Plant height (cm)	No of Branches	No of fruit per plant	Fruit weight (g)	No of days to flowering	No of days to first fruit set	No of days to plant maturity	Fruit diameters (cm)
Treatments	2	228.92*	1.00*	1520.33*	36424.28*	907.00*	562.33*	652.00*	18.54*
Replication	2	1.40ns	0.33*	14.33*	2.21ns	1.33*	0.33ns	0.33*	0.05*
Error	4	2.83	0.33	2.17	27.69	0.33	0.67	0.33	0.02
		32.34	6	37	132.15	61.33	80	101.33	6.15
CV		8.75	5.5	5.86	20.96	0.54	0.84	0.33	0.33

Table 2: Estimate of genetic parameters on eight quantitative traits in egg plant

Characters	GCV	PCV	ɦ2	GA	GAM
Plant height (cm)	26.84	27.34	96.38	17.56	54.29
No of branches	7.82	12.36	40.00	0.61	10.17
No of fruits per plant	60.77	60.93	99.57	46.24	124.97
Fruit weight (g)	83.35	83.44	99.97	226.64	171.50
No of days to flowering	28.35	28.36	99.89	35.79	58.36
No of days to first fruit set	17.10	29.63	99.64	28.13	35.16
No of days to fruit maturity	14.54	14.56	99.85	30.34	29.94
Fruit diameter (cm)	40.39	40.46	99.68	5.11	83.09

GCV: Genetic coefficient of variation; PCV: Phenotypic coefficient of variation; ɦ²: Heritability in broad sense; GA: Genetic advance; GAM: Genetic advance in percent of mean/Expected genetic.

Table 3. Phenotypic Correlation coefficient of eight quantitative traits in egg plant

Parameters	NOB	NFPPT	FW	NDFF	NDF	FD	NDFM
PLHT	0.66	0.97**	-0.98**	-0.94**	-0.93**	-0.939	-0.98
NOB		0.67*	-0.71*	-0.68*	-0.66	-0.68	-0.68
NFPPT			-0.96**	-0.88**	-0.86**	-0.88**	-0.96*
FW				0.98**	0.97**	0.98*	0.99*
NDF					0.98**	0.99**	0.97*
NDFF						0.99**	0.99
NDFM							0.97*

*, ** significant at 0.05 and 0.01 levels of probability PLHT = Plant height, NOB = Number of branches, NFPPT = Number of fruits per plot, FW = Fruit weight, NDF = Number of days to flowering, NDFF = Number of days to first fruit set, NDFM = Number of days to fruit maturity, and FD = Fruit diameters

Table 4: Reliability analysis for parameter covariance matrix in eight quantitative traits of egg plant

Traits	PLHT	NOB	NFPPT	FW	NDF	NDFF	NDFM	FD
PLHT	58.99	3.58	146.45	-720.21	-108.97	-84.51	-92.19	-16.23
NOB	3.58	0.50	9.25	-48.13	-7.25	-5.50	-6.13	-1.04
NFPPT	146.45	9.25	384.75	-1789.89	-260.75	-199.50	-220.75	-40.70
FW	-720.21	-48.13	-1789.87	9120.47	1405.88	1095.72	1190.50	205.27
NDF	-108.97	-7.25	-260.75	1405.88	227.25	178.50	192.38	31.53
NDFF	-84.51	-5.50	-199.50	1095.72	178.50	141.00	151.38	24.58
NDFR	-92.19	-6.13	-220.75	1190.50	192.38	151.38	163.25	26.71
FD	-16.23	-1.04	-40.70	205.29	31.53	24.58	26.71	4.66

PLHT = Plant height, NOB = Number of branches, NFPPT = Number of fruits per plot, FW = Fruit weight, NDF = Number of days to flowering, NDFF = Number of days to first fruit set, NDFM = Number of days to fruit maturity, and FD = Fruit diameters

YIELD PERFORMANCE AND STABILITY OF SOME PROMISING LARGE SEEDED CASTOR GENOTYPES ACROSS EIGHT LOCATIONS IN NIGERIA

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ABSTRACT

Castor (*Ricinus communis* L.) expresses a wide-range of plasticity to changing in environment, hindering effective ranking of genotypes by mean performance. In the present trial assessment of performance and stability of some promising large seeded castor genotypes at eight locations in Nigeria. The trial was laid out on randomized complete block design with three replications. Results showed significant effects of genotypes, locations as well as genotype by locations interaction for seed yield, height at maturity, spike per plant and seed oil content. Pool means showed a range between 781.16 kg/ha and 1263.53 kg/ha among the genotypes. The GGE Biplots revealed that the eight locations could be grouped into two clusters. The genotype Acc001 (Gen3) out yielded others at five out of the eight locations. Genotype Acc001 and Genotype Acc045 showed better performance and stability among the evaluated castor genotypes.

Keywords: castor, GGE Biplot, stability, yield performance

INTRODUCTION

Castor has a wide-range of variability for characteristics such as seed size (Wiess, 2000). The small seeded castor is commonly chosen if the interest is on the seed oil while the large seeded ones are preferred if the interest is on the product derived from seed endosperm (Salihu *et al.*, 2015). In Nigeria and some other parts of West Africa, the large seeded castors are used to produce '*Ogiri*' - a local condiment (Gana, 2015). The small seeded are not used for the condiment due to the drudgery involved in the removal of the seed coat and low endosperm yield. The condiment is a highly proteinous fermented food supplement traditionally consume by about 20% of the Nigerian population (Okeke *et al.*, 2009). The castor condiment has been reported to have 5.70 and 2.57-times higher protein content than pumpkin and snail respectively (Okeke *et al.*, 2009). The seed may also contain up to 60% oil content. The castor oil has a unique fatty acid composition which provide expanding utilization in many industries.

Despite the economic potential, castor improvement programme in Nigeria has not been receiving much attention, resulting in lack of improved production practices to the farmers (Amosun *et al.,* 2013). Low yield is a major limitation of production in Nigeria (Gana, 2015). Against average yield of 1,200 – 3,000 kg/ha obtainable in other countries like India, China and Brazil; the average yield among farmers in Nigeria ranges between 300 kg/ha and 600 kg/ha (Amosun *et al.,* 2013). Another major limitation in the country is poor and unorganized castor market (Salihu *et al.*, 2015). The major off take of castor seed in Nigeria presently are the local condiment producers and some cottage oil industries; thus, farmers have preference for the large seeded castor because of the available market. Therefore, the objectives of this research were to assess the yield performance as well as stability of some promising large seeded castor genotypes across eight locations in Nigeria.

MATERIALS AND METHODS

Eight (8) large seeded genotypes (including a check) were evaluated in 2016 and 2017 raining seasons. The trials were arranged in a randomised complete block design with three replications. The genotypes were evaluated on plot size of 5 m x 6 m with a plant spacing of 1.00 m by 0.75 m. Two seeds were sown and later thinned to one stand per hill. Fertilizer at 60:30:30 kg/ha of N:P:K respectively was applied. Weeding was carried out at 3, 7 and 11 weeks after planting. The locations used were Badeggi, Minna, Zuru, Mokwa, Bacita, Riyom, Ibadan and Amakama. Yield Performances and Stability Analysis (GGE Biplot) for the multi-locational data was done following the procedure of a statistical package PBTools 1.3 version

Statistical analyses

Data were analysed with the Statistical Package for Agricultural Research using descriptive statistics and analysis of variance at p=0.05. Yield Performances and Stability Analysis (GGE Biplot) was done following the procedure of a statistical package PBTools 1.3 version

RESULTS AND DISCUSSION

A Significant contribution of genotypes to the variation in seed yield was recorded in all the locations (Table 1). Also, the pool ANOVA showed that there were significant differences in the seed yield and all other traits considered among the genotypes (Table 1). Significant effects of environments as well as genotype by environment were observed for seed yield and height at maturity (Table 1). Pool means showed a range between 781.16 kg/ha and 1263.53 kg/ha among the genotypes. The genotype Acc001 recorded the highest average seed yield of 1263.53 kg/ha while the least mean was recorded by the local check (i.e popular farmers' accession – not standard check). The significant effects of locations as well as G × L interactions observed for the seed yield and height at maturity have also been reported by Solanki and Joshi (2003) and Aher *et al.* (2015).

According to the GGE Biplots, a total of 84.3% (PC1 - 61.1% + PC2 - 23.3%) variation was attributed to the Principal Component Axis 1 and 2 (Figures 1, 2, 3). Ibadan and Mokwa locations showed the highest discriminating ability among the locations in the two clusters respectively (Figure 1). In term of representativeness, Zuru (E8) Bacita with least angle to the average environmental axis (AEA) are the most representative of the two groups (1). The genotype Acc001 (Gen3) showed good stability and falls within the concentric cycle of ideal genotype, representing the most ideal genotype among the entries (Figure 2). The which-won-where biplot for the entries is presented in Figure 3. The genotype Acc001 (Gen3) out yielded others in Amakama (E1), Bacita (E2), Mokwa (E6), Riyon (E7) and Zuru (E8). Genotype Acco040 (Gen6) out yielded all others at Badeggi (E3) and Ibadan (E4). From the results of the performance and stability assessments, it is logical to recommend both Acc001 and Acc045 for on farm trials in both identified clusters of environments so as to exploit the opportunity of both broad adaptation and specific adaptation to the environments if any

Conclusion

The results revealed wide range of yield performance means among the genotypes evaluated. Out of the 8 genotypes evaluated, genotype Acc001 and Acc045 were two best performing genotypes and could be recommended for on-farm yield trials for farmers selection and adoption.

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Table 1. Pool means for seed yield and other agronomic traits of eight castor genotypes across eight (8) locations in Nigeria, 2016-2017

Genotypes	Day to Maturity	Height at maturity (cm)	Seed Yield (kg/ha)
Acc.048	106.77	159.37	938.85
Acc.050	102.18	145.92	902.2
Acc001	109.45	141.12	1263.53
Acc020	171.37	250.85	815.7
Acc024	161.32	149.07	863.2
Acc040	98.16	186.7	992.18
Acc045	99.25	240.94	1060.85
Local Check	143.72	212.41	781.16
Mean	124.03	185.8	952.2
Mean square			
Location (L)	8114.95	660.17**	2602095.24**
Block (L)	29158.25	301.52	15467.5
Genotype (G)	43138.24*	93365.11**	1070249.84**
Year (Y)	2299.71	42.68	988173.33**
G x Y	7519.86	153.21	45577.42**
L x G	15042.92	1204.17**	274992.73**
L x Y	12880.17	26.02	179918.27**
L x G x Y	22775.72	282.13*	43398.35**
Pooled Error	19361.13	190.95	9830.41

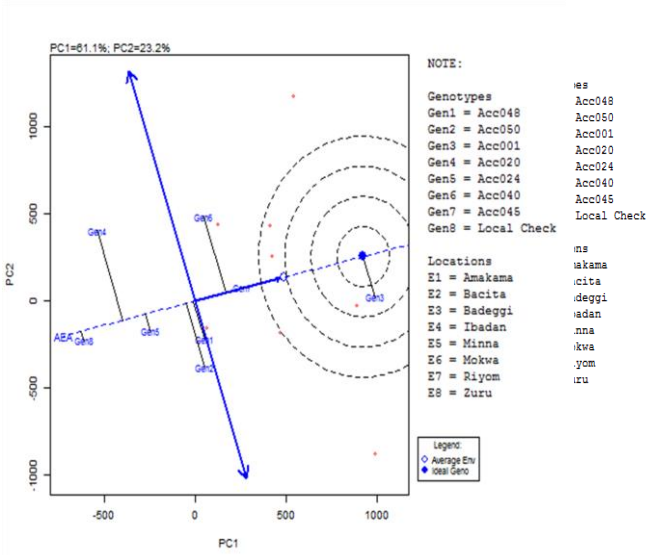

Figure 2. Mean performance and stability of the 8 castor genotypes evaluated across 8 Locations in Nigeria

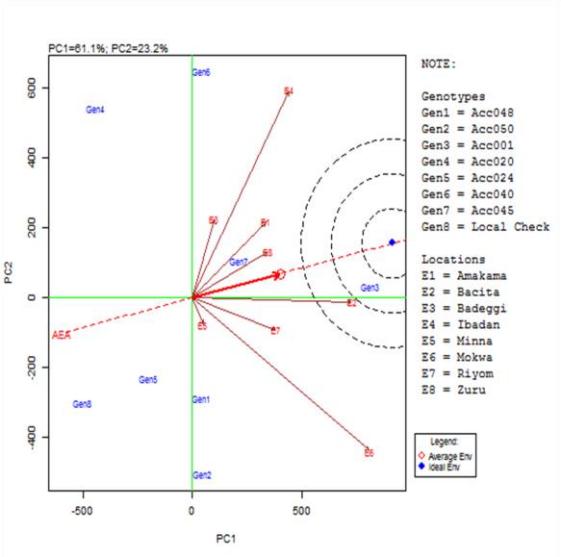

Figure 1. GGE Biplot showing representative and discriminating abilities of the eight locations considers

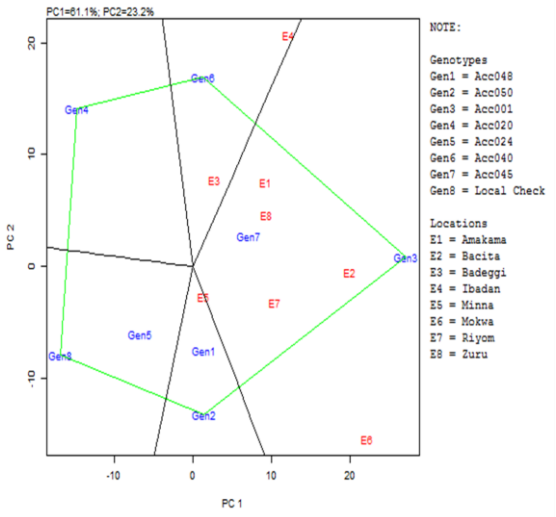

Figure 3: The which-won-where view of the GGE biplot

GENETIC VARIATION IN SOYBEAN (*Glycine max* L. Merril) GENOTYPES

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ABSTRACT
Eighteen genotypes of soybean were evaluated for genetic variation, heritability and genetic advance on the field using randomized complete block design in two (Ogun and Oyo) States. The analysis of variance showed that there was significant ($p < 0.01$) variation among the genotypes for the characters studied except for plant height and number of branches. Effect of locations was significant ($p < 0.01$) except for days to maturity and seed yield. The highest phenotypic coefficient of variation in Ibadan was observed for days to emergence (64.63) while, In Abeokuta, 100-seed weight (19.28 g) recorded the highest for PCV respectively. High heritability and high genetic advance observed in all the characters except for days to emergence, plant height and number of branches revealed that selection for these traits will be favourable because they are governed by additive gene. At phenotypic correlation, yield correlated significantly ($p<0.05$) with number of branches in the two locations. Therefore, this character can be used as selection index for seed yield improvement in soybean

Keywords: genetic variation, heritability, traits, yield

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INTRODUCTION
Soybean is a legume that is widely grown for its edible seed which is rich in oil and protein. It is native to East Asia particularly China (Tian *et al.*, 2010). The cultivated type *Glycine max* (L.) is an annual crop, while some related wild type species are perennial in nature (Mullen *et al.,* 2003). According to FAO (2018), soybean is globally produced on about 125 million hectares, yielding about 349 million tonnes at the rate of 2.79 tons/ ha. Africa contributes about 3.6 million tonnes at the rate of 1.36 tons/ha on a total land area of 2.6 million hectares. Nigeria is only second to South Africa in the continent yielding about 0.76 million tonnes on a total harvested area of 0.78 million tonnes at the rate of 0.97 tons/ha. The success of breeding programmes can be enhanced when variability within the existing germplasm is high, which allows the plant breeder to more rapidly produce new varieties or improve existing ones (Meena and Bahadur *et al.*, 2013). Effective selection of genotypes for desirable traits is best done when the heritability score is considered alongside that of genetic advance and GCV (Abebe*et al.*, 2017). Hence, this study was carried out to estimate genetic variation, heritability, genetic advance and character associations among yield and yield contributing traits of 18 soybean genotypes.

MATERIALS AND METHODS
Eighteen genotypes of soybean used for this study were sourced from the International Institute of Tropical Agriculture (IITA), Ibadan, Oyo State, Nigeria. The experiment was conducted in two locations, experimental field of National Cereals Research Institute, Moor Plantation, Ibadan, Oyo State (Latitude 8.15°N, Longitude 3.61°E) and Teaching and Research Farm, Federal University of Agriculture Abeokuta, Ogun state (Latitude 6.99°N, Longitude 3.4 °E). The experiments were established in June 2016 and laid out in a randomized complete block design in three replications. Each variety was planted in a two-row plot of 2 m long. The seeds were planted by drilling method and later thinned to 5 cm between plant after about 2 weeks the spacing between rows were maintained at 75 cm with an alley of 1 m between plots. Data were collected on the following traits, days to emergence, days to 50% flowering, plant height, number of branches, days to maturity, number of pods per plant, plant height of first pod, 100-seed weight and seed yield. Data were subjected to analysis of variance (ANOVA) using SAS 1999 statistical package. The treatment means were separated using Turkey's HSD test at 5% probability level. Phenotypic correlations were obtained using the formula of Miller *et al.*, 1958. Broad-sense

heritability and genetic advance were also computed

RESULTS AND DISCUSSION

A significant varietal effect was observed for all characters except for plant height and number of branches. The effect of location was significant for all characters except for days to maturity and seed yield. Significant effect of genotype x location was observed for all characters except for number of branches, number of pods per plant, plant height of first pod and seed yield (Table 1). The phenotypic variances were generally greater than the genotypic variances; in some traits their difference was small and negligible while in others their differences were quit much. The highest Phenotypic Coefficient of Variation (PCV) and Genotypic coefficient of variation (GCV) in Ibadan was observed for number of days to emergence (64.63, 63.24 respectively) while the lowest scores were obtained from number of days to maturity (2.32, 2.30) respectively. Similarly, in Abeokuta, number of days to maturity also recorded the lowest PCV and GCV respectively (2.54, 2.52), While 100 seed weight (19.28, 19.24) recorded highest value for the parameters, respectively. The estimate of broad sense heritability for Ibadan ranged from 8.00% in number of branches to 99.86% in days to 50% flowering, whereas, in Abeokuta, the estimate ranged from 15.56% for plant height to 99.54% for 100 seed weight. Number of days to emergence had the highest genetic advance (127.46%) in Ibadan while 100 seed weight was the highest (39.54%) in Abeokuta. The lowest genetic advance estimate was obtained in number of days to maturity (4.69%) in Ibadan and for plant height (3.16%) in Abeokuta (Table 2).

Phenotypic correlation among nine characters of soybeans in two locations showed that Seed yield has significant positive correlations with number of branches (0.40**) in Ibadan and significant negative correlations with plant height (-0.32*) and plant height of first pod (-0.41**) in Abeokuta. Number of days to emergence (0.39**) in Ibadan, plant height of first pod (0.38**, 0.41**) in the two locations significantly correlated positively with 100 seed weight while it has significant negative correlations with plant height (-0.29*) in Ibadan, number of days to maturity (-0.55**, -0.58**) and number of pods per plant (-0,50**, -0.31*) in the locations respectively. Plant height of first pod has significant positive correlations with days to emergence (0.29*) in Ibadan and with plant height (0.31*) in Abeokuta, it significantly correlated negatively with number of days to maturity (-0.35*, -0.47**) in the locations respectively. Number of days to maturity has significant negative correlations with number of days to emergence (-0.46**) in Ibadan and number of branches (-0.30*) in Abeokuta it however correlated positively with plant height (0.62**) (Table 3)

DISCUSSION

Significant variability was observed for most of the characters indicating sufficient variations among the genotypes. Similar result was obtained by Sawale *et al.* (2014) when they assessed 12 genotypes of soybean for genetic variability. The inconsistence of genotypes from location to location suggests the presence of genotype x environment interaction. This indicates that selection among these genotypes has to be location specific. Expectedly the phenotypic coefficients of variation (PCV) were generally higher than the genotypic coefficients of variation (GCV) across the locations. In cases where the difference is small it suggests a minimal effect of the environment in the expression on the observed phenotype, hence selection based on the phenotypic variations will be promising; while in cases where the difference of PCV and GCV is quite much, it suggests a greater effect of the environment in the phenotype. The higher heritability estimates for number of days to 50% flowering, number of days to maturity, number of pods per plant, plant height of first pod, 100-seed weight and seed yield in both locations as well as number of days to emergence in Ibadan, indicate that their expression was largely determined by genetic factors. Similar observations were made by Parameshwar 2006 (number of days to 50 % flowering); Sawale *et al.*, 2014 (number of pods per plant); Agarwal *et al.*, 2001 (number of days to maturity); Aditya *et al.*, 2011 (100 seed weight) and Bangar *et al.*, (2003) for seed yield. Therefore, selecting for these characters on the basis of phenotypic performance is likely to be reliable and effective. The difference in heritability estimates of the characters between locations suggests their response to environments. Moderate to high estimates of genetic advance observed for number of days to 50% flowering, number of pods per plant, plant height of first pod, 100 seed weight and yield in both locations and days to emergence with plant height both in Ibadan, suggests good prospect for genetic gain during selection.

Abebe *et al.*, 2017, suggested that a trait with high GCV, heritability and genetic advance will be predictable in performance because such trait is governed by additive gene. The moderate to high values of GCV, heritability and genetic advance observed for number of days to 50% flowering, number of pods per plant, 100-seed weight and seed yield in the two locations, and days to emergence in Ibadan could be attributed to addictive gene action, thus making selection for them shall be effective. Cruz *et al.,* 2004 postulated that phenotypic and genotypic correlation coefficients with the same arithmetic sign indicate the absence of error in sampling and evaluation; similar signs could be observed for most of the character correlation especially for seed yield with all the characters in both coefficients. Arshad *et al.,* 2006, reported positive and significant correlation between number of branches and seed yield in soybean. Similarly, if there exist a negative correlation between characters, the effect of their improvement will be inverse (Nogueira et al., 2012); these relationships were observed between seed yield with plant height and plant height of first pod in Abeokuta.

Conclusion

This experiment revealed that there is sufficient variation among the characters of the 18 genotypes of soybean evaluated; it further indicated that because of the significance of the characters under location, selection has to be location specific. High heritability and genetic advance which implies that selection for these characters for hybridization will be profitable because they are governed by additive gene component and are stable. Character correlations further reveals that an attempt to improve or select for genotypes with a greater number of branches, this character can be used as selection index for seed yield improvement in soybean

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Table 1. Combined analysis of variance of seed yield and related characters in Ibadan and Abeokuta for eighteen soybeans genotypes

Sources of variation	Blocks (df = 4)	Genotype (G) (df = 17)	Location [L] (df = 1)	G x L (df = 17)	Error (df = 68)
Days to emergence	0.55	15.44**	12.00**	15.16**	0.76
Plant height (cm)	220.64**	67.71	1105.92**	105.97**	46.9
Number of Branches	6.20**	1.81	161.03**	1.93	1.39
Days to 50% flowering	10.88**	243.77**	131.12**	18.02**	2.46
Days to Maturity	0.18	47.62**	0.01	1.64**	0.44
Number of pods/plant	5.12	136.32**	131.12**	11.87	7.73
Plant height of first pod (cm)	0.67	10.43**	9.60**	0.77	0.73
100-seed weight (g)	0.04	53.14**	5.01**	0.74**	0.12
Seed yield (kg/ha)	17286.01	603659.10**	45797.93	26699.04	17018.29

** $p < 0.01$, *$p < 0.05$

Table 2. Mean, genotypic and phenotypic coefficient of variability, broad sense heritability and Genetic advance expressed as percentage of the mean in Ibadan and Abeokuta for 18 soybean genotypes

Character	Location	Mean	PCV	GCV	HB (%)	GA
Days to emergence	Ibadan	4.93	64.63	63.24	95.74	127.46
	Abeokuta	4.26	6.47	4.04	39.04	5.20
Plant height (cm)	Ibadan	23.06	30.89	22.92	55.06	35.04
	Abeokuta	29.46	9.87	3.89	15.56	3.16
Number of branches	Ibadan	2.96	29.42	8.32	8.00	4.85
	Abeokuta	5.40	12.92	9.42	53.11	14.14
Days to 50% flowering	Ibadan	54.15	13.14	13.13	99.86	27.03
	Abeokuta	56.35	10.74	10.51	95.72	21.18
Days to maturity	Ibadan	117.78	2.32	2.30	98.42	4.69
	Abeokuta	117.80	2.54	2.52	98.04	5.14
Number of pods/plant	Ibadan	26.56	18.12	17.29	91.06	33.98
	Abeokuta	28.76	17.81	16.73	88.26	32.39
Plant height of first pod (cm)	Ibadan	9.49	14.36	14.25	98.40	29.12
	Abeokuta	10.09	13.59	11.82	75.68	21.18
100 seed weight (g)	Ibadan	14.98	20.17	20.13	99.55	41.37
	Abeokuta	15.41	19.28	19.24	99.54	39.54
Seed yield (kg/ha)	Ibadan	1920.22	15.72	15.38	95.73	30.99
	Abeokuta	1961.41	17.59	17.03	93.74	33.97

Phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV), heritability in broad-sense (HB), genetic advance (GA)

Table 3. Phenotypic correlation coefficient among eight characters in soybean in Ibadan and Abeokuta

Characters	Location	Plant height	Number of branches	Days to 50% flowering	Days to Maturity	Number of pods/ plant	Plant height of first pod (cm)	100-seed weight (g)	Seed yield (kg/ha)
Days to emergence	IB	-0.73**	0.48**	0.19	-0.46**	-0.06	0.29*	0.39**	0.24
	AB	0.02	0.18	0.16	-0.02	-0.04	0.25	0.06	0.11
Plant height (cm)	IB		-0.04	-0.38**	0.62**	-0.04	-0.05	-0.29*	-0.05
	AB		-0.17	0.46**	0.07	0.11	0.30*	0.04	-0.32*
Number of branches	IB			0.06	0.22	0.26	0.07	-0.25	0.40**
	AB			0.45**	-0.30*	-0.21	0.08	0.23	0.21
Days to 50% flowering	IB				-0.15	-0.18	0.24	0.13	-0.21
	AB				-0.12	-0.07	0.14	0.19	-0.15
Days to maturity	IB					0.16	-0.35*	-0.55**	0.07
	AB					-0.11	-0.47**	-0.58**	0.02
Number of pods/plant	IB						0.06	-0.50**	-0.1
	AB						0.09	-0.31*	-0.22
Plant height of first pod (cm)	IB							0.38**	-0.21
	AB							0.41**	-0.41**
100 seed weight (g)	IB								0.01
	AB								0.19

IB-Ibadan, AB-Abeokuta

DISTRIBUTION AND DIVERSITY OF COWPEA GERMPLASM IN NIGER STATE

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ABSTRACT: Biodiversity loss have emerged as bottleneck befalling the agricultural production including cowpea. Rising insecurities, socio-economic changes, abnormal onset and cessation of rainfall and soil conditions has led to a dramatic reduction of cowpea landraces cultivated recently and probably to the disappearance of local populations. Germplasm exploration is the basis for crop improvement and foundation of agricultural production. This study was designed to evaluate the distribution and diversity of cowpea germplasm using seeds morphology. The study was conducted between the months of November to December 2021. A total of 43 germplasm was collected. The germplasms were randomly collected across the three Geopolitical zones of Niger state. The data was collected using participatory research tools and techniques such as direct observation, group discussions, individual interviews, field visits and questionnaires. The results revealed that *Vigna unguiculata. Vigna unguiculata* recorded the highest accessions (39), followed by *Vigna angularis* (1), *Vigna mungo* (2), *Vigna radiata* (1). *Vigna unguiculata* showed the highest occurrence in most parts of the three geopolitical zones while *Vigna angularis* and *Vigna radiata* were found in Zone A), *Vigna mungo* were found in Zone A and zone B. Zone A had the highest germplasm accessions (22), zone C (13). Zone B (8). This result showed an uneven distribution of the species of cowpea and this could be as a result of the increasing insecurity ravaging some parts of the state. There by promoting the movement of the farmers from one area to another. Hence germplasm collection can serve as means of conserving crop diversities from total loss.

Keywords: cowpea, food security, genetic diversity, germplasm

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INTRODUCTION

Cowpea (*Vigna unguicuilata* L. Walp.) (2n = 2x =22) belongs to the family Fabaceae and is a warm annual crop that is adapted to drier regions of the tropics (Agbogidi, 2010). Cowpea is mainly consumed as dry grain or fresh vegetable. The grain contains high protein, carbohydrate, vitamins, and fibre (Hall, 2012). Boukar *et al.* (2019), revealed that the protein content of cowpea is about 250 mg/g, which is comparable to soybeans. Boukar *et al.* (2016), reported that Nigeria is the largest producer of cowpea worldwide followed by Niger, Burkina Faso, Cameroon, and Mali. The North West and North East regions of Nigeria such as Borno, Bauchi, Gombe, Jigawa, Kaduna, Kano, Katsina, Kebbi, Sokoto, and Zamfara States are the most productive, accounting for 75% of the cowpea production in Nigeria (Manda *et al.,* 2019). Niger state has high diversity of cowpea however, it has not been collected and assessed extensively thus leading to the disappearance of many varieties, as earlier reported by Gbaguidi *et al.,* 2013).

Socio-economic changes and drought however, has led to a dramatic reduction of cowpea landraces cultivated recently and probably to the disappearance of local populations (African Centre for Biodiversity, 2015). Similarly, the current insecurities in Nigeria have been identified by Aluko *et al.* (2016) as a major factor behind the reduction in cowpea production. Germplasms are living genetic resources that are maintained for animal and plant breeding, preservation, and other research uses. Gado *et al.* (2019), opined that germplasm collections ranges from collections of wild species to elite, domesticated breeding lines that have undergone extensive human selection. Germplasm collection plays a critical role in supporting conservation and crop genetic enhancement strategies. It is important for the maintenance of biological diversity and food security. Genetic diversity of crops plays an important role in sustainable development and food security, as it serves as a source of genes needed in the development of better performing and well adapted varieties (Dossa *et al.,* 2016).

The aim of this study was to evaluate the distribution and diversity of cowpea germplasm in the geopolitical zones of Niger state using seeds morphological traits of varieties.

MATERIALS AND METHODS

The germplasm collection was done following the methods described by Kombo *et al.* (2012) and Gado *et al.* (2019). The germplasms were collected between the months of November to December 2021 across the growing local government in the three Geopolitical zones of Niger state. The data were collected through participatory research tools and techniques such as direct observation, group discussions, individual interviews and field visits using a questionnaire. The varieties available with the producers were collected in paper bags and labelled following the methods of Gado *et al.* (2019). The germplasms were characterise using standard descriptors developed by the International Board for Plant Genetic Resource IBPGR1 (1983).

RESULTS AND DISCUSSION

A total of 43 accessions of the genus *Vigna* and four species; *unguiculata, angularis*, *mungo*, *radiate* where collected. After the sorting, *V. unguiculata* recorded the highest accessions (39), *V. angularis* (1), *V. mungo* (2), *V. radiata* (1) (Table 1, Figure 1). The specie *V. unguiculata* showed the highest occurrence in most parts of the three geopolitical zones while *V. angularis* and *V. radiata* were found in Bida (Zone A), *V. mungo* was found in Bosso (Zone B) and Bida (Zone A). Mokwa and Bida (Zone A) had the highest number of accessions 22, Kontagora and Wushishi (Zone C) 13, Shiroro and Bosso (Zone B) 8. These findings entails that there was uneven distribution of the species of cowpea across the geopolitical zones of Niger state.

The un-uniform distribution and confinement of some species to one particular area or zone of the state could be attributed to the varying availability of rainfall or other edaphic conditions. This can be corroborated by the findings of Adojutelegan *et al.* (2015) who highlighted that rainfall and soil conditions among others limit production of watermelon. According to Oyinloye *et al.* (2018), the outcomes of climate change has led to the disruption in the seasonal pattern of food production and distribution. The low occurrence of *V. unguiculata* in zone C and parts of zone B could be attributed to the rising insecurities which has crippled farming activities in the zones. This is supported by the findings of Aluko *et al.* (2016), who reported that increasing insecurities spread in parts of country could limit the production of cowpea. Similarly, Agri *et al.* (2019), mentioned that the escalation of insurgency and other forms of conflicts has caused many farmers to abandon their farms thus affecting the production and diversity of cowpea in Nigeria.

The occurrence of *V. ungiculata* across the zones might be linked to in and out flow of germplasms in the regions which could be facilitated by Agricultural Development Projects (ADPs) as reported by Gado *et al.* (2019). Similarly, Mahesh and Ronnie (2017), reported that one of the routes through which germplasms get in to the region is by donor-assisted projects involved in agricultural development.

Conclusion

Niger state houses substantial diversity of cowpea *Vigna unguiculata* is of outmost importance to the economy and the livelihood of the farmers and the populace. The *V. unguiculata* showed the highest occurrence in most parts of the three geopolitical zones while *V. angularis* and *V. radiata* was found in Bida (Zone A), *V. mungo* were found in Bida and Bosso (Zone A and B).

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Figure 1. Seed morphology of cowpea species in Niger State

Table 1. Sources and description of cowpea in Niger State

Accession	Local name	Scientific name	Coat colour	Hilum colour	Shape	Length (cm)	Diameter (mm)	Location	L.G	Zone
NGA-BD-01	Kapangi	*V. unguiculata*	Cream white	Yellow	Rhomboid	0.8	5	Edokota	Bida	NA
NGA-BD-02	Ezo miliki	*V. unguiculata*	Cream	White	Kidney	1.0	7	Bida	Bida	NA
NGA-BD-03	Kapangi	*V. unguiculata*	Cream white	Black	Globose	0.5	4	Batati	Bida	NA
NGA-BD-04	Ezo sobo	*V. unguiculata*	Brown	White	Rhomboid	0.9	5	Bida	Bida	NA
NGA-BD-05	Bossa	*V. unguiculata*	White	Black	Ovoid	1.3	7	Bida	Bida	NA
-NGA-BD-06	Egwakangi	*V. angularis*	Red	White	Rhomboid	0.6	4	Kutigi	Bida	NA
NGA-BD-07	Dan misra	*V. unguiculata*	White	White	Rhomboid	1.2	7	Bida	Bida	NA
NGA-BD-08	Kapangi	*V. unguiculata*	White	Yellow	Kidney	0.9	5	Bida	Bida	NA
NGA-BD-09	Kapangi	*V. unguiculata*	Cream white	Black	Kidney	0.8	4	Kangi Bororo	Bida	NA
NGA-BD-10	Kebbiwhite	*V. unguiculata*	Cream white	Brown	Ovoid	0.9	5	Bida	Bida	NA
NGA-MK-11	Ezo sobo	*V. unguiculata*	Neples yellow	White	Kidney	1.3	7	Kudu	Mokwa	NA
NGA-MK-12	Ezo sobo	*V. unguiculata*	Light brown	White	Rhomboid	1.2	4	Kudu	Mokwa	NA
NGA-MK-13	Ezo sobo	*V. unguiculata*	Golden yellow	White	Rhomboid	1.0	5	Ibbah	Mokwa	NA
NGA-MK-14	Ezo milki	*V. unguiculata*	Cream	White	Ovoid	1.0	4	Mokwa	Mokwa	NA
NGA-MK-15	Ezo miliky	*V. unguiculata*	Cream	White	Rhomboid	0.9	6	Kudu	Mokwa	NA
NGA-MK-16	Ezo sobo	*V. unguiculata*	Golden brown	White	Rhomboid	1.3	6	Ibbah	Mokwa	NA
NGA-MK-17	Ezo kenchi	*V. unguiculata*	White	Brown	Ovoid	1.1	6	Kudu	Mokwa	NA
NGC-KT-18	Waken milk	*V. unguiculata*	Cream	White	Rhomboid	1.0	6	Kontagora	Kontagora	NC
NGC-KT-19	Danmarkinsoja	*V. unguiculata*	Black &White	White	Rhomboid	1.0	4	Kontagora	Kontagora	NC
NGC-KT-20	Waken sobo	*V. unguiculata*	Bright yellow	White	Rhomboid	1.0	6	Kontagora	Kontagora	NC
NGC-KT-21	Waken sobo	*V. unguiculata*	Yellow	White	Kidney	1.3	5	Kontagora	Kontagora	NC
NGC-KT-22	Kananado	*V. unguiculata*	White	Brown	Ovoid	1.0	6	Kontagora	Kontagora	NC
NGC-KT-23	Dan misra	*V. unguiculata*	White	White	Rhomboid	1.0	4	Kontagora	Kontagora	NC
NGC-ZG-24	Olanyo	*V. unguiculata*	Yellow	White	Rhomboid	1.3	5	Zungeru	Wushishi	NC
NGC-ZG-25	Kananado	*V. unguiculata*	White	Brown	Rhomboid	1.1	5	Zungeru	Wushishi	NC
NGC-ZG-26	Iron beans	*V. unguiculata*	White	Black	Rhomboid	1.2	4	Zungeru	Wushishi	NC
NGC-ZG-27	Waken sobo	*V. unguiculata*	Raw sienna	White	Rhomboid	1.3	7	Zungeru	Wushishi	NC
NGC-ZG-28	Dan muzakari	*V. unguiculata*	Cream white	White	Ovoid	1.1	5	Zungeru	Wushishi	NC
NGC-ZG-29	Dan misra	*V. unguiculata*	White	White	Rhomboid	1.0	7	Zungeru	Wushishi	NC
NGC-ZG-30	Waken milk	*V. unguiculata*	Cream	White	Rhomboid	1.0	6	Zungeru	Wushishi	NC
NGB-SH-31	Kananado	*V. unguiculata*	White	White	Rhomboid	0.9	4	Mutun daya	Shiroro	NB
NGB-SH-32	Kananado maidoro	*V. unguiculata*	White	Brown	Kidney	1.3	5	Gwada	Shiroro	NB
NGB-SH-33	Waken gwari	*V. unguiculata*	White	Black	Ovoid	0.8	4	Kuta	Shiroro	NB
NGB-SH-34	Kananado	*V. unguiculata*	White	Brown	Rhomboid	0.7	5	Kuta	Shiroro	NB
NGB-BS-35	Waken gwari	*V. unguiculata*	White	Black	Rhomboid	1.3	7	Minna	Bosso	NB
NGB-BS-36	Zappa	*V. unguiculata*	White	White	Rhomboid	I.2	5	Minna	Bosso	NB
NGB-BS-37	Dan misra	*V. unguiculata*	White	White	Rhomboid	1.0	7	Minna	Bosso	NB
NGB-BS-38	Achishiru	*V. mungo*	Black	White	Ovoid	0.6	4	Maikunkele	Bosso	NB
NGA-BD-39	Ezo yere	*V. unguiculata*		White	Rhomboid	1.0	6	Sachi	Bida	NA
NGA-BD-40	EzoK ampala	*V. unguiculata*	White & brown		Ovoid	0.9	5	Barak	Bida	NA
NGA-BD-41	Asuwayin	*V. radiata*	Green	White	Ovoid	0.6	5	Ndawangwa	Bida	NA
NGA-BD-42	Egwakangi	*V. mungo*	Black	black	Ovoid	0.7	6	Gbazhi	Bida	NA
NGA-BD-43	Fenzo	*V.unguiculata*	Brown	white	Rhomboid	0.9	7	Gbazhi	Bida	NA

NGC – KT – 23 Dan Misra (*Vigna unguiculata*)

NGC – ZG-24 Olanyo (*Vigna unguiculata*)

NGB – ZG-35 Waken gwarri (*Vigna unguiculata*)

NGB –BS – 38 Achishiru (*Vigna mungo*)

NGB – BS – 36 Zappa (*Vigna unguiculata*)

NGA –BD-39 Ezo Yere (*Vigna unguiculata*)

NGA –BD-40 Ezo Langba (*Vigna unguiculata*)

NGA –BD – 41 Asunwayin (*Vigna radiate*)

NGA- BD -42 Egwakangi Kin (*Vigna mungo*)

NGA-BD-43 Fenzo (*Vigna unguiculata*)

Figure 1. Contd.

IDENTIFICATION OF SIMPLE SEQUENCE REPEAT (SSR) MARKERS UNIQUE TO SOMATIC EMBRYOGENESIS COMPETENT WHITE YAM GENOTYPES

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ABSTRACT
Somatic Embryogenesis (SE) is an important tool in improving yam propagation. However, there is inadequate information on genes regulating yam SE necessary for optimizing protocols for target genotypes. This study identified Simple Sequence Repeat (SSR) markers associated with SE in three *Dioscorea rotundata* (Kpamyo, Ekiti2a and Asiedu) genotypes subjected to SE regeneration stages. At Callus Induction (CI), Embryo Formation (EF) and Plantlet Regeneration (PR) stages, RNAs were extracted from the genotypes and cDNAs were synthesised using standard procedures. Four SSR markers (YM08, YM18, YM30 and SERK) and the cDNAs were used for gene expression profilling using qRT-PCR. Only YM08 and SERK were expressed. The YM08 was upregulated at EF and PR of Asiedu, CI and EF of Kpamyo and Ekiti2a, respectively, while SERK was upregulated at CI of Asiedu, CI and EF of Ekiti2a, but downregulated at EF of Kpamyo. The YM08 and SERK markers expressions were stage and genotype-specific.

Key words: *Dioscorea* species, somatic embryos, plantlet regeneration, SSR markers

INTRODUCTION
Yam is a tuberous crop consumed by millions of people worldwide (FAO, 2014). It is traditionally propagated through tuber which is also the edible part. This provides a competition on the tuber part as a means of propagation and consumption coupled with its low multiplication rate (Maroya *et al*., 2014). The direct implication of the above constraints is the scarcity of quality planting materials leading to the high cost of purchasing seed yam for cultivation. In addressingthis growing demand for clean seed yam, different propagation methods such as yam miniset technique, vine cutting, aeroponics, hydroponics and tissue culture techniques have been developed with an improved propagation rate relative to the traditional system (Aighewi *et al*., 2015). However, tissue culture techniques have been the fastest among the systems majorly through organogenesis where yam is propagated from organs having pre-existing meristem (Balogun and Gueye, 2013).

Recently, the successful technique of embryo production from somatic parts and the subsequent regeneration of plantlets from the embryos (Somatic Embryogenesis-SE) has shown potential to further improve the propagation ratio of yam (Manoharan *et al*., 2016). However, the system is constrained by the genotype-dependence response (Ossai *et al*., 2018). This signifies differences in gene functions in the evaluated genotypes, but the molecular basis of SE in plants and its pathway remain unclear (Fehér *et al.,* 2003). Reports have shown that different genes such as the somatic embryogenesis receptor-like kinase (SERK) and Baby boom were expressed during SE in potato, another clonally propagated crop (Sharma *et al*., 2008). This finding was possible with the use of marker-assisted breeding that it utilizes. However, it is important to look at the different marker types currently used in the study of SE as they help in establishing embryogenic potentials in plant cells (Feher, 2008). Based on their polymorphism and detection techniques, the markers include Amplified Fragment Length Polymorphism, Random Amplified Polymorphic DNA and Simple Sequence Repeat (SSR). However, SSR markers has shown superior reproducibility and reveals more genetic information within a target loci compared to other marker in SE studies (Kamle *et al*., 2013). This study thus identified some SSR markers that are unique to the SE competent yam genotypes as a guide in constructing SE-specific markers for early assessment of yam competence to SE.

MATERIALS AND METHODS
Study location:
The tissue culture experiments were carried out at the Cell Biology Unit of the Bioscience Center, International Institute of Tropical Agriculture (IITA).

Plantlet Regeneration
Axillary bud explants, excised from two weeks old plantlets of Kpamyo, Asiedu, Ekiti2a were

cultured into Murashige and Skoog (MS) medium modified with 9.1 µM 2,4-Dichlorophenoxylacetic acid and 5.4 µM Naphthaleneacetic acidunder laminar flow hood. The cultures were incubated in a dark condition for 4 weeks for callus induction. The induced calli were transferred to hormone-free MS, incubated at 16 h photoperiod and 25±1°C for 3 weeks for embryo formation and maturation. The embryos were thereafter transferred to Plantlet Regeneration Medium: MS + 4.4 µM Benzyl Amino Purine + 34 µM Uniconazole-P and kept at 16 h photoperiod at 25±1 °C for plantlet regeneration.

RNA Isolation

Cultures of Asiedu, Ekiti2a, Kpamyo were taken from 4 (CI), 6 (EF) and 8 (PR) weeks of culturing (Fig. 1), and RNAs were extracted from the samples using the RNeasy Plant Mini Kit (Qiagen) following the manufacturers' instructions. The integrity and purity of the extracted RNA's were checked using 2% agarose gel electrophoresis and nanodrop machine.

Synthesis of cDNA and differential gene expression by qRT-PCR

Isolated RNAs (100 ng/µL) were converted to cDNAs using the Superscript one-Step RT-PCR method (Qiagen). The cDNA's and polymorphic SSR markers (YM08, YM18, YM30) (Table 1) with flanking regions in both yellow and white yams (Muluneh *et al.*, 2015), and SERK marker designed to amplify conserved SERK target genes in rye (Gruszcynska and Rakoczy-Trajanowska, 2011) were mixed and amplified using PCR according to the manufacturer's instructions. The reaction component includes: 2 µL RNase-free water, 10 µl Qiagen One-Step RT-PCR Buffer, 2 µl dNTP Mix, 0.6 µM forward and reverse primers, 2 µL Qiagen One-Step RT-PCR enzyme mix and 2 µg template RNA. The PCR thermal cycling conditions was set at 95°C for 10 minutes and 30 seconds for denaturation, annealing at 60°C for 1 minute, and extension at 72°C for 1 minute. To separate amplified PCR products, 2% agarose gel electrophoresis was used. Expression levels of the SSR markers were normalized to a housekeeping gene (Dr-Actin). The qRT-PCR was conducted using SuperScript SYBER Green One-Step qRT-PCR (Qiagen) kit and a Roche system (LightCycler with the software v. 3.5) following the procedure of Nolan *et al.* (2006). A 25 µL mixture containing 2 µL diluted cDNA, 12.5 µL SYBER Green master mix, and 20 ϱM each of forward and reverse primer (YM08, YM18, YM30, SERK and Dr-Actin) was prepared for each qRT-PCR reaction. The template cDNA (5 µL) and 20 µL of the master mix were added to the reaction wells. A blank well containing only water was also loaded. The well cap was carefully covered, and spanned. The well plate was placed in the real-time thermal cycler for quantitative assay of the reference gene and the expression plots were generated.

RESULTS AND DISCUSSION

Integrity and purity check of the cDNA

The YM08 and YM18 were amplified at 250 base pairs, while YM30 was amplified at 200 base pairs at 4-, 6- and 8-week-old cultures of Asiedu, Ekiti2a and Kpamyo. This agrees with Muluneh et al. (2015) that the markers have flanking regions in white and yellow yams. However, the SERK had a visible amplification on 6-week-old culture of Kpamyo at 250 base pairs with faint bands at 300 base pairs (Fig. 2). This could be because the SERK was constructed from rye (Gruszcynska and Rakoczy-Trajanowska, 2011).

Expressions of SSR YM08 and SERK in SE stages of Asiedu, Kpamyo and Ekiti2a Using RT-PCR

In the RT-PCR analysis, only YM08 and SERK markers were amplified in the samples. The YM08 showed a progressive increase in the expression level in Asiedu cultures. The CI (1.0) < EF (6.0) < PR (11.7) (Table 2), with a threshold range of 27.73 to 29.42 (Figs. 4 - 5). In Ekiti2a, it ranged from CI (2.6) < EF (2.3) >PR (0.3), with a threshold range of 28.74 to 29.19. In Kpamyo, its expression was CI (2.3) > EF (1.1) > PR (0.5) with a threshold range of 29.04 to 29.52. The SERK was only expressed at CI in Asiedu (1.0) at a threshold level of 5.6. In Ekiti2a, the expression trend was CI (4.06) >EF (4.0) > PR (0.11). In Kpamyo, it was undetermined at CI but was expressed at EF (0.01) at a threshold of 6.2 cycles, which increased slightly at PR to 0.03 at a threshold of 9.99 cycles.

The YM08 got upregulated at the early stages of SE in Ekiti2a and Kpamyo and became downregulated at the plantlet regeneration stage, but in Asiedu, it was downregulated at the early stage and became upregulated at plantlet regeneration. Unlike the YM08, the SERK marker was only fully expressed in all the SE stages of Ekiti2a with a trend of upregulation at the early stages of SE and downregulated at the plantlet regeneration stage. Several reports of the genes controlling SE expressed at the early phase of SE (callus induction) until the globular stage of embryo formation in competent cells exists (Baudino *et al.*, 2001). The expression of the SERK marker was undetermined at the plantlet

regeneration stage of Asiedu, which could be that the gene switched off at the later stages of SE in the genotype (Feher, 2008). The SERK genes are mostly expressed in cells that are capable of responding to hormonal signals and competent to form somatic embryos and not after embryo formation (Hecht *et al*., 2001). In this study, the variation in the expression pattern between the three white yam genotypes could be due to the relative differences in their inherent physiological factors and stage cycles (Matsumoto *et al*., 2015). This could be that Ekiti2a and Kpamyo attains maturity earlier than Asiedu.

Conclusion

The expression pattern of the two SSR markers YM08 and SERK varied among the white yam genotypes. In Ekiti2a and Kpamyo, both markers showed upregulation at early stages of somatic embryogenesis and dropped at the plantlet regeneration stage. However, the expression trend in Asiedu was an upregulation at the plantlet regeneration stage. It is then important to construct and validate more genotype-specific markers for the detection of somatic embryogenesis competence in yam.

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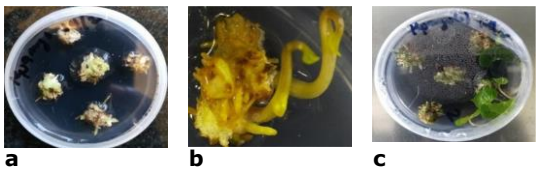

Fig 1: Somatic embryogenesis stages in yam
Keys: a: callus induction b: somatic embryos d: Plantlet regeneration

Table 1: Primer sequences used in qRT-PCR analysis

Primers	Nucleotide sequences
SERK (Forward)	TTGCTGGAGGTGTTGCTG
SERK (Reverse)	TACACCTTTCCAAAGCCAC
YM08 (Forward)	TCTTAGGCTTTGGGCAGGG
YM08 (Reverse)	AGTATGCCTACCCTGTTCTTC
YM18 (Forward)	GACATTGGGGATCTCTTATCAT
YM18 (Reverse)	TAGCAGCAGTAACGTTAAGGAA
YM30 (Forward)	CCACAACTAAAAACACATGGAC
YM30 (Reverse)	GTGGTAGGGTGTGTAGCTTCTT
Actin (Forward)	CAGGGAAAAGATGACCCAAATC
Actin (Reverse)	CCATCACCAGAATCCAGCAC

Gruszcynska and Rakoczy-Trajanowska, 2011; Muluneh *et al.*, 2015

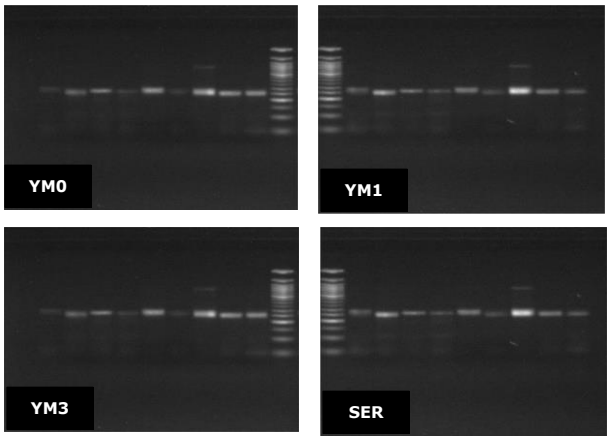

Fig 2: Gel images of cDNAs PCR amplified products using YM08, YM18, YM30 and SERK primers
Keys: 1-3 wells from the base pairs represent Asiedu at 4, 6 and 8 WOC, 4-6: Ekiti2a at 4, 6 and 8 WOC and 7-9: Kpamyo at 4, 6 and 8 WOC.

Table 2: RT-PCR quantification of YM08 and SERK markers in SE stages of white yam

Genotypes	Stage	YM08		SERK	
		RQ	Ct	RQ	Ct
Asiedu	CI	1*	29.42	1*	5.6
Asiedu	EF	6	28.79	-	-
Asiedu	PR	11.7	27.73	-	-
Ekiti2a	CI	2.6	29.01	4.06	4.5
Ekiti2a	EF	2.3	28.74	4	4.07
Ekiti2a	PR	0.3	29.19	0.11	6.9
Kpamyo	CI	2.3	29.04	-	-
Kpamyo	EF	1.1	29.50	0.01	6.2
Kpamyo	PR	0.5	29.52	0.03	9.99

CI: Callus Induction, EF: Embryo Formation, PR: Plantlet Regeneration, RQ: Relative Quantification, Ct: Threshold cycle, *: Calibrator, -: Undetermined

GENOME-WIDE DETECTION OF SNP MARKERS ASSOCIATED WITH FE, ZN AND PHYTIC ACID CONTENTS IN SORGHUM

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ABSTRACT: Mineral malnutrition is a major challenge worldwide, particularly in developing countries where approximately 50% of the children are reported to be deficient in several micronutrients, particularly Fe and Zn. Biofortification remains a cost-effective and sustainable solution for tackling micronutrient deficiencies, particularly in. In sorghum, unlike other crops, the approach is still limited by the presence of many anti-nutritional factors such as phytic acid (PA). This study was conducted to determine the variability in Fe, Zn and PA and determine important genetic loci associated with these traits in sorghum. The PA content ranged from 0.0048 to 9.65 (g/100 mL) with a mean of 1.48. The cluster analysis revealed three groups for PA content with cluster 1 having the highest mean value of PA (4.27) while cluster 3 had the lowest PA. The mean Fe and Zn contents of the accessions were 67.2 and 15.98 mg/kg, respectively. The Fe content ranged from 10 – 1172 mg/kg while the Zn content ranged from 2 – 57 mg/kg. The marker-trait association (MTA) revealed significant SNP markers associated with PA. Four significant loci were associated with PA and have PVE ranging from 4 – 8%. The loci had allelic effects ranging from 0.53 – 0.96. This study provides information on some important genetic loci for the improvement of quality traits in sorghum.

Keywords: Biofortification, genome-wide association, sorghum, phytic acid, micronutrients

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INTRODUCTION

Sorghum is the 5th most important grain crop in the world with a total production of 58.4 million metric tons (USDA, 2019). It is a highly reliable and resilient crop, and often called "climate change-ready". Sorghum contributes to food security and income for millions of resource poor people living in arid and semi-arid dryland regions of sub-Saharan Africa (SSA) and South Asia (Kumar *et al.*, 2013). Over half a billion people rely on sorghum as a dietary mainstay, given its diversity of uses, as an important source of income. The crop is among the cheapest sources of energy and nutrients; the grain is rich in starch, protein, micronutrients, and crude fiber (Chavan and Patil, 2010). It provides more than 50% of the dietary micronutrients to low-income groups, particularly in rural SSA and South Asia where both physical and economic access to nutrient-rich foods is limited (Ashok-Kumar *et al.*, 2015).

Mineral malnutrition is a major challenge worldwide particularly in developing countries where approximately 50% of the children are reported to be deficient in several micronutrients, particularly Fe and Zn (FAO, IFAD, UNDP, 2020). Globally, the problem of malnutrition is addressed through dietary diversification, mineral supplementation, food fortification, or increasing the concentration and/or bioavailability of mineral elements (Aggarwal *et al.*, 2018) in the genetic background of most staple crops. However, approaches involving mineral supplementation and food fortification have not been very effective in several crops. Biofortification involving enhancement of bioavailable micronutrient concentrations and increasing micronutrients in food crops through decreasing the concentration of anti-nutrients and other secondary metabolites remains a cost-effective and sustainable solution for tackling micronutrient deficiencies, particularly in developing countries. In sorghum, unlike other crops, the approach is still limited by the presence of many anti-nutritional factors such as phytic acid (PA), cyanogenic glucoside, polyphenols, oxalate, amylase and trypsin inhibitors, as well as tannins (Ashok-Kumar *et al.*, 2015). Phytic acid (myoinositol-1, 2, 3, 4, 5, 6-hexakisphosphate, InsP6) is one of the major anti-nutrients in grains of wheat, rice, soybean, sorghum and other crops that limit the bioavailability of certain micronutrients. It is a major storage form of phosphorous in seeds, making up to 85% of the

total P in some seeds (Sparvoli and Cominelli, 2015).

The highly charged phosphate groups make phytic acid very reactive, and if present in foods, binds the divalent cations, such as calcium, iron, zinc, and magnesium, rendering them nutritionally unavailable. In addition, phytic acid binds to protein and forms insoluble complexes (Wanasundara, 2011). Consequently, the effect of phytic acid in diminishing bioavailability of numerous minerals (P, Ca, Cu, K, Mg, Fe, and Zn) and biomolecules have been established (Gibson *et al*., 2015). In view of these adverse effects, attempts have been made to reduce the content of PA in crop plants (Aggarwal *et al*., 2018). In view of these anti-nutritional effects of phytic acid many attempts have been made to eliminate phytic acid from foods by several methods such as soaking, fermentation, storing, cooking, germination, dehulling, but these have been implicated in the losses of several other essential nutrients (Sathe *et al*., 2001). Advances in biotechnology have opened a promising strategy to develop crops with high nutritive values by manipulating the PA biosynthetic pathway using transcriptomics, proteomics and metabolomics approaches to identify and characterize various genes involved in its biosynthesis. Thus, the aim of this research is to improve the nutritive value of sorghum through the identification of genes associated with PA content.

MATERIALS AND METHODS

Phytic acid extraction

Given the complexities of the purification and measurement of phytic acid separate from lower myo-inositol phosphate forms, Megazyme has developed a simple, quantitative method (K-PHYT) to measure total "available phosphorus" released from food and feed samples that is amenable to high numbers of samples and does not require tedious anion-exchange purification. This method involves acid extraction of inositol phosphates followed by treatment with a phytase that is specific for phytic acid (IP6) and the lower myo-inositol phosphate forms (i.e., IP2, IP3, IP4, IP5). Subsequent treatment with alkaline phosphatase ensures the release of the final phosphate from myoinositol phosphate (IP1) which is relatively resistant to the action of phytase. The total phosphate released is measured using a modified colourimetric method and given as grams of phosphorus per 100 g of sample material.

The absorbance (A655) for both the "Free Phosphorus" sample and the "Total Phosphorus" sample were determined. Subtract the absorbance of the "Free Phosphorus" sample from the absorbance of the "Total Phosphorus" sample, thereby obtaining ΔAphosphorus. The concentration of phosphorus was calculated as follows:

c = (mean M x 20 x F/10,000 x 1.0 x v) x ΔAphosphorus [g/100 g]

where:

mean M = mean value of phosphorus standards [μg/ΔAphosphorus], 50 = original sample extract volume [mL], F = dilution factor, ΔA = absorbance change of sample, 10,000 = conversion from μg/g to g/100 g

1 = weight of original sample material [g], v = sample volume (used in the colourimetric determination step).

Iron and Zinc determination

3 g of sorghum grain from each of the selected 282 germplasm was grinded with a ceramic stone mill, sieved with a plastic sieve and put into small holders. The Iron and Zinc contents then determined by X-RAY Florescence (XRF) Machine.

DArT-Based Genotyping by Sequencing

282 samples of sorghum were sent to Beca-ILRI (SEQART), Nairobi Kenya for sequencing. Genotyping of the sorghum accessions was performed using the DArT-based GBS platform of SEQART AFRICA. Briefly, genomic DNA was extracted from young, fresh sorghum leaves using the NucleoMag Plant genomic DNA extraction kit (Takara Bio, Shiga, Japan). The quality and quantity of DNA in each sample were checked via 0.8% *w/v* agarose gel and a NanoDrop spectrophotometer, respectively. Genomic DNA was digested using the DArT-seq complexity-reduction method and ligated to the barcoded adapters, after which PCR amplification of adapter-ligated fragments was performed (Shaibu *et al*., 2022).

Statistical analysis

The SNP characteristics (missing rate, PIC and frequency of heterozygosity) were generated by the DArT GBS platform. The filtering of the SNPs was performed in two stages; the first stage filtering removed all SNPs that were unmapped to any of the 10 sorghums chromosomes, while the second stage filtering removed the redundant markers. The redundant markers were markers with missing rates of more than 10%, MAF below 5% and PIC < 10%. The genome

summary plugin in the TASSEL v.5.2.37 software was used to generate the allele frequency and MAF of the markers.

RESULTS AND DISCUSSION

Descriptive analysis of Fe, Zn and phytic acids

Highly significant differences ($p<.001$) were observed among the genotypes for P, PA, Fe and Zn (Table 1). Significant differences in PA have been reported in sorghum (Ashok *et al.*, 2015). The P content ranged from 0.0013 to 2.72 (g/100 mL) with a mean of 0.42. The PA content ranged from 0.0048 to 9.65 (g/100 mL) with a mean of 1.48 (Table 1). The PA contents were higher than the PA contents reported by Ashok-Kumar *et al.* (2015) and this may be attributed to the high number of accessions screened in our study. The mean Fe and Zn contents of the accessions were 67.2 and 15.98 mg/kg, respectively (Table 1). The Fe content ranged from 10 – 1172 mg/kg while the Zn content ranged from 2 – 57 mg/kg. The concentrations were within the range reported for sorghum and wheat (Cakmak *et al.*, 2010).

Marker-trait association analysis

A total of 115,610 SNPs and 42,827 DArT markers were generated for the 282 sorghum accessions. After the first stage of filtering, which excluded unmapped markers, 13,229 SNPs and 24,537 DArT markers were obtained. The second stage filtering returned 3967 SNPs and 2486 DArT markers. The polymorphism information content (PIC) and minor allele frequency (MAF) ranged from 0.1–0.5 and 0.05–0.50, respectively for both SNP and DArT markers while their reproducibility ranged from 0.95–1.00. The marker trait association revealed significant SNP markers associated with phytic acid (Table 2 and Figure 1). Four significant loci were associated with PA and have PVE ranging from 4 – 8%. The loci had allelic effect ranging from 0.53 – 0.96.

Gene identification and protein regulating phytic acid

Based on the LD decay distance, 5 bp upstream and downstream of regions where significant MTAs were detected were explored to identify genes whose functional annotations are related to phytic acid in the sorghum reference genome using phytozome (https://phytozome-next.jgi.doe.gov/). The descriptions of the genes were retrieved from phytozome (https://phytozome-next.jgi.doe.gov/). Three genes were identified each in SM6054 (chr. 09), SM3027 (chr. 04) and SM55446 (chr. 09) (Table 3). For SM6054, the gene identified was Sobic.009G143100 which lies within Chr09:50039521..50041289 reverse. The gene has a protein description similar to Cytochrome b6-f complex iron-sulfur subunit, chloroplast precursor. Sobic.004G121200 was associated with SM3027 and lies within Chr04:13274662..13278061 reverse. It is similar to UCW116, putative lipase with a function of zinc finger five domain containing protein. It is co-expressed with genes in roots specific co-expression subnetwork, Phosphatidylinositol 3-phosphate-binding protein required for the abscission step in cytokinesis: recruited to the midbody during cytokinesis and acts as a regulator of abscission. May also be required for efficient homologous recombination DNA double-strand break repair. For SM55446, Sobic.009G060700 was identified and lies within Chr09:6363727..6367521 forward. This gene is similar to Putative receptor protein kinase and have the Protein kinase domain (Pkinase) // Leucine Rich Repeat (LRR_1) // Leucine rich repeat N-terminal domain (LRRNT_2) // Leucine rich repeat (LRR_8) functions.

Conclusion

The study revealed high variability in PA, Fe and Zn contents of the germplasms. The significant regions identified in this study will assist in developing markers for selection and the identification of important genes regulating PA. Elite breeding materials can also be selected for biofortification of sorghum.

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Table 1. Descriptive statistics of P and PA in the sorghum accessions. P and PA were measured in g/100 mL while Fe and Zn were measured in mg/kg

Traits	Mean	Min	Max	Std Err	CV	P-value
P	0.42	0.001	2.72	0.02	93.21	<.001
PA	1.48	0.005	9.65	0.06	93.2	<.001
Fe	67.2	10	1172	2.86	95	<.001
Zn	15.98	2	57	0.31	43.34	<.001

Table 3. Putative candidate genes associated with the SNP markers

SNP	Chr.	Gene	Region
SM6054	Chr09	Sobic.009G143100	50039521..50041289
SM3027	Chr04	Sobic.004G121200	13274662..13278061
SM4996	Chr07	-	-
SM5546	Chr09	Sobic.009G060700	6363727..6367521

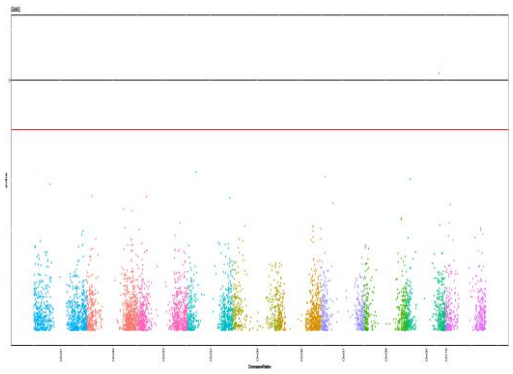

Figure 1. Manhattan plots of SNP for PA

Table 2: Marker-trait association for the SNP markers

SNP	Chr.	Pos.	P value	R square	Ae
SM6054	Chr09	50040334	7.28E-06	0.074632	0.96
SM3027	Chr04	13276725	0.000679	0.033845	0.57
SM4996	Chr07	5944251	0.00085	0.0319	0.66
SM5546	Chr09	6363925	0.000949	0.030949	0.53

Chr. = chromosome; Pos. = position; Ae = allelic effect

EFFECTS OF GENETIC VARIATION ON HOMOSEXUALITY ARE MODELED MATHEMATICALLY USING POPULATION GENETICS

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ABSTRACT

This study considers a testable genetic prediction, through the use of mathematical model. Paternal, maternal, environment, idiopathic are some of genetic impacts in the human population. One of the determining factors used to measure genetic features is environment. The study concentrated on the first three criteria because the fourth one only influences a small portion of the population. In order to create testable theories that have an impact on homosexuality, this study provides a genetics and evolutionary foundation. Previous research concentrated on paternal and maternal connections, with little attention paid to the environment's role. Environmental impacts with direct selection and direct, maternal, and environmental effects with combine selection are two separate methodologies that are taken into consideration. The aim of this research is to measure the genetic variance between genotypes of men and women. The use of various methods for homosexuality prediction is combined with consideration of environmental factors. Empirical evidence indicates that maternal and environmental effects (i.e. phenotype) have great influence for male's homosexuality. It is measured how much genetic diversity contributes to homosexuality. The model is discrete, non-overlapping, with genotypes **AA**, **Aa**, and **aa**, and it takes into account populations of any size. A possibility of surviving to reproduce is also based on fitness. Mating success is the probability of joining the breeding population, and fertility is the quantity of offspring whose mother and paternal effects interact several times. A numerical example is given to support the outcome. To understand the effects of homosexuality on fitness gain and loss, sensitivity analysis is performed.

Keywords: evolution, genetic, genotype, homosexuality

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INTRODUCTION

Mathematical genetics is the study of genetic variation in a population as a result of different evolutionary forces including paternal, maternal and environmental factors. Analysis of generation, gene nature and maintenance of genetic variations constitute mathematical genetics. Selection, mutation, migration and recombination are the basics of evolutionary biology. Separate researches were made to portray homosexuality through several techniques. Principles of genetic and evolution were developed before the discovery of DNA in 1953. During the first half of the 20th century, scientists explore the mathematical principles of mutation, selection and evolutionary genetics after Mendel's theory. Rough garden *et al.* (2017) gave antagonistic genes and of maternal and parental selections to the context of homosexuality. The information about human genetics has provided the way for gene variation with various associations, and various investigations about gene variation explain the levels of homosexuality (Cook, 2018).

Bailey (2016) state that, a unifying etiological theory attributes the expression of sexual orientation to genes that shapes the central nervous system's development, organization, and structure via prenatal sex steroids. Psychosocial development models describe initial stages of awareness and confusion about same-sex attractions, followed by acknowledgement of homosexuality and integration into a comprehensive sense of self, Dickson (2013). The study considers the selection of genes that cause for long standing interest among evolutionary biologist. There are three types of basic selection: direct selection, maternal effects and environmental interaction. The over dominance and sexual antagonism are taken into account for explaining the genetic evidence from generation to generation.

THE MODEL DESCRIPTION

The term fitness is described as the probability of surviving to reproduction; the probability of entering the mating pool is known as mating success and the number of offspring with maternal and paternal effects interact multiplicatively is considered as fertility. Population of infinite size is considered in describing the models, discrete and non-

overlapping with genotypes **AA**, **Aa** and **aa**, where **A** is an allele that has no influence on sexual orientation and allele **a** feminizes both sexes and increases the probability of homosexuality. Let f_1, f_2 and f_3 be female finesses and m_1, m_2 and m_3 be male fitnesses in genotypes **AA**, **Aa** and **aa**, respectively. We assume that G'_{od} is the overdominant fitness gain of heterozygous males E' is the fitness loss due to the environmental effects and C^I is the fitness loss of homozygous males. r be the fraction of effectiveness for environment and h be the measure of dominance of allel **a** in females such that $0 \leq r \leq 1, 0 \leq h \leq 1$and $1 \geq C^I \geq 0$. G and E are the maximum fitness gains in females from sexual orientation and from favourable effects of environment respectively. Also $f_1 \leq f_2 \leq f_3$ and $m_2 \geq m_1 \geq m_3$. For the analysis purpose, we develop the following two models: (i) Direct selection model with environmental effect and (ii) Combined selection model with maternal and environmental effects.

Direct selection model with environmental effect

In this model, the fitness of both sexes is considered by the direct genetic effects of genes in a zygote. Here, we consider two cases such as: (i) fitness for autosomal gene and (ii) fitness for X-linked gene which are described as follows:

(i) Fitness for autosomal gene: The condition of successful invasion of allele **a** in a population initially monomorphic for allele **A** is obtained by (cf. Gavrilets and Rice (2006))

(ii) $$\frac{m_2}{m_1} + \frac{f_2}{f_1} > 2 \quad \textbf{i}$$

Similarly, the condition of successful invasion of allele **A** in a population initially monomorphic for allele **a** is (cf. Gavrilets and Rice (2006)).

$$\frac{m_2}{m_3} + \frac{f_2}{f_3} > 2 \quad \textbf{ii}$$

In this case the following three conditions arise:

(a) Over dominance in both sexes

If $m_2 > m_1$ and $m_2 > m_3$ **iii**

And $f_2 > f_1$ and $f_2 > f_3$ **iv**

then inequalities (**i**) and (**ii**) are satisfied i.e., heterozygote have the highest fitness in both sexes and overdominance in both sexes is possible.

(b) Overdominance in one sex and directional selection in the other sex.

If we assume

$$m_1 = 1, m_2 = 1 + G'_{od} - rE', m_3 = 1 - C' - E' \quad \textbf{v}$$

And $f_1 = 1, f_2 = 1 + hG + rE, f_3 = 1 + G + E$ **vi**

Then from eqn. (**i**), we get

$$G > \frac{r(E'-E) - G'_{od}}{h} \quad \textbf{vii}$$

And from eqn. (**ii**), we have

$$G > \frac{C^I + G^I{}_{od} - rE^I + (r-1)E + (2-r-h)EC^I + (1-2r)EE^I}{(1-h) - (2-h)C' - (1-r-h)E^I} \quad \textbf{viii}$$

i.e., the allele **a** is a feminizing allele and increases female fitness, so that one copy of allele **a** increases male fitness but two copies of **a** reduce male fitness because of homosexual behaviour. In other words, we can say that increasing the fitness loss to homozygous males (C^I) promotes the maintenance of genetic variation. If $C^I = 1$ i.e., homozygous males have zero fitness then variation of genetic evident is always maintained.

(c) Sexually antagonistic selection

Let us suppose that

$$m_1 = 1, m_2 = 1 - hC^I - rE^I, m_3 = 1 - C^I - E^I \quad \textbf{ix}$$

And $f_1 = 1, f_2 = 1 + hG + rE, f_3 = 1 + G + E$ **x**

Then from equation (**i**), we get

$$G > \frac{hC^I + r(E^I - E)}{h} \quad \textbf{xi}$$

Also, from equation (**ii**), we get

$$G = \frac{(1-h)C^I - rE^I + (r-1)E + (2-r-h)EC^I + (1-2r)EE^I}{(1-h) - (2-h)C^I - (1-r-h)E^I} \quad \textbf{xii}$$

i.e., the fitness gain to females is larger and the fitness loss to males is sufficiently large. Here, the degree of dominance is equal for both sexes and if allele **a** dominant in the sexes, the variation is maintained.

(ii) Fitness for X-linked gene

Suppose that the locus is X-linked and the fitnesses in both sexes are determined by direct selection. Then the condition of successful invasion of allele **a** in a population initially monomorphic for allele **A** is given by

$$\frac{f_2}{f_1} > \frac{m_1}{\bar{m}} \quad \textbf{xiii}$$

and the condition of successful invasion of allele **A** in a population initially monomorphic for allele **a** is as follows

$$\frac{f_2}{f_3} > \frac{m_2}{\bar{m}} \quad \textbf{xiv}$$

where, $\bar{m} = \frac{m_1 + m_2}{2}$ is the average male fitness. In this case the following three conditions arise.

(a) Overdominance in homogametic sex

$$m_1 = 1, \; m_2 = 1 - C^I - E^I \quad \textbf{xv}$$

And $f_1 = 1, f_2 = 1 + G_{het} + rE, f_3 = 1 + G + E$ **xvi**

Where $G^I{}_{het}$ is the fitness gain of heterozygous females and if $f_2 > f_1, f_3$ and $m_1 > m_2$, then from equation (**xiv**), we get

$G^I{}_{het} > \frac{2rE+(1+rE)C^I+(1+rE)E^I}{2-C^I-E^I}$ **xvii**

From equation (**xiv**), we have

$G^I{}_{het} > \frac{2G-2(C^I+E^I)G-(C^I+E^I)+2(1+r)E-(2+r)(C^I+E^I)E}{2-(C^I+E^I)}$ **xviii**

i.e. the allele **a** is a feminizing allele and maximizes female fitness because of homosexual behaviour.

(b) Sexually antagonistic selection for feminization allele

Let $m_1 = 1, \quad m_2 = 1 - C^I - E^I$ **xix**

And $f_1 = 1, f_2 = 1 + hG + rE, f_3 = 1 + G + E$ **xx**

Then from equation (**xiii**) and (**xiv**), we have

$G > \frac{C^I+E^I+rE(C^I-2)+rE^2}{h(2-C^I-E^I)}$ **xxi**

And

$G > \frac{2(2+2h-h^2)-(2+h-h^2)(C^I+E^I)-(1-4r+5h-2hr)E+(1+2h-2r-rh)EC^I+(1-2r+rh)EE^I}{2h(C^I+E^I-3)}$ **xxii**

This shows that the fitness gain to females is larger and the maintenance of feminizing allele requires fitness advantage to be sufficiently large.

(c) Sexually antagonistic selection for masculinization allele

Let $m_1 = 1, \ m_2 = 1 + G_m + E_m$ **xxiii**

And $f_1 = 1, f_2 = 1 - hC^I{}_f - rE^I{}_f, f_3 = 1 + C^I{}_f + E^I{}_f$ **xxiv**

where $E^I{}_f$ and $C^I{}_f$ denote the females fitness losses due to the environment and sexual orientation respectively, such that $0 \leq E^I{}_f \leq 1$ and $0 \leq C^I{}_f \leq 1$. G_m and E_m are the maximum fitness gain of males from sexual orientation and from favourable environment, respectively. From Equations (**xiii**) and (**xiv**), we have

$G_m > \frac{2hC^I{}_f+(hC^I{}_f-1)E_m}{1-hC^I{}_f-rE^I{}_f}$ **xxv**

$G_m > \frac{4hC^I{}_f+4(r-1)E^I{}_f+2E_m+2(h-2)E_mC^I{}_f+2(r-2)E_mE^I{}_f}{2((2-h)C^I{}_f+(2-r)E^I{}_f-1)}$ **xxvi**

Thus, the fitness loss to females is larger and the fitness gain to males is also sufficiently large, but the allele **a** has to be recessive.

Combined selection model with maternal and environmental effects

In this model, we assume that the finesses in both sexes are obtained by considering direct, maternal and environmental effects. For this model we let $m^I{}_1$, $m^I{}_2$ and $m^I{}_2$ be the maternally determined fitnesses of males for allele **AA**, **Aa** and **aa**, respectively. Then the condition of successful invasion of allele **a** in a population initially monomorphic for allele **A** is

$\frac{f_2}{f_1} + \frac{f_2}{f_1}\frac{m_2{}^I}{m^I{}_1} > 2$ **xxv**

$\frac{f_2}{f_3} + \frac{f_2}{f_3}\frac{m_2{}^I}{m^I{}_3} > 2$ **xxvi**

The following three cases for this model arise:

(a) Overdominance in both sexes

Let $m_2{}^I > m_1{}^I$ and $m_2{}^I > m_3{}^I$ **xxvii**

And $f_2 > f_1$ and $f_2 > f_3$ **xxviii**

Now inequalities (**xxv**) and (**xxvi**) are satisfied i.e., highest fitness in both sexes is possible. (b) Overdominance in one sex and directional selection in the other sex

Assuming

$m_1{}^I = 1, \ m_2{}^I = 1 + G^I{}_{od} - rE^I, \ m_3{}^I = 1 - C^I - E^I$ **xxix** and $f_1 = 1, f_2 = 1 + hG + rE, f_3 = 1 + G + E$ **xxx**

From equation **xxv**) and (**xxvi**), we get the following inequality

$G > \frac{rE^I-G^I{}_{od}-2rE-rEG^I{}_{od}+r^2EE^I}{2\pm G^I{}_{od}-rE^I}$ **xxxi**

And $G > \frac{G^I{}_{od}-2E+(C^I-E^I)-(r-2)(C^I+E^I)E+rEG^I{}_{od}-hrE^2}{2(1-h)-(2-h)(C^I+E^I)-hG^I{}_{od}+hrE}$ **xxxii**

Thus, the fitness gain to females is larger than the fitness loss to males which is sufficiently large. In this case, the female fitness is determined by her genotype whereas male fitness is determined by maternal effect. It is noticed that the variation is maintained if allele **a** is recessive.

Example

There are two models invoked to explain the persistence of genetic disease in human populations. The first explanation is that the alleles which cause disease when homozygous confer some benefit when heterozygous: this is the overdominance model. The second explanation is that the alleles are present at a balance caused by their input by mutation and their removal by natural selection: this is the mutation or selection model. Infectious diseases are one of the major selective forces affecting human evolution and are known to have caused genetic responses in human populations. The best known example is that of the sickle cell gene. The sickle cell homozygote suffers from **lethal anaemia**, the heterozygote is phenotypically

abnormal and apparently protected from fatal malaria, while the homozygote wild-type is phenotypically normal but at risk from developing fatal malaria. The sickle cell allele is maintained in a population at a frequency determined by the certainty (in the absence of medical care) of the sickle cell homozygote dying from anaemia. Its frequency can be used to infer historic malaria mortality rates.

Conclusion

The present study indicates that genes influencing homosexuality can be spread and become polymorphic under a wide range of conditions. The main goal of this investigation is to provide genetic analysis of homosexuality with regards to effects of genes. We have provided various prediction methods of homosexuality by incorporating environmental effects. In fact, the empirical evidence indicates that maternal and environmental effects (i.e., phenotype) have significant influence at least for male's homosexuality. It is also clear that the genetic characteristics of genes are informative and maintain their polymorphism. It is possible that homosexuality can appear in many other species. We have developed this analysis to illustrate a hypothesis under the pheno-genotype paradigm. However, we find that genetic variations appear dependent on the variation of environment, which is shown by fitness loss and fitness gain in each of the experiment. A more sophisticated analysis incorporating the variation of environment is definitely effective to next generation.

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CONSERVATION AND IMPROVEMENT OF CASSAVA GERMPLASM: A SIGNIFICANT STEP TO AVOID FUTURE FOOD CRISES IN AFRICA (A REVIEW)

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ABSTRACT
Cassava is an essential staple food in sub-Saharan Africa. The importance of Cassava to food security cannot be over-emphasised. The recognition of these must have informed the use of Vitamin A bio-fortified cassava to combat hidden hunger by Harvest Plus. However, Cassava is bedevilled by various pests and diseases apart from the danger posed by population increase, wars, terrorism, and climate change. Various needs why one variety or the other was bred and released in various countries in Africa include high yielding, low cyanide, early bulking, resistance to pests and diseases, non-branching, good gari and lafun, high dry matter, preservation and longevity of tubers in the soil without spoilage, suitability for mixed cropping, high biomass, resistance to Cassava Mealy Bug (C.M.D.), early maturing, suitable for food and industry, increased or high beta carotene, suitability for intercropping, suitability for particular agro-ecology or group of agro-ecologies, tolerance to acidic soils, ability to smother weeds, suitability for fufu, suitability for a dense population in plantation, tolerance for drought, suitability for high-quality cassava flour due to low fibre content, high starch yield, high dry matter, high dry root yield, broad adaptation, and erect plant type. In the future, apart from the pressure for increased food production due to population, there may be a need to breed to address specific problems such as flood or submergence; therefore, there is a need for collective responsibility in the conservation of cassava germplasm, especially landraces and wild varieties to have broad base germplasms with various genes that can address myriads of problems militating against cassava production.

Keywords: agro-ecology, cassava mealy bug, germplasms, vitamin A bio-fortified cassava

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INTRODUCTION
Cassava (*Manihot esculenta*) is an important food crops in sub-Saharan Africa. It is accounted to be a third (1/3) of 33% of all the staple foods produced in sub-Saharan Africa (F.A.O., 1986; Eggleston et al., 1989). One of the foods derived from the processing of Cassava is Gari. The various nicknames given to this Gari among the students of secondary schools and higher institutions in Nigeria underscore the importance of this food. These nicknames include "Student power", Garium sulphate", and so on.

The root of Cassava is said to form an essential diet of over 800 million people in the tropical World (Bokanga, 1989). In 1986, the Food and Agriculture Organization (F.A.O.) of the United Nations estimated that 44% of the world output of Cassava came from Africa and that Zaire and Nigeria accounted for half of this (F.A.O., 1986; Bokanga, 1989).

Population increase – the need for increased food production
The World Bank's twin goals are ending extreme poverty and boosting shared prosperity. The new World Bank president David Malpass stressed that their mission is more urgent than ever. He noted that with over 700 million people living in extreme poverty, income growth is insufficient to ensure shared prosperity (World Bank 2019). The African population is a significant concern. The population of Africa is expected to double by the year 2050. Ibrahim (2017) stressed the importance of food security vis-à-vis the population of Africa. According to him, the population of Nigeria will be 400 million people by 2050. Even though various governmental and Non- governmental Organizations in Africa have been putting on various efforts to address food insecurity in Africa but challenges and threats such as terrorism, war, drought, flood, climate change, human pestilence, Cataclysmic events, plant and animal diseases outbreak,

environmental pollution and degradation and other challenges springing up daily have made food security a problem. Added to this is the fact pointed out by Gbile (1987) and Fawusi (1993) that of 250 000 plant species on earth, about 20,000 are known to be edible, and perhaps, 3000 have been used as food. Fawusi further stated that almost the World's food supply comes from about 20 plant species. For Africa, one of the major crops that supply food to her populace is Cassava. That must have informed the use of bio-fortified Cassava to address hidden hunger by Harvest – plus in Africa.

Cassava agronomy

Cassava is adaptable to a wide range of soils but does well on well-drained, rich, friable loamy soil. Cassava can be propagated by seeds. Nevertheless, the seeds typically give thin, slender stems, which may not give good tubers, the primary food derived from Cassava. Seeds are usually good for research purposes. The Seeds also are recalcitrant. However, propagation is better done with mature stem cuttings of between 20 cm to 30 cm that is dipped in rigour before planting between April and October in Nigeria (Akinsanmi, 2003). However, because of its hardiness, Cassava can partially survive extreme late planting in October to November in Southern Nigeria. Cassava plant density is about 1200 plants per hectare with a plant spacing of 90 cm within rows and 100 cm to 150 cm between rows. The planting of Cassava is done by placing the stem in a slanting position or horizontal position. The ones planted in a slanting position must have about 10 cm above the soil with cassava buds pointing upwards. The harvesting is done by uprooting the stems. Cassava food is stored as gari or as cassava flour. Cassava tubers harvested can spoil within two to three days; therefore, it is better left on the field if the farmer is not ready to process them into food immediately. There is a market for Cassava both locally and abroad. The starch can be extracted and sold locally and exported. Tuber flour and gari are also sold locally. Cassava tubers are also processed and sold locally as dough and also exported as tapioca".

Some varieties that have less hydrocyanide (H.C.N.) and are sweet are eaten cooked or eating pounded like pounded yam. Various parts of Cassava are helpful. These include the tubers processing as gari or starch into tapioca. Starch is also used in the food and in textile industries. Terminal shoots and leaves are used as vegetable soup.

Threats to Cassava production and various efforts

The mottled cassava virus caused cassava mosaic disease (C.M.D.). This started in Uganda in the mid-1990s and has spread to neighbouring countries and beyond (Dixon et al., 2010). Severe strains of this Cassava mottled virus also spread to Nigeria. To avoid food insecurity, the save our soul strategy under the Cassava Mosaic Disease (C.M.D.) project financed by the Federal Government of Nigeria (F.G.N.), United States Aid (USAID), Shell Petroleum Development Company (SPDC), Niger Delta Development Commission (NDDC) and International Institute of Tropical Agriculture (IITA) was put in place. This has aided the development of various Cassava germplasms by IITA and the National Root Crops Research Institute (NRCRI) (Dixon et al., 2010). IITA and NRCRI both have nothing less than 59 varieties in their custody, some of which have been released in Africa while some have not been released in Africa. However, other efforts that have been put in place since 1984 include the contribution by both IITA, NRCRI and IITA Institute of Agricultural Research and Training (IAR&T), Obafemi Awolowo University (O.A.U.), Ibadan.

Some of the varieties were developed with the mindset that, along with some other traits, they would be resistant to Cassava green mite, cassava mealy bug, red spider mite, Spiraling whitefly, Cassava anthracnose disease and Cassava bacterial blight. Some of these varieties are developed to decrease Cyanogenic potential (C.N.P.). The more cyanide, the more the Cassava is unfit for consumption. Some improvements were made to increase the fresh yield in tonnes per hectare (t/ha). Some improvements were made to increase dry matter content (D.M. %). Some improvements were made to increase starch content (Starch %). However, some cassava varieties were improved to increase protein content (Protein %). Those improved to increase protein content were called yellow Cassava because of the beta-carotene content. These cassava varieties bio-fortified are being used by Harvest plus to combat hidden hunger in Africa. The various attributes calling for improvement necessitate the conservation of cassava germplasms to avoid food insecurity in Africa in the future.

List of Cassava germplasms owned by IITA and NRCRI According to Dixon et al. (2010)

The following varieties are owned by IITA and NRCRI

(1) T.M.S. 4 (2)1425 (2) T.M.S. 82/00058 (3) T.M.S. 91/02324 (4) T.M.S. 92/0057 (5) T.M.S. 92/0067 (6) T.M.S. 92/0325 (7) T.M.S. 92/0326 (8) T.M.S. 92b/00061 (9) T.M.S. 92b/00068 (10) T.M.S. 94/0026 (11) T.M.S. 94/0039 (12) T.M.S. 94/0561 (13) T.M.S. 95/0166 (14) T.M.S. 95/0289 (15) T.M.S. 95/0379 (16) T.M.S. 96/0523 (17) T.M.S. 96/0603 (18) T.M.S. 96/1089a (19) T.M.S. 96/1565 (20) T.M.S. 96/1569 (21) T.M.S. 96/1632 (22) T.M.S. 96/1642 (23) T.M.S. 97/0162 (24) T.M.S. 97/0211 (25) T.M.S. 97/2205 (26) T.M.S. 97/3200 (27) T.M.S. 97/4763 (28) T.M.S. 97/4769 (29) TMS97/4779 (30) T.M.S. 98/0002 (31) T.M.S. 98/0505 (32) T.M.S. 98/0510 (33) T.M.S. 98/0581 (34) T.M.S. 98/2101 (35) T.M.S. 98/2226 (36) T.M.S. 99/2123 (37) T.M.S. 99/3073 (38) T.M.S. 99/6012 (39) TMS 30572 (40) TMS M98/0028 (41) TMS M98/0040 (42) TTMS M98/0068 (43) TME 419 (44) TMS 90257 (45) TMS 91934 (46) T.M.S. 81/00110 (47) T.M.S. 82/00661 (48) TMS 30001 (49) TMS 30555 (50) TMS 50395 (51) TMS 84537 (52) NR 87184 (53) NR 41044 (54) NR 8082 (55) NR 8083 (56)NR 8208 (57) NR 8212 (58) NR 930199 (59) NR 8310

Conclusion

The breeding needs of Cassava, like any other crop, are driven by outstanding characteristics such as those mentioned in Table 1. These outstanding characteristics can only be achieved if there are broad base germplasms. These outstanding characteristics ranged from high yielding, low cyanide, early bulking, resistance to pests and diseases, non-branching, good gari and lafun, high dry matter, preservation and longevity of tubers in the soil without spoilage, suitability for mixed cropping, high biomass, resistance to Cassava Mealy Bug (C.M.D.), early maturing, suitable for food and industry, reasonably suitable for industry, increased or high beta carotene, suitability for intercropping, suitability for particular agroecology or group of agro-ecologies, tolerance to acidic soils, ability to smother weeds, suitability for fufu, suitability for a dense population in plantation, tolerance for drought, suitability for high-quality cassava flour due to low fibre content, high starch yield, high dry matter, high dry root yield, broad adaptation, and erect plant type. The reason for the release of different varieties of Cassava for different countries is that varieties released are determined by the needs, agroecologies and other socio-economic factors (Table 2).

Agricultural problems are dynamic, however, due to climate change, pestilence, wars, terrorism, population increase etc. For instance, there was a report of the recent outbreak of Cassava Brown Streak Disease (CBSD), currently destroying Cassava in East and Central Africa and is threatening to break in West Africa like C.M.B. This disease is said to be vectored by insects which can migrate to new regions and can cause problems to Countries yet to be affected (Eni, 2019). There is, therefore, a need for the conservation of germplasms, particularly landraces and possibly wild varieties, which may contain unique genes that may be used to address specific problems through conventional breeding or the use of modern biotechnological tools such as clustered regularly interspaced short palindromic repeats (CRISPR cas 9, CRISPR cas 3, CRISPR cas 12). Likewise, due to climate change, there may be a need to breed for resistance to flood or the need to breed for submergence, as in rice (*Oryza sativa*) in the future.

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Table 1. List of cassava released and registered in Nigeria from 1984 to 2014

S/No	Variety Name	Original Name	National Code	Original Source	Developing Institute	Outstanding Characteristics	Year of Release	Year of Registry
1	NICASS 1	T.M.S. – 30572 (Idi – Ose)	NGME 91-1	IITA, Ibadan	IITA, Ibadan	High Yielding	1984	1991
2	NICASS 2	T.M.S. – 4 (2) – 1425	NGME 91-2	IITA, Ibadan	IITA, Ibadan	High-yielding, low cyanide	1986	1991
3	NICASS 3	T.M.S. - 90257	NGME 96–3	IITA, Ibadan	IITA, Ibadan	Early bulking, high yielding	1986	1996
4	NICASS 4	TMS 84537	NGME 96- 4	IITA, Ibadan	IITA, Ibadan	High yielding	1986	1996
5	NICASS 5	T.M.S. 82/00058	NGME 96- 5	IITA, Ibadan	IITA, Ibadan	High yielding	1986	1996
6	NICASS 6	T.M.S. – 82/00661	NGME 96- 6	IITA, Ibadan	IITA, Ibadan	High yielding	1986	1996
7	NICASS 7	T.M.S.- 81/00110	NGME 96- 7	IITA, Ibadan	IITA, Ibadan	High yielding	1986	1996
8	NICASS 8	MS- 6 (Antiota)	NGME 96- 8	IAR&T, Ibadan	IAR&T, Ibadan	Non-branching, high yielding, resistant to pests and diseases, low cyanide, good gari and lafun	1986	1996
9	NICASS 9	MS-3 (odongbo)	NGME 96-9	IAR&T, Ibadan	IAR&T, Ibadan	Non-branching, high dry matter, good gari qualities, keep well in the soil. Good for mixed cropping.	1986	1996
10	NICASS 10	T.M.S. – 30555	NGME 96-10	IAR&T, Ibadan	IAR&T, Ibadan	Moderate Yielding	1976	1996
11	NICASS 11	NR-8208	NGME 96-11	NRCRI, Umudike	NRCRI, Umudike	High yielding	1988	1996
12	NICASS 12	NR-8083	NGME 96-12	NRCRI, Umudike	NRCRI, Umudike	High yielding	1986	1996
13	NICASS 13	NR-83107	NGME 96-13	NRCRI, Umudike	NRCRI, Umudike	High resistance to pests and diseases	1989	1996
14	NICASS 14	NR-8082	NGME 96-14	NRCRI, Umudike	NRCRI, Umudike	Very high yielding and resistant to pests and diseases	1986	1996
15	NICASS 15	TMS-50395	NGME 96-15	IITA, Ibadan	IITA, Ibadan	High biomass	1986	1996
16	NICASS 16	NR-8212	NGME 96-16	NRCRI, Umudike	NRCRI, Umudike	High yielding	1986	1996
17	NICASS 17	NR-41044	NGME 96-17	NRCRI, Umudike	NRCRI, Umudike	High yielding	1986	1996
18	NICASS 18	TMS-30001	NGME 96-18	IITA, Ibadan	IITA, Ibadan	Moderate yielding	1986	1996
19	NICASS 19	TMS-91934	NGME 96-19	IITA, Ibadan	IITA, Ibadan	High yielding	1986	1996
20	NICASS 20	TME-419	NGME 05-20	IITA, Ibadan	IITA, Ibadan	High yielding, resistant to C.M.D.	2005	2005
21	NICASS 21	T.M.S. 97/2205	NGME 05-21	IITA, Ibadan	IITA, Ibadan	High yielding, resistant to C.M.D.	2005	2005
22	NICASS 22	T.M.S. 98/0505	NGME 05-22	IITA, Ibadan	IITA, Ibadan	High yielding, resistant to C.M.D.	2005	2005
23	NICASS 23	T.M.S. 98/0510	NGME 05-23	IITA, Ibadan	IITA, Ibadan	High yield, resistant to C.M.D.	2005	2005
24	NICASS 24	T.M.S. 98/0581	NGME 05-24	IITA, Ibadan	IITA, Ibadan	High yield, resistant to C.M.D.	2005	2005
25	NICASS 25	NR 87184	NGME 06-25	NRCRI, Umudike	NRCRI, Umudike/ RMRDC, Abuja	Early maturing, high yielding, suitable for food and industry (34.6 t/ha)	2006	2006
26	NICASS 26	T.M.S. 92/0057	NGME 06-26	IITA	IITA/NRCRI Umudike	Reasonably suitable for mixed cropping, high yielding, suitable for food and industry (37.7 t/ha)	2006	2006
27	NICASS 27	T.M.S. 92/0326	NGME 06-27	IITA	IITA, NRCRI Umudike and RMRDC Abuja	Early maturing, suitable for mixed cropping, high yielding, suitable for food and industry (39.5 t/ha)	2006	2006
28	NICASS 28	T.M.S. 96/1632	NGME 06-28	IITA	IITA, NRCRI Umudike	Reasonably suitable for mixed cropping, high yielding, suitable for food and industry (43.2 t/ha)	2006	2006
29	NICASS 29	T.M.S. 98/0002	NGME 06-29	IITA	IITA, NRCRI Umudike and RMRD Abuja	Early maturing, reasonably suitable for mixed cropping, high yielding, suitable for food and industry (48.4t/ha)	2006	2006
30	NICASS 30	N.R. 93/0199	NGME 08 -30	NRCRI, Umudike	NRCRI, Umudike	Very suitable for food and industry	2008	2008

Source: Catalogue of crop varieties released and registered in Nigeria. Volume No. 6 updated as of September 2014 (NACGRAB) publication

Table 1. contd.

S/No	Variety Name	Original Name	National Code	Original Source	Developing Institute	Outstanding Characteristics	Year of Release	Year of Registry
31	NICASS 31	T.M.S. 96/1089A	NGME 08 -31	IITA	IITA, NRCRI, Umudike	Contains moderate level of beta-carotene, high yielding, suitable for food and industry	2008	2008
32	UMUCASS 32	N.R. 01/0004	NGME 10 -32	NRCRI, Umudike	NRCRI, Umudike	Early maturing, moderately suitable for intercropping, high yielding, suitable for food and industry and tolerant to drought (48.4t/ha). Suitable for southern and Northern Guinea Savanna agro-ecology	2010	2010
33	UMUCASS 33	C.R. 41-10	NGME- 10 -33	CIAT, Colombia	NRCRI, Umudike	Very suitable for intercropping, early maturing, high yielding, suitable for food and industry and tolerance to acidic soils (46.4 t/ha). good for southern and Northern Guinea Savanna agro-ecology	2010	2010
34	UMUCASS 34	T.M.S. 01/0040	NGME-10-34	IITA, Ibadan	NRCRI, Umudike	Moderate branching that can smother weeds, early maturing, high yielding, suitable for food and industry (51.7t/ha). Suitable for Southern and Northern Guinea Savanna agroecologies.	2010	2010
35	UMUCASS 35	TMS 00/0203	NGME 10- 35	IITA, Ibadan	NRCRI, Umudike	Suitable for smothering weeds in sole cropping, early maturing, high yielding suitable for food and industry (43.3t/ha). Suitable for Southern and Northern Guinea Savanna agro-ecologies		
36	UMUCASS 36	IITA TMS 1011368	NGME-11-36	IITA, Ibadan	NRCRI, Umudike	High beta carotene, high yield, suitable for gari and fufu, and high-quality cassava flour (46.5t/ha). Suitable for Humid Forest/ Savanna ecological zones		
37	UMUCASS 37	IITA TMS 1011412	NGME – 11 – 37	IITA, Ibadan	NRCRI, Umudike	High beta carotene, high yielding, suitable for gari and fufu, broad adaptation (59.1 t/ha). Good for Southern and Northern Guinea Savanna agro-ecologies	2011	2011
38	UMUCASS 38	IITA TMS 1011371	NGME-11-38	IITA, Ibadan	NRCRI, Umudike	High beta carotene suits gari, fufu, and high-quality Cassava flour (39.3t/ha). Good for Southern and Northern Guinea Savanna agro-ecologies	2011	2011
39	UMUCASS 39	N.R. 03/0211	NGME-11-39	NRCRI, Umudike	NRCRI, Umudike	Early maturing, high yielding, and high starch yield are suitable for high-quality cassava flour (42.5 t/ha). Suitable for Southern and Northern Guinea Savanna agroecologies.	2011	2011
40	UMUCASS 40	NR 03/0155	NGME -11-40	NRCRI, Umudike	NRCRI, Umudike	Early maturing, high yielding, suitable for gari and fufu, tolerance to drought (53.7t/ha). Suitable for Southern and Northern Guinea Savanna agro-ecologies	2011	2011
41	UMUCASS 41	C.R. 36 – 5	NGME – 12 -- 41	International Centre for Tropical Agriculture (CIAT), Cali Colombia	NRCRI, Umudike	High starch yield, high dry matter, erect plant type. Suitable for the intercropping and dense population in plantations and suitable for gari and fufu (42t/ha). Suitable for Southern and Northern Guinea Savanna agro-ecologies		
42	UMUCASS 42	IITA TMS 1982132	NGME -12-42	IITA, Ibadan	IITA, Ibadan, NRCRI, Umudike	High root yield, dry matter, and moderate carotene content (49.5t/ha). Suitable for Rainforest and Southern Guinea Savanna	2012	2012
43	UMUCASS 43	IITA TMS 1011206	NGME – 12-43	IITA, Ibadan	IITA, Ibadan, NRCRI, Umudike	High root yield, high dry matter content, drought tolerance (leaf retention in the dry season), and suitability for high-quality cassava flour due to low fibre content and high starch of dry roots (53t/ha). Suitable for Rainforest and Southern Guinea Savanna	2012	2012
44	UMUCASS 44	N.R. 07/0220	NGME – 14-44	NRCRI, Umudike	NRCRI, Umudike/ IITA, Ibadan	High beta carotene content and yielding (36 t/ha). Good for Rainforest and Southern Guinea Savanna	2014	2014
45	UMUCASS 45	IITA TMS107/0593	NGME – 14-45	IITA, Ibadan	IITA Ibadan/NRCRI Umudike	High carotene content and high yielding (34t/ha). Good for Rainforest and Southern Guinea Savanna	2014	2014
46	UMUCASS 46	IITA TMS 107/0539	NGME-14-46	IITA, Ibadan	IITA Ibadan/NRCRI Umudike	High carotene content and high yielding (32 t/ha). Good for rainforest and Southern Guinea Savanna	2014	2014

Source: Catalogue of crop varieties released and registered in Nigeria. Volume No. 6 updated as of September 2014 (NACGRAB) publication

Table 2. NARS cassava variety released from 2000 – 2009 in Africa

Year	Country	Cassava variety released
2000	Niger	T.M.S. 4 (2) 1425, TMS 085/01887, T.M.S. 92/0067, T.M.S. 91/02324, T.M.S. 98/0581
	Uganda	NASE 10, NASE 11 and NASE 12
2002	Angola	M 96000910, T.M.S. 92/0326
	Central African Rep	T.M.S. 91/02322 and T.M.E. 1
	Gambia	T.M.S. 98/00959, T.M.E. 90/01204, TMS91/02313 and T.M.E. 12
	Malawi	CH92/077 (Sauti) and CH92/112 (Yizaso)
	Sierra Leone	SLICASS 1, SLICASS 2, SLICASS 3, SLICASS 4 and SLICASS 5
	South Africa	(1995). – 13 – 2, 1989 – 17 – 1, 1987 – 16 – 1, 1995-10-1, 1995-6-3
	Togo	T.M.S. 92/0326
2003	Burkina Faso	T.M.S. 91/02312, T.M.S. 92/0067, TMS92/0427, T.M.S. 92/0325, T.M.S. 92/0325, T.M.S. 4 (2) 1425, T.M.S. 94/0270, T.M.S. 92B/00061, TMS M94/0177
	Cameroon	T.M.S. 92/0326 and T.M.S. 96/1414
	Ghana	T.M.S. 91/02327, T.M.S. 91/02324, TMS92/00067 and T.M.S. 92/0427
	Sierra Leone	80/40, 80/32, 83/15, 86/1, 87/29
	Tanzania (Costal Zone)	N.D.L. 90/034
	Chad	TME 225, TMS 94/D23, TMS 94/D66, TMS 94/D54, TMS 94/D70 and TMS 92/0236
2004	Cameroon	870713, 880477-2, T.M.S. 96/0023, 8085
	Swaziland	Clones 160, 48 and 65, 192/0326 and Rushinga
2005	Benin	TMS 91/02322 (Manina), TMS 92B/0061(Ina – H), TMS 92/0427 (Ina- Premier), TMS 92/0067 (MR – 67), TMS 91/2327, TMS 92/0057, TMS 92B/0068
	Cameroon	B- Bulk P6, T.M.S. 92/0057, T.M.S. 95/0109, and T.M.S. 96/1762
	Ghana	TMS 97/4962 (Abglifa), TMS 97/4414 (Bankyehemaa), TMS 97/3982 (Esambankye), and TMS 97/4489 (Doku duade)
	Nigeria	T.M.S. 98/2205, T.M.S. 98/0505, T.M.S. 98/0510, T.M.S. 98/058 and TME 419
	DR Congo	Butamu, Disanka, Mvuazi, Nsansi, and Zizila
2006	Burundi	MM96/0287, MM96/3920, MM96/7204, MM96/7866
	Guinea Conakry	TMS 92/0326, TME 419
	Kenya	MM96/7688, TMS 30567, MM96/4466, MM96/1871 and MH95/0183
	Nigeria	T.M.S. 92/0326, T.M.S. 92/0057, T.M.S. 96/1632, T.M.S. 98/0002, and NR 87184
	Rwanda	TMS 192/0057, 95/NA/00063, T.M.E. 14
2006	Sierra Leone	T.M.S. 92/0057 (SLICASS 6)
	Tanzania (Lake Zone)	MM 96/4684, MM96/8450, MM96/4619, MM96/5725, MM96/8233, MM96/3075B,TMS 191/00063, TMS 192/0057, TMS 192/0067, T.M.E. 14
	Tanzania (Zanzibar)	KBH 2002/482, KBH2002/482,KBH2002/494,KBH2002/517
	Uganda	MH9712961
2007	Guinea Conakry	T.M.S. 96/1632, T.M.S. 98/0581, T.M.S. 91/02324, T.M.S. 92B/00061
	Madagascar	A (094)/99, A 137/99, A 190/00
2008	DR Congo	Mbankana (196/0067), 94/0330, 01/1661, 01/1229, Obama je t'aime (TME 419), Liyayi, Namale and Mayombe
	Liberia	TME 693, TME 419, T.M.S. 01/0040, T.M.S. 95/0211, T.M.S. 98/0510, T.M.S. 92/0067, T.M.S. 96/1632, T.M.S. 98/0581
	Malawi	LCN 8010 AND 83350
	Nigeria	TMS 96/1089A, NR 930199
	Rwanda	MM96/0287, MM96/3920 and MM96/7204
	Togo	TMS 96/1642, TMS 96/0529, TMS 95/0166, TMS 96/0191, TMS 96/1632, TMS 96/1569, TMS 96/0409, TMS 96/0102, TMS96/0603, and TMS 95/0211
2009	Cameron	TMS 92/0067
	Cote d'Ivoire	88/00158

Source: Improved Cassava variety handbook (Dixon et al., 2010); T.M.S. = Tropical Manihot Species; MM = Midaltitude and medium rainfall – adapted selection; M.H. = Midaltitude and high rainfall – adapted selection

INSIGHT TO THE GENETIC ARCHITECTURE OF TEA PLANT [*Camellia sinensis* (L.) O. KUNTZE] IN MAMBILLA PLATEAU, TARABA STATE USING PHENOMICS AND SINGLE NUCLEOTIDE POLYMORPHISM DATA

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ABSTRACT

Tea plant [*Camellia sinensis* (L.) O. Kuntze] is a tropical tree with great economic and therapeutic potentials. Unfortunately, these potentials have not been adequately maximized and harnessed in Nigeria due partly to the low commercialization and partly due to the lack of genomic information, which has hindered the breeding, improvement and development of superior varieties. The combination of phenomic and single nucleotide polymorphism data in deciphering the genetic diversity are preferred for genetic and plant breeding applications/programmes, especially in tea plants. We investigated the genetic diversity in 46 tea plant clones obtained from tea growing communities in Mambilla Plateau as it relates to the bioactive compound composition in the leaves, leaf traits as well as using SNP markers. Varying bioactive compounds were identified in varying quantities but observed that caffeine was not present in all the leaves sampled. Leaf traits such as leaf length, leaf width, leaf area, shoot length, internode length and leaf biomass showed significant differences ($p < 0.05$), comparatively. From the molecular results, we report 232 segregating/polymorphic sites with nucleotide diversity of 0.095290 and Tajima neutrality test of -1.077234. Linear genetic distance ranged from 0.000- 0.6780. Phylogenetic analysis using leaf traits and SNP data showed inconsistency in the clustering pattern, which was not location-specific. This was corroborated by the principal coordinate analysis (PCoA) that showed a total variation of 43.87%. Analysis of molecular variance (AMOVA) revealed 100% within population and 0% among population variances. Taking the results together, there is urgent need therefore, to introduce elite varieties into the Mambilla tea population to widen the genetic base given that the genetic diversity is abysmally low. Additionally, the common practice of combining the leaves of all the clones during tea processing and production should be critically investigated for the optimal benefits of tea consumers.

Key words: economic, genetic diversity, diversification phenomics, tea plant, SNP

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INTRODUCTION

Food and nutrition insecurity is one of the major challenges in the developing countries, especially in Sub-Saharan Africa (SSA). Another critical challenge in this region is the healthcare where high death rate as a result of some preventable diseases are prevalent. Among these killer diseases, cardiovascular disorder accounts for about 3.76% of total deaths in Nigeria as at 2018 and is projected to increase by 20% by year 2020 (Oluseyi *et al.*, 2018). Interestingly, the medicinal properties of the tea plant [Camellia sinensis (L.) O. Kuntze] have scientifically been validated and known to treat a wide range of health conditions, including: cardiovascular diseases, obesity, immune enhancement, cancer, type 2 diabetes, neuralgic headaches, diarrhea, fatigue, sluggishness and asthma (Zhen Youn, 2002). The tremendous therapeutic, nutritional and economic importance of the tea plant should further strengthen the large-scale cultivation, which is an incredibly important industry in several countries such as China, Japan, India, Vietnam and Indonesia. Despite this obvious significance of tea, negligence in breeding, improvement as well as lack of effective conservation strategies have robbed most African countries, especially Nigeria the economic and therapeutic benefits that comes with tea production (Chen *et al.*, 2019) and current clones may soon face genetic erosion if nothing strategic is done. Regrettably, of the 33 clones acquired by Cocoa Research Institute of Nigeria from Nigerian Beverage Production

Company (NBPC) (Olaniyi *et al*., 2014) only 6 clones are currently under cultivation in the Kakara Tea plantation, Taraba State. However, vegetative means of propagating tea, which is currently being practiced in Kakara Tea Plantation and selection pressure for high yielding clones have posed serious problem leading to genetic erosion. Informatively, plant genetic resources are key to crop genetic improvement giving that the success of plant breeding and conservation is largely dependent on the amount and distribution of genetic variations present in plant collections. As been reported by Mutai *et al.* (2015) and corroborated by our findings there is no information on the genetic analysis and improvement of tea plant using genomic/ molecular tools in Nigerian tea germplasm. It is this premise that this current research is hinged.

MATERIALS AND METHODS

Samples were collected from Mambilla Plateau, Taraba State, which is located at coordinates range of 7°20'N and 11 ° 43'E. A total of forty-six (46) tea samples were collected; 6 samples from the six original clones [CBB36, C68, C143, C236, C318 and C1212] while 40 samples were randomly collected 10 from germplasm (G1-G10), 10 from Kusuku (KU1-KU10), 10 from Bangoba (BA1-BA10) and 10 from Kasalasa (KA1-KA10). All leaf parameters were collected in situ based on the outcomes of previous studies conducted on tea plant (Gunasekare *et al*., 2001; Piyasundara *et al*., 2006). Analysis of bioactive compounds were performed on the leaf samples of (clones BB36, 68, 143, 236, 318 and 1212 and the combination of the 6 clones being the practice in the company using GC/MS protocol according to Adamu *et al.* (2018) and Ananthi and Giri, (2018). For the molecular analysis, total genomic DNA (gDNA) of each dried tea leaf was extracted using NucleoSpin® Plant II kits (Macherey-Nagel, Gauteng, South Africa) according to the manufacturer's instructions and modified based on previous publications reported (Udensi *et al*., 2021; Udensi *et al*., 2022). Specific sets of primers were used to amplify the expressed sequence tags (ESTs) as previously documented by researchers Chen *et al*., 2000 and Ma *et al*., 2010. All PCR amplification's reaction (25 µl) consisted of 15 ng of template DNA, 0.3 µM of each primer (forward and reverse primers), 2.5 mM of $MgCl_2$, 0.3 mM of each dNTP, and 1 U KAPA HiFi HotStart DNA Polymerase (Kapa Biosystems-Roche, Basel, Switzerland). The bidirectional sequencing of all purified PCR amplicons was carried out at Inqaba Biotech Laboratory, South Africa using the same primer pair that was used for amplification of region under investigation. The purified sequencing products were analyzed with ABI 3500 xl Genetic Analyser (Applied Biosystems), using standard protocols. Leaf parameters were analyzed using PASW version 20 while molecular data were computed using MEGA X software (Kumar *et al*., 2018) and GenAlex 6.51 software (Peakall and Smouse, 2012), respectively.

RESULTS AND DISCUSSION

Leaf traits such as leaf length, leaf width, leaf area, shoot length, internode length and leaf biomass showed significant differences ($p < 0.05$), comparatively. We observed differences in leaf traits when compared our results with other researchers from other tea growing countries. These differences in morphological traits in our population and other populations may be due to the variations in genetic architecture of different clones of tea cultivars and prevailing environmental conditions. Varying bioactive compounds were identified in varying quantities but observed that caffeine was not present in all the leaves sampled. This result has been reported by several authors in different tea growing countries. This implies that tea producing companies can produce tea without caffeine and label it as such. From the molecular results, we report 232 segregating/polymorphic sites with nucleotide diversity of 0.095290 and Tajima neutrality test of -1.077234. Linear genetic distance ranged from 0.000 - 0.6780. Phylogenetic analysis using leaf traits and SNP data showed inconsistency in the clustering pattern, which was not location-specific. This was corroborated by the principal coordinate analysis (PCoA) that showed a total variation of 43.87%. Analysis of molecular variance (AMOVA) revealed 100% within population and 0% among population variances. Since tea plant is an outcrossing crop with high heterozygosity, it was surprising that after over 3 decades of introduction in Mambilla Plateau, there was little or no significant introgression, mutation and recombination that have taken place, leading to low genetic diversity. Local farmers in the adjoining community's source their planting materials from the Kakara Tea plantation/germplasm, which must have led to the result obtained from the AMOVA. Taking

the results together, there is urgent need therefore, to introduce elite varieties into the Mambilla tea population to widen the genetic base given that the genetic diversity is abysmally low. Additionally, the common practice of combining the leaves of all the clones during tea processing and production should be critically investigated for the optimal benefits of tea consumers.

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GENETIC VARIATIONS IN THREE SPECIES OF TILAPIA (*Oreochromis niloticus, Oreochromis aureus* AND *Oreochromis mossambicus*) IN SOME RIVERS OF SOUTH-SOUTH NIGERIA

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ABSTRACT
The understanding of genetic variation within and between species is the preliminary requirement for proper selection and breed improvement. This research aimed at evaluating the genetic variation in three species of tilapia fish in some rivers of South-South, Nigeria. From mt DNA, *O. aureus* had the highest polymorphism with 225 polymorphic sites followed by *O. niloticus* and *O. mossambicus* with 129 and 84 polymorphic sites, respectively. Haplotype numbers were five in *O. niloticus* and three in both *O. aureus* and *O. mossambicus*. The highest haplotype diversity was recorded in *O. niloticus* (0.796±0.001) while the highest nucleotide diversity was recorded in *O. aureus* (0.139±0.001). The highest genetic distance was between *O. aureus* and *O. mossambicus* (0.388) while the lowest genetic distance was between *O. niloticus* and *O. mossambicus* (0.217). Selective breeding of tilapia fish from Itu, Ethiope and Ikwere Rivers that showed high variation may enhance tilapia production.

Keywords: tilapia, variation, phylogenetics, South-south

INTRODUCTION
The production rate of fish in Africa has been very slow despite its increasing demands (Chan *et al.*, 2019). Indiscriminate fishing, lack of effective management, water and land use damage have caused many fishes in Africa to decline (Tran *et al.*, 2019) and their important species may soon face genetic erosion. In view of this pending doom, there is urgent need for government, policy makers and research institutions to put measures on ground to explore, exploit and conserve fish. This will demand keeping of proper track records of fish genetic resources and assessment of the different water bodies of their inhabitant, identification and classification of these resources to estimate their direct and indirect economic values as well as utilization in overall genetic improvement of fish (Hassanien *et al.*, 2011). Understanding the genetic variations in fish including tilapia in their natural habitats will promote selection of stock for breeding improvement. Sequence variation in mitochondrial D-loop has been used in related studies to discriminate tilapia species (Agbebi *et al.*, 2016). Therefore, unveiling the genetic diversity of tilapia species using mt D-loop will grant indebt understanding of tilapia stock variations which is preliminary requisite for selective breeding, genetic improvement and conservation.

MATERIALS AND METHODS
Sampling
Hundred tilapia fish species (*Oreochromis niloticus*, *Oreochromis aureus* and *Oreochromis mossambicus*) were collected from five locations. These included Itu River in Akwa Ibom State at approximately 5°12'5"N and 7°58´39"E, Anangtigha River in Cross River State at 4°54´54"N and 8°19´12"E, Ikwere in Rivers State at 4°59´92"N and 6°53´75"E, Kpansia River in Bayelsa State at 4°56´55"N and 6°19´52"E and River Ethiope in Delta State at 5°54´25"N and 5°40´58"E.

DNA extraction
Extraction of mtDNA was carried out in Biotechnology Laboratory Unit of Animal Science Department, Federal University of Agriculture, Abeokuta, Ogun State, Nigeria. The DNA was extracted from whole blood of the fishes using Quick-DNA MiniPrep kit from Zymo Research, USA.

Sequencing of D-loop
D-loop of the mtDNA was sequenced for all tissue-DNA extracts using the primers Forward (5'-GGATTYTAACCCYTRCCCC-3') and Reverse (3'-AGTAAAGTCAGGACCAAGCC-5').

Statistical analysis
ChromasPro version 2.6.6 was used to view and edit the sequences. MEGA 6.06 was used for

multiple sequence alignment of all the samples (Tamura *et al*., 2013) excluding all the gaps. Estimation of polymorphism in the aligned regions including nucleotide diversity (π) and haplotype diversity (Hd) values was carried out using DnaSP 5.1 software (Librado and Rozas, 2009). Genetic distance analysis of samples from the locations was carried out using MEGA 6.06 (Tamura *et al*., 2013).

RESULTS AND DISCUSSION

Comparative assessment of the three species showed that the highest polymorphism was recorded in *O. aureus* with 225 polymorphic sites followed by *O. niloticus* and *O. mossambicus* with 129 and 84 polymorphic sites, respectively (Table 1). The number of haplotypes were five in *O. niloticus,* three in *O. aureus* and three in *O. mossambicus*. Haplotype diversity was highest in *O. niloticus* (0.796±0.001), followed by *O. mossambicus* (0.703±0.004) and *O. aureus* (0.692±0.002), while nucleotide diversity was highest in *O. aureus* (0.139 ± 0.001) followed by *O. niloticus* (0.058±0.00012) and *O. mossambicus* (0.052 ± 0.0002). The implication here is that *O. niloticus* shared more conserved genes and therefore had more relatedness within the species as compared to *O. aureus* and *O. mossambicus*. Abdel-Hamid *et al.* (2014) reported five haplotypes in *O. niloticus* and *O. aureus*. In a similar study by Agbebi *et al.* (2016), six haplotype were identified in population of *O. niloticus* in South West Nigeria, which is in close similarity to the number of haplotypes identified in the present study. From the results obtained on genetic distance estimate of the three tilapia species (Table 2), *O. aureus* was different from *O. niloticus* and *O. mossambicus* with genetic distance of 0.294 and 0.388, respectively while *O. niloticus* and *O. mossambicus* had a lower genetic distance of 0.217. The implication here is that *O. aureus* from the different locations were more dissimilar to *O. nilotius* and *O. mossambicus*. This can be attributed to the higher degree of variable alleles in *O. aureus* which were reflected in the higher polymorphic sites, nucleotide diversity and low sequence conservation in their mt D-loop sequences.

Conclusion

The results showed existence of genetic variation among the three tilapia species. Therefore, tilapia from the rivers where samples were obtained for this research may serve as profitable breeding stock for selection and breeding improvement of tilapia.

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Table 1. Mitochondrial DNA Polymorphism among three species of tilapia fish

Polymorphism indices	*O. niloticus*	*O. aureus*	*O. mossambicus*
Monomorphic sites	684	582	692
Polymorphic sites	129	225	84
Singleton variable sites	08	14	10
Parsimony information sites	121	211	74
Number of haplotype	5	3	3
Haplotype (gene) diversity	0.796±0.001	0.692±0.002	0.703±0.004
Nucleotide diversity	0.058±0.00012	0.139±0.001	0.052±0.0002

Table 2. Genetic distance between three species of tilapia fish

Species	*O. niloticus*	*O. aureus*	*O. mossambicus*
O. niloticus	0	0.294	0.217
O. aureus	0.294	0	0.388
O. mossambicus	0.217	0.388	0

EFFECTS OF STOCKING DENSITY AND ENVIRONMENTAL COLOUR ON MOLECULAR STRESS RESPONSES AND ZOOTECHNICAL PERFORMANCE IN AFRICAN CATFISH (*Clarias gariepinus*) (BURCHELL, 1822)

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ABSTRACT

The effects of stocking density and environmental colour on the molecular stress indicators and zootechnical performance in African catfish (*Clarias gariepinus*) (Burchell, 1822) were assessed in this study. Fish with average weight of 15.00 ± 0.10 g were stocked into glass tanks of 60 cm x 45 cm x 45 cm dimension in triplicate at stocking densities of 10, 20 and 30 biomass in White, blue and black respectively. They were fed commercial diets containing 40% crude protein to meet the requirements for *C. gariepinus* fingerlings. After eight weeks of the feeding trial, molecular stress indicators (abundance and diversity) of stress protein genes (heat shock protein, HSP70) and zootechnical performance were assessed in the experimental fish. Result showed that growth and nutritional parameters mortality were significantly reduced ($p < 0.05$) with increasing stocking density. Colours of the container also significantly influenced the molecular stress markers and growth indicators in experimental fish. Molecular analyses of the HSP 70 genes showed that colour and stocking density significantly affected the stocking density and zootechnical performance of African catfish. The stocking density of 10 fish regarded as the low density which gave the best growth and zootechnical performance with least stress responses from fish is therefore regarded appropriate for intensive culture of African catfish. It was also demonstrated that African catfish zootechnical performance and stress responses were better in black rearing tanks than the in more contrasting background like blue and white backgrounds.

Keywords: catfish, densities, fish growth, HSP genes, welfare

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INTRODUCTION

The stagnating global capture fisheries has led to an ever-increasing focus on fish farming to meet the shortage of fish products and cater for the growing demand of the ever – increasing population (FAO, 2015). The overall effect of the global growth in fish farming and the increase in world population means that effective fish farming requires good management, including a focus on maintaining fish welfare. Stocking density is recognized as an important technical factor with a high impact on fish welfare and productivity. Therefore, fish farmers try to attenuate fish stress by applying several techniques such as reduction of handling and lower stocking densities (Conte *et al.*, 2014). Several environmental factors can alter the behavior and physiology in fish , among them: the photoperiod and rearing environmental colour (Papoutsglou *et al.,* 2010), which has great influence on the biorhythm of the animals influencing in the weight gain (Volpato and Barrento, 2012), food intake (Ellis *et al.,* 2012), energy expenditure, locomotor activity, among other physiological parameters (Mazeund *et al.*, 1977), such as light intensity (Pickering, 1981) and environmental color (Tort *et al.,* 1996).

Stocking density may act as a biological stressor, causing the development of a physiological response for the maintenance of internal homeostasis (Liu *et al.,* 2014). The visual environments of fish are blue, green or near infrared (Shreck and Tort, 2009) and fish have cone cells which enable them to discriminate colours (Shreck, 2009). Despite this, very few studies have been devoted to understanding the effects of stocking density and background or light color on fish biology. Even so, some interesting effects have been reported. In fisheries and aquaculture, the environmental conditions should undoubtedly be monitored to guarantee fish welfare. In these attempts, however, compatibility with tank colour has been largely neglected. Actually, the internal-wall color of the artificial fish environment has been chosen almost by chance. The African catfish (*Clarias gariepinus*) (Burchell, 1822) is commonly used in homestead fish culture because it takes up oxygen from the air, has a high growth rate and is often disease resistant (Gbadamosi *et al.,* 2016). Studies have reported the importance of color vision of the feeding behavior, survival and performance of fish, especially in the larval period of several species. However, there are few studies focusing on possible changes in behavior

or maintenance of physiological parameters of the fish with respect to the stocking density and colouring of the environment (Marandi *et al.,* 2018). The present study aims to understand the effect of stocking density and environmental colour in the African catfish (*Clarias gariepinus*) (Burchell, 1822), to the molecular levels of the heat shock proteins.

MATERIALS AND METHODS

Experimental design and fish feeding trial

The experiment was set up in a 3 x 3 factorial design to consist of 3 stocking densities (ten fingerlings termed as the low density, twenty fingerlings termed as the medium densities and thirty fingerlings termed as the high density) and 3 background colours (white, blue and black plastics tanks) designated as treatment 1 (T_1), treatment 2 (T_2) treatment 3 (T_3) respectively. *C. gariepinus* fingerlings were obtained from a reputable hatchery, prior to the feeding trial. Fish fingerlings with initial weight of 15.10 ± 0.10 g were stocked into plastics tanks of 60 cm x 45 cm x 45 cm dimension in triplicate treatment. A commercial diet, Nutreco ® (40% crude protein) was fed to all fish for 56 days. All groups were fed their respective diets at the same fixed rate (initially 5% of body weight per day). This rate was adjusted each week. Fish were fed by 0900-1000 and 1700-1800 h GMT, for 7 days each week. Growth was monitored weekly by batch weighing of fish from each tank.

Physico-chemical water parameters

Dissolved oxygen was monitored using HANNA 98103SE (HANNA instruments, Rhode Island). Temperature and pH were monitored using YSI-IODO 700 Digital probe (IFI Olsztyn, Poland). The water was maintained at 27 - 30°C, dissolved oxygen at 6.5 - 7.3 mg/Land Ph of 6.0 - 7.2.

Growth performance and nutrient utilization parameters

After 56 days, the total biomass of fish will be weighed and the final mean weight, daily weight gain, yield and survival rates will be calculated. The total amount of feed given in each treatment will also be added up at the end of the study. The following formulas will be used to calculate growth performance and nutrient utilization:

Growth performance and nutrient utilization were determined as follows:

Daily weight gain (g/fish/day) = (final BW (g) - initial BW (g)) / days

Feed Intake (g /fish) = total feed consumption during the experimental period (56 days).

Feed conversion ratio (FCR) = feed consumed (g)/ (final BW (g) - initial BW (g))

Specific growth rate (%/day) = 100 × (ln [final body weight] – ln [initial body weight])/no. of days of trial.

Molecular expression (abundance and diversity) of stress protein genes (Heat Shock Protein, HSP70) in African Catfish

Extraction of DNA and PCR-TGGE of fish liver were performed using the Qiagen® blood + tissue through the spin column protocol, the gram-positive optimisation was used in this kit to enhance the lysis of cells with complex cell walls. Extracted DNA was checked for quality and quantity by agarose electrophoresis and UV spectrophotometry using Nanophotometer P-class (IMPLEN®, USA).

Polymerase Chain Reaction (PCR) conditions

Primers were sourced from literature and emphasis was laid on primers suitable for Temperature gradient gel electrophoresis (TGGE) (Table 1). PCR of the V3–5 region of the liver 16S rDNA genes was performed using primer 968-f (Ojima *et al.,* 2005) as shown in Table 1. PCR of extracted DNA was performed with a 15-mL reaction mixture containing 7.3 mL Mango mix (Qiagen®). Thermocycling conditions were as follows: initial denaturation at 94°C for 2 minutes 30 seconds, followed by 60°C for 30 seconds at -0.7 per cycle for the annealing and elongation was at 72°C for 1 min. Denaturation was done again at 94°C for 30 seconds for 15 cycles, then 49°C for 30 seconds and elongation at 72°C for 30 seconds. Final denaturation was done for 18 cycles and final elongation for 5 minutes and cooled down to 4°C.

TGGE gels electrophoresis, staining and photographing the gel

Control gels and Quick load® DNA ladders (Biolabs, New England) were run on every gel. The condition for TGGE machine was at a constant voltage of 65 V for 16 h, the ramp temperature and increasing rate ramp (output change) was at 0.9°C per hour from 55.6 to 69.6°C using a DCode system (BioRad). Photograph was documented with Gel documentation equipment, Gene genius by Syn gene® and processing was done using gene genius snap 6.0 software.

Statistical analysis

Evaluation of growth performance and nutrient utilization parameter were subjected to multivariate analysis of variance (ANOVA) using SPSS 16 for windows software package. A P-

value 0.05 was used as the level of statistical significance. The significant differences among mean were determined by the subsequent use of Duncan's multiple range test (DMRT). Photographed gel after TGGE was processed for gel diversity and migration pattern using GelAnalyzer 2010a®, gel electrophoresis image analysis software.

RESULT AND DISCUSSION

Influence of stocking density and environmental colour on growth performance and nutrient utilization

In the current study, stocking density has direct effect on growth and survival of fish. In the current research, the environmental colour is another factor that affect different stocking density. The lowest stocking density was observed to have the best growth and nutritional performance, it also resulted into higher survival rate as shown in Table 2. On the other hand, the, the higher the stocking density, the lower the growth performance and nutrient utilization as it was observed in the present study furthermore, mortality rate increased and the feed conversion rate increases. It was also found that growth performance and other zootechnical parameters improved with as the contrast in the environment colours reduced in this form Black > Blue>White. This is agreement with the work of Ferosekhan *et al.* (2020) who reported that contrasting and deep colours of rearing tank improved zootechnical performance in Asian catfish, Pangas (*Pangasius pangasius*) larval growth and survival.

In understanding the effect of tank colour and stocking density on the growth performance of the fish, this study revealed that the blue tank with 10 stocking density shows a very good result as the growth performance was observed to exceed the other in which the 10 stocking density are also higher. This is in accordance with Herrera (2015) who stated that the growth performance at the low and intermediate density was significantly better than that of fish reared at the highest density. Also increased stocking density result in competition for space, food and oxygen, increase activity level and fish use more energy deriving in high metabolic rates and then growth decrease. (Ellis *et al.,* 2002). Under culture conditions, the fish for obtain food increase the swimming speed, these activities require energetic cost, which increase due to agonistic interactions. (Thorarensen & Farrell, 2010). This study also signifies that the black colour is a good environmental colour for African Catfish rearing as it was observed that at different stocking density the black colour reduce the fish stress thereby creating a good growth performance and feed utilization. This may be due to the physiological adaptation of fish to dark environment as opined by Andrade *et al* (2004). It was observed that lower weight uniformity occurred in *Leporinus macrocephalus* kept in environments with containers of brown, green, black and red colours. The authors also found that the use of containers of the black colour showed better weight uniformity than white colour and better length uniformity than red colour background. The zootechnical performance of the Catfish varies with the environmental. The performance of catfish reared in the blue tank was observed to better than every other one reared in the remaining two tank colours. Likewise, in nature, light intensity and background colour can affect feed detection, feed conversion rate and feeding success of cultured fish. Therefore, all these factors can affect the fish growth and mortality (Henne and Watanabe, 2003). Under culture conditions, tank color and light intensity can cause stress to the fish (Papoutsoglou *et al*., 2005) resulting in behavioural changes such as swimming performance, activity level, and habitat utilization (Schreck *et al.,* 1997). Farmers grow fish in high stocking density in order to maximize productivity (Iguchi et al., 2003). Stocking density may affect fish growth performance, physiology and fish behavior as shown in the current study this is in agreement with Marandi *et al* (2018) who reported that tank colour and rearing density significantly affected the growth and nutrient utilization of Common carp, *Cyprinus carpio*, influences of the interaction of the two factors were also reported.

Values in a row with different superscripts denote significant difference ($p<0.05$). Each value represents the mean ± SD
Initial weight=IW, Final weight=FW, Specific Growth Rate=SGR, Feed Intake = FI, Feed Conversion Ration= FCR.

Similarity and richness of the Heat Shock Protein 70 (HSP 70) genes and PCR-TGGE of the liver of experimental Clarias gariepinus

The similarity and richness of the HSP 70 from the PCR-TGGE fingerprints gel within the *C. gariepinus* liver is presented in Figure 1. The band represents one gene of HSP 70, dietary effects were observed in the banding patterns, with fish reared in white tanks showing the highest

expression of the HSP genes on the gel (Figure 1). Fish from the high stocking density tanks showed an increase in the expression of the HSP genes on the banding profile compared with the control. The fingerprints gel showed that lower diversity of the HSP 70 genes in *C. gariepinus* were recorded in fish reared in black tanks and diversity of shock genes increased with contrast of colours. Higher expression of the HSP genes were also recorded with increasing stocking density in the present study. In another study on HSP expression three HSP genes (HSP90, HSP70 and HSP60) were up-regulated with the significant up-regulation being detectable as early as 3 h after stress challenge in channel catfish (Liu *et al*., 2014). Under stressful conditions such as heat shock, pH shift or hypoxia and confinement, increased expression of HSPs protect the cell by stabilizing unfolded proteins, giving the cell time to repair or re-synthesize damaged proteins (Ojima et al 2005). Cha et al (2014) found higher levels of HSP gene expression at early stages of pathogenesis in olive flounder kidney and concluded that it was needed for chaperone activities to reduce stress effects. The highly conserved heat shock proteins (HSPs) are expressed and function as molecular chaperones which facilitate the synthesis and folding of proteins (Giri et al 2014). This is in agreement with the more abundant expression and up-regulation of HSP70 in *C. gariepinus* used in the current study which corresponds with fish reared in white and blue tanks having more due to stressful conditions than the black tank. This trend is also found to be applicable to increasing stocking density in the current study this is consistent with the findings of Webster *et al* (2020) which opined that exposure to a reoccurring, high-level aquaculture-relevant stressor (confinement) increased cortisol up regulated concentration in the juvenile salmon compared to low-level confinement.

Conclusion

In aquaculture ponds, growth rates of fish are related to a variety of factors, such as stocking density, nutrition, water quality, and health. In the case of indoor recirculating water systems, producers attempt to maximize productivity by optimizing the above parameters as well as other aspects of the environment. This study revealed the effect of stocking density and environmental colour on stress response and zootechnical performance in African catfish. Stocking density is a major factor in determination of successful aquacultural practices. With the high human population and increased demand for fish and fish products, it is necessary to increase stocking density of ponds to enhance productivity. The black colour was observed to promote growth and performance of African catfish and was observed to have reduced the effect of stress on the fish compared with the blue and white tanks. It can be deduced from this study that stocking density affect fish consumption rate, mortality rate, growth and performance of African catfish. The study shows that an increase in the concentration of Heat Shock regulated genes in the blue and blank tanks and also as the stocking density increases. Given the fundamental influence of stocking density and environmental colours as shown in this study, these results have important implications for health and welfare of fish.

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Table 1. The Sequence and conditions of primers used in this study. PCR of the V3–5 region of the African catfish targeting the 16S rDNA genes was performed using universal primers Gbadamosi *et al*., (2016) for African catfish

Oligo Name	Primer	Sequence (5'-3')	Amplicon size	Region	GC-contents
GUO-	PRBA338f (forward)	HSP70-F: TGGAGGAGGGTCTTCTGGAC	514	V5	57%F
	PRUN518r (Reverse)	HSP70-R: CACCAAAGAAAACAAACGGACTG			55%R

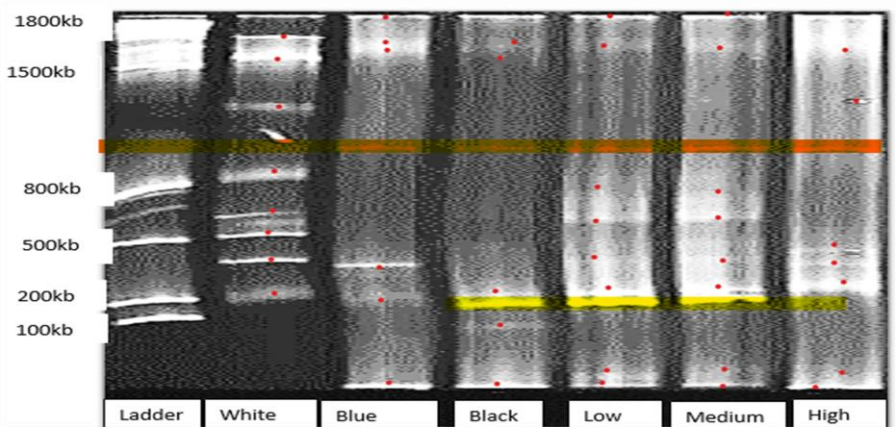

Figure 1. PCR-TGGE gels showing diversity of the HSPs from the PCR-TGGE fingerprints gel within the *C. gariepinus* liver after the feeding trials. Lane 1 = Ladder (arbitrary markers)

Table 2. Growth and feeding performance on African catfish reared in three tanks colors (white, blue and black) with three different Stocking densities (10, 20, 30) for 56 days

Growth	White			Blue			Black		
	10	20	30	10	20	30	10	20	30
IW (g)	15.14±0.03a	15.13± 0.03a	15.14± 0.01a	15.0±0 .09 a	15.14± 0.00a	15.11± 0.00a	15.03± 0.02a	15.05± 0.03a	15.04± 0.07a
FW(g)	88.37±0.31c	76.55± 3.85b	68.15± 0.94a	84.41± 2.32c	72.83± 2.24b	64.93± 2.55a	89.39± 0.54c	84.64± 0.47b	81.72± 0.58a
WG (g)	73.23±0.31c	61.42± 87b	53.01± 0.93 a	69.36± 2.36c	57.69± 2.26b	49.82± 2.55a	74.36± 0.55c	69.59± 0.49b	66.70± 0.54a
SGR (%/day)	3.15±0.10c	2.89±0 .09b	2.68±0 .02a	3.07±0 .55c	2.80±0. 06b	2.60±0. 10 a	3.18±0. 11c	3.09±0. 11b	3.02±0. 0a
FI	92.19±0.93c	85.63± 1.26b	75.95± 5.95a	87.49± 1.57c	82.00± 0.49b	70.25± 2.91a	94.29± 0.53c	94.07± 0.53b	88.18± 0.46a
FCR	1.26±0.01a	1.39±0 .76b	1.43±0 .09b	1.26±0 .02a	1.42±0. 06b	1.42±0. 12b	1.27±0. 15a	1.35±0. 01b	1.32±0. 01b
Mortality (%)	7.00±1.00a	8.00±0 .00a	11.33± 0.57a	6.66±0 .57a	8.33±1. 52a	9.00±1. 00a	6.33±0. 57a	8.00±0. 00a	9.33±0. 57a

PERIPHERAL BLOOD MONONUCLEAR CELLS: A CELLULAR SYSTEM REPUTABLE FOR EXTRAPOLATING HOW CATTLE RESPONDS TO HEAT SHOCK WHEN EXPOSED TO DIFFERENT ASSAULTS OF THERMAL CONDITIONS

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ABSTRACT

When livestock animals including cattle are exposed to toughed thermal conditions for a long time, thermal assault inflicted heat shock on them and this consequently impairs production performance such as fertility, feed consumption, milk yield, growth, health, physical and metabolic activities. Heat shock is one of the grave consequences of climate change and global warming on production and management of livestock animals. We subjected PBMCs from Indian Gir Zebu Cattle to *in vitro* thermal stress stimulation (TSS) of various dosages of thermal assault conditions, including normal to extreme temperatures and different durations of thermal exposures, in order to understand how PBMCs respond to various dosages and durations of heat shock. Understanding how PBMCs as a cellular system react to *in vitro* heat shock/thermal assault can help manage and decrease the effects of thermal stress on mammalian species. Our research found a significant ($P<0.0001$) correlation between the drop in PBMC count and decrease in PBMC count during *in vitro* TSS as thermal assault and heat shock intensified. The results of this study can be used to learn how mammalian species respond to various environmental thermal conditions *in vivo* and how to improve their capacity for adaptation, survival, and productivity.

Keywords: Cattle, heat shock, PBMCs, thermal assaults

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INTRODUCTION

According to Onasanya *et al.* (2022), one of the effects of thermal assaults on animals, particularly when subjected to prolonged-extreme thermal conditions, is heat shock (HS). Long-term exposure to harsh thermal conditions causes livestock animals, such as cattle, to experience heat shock, which negatively affects their ability to produce in terms of fertility, feed consumption, milk yield, growth, health, and physical and metabolic functions (Onasanya *et al.*, 2022 and Onasanya *et al.,* 2017). One of the severe effects of climate change and global warming on the production and management of livestock animals is heat shock which impairs cellular functions and performance of livestock animals (Onasanya *et al.*, 2021). Thermal stress is caused when an animal's body temperature is raised over typical physiological levels and this must be regulated to enable animals maintain a stable internal body temperature regardless of external thermal influences (homeostasis). Homeothermy in animals is the thermoregulation of the internal body temperature regardless of outside thermal assault challenges (Onasanya *et al.*, 2022). The existence of farm animals, including cattle, has been threatened by heat stress that can be reduced and mitigated by heat shock protein genes' thermoregulatory mechanisms in the face of the existential threat posed by global warming (Onasanya *et al.*, 2020 a; Onasanya *et al.*, 2021).

In *in vitro* study of peripheral blood mononuclear cells (PBMCs), Onasanya *et al.* (2023), Kishore *et al.* (2016), Sodhi *et al et al.* (2013) and Kapila *et al.* (2013) reported PBMCs as a cellular system which can be used to understand how animals respond to assaults of thermal conditions and environmental HS. Under prolonged and intense

thermal assault conditions (TACs) such as high tropical temperatures, the cellular systems of livestock animals are vulnerable to HS, which inhibits normal cell performance and may potentially result in cell death or trigger apoptosis. The goal of this report is to present advancement in the use of PBMCs as a cellular system in the study and understanding of how mammalian species, particularly bovine species in the tropics respond to assaults of thermal stimulation (TS) and HS occasioned by intense sunshine intensity for better management of heat stress and production.

MATERIALS AND METHODS

Study Animals, collection of blood samples Isolation of PBMCs

Blood samples (10 mL per animal) were collected aseptically from 65 Indian Gir zebu cattle breed aged 5–6 years kept under intensive system fed concentrates and water *ad libitum*. After blood collection, the blood samples were immediately processed for isolation of PBMCs. Fractional Separation of PBMCs from fresh whole blood using Histopaque-based procedures as earlier published by Onasanya *et al*., 2022 and Onasanya *et al*., 2023).

Thermal Stress Stimulation and Durations Different Thermal Assault Conditions, Estimation of the PBMC Count/Viability and Statistical Analyses

Blood samples of the 65 Indian Gir zebu cattle were used to obtain 65 aliquots of PBMCs, both stressed and unstressed groups contained 5 aliquots of PBMCs per each of the 13 treatment groups including the control group. The PBMCs received three TACs (0°C: Normal, 37°C: Normal body temperature and 45°C: Extreme) for 1 h, 2 h, 3 h, and 4 h with the exception of 0°C TAC which received no TS (0°C) for 0 h-DTE as shown in Figure. 1. Before the thermal TSS procedure, the average number of viable PBMCs were about 8.00-7.86 × 10^7 cells/msL. TSS was performed *in vitro* and, measurement of PBMCs pre- and post-TSS were performed using Trypan blue dye and haemocytometer, and viewed under microscope (Onasanya *et al*., 2023; Onasanya *et al*., 2022) as presented in Figure 2. TACs, TSS procedures, estimations of PBMCs and statistical analyses were performed according to previously published procedures reported by Onasanya *et al.* (2023) and Onasanya *et al.* (2022)

RESULTS AND DISCUSSIONS

We reported that HS had the greatest impact ($p < 0.0001$) on the PBMCs of Indian Gir cattle breed at 45°C–4 h-DTE (1.45 × 10^6), leading to increase in PBMCs death compared to PBMCs from other thermal conditions investigated (Figure 3). As the TACs toughen and DTEs progresses, we observed an increased reduction in PBMC count across the treatment groups ranging from 0^0C to 45^0C (Figure 3). However, PBMCs that were exposed to no TS (0^0C) and 0-h had the highest cell viability and PBMC count (7.86 × 10^7) hence they suffered no HS. Next to this were PBMCs exposed to normal body temperature of 37°C which had better cell count and viability than those exposed to 40^0C and 45^0C TACs (Figure 3), this suggests that 37°C mimics normal mammalian body temperature, hence PBMCs at this temperature had conducive cellular environment for better cell viability, growth and proliferation (Onasanya *et al*., 2022 and Onasanya *et al*., 2023; Siddiqui *et al*., 2021; Wang *et al*., 2017). PBMCs have been found to be an effective biological model for examining how cattle and other animals respond to TACs and heat stress (Onasanya *et al*., 2023; Onasanya *et al*., 2022; Kishore, *et al.* 2016). Circulating PBMCs, can be used as cellular system to learn more about the effects of HS on an animal's body and how thermal assault causes chronic inflammation and increases the risk of developing many diseases in cattle and other mammalian species (Dado-Senn *et al*., 2020; Kornienko *et al*., 2019; Kheirandish *et al*., 2017; Sheikh *et al*., 2017)

Conclusion

Climate change has significant consequences on the performance and survival of livestock animals. To accomplish this, it is essential to comprehend how animals respond to various assaults of environmental thermal conditions. The extended-extreme TACs, such as the high tropical temperatures, subject the cellular systems of livestock animals to heat shock, which hinders normal cell performance and may cause cell death or quickly induce apoptosis. Because of this, severe TACs-DTE combinations are harmful to cell count, viability and survival. PBMCs can be used as a cellular model in both *in vitro* and *in vivo* thermal environments to better understand the ability for thermotolerance in farm animals under actual environmental conditions for adaptation and improved productions.

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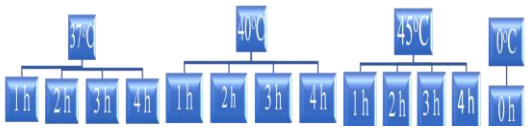

Figure 1. Experimental design showing different TACs and DTEs for stressed and unstressed peripheral blood mononuclear cells of Indian Gir Zebu cattle breed

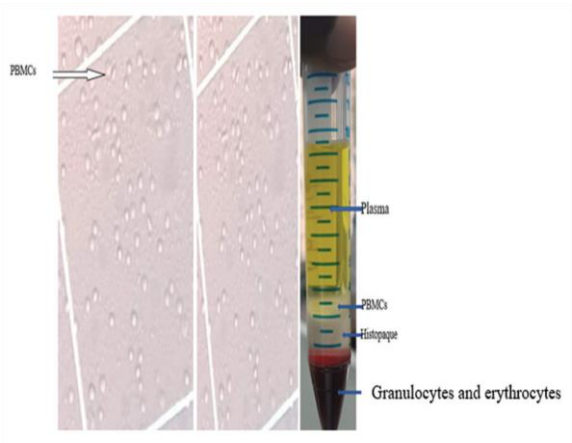

Figure 2. (a) Microscopic detection of peripheral blood mononuclear cells using hemocytometer viewed under microscope, (b) Fractional separation of bloods sample showing peripheral blood mononuclear cells and other fractional layers

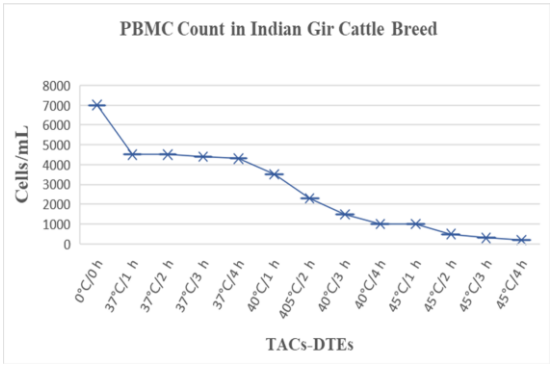

Figure 3. Assessment of Comparative Reduction and Viability of PBMC Count at different TACs-DTEs across PBMCs of Indian Gir Zebu Cattle breed and were significant at ****$p < 0.0001$

HERITABILITY ESTIMATES OF REPRODUCTIVE TRAITS OF TWO STRAINS OF INDIGENOUS TURKEY *(Meleagris gallopavo)* OVER TWO GENERATIONS OF SELECTION IN ZARIA, NIGERIA

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ABSTRACT
The local gene pool of poultry provides the basis for genetic improvement due to their fitness and resistance to local diseases. This study therefore estimates the heritability for reproductive traits of indigenous turkey. Two breeding group of white and black are formed with 18 adult turkeys (6 males and 12 females). A total of 90 poults were hatched from their eggs as the first generation G_1. At 8 weeks, 6 toms and 12 hens were selected and used as the parents of second generation G_2. Similar procedure used in G_1 was adopted for G_2. Egg number, fertility, hatchability, age and body weight at first egg lay were measured in both generations. SAS package was used to estimate variance components. The heritability estimate ranged from h^2 = 0.02-0.42 and 0.07-0.58 in white and h^2= 0.25-0.47 and 0.05-0.79 in black strain in generation one and two with most of the estimates been low. Lower heritability estimates observed shows that the trait had low genetic response hence it can only be improved through environment.

Keywords: heritability estimates, reproductive traits, Nigerian indigenous turkey,

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INTRODUCTION
In Nigeria, turkey production remained at small holder level and not popular. But it is considered significant next to chicken, duck, guinea fowl, pigeon and quail in contributing to the national economy, nutritional status and food security of the increasing population of the country (Kabir *et al.*, 2015). Heritability is the extent to which phenotype is genetically determined (Aboul-Seoud, 2008). It is essential in given an indication of the ability of a species to respond to selection, is also important to understand traits that change over generation to predict the breeding value of individual for effective breeding plan (Aboul-Seoud, 2008).

The local gene pool still provides the basis for genetic improvement and diversification to produce breeds adapted to local conditions (Hoffman 2005). The main aim of turkey breeder production is to increase the number of poults produced. Egg number, fertility and hatchability are the major determination of profitability in turkey breeding farm (Adebiyi *et al.*, 2014). This study is therefore aimed at estimating the heritability for reproductive traits of two strains of indigenous turkey.

MATERIALS AND METHODS
Experimental site
The research was conducted at the Teaching and Research Farm of Department of Animal Science, Faculty of Agriculture, Ahmadu Bello University Zaria. Detail of description of the site was as given by (IAR, 2018)

Mating design and management of experimental birds:
Two breeding group of white and black strain are formed with 18 adult turkeys (6 males and 12 females). A total of 90 poults were hatched from their eggs as the first generation G_1. At 8 weeks, 6 toms and 12 hens were selected and used as the parents of second generation G_2. Similar procedure used in G_1 was adopted for G_2. Egg number, fertility, hatchability, age and body weight at first egg lay were measured in both generations.
The birds were fed starter diet that contains 2800 kcal ME/kg with 28% CP, grower diet of 2900 kcal ME/kg with 18% CP and breeder diet of 2900 kcal ME/kg with 15% CP. They were fed *ad libitum*, clean drinking water provided. Necessary medications and vaccinations were administered as when due.

Data collection

Egg number: Is the number of eggs laid per week by each genotype.

Age at first egg lay: Age of hens at first egg laid.

Body weight at first egg lay: weight of dam at first egg laid by each genotype

Fertility (%) = $\frac{Number\ of\ fertile\ eggs}{Total\ number\ of\ eggs\ incubated} \times 100$

Hatchability (%) = $\frac{Number\ of\ chicks\ hatched}{Number\ of\ fertile\ eggs} \times 100$

RESULTS AND DISCUSSION

Table 1 shows the heritability (± SE) estimates for reproductive traits in white strain of turkey in generations 1 and 2. Egg number had lower estimates (0.02±0.06, 0.07±0.11) while, fertility (0.25±0.07, 0.11±0.02) and Hatchability (0.23±0.12, 0.13±0.05) had moderate to low estimates in generation one and two respectively. In Table 2 black strain, had non estimable heritability in Egg number in generation one with lower estimates (0.05±0.10) in generation two, fertility (0.25±0.06, 0.10±0.02) and hatchability (0.33±0.12, 0.19±0.11) are moderate to low in generations one and two. Lower heritability estimates observed in egg number and moderate to low estimates observed in fertility and hatchability in both strains in this study shows that variability due to additive genetic values was low. Hence, the trait is more influenced by environment. This was similar to the study of Wawro *et al.* (1996) who observed a lower heritability in reproductive traits of turkey, they concluded that the traits are among low-heritable ones and therefore, are highly influenced by the environment.

In Table 1, white strain had higher estimate for age at first lay in both generations (0.42±0.23, 0.58±0.17), whereas, body weight at first lay is moderate to high (0.32±0.04 and 0.54±0.03) in generations one and two. Similarly, in Table 2 black strain had moderate to high estimate for age at first lay (0.25±0.23, 0.42±0.23) and body weight at first lay was highly estimated (0.47±0.04, 0.73±0.03) in both generations. The higher estimates observed in age and body weight at first lay in both strains were in line with the report of (Emamgholi Begli *et al.*, 2018) where they reported higher heritability for age and body weight at first egg of turkey. There is an increase in heritability from generation one to two in age and body weight at first egg lay in both strains. This indicates an increase in additive genetic variance across generations as stated by (Falconer, 1989). Hence selection for increased 8-weeks body also reduced age and increased body weight at maturity.

Conclusion

Lower heritability estimates observed in most of the reproductive traits studied (egg number, fertility and hatchability) shows that the traits are influenced by environment. Environmental factors should be improved to enhance these traits, while, age and body weight at first lay had higher heritability, therefore, can be improved by selection for increased 8-weeks body weight.

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Table 1. Heritability (± SE) estimates of reproductive traits of white turkey in generations 1 and 2

Traits	Generation 1	Generation 2
Egg number	0.02±0.06	0.07±0.11
Fertility	0.25±0.07	0.11±0.02
Hatchability	0.23±0.05	0.13±0.12
Age at maturity	0.42±0.23	0.58±0.17
BW at maturity	0.42±0.04	0.54±0.03

BW= body weight; NE= not estimable.

Table 2. Heritability (± SE) estimates of reproductive traits of black turkey in generations 1 and 2

Traits	Generation 1	Generation 2
Egg number	-	0.05±0.10
Fertility	0.25±0.11	0.10±0.02
Hatchability	0.43±0.11	0.19±0.12
Age at maturity	0.25±23	0.42±0.27
BW at maturity	0.47±0.04	0.79±0.03

BW= body weight; NE= not estimable.

CANONICAL VARIATE ANALYSIS OF THREE NIGERIAN INDIGENOUS AND EXOTIC CHICKENS

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ABSTRACT
Multivariate Analysis was conducted on body weight and morphological traits to characterize 180 three Nigerian indigenous (normal feathered (60), naked neck (60), frizzle feathered (60) and 60 exotic (Ross 308 broiler) chickens reared in Maiduguri, Borno State, Nigeria. The traits examined were body weight, shank length, shank circumference, keel length, back length, thigh length and shank diameter. Chicken types were used as separation criterion and data analyzed using SPSS. The results indicated superiority of Ross 308 broiler chicken over indigenous types and naked neck was distinguished from other local chickens. First Canonical function accounted for 98.4%, second and third accounted for 1.0% and 0.6%. Overall percentage of correctly classified cases is 75.8%. Proportion of individual chickens correctly classified to original group was 100% in Ross 308 and 76.7% in naked neck; indicating distinctness of exotic breed from indigenous and best potential of naked neck for genetic improvement among the locals.

Key words: canonical, exotic, indigenous, morphological traits, Dendrogram

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INTRODUCTION
Chickens have been described to contain a highly conserved genetic reservoir rich in high level of heterozygosity required for the development of genetic stocks with improved adaptability (Ajayi *et al.,* 2012). In other words, it is the genetic variation fond in these chickens that justifies their future improvement and sustainability of their production systems (Benitez, 2002). The first approach to a sustainable use of animal genetic resource is characterization of a group of livestock. To achieve this, knowledge of variation of morphological traits in these animals is pertinent (Delgado *et al.,* 2001). For years, morphological measurements have been in use to characterize various breeds of animals including chickens and this could provide useful information on the suitability of animal for selection. Series of attempts have been made to improve the indigenous chickens for body weight; one of these is cross breeding between local and exotic breeds especially broilers. Although chickens have been characterized based on morphological traits, however, incorporation of exotic meat-type breeds using multivariate analysis is rear especially in this part of the country. The objective of this study therefore was to characterize three Nigerian indigenous chickens and one exotic meat-type (Ross 308 broiler) breed using multivariate Canonical variate Analysis.

MATERIALS AND METHODS
Experimental Area
The work was conducted in Maiduguri, Borno State. The state lies between Latitudes 10 and 13^0 N and Longitudes 12 and 15^0E. The annual rainfall varies from 700 to 1000 mm in the Southern part and 300 to 500 mm in the north (Ayuba *et al.,* 2003). There are three seasons namely, dry cold (October to March); hot dry (April - June); and rainy season (July - September). Temperatures are high all year round with hot season mean ambient temperatures ranging between 39 and 40^0 C. (Mohammad and Ahmed, 2014).

Experimental birds and data collection
Indigenous chickens were collected from different parts of Maiduguri, Borno State. A total of 180 chickens comprising 60 each of naked neck, normal- and frizzle feathered were randomly selected therein and 6 and 8 weeks old Ross broiler chickens were selected from a group of birds. They were characterized for morphological traits; body weight, shank length, back length, keel length, thigh length, shank circumference and shank diameter. These were measured using methodology of Francesch *et al.* (2011).

Statistical analysis

Data collected were first subjected to Descriptive statistics. Body weight and Morphological characteristics were subjected to Canonical Variate analysis with type of chicken as a separation criterion using SPSS version 20.0 (SPSS, 2011). Data collected on the body measurements were analyzed using the fixed model:

$$Y_{ij} = \mu_o + A_i + e_{ij}$$

Where Y_{ij} = observation belonging to $_{ij}$ classification

μ_0 = Overall mean

A_i = effect of ith genotype (i =1, 2, 3, 4)

e_{ij} = random error

RESULTS AND DISCUSSION

Ross broiler chicken was distinguished from the local strains in four morphological traits; body weight, keel length, back length and thigh length (Table 1). An indication that keel, back and thigh lengths constitute the major parts of broiler body weight. However, the indigenous strains expressed better shank qualities. Distinguished characteristics of Ross are expected because it is a breed exclusively developed for table meat. On the other hand, generally lower body weights and dimensions shown by indigenous strains confirm that indigenous chickens are light birds compared with the exotic (Adeleke *et al.,* 2011). Meanwhile, naked neck among the indigenous types was identified with heaviest body weight, longest keel and back as well as best shank diameter. Since these traits are most important in meat quality of a bird, the result indicates that naked neck could be the best for cross-breeding programme with Ross broiler. This is in line with the work of Abdulraheem *et al* (2021) and Ajayi *et al.* (2012).

The first Canonical function (Table 2) accounted for largest amount between group variability (98.4%) while second and third functions accounted for 1.0% and 0.6%, respectively. The Discriminant analysis results based on type of chicken as separation criteria are given in Table 3**.** The overall percentage of correctly classified cases is 75.8%. The proportion of individual chicken-types correctly classified into their original group was 100% in the Ross broiler; followed by naked neck (76.7%). This indicated distinctness of exotic breed and suggested naked neck for best potential for genetic improvement among local chickens. Tauran *et al.* (2005) reported that, it is difficult to obtain 100% prediction of group membership. However, Herrera *et al.* (1996) obtained 100% classification for Andalusia goats.

Conclusion

Ross broiler chicken was distinguished from the local strains in major traits. Naked neck was identified with heaviest body weight, longest keel and back and best shank diameter among its peers. The proportion of individual chickens correctly classified into their original group was highest in the Ross broiler and then in naked neck, an indication of distinctness of exotic breed from indigenous and good potential of naked neck for genetic improvement.

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Table 1. Descriptive statistics of three indigenous and one exotic broiler chickens

	Normal feathered chicken		Frizzle feathered chicken		Naked neck chicken		Ross 308 broiler	
Trait	Mean	SD	Mean	SD	Mean	SD	Mean	SD
BW(g)	1543.67	289.67	1271.67	179.54	1613.33	165.49	2377.58	345.39
SL(cm)	9.76	1.59	8.87	1.19	9.63	1.16	7.47	0.57
SC(cm)	5.28	0.76	5.17	0.69	5.23	0.56	5.17	0.53
KL(cm)	11.84	0.99	11.43	1.46	13.49	1.57	15.80	0.79
BL(cm)	21.34	2.29	19.62	1.81	22.38	1.79	43.05	1.84
THL (cm)	13.94	1.77	12.20	1.86	13.34	1.64	18.85	0.86
ShD(cm)	1.69	0.24	1.61	0.134	1.75	0.22	1.63	0.13

BW=Body weight, SL=shank length, SC=shank circumference, L=keel length, BL=back length, THL=thigh length, ShL=shank diameter SD= Standard Deviation

Table 2. Summary of canonical discriminant functions and eigen values

Function	Eigen value	% Variance	Cumulative %	Canonical correlation
1	33.213	98.4	98.4	0.985
2	0.344	1.0	99.4	0.506
3	0.185	0.6	100.0	0.404

Table 3: Classification results of discriminant analysis

Classification		Predicted Group Membership				Total
	Type	1	2	3	4	60
Count	1	38	15	7	0	60
	2	14	38	8	0	60
	3	6	8	48	0	60
	4	0	0	0	60	60
Original %	1	63.3	25.0	11.7	0	100
	2	23.3	63.3	13.3	0	100
	3	10.0	13.3	76.7	0	100
	4	0	0	0	100	100

75.8% of original grouped cases correctly classified

Table 2: General combining ability effects of parents for the studied characters evaluated at Maiduguri and Benisheikh combined, 2022

Genotype	DFF	PLH	NPP	GYD	SCH	DMI
Testers						
PS202	4.58	11.8	32.74	169.9	22.14	-10.42
Ex-Monguno	0.75	-23.63	-8.76	112.7	-4.19	4.69
Ex-Baga	-2.88	5.14	-12.16	-141.3	-16.56	3.36
Ex-Gubio	-2.45	6.69	-11.83	-141.3	-1.39	2.37
SE±	0.79	9.91	4.03	79.37	5.56	2.7
Lines						
PEO 5684	0.63	10.59	9.96	246.02	3.58	-8.09
Zango	0.13	-5.48	-4.04	-7.94	-7.72	0.76
LCIC9702	-0.16	-7.87	-2.42	-119.07	-7.88	0.68
SOSAT C-88	-0.83	17.82	-2.83	-118.98	11.49	2.34
Ex-Borno	0.22	-15.06	-0.67	-0.03	0.53	4.32
SE±	0.71	8.87	3.6	70.99	4.97	2.42

DFF= Days to 50% flowering, PLH= Plant height, NPP= Number panicles per plant, GYD= Grain yield, SCH= Striga count, DMI= Downey mildew incidence

Table 3. Specific combining ability effects of hybrids for the studied characters evaluated at Maiduguri and Benisheikh combined, 2022

Hybrid	DFF	PLH	NPP	GYD	SCH	DMI
PEO 5684 × PS202	0.00	3.80	-6.99	-138.2	-9.14	7.01
Zango × PS202	-0.33	-19.85	-0.82	179.3	-19.52	-0.32
LCIC 9702 × PS202	-0.54	14.48	6.38	131.9	-13.35	-7.91
SOSAT-C88 × PS202	-0.21	-4.82	2.8	-185.8	30.78	-5.12
Ex-Borno × PS202	1.08	6.12	-1.36	12.7	11.23	6.33
PEO 5684 × Ex-Monguno	1.5	38.9	28.17	585.9	37.03	-20.56
Zango × Ex-Monguno	2.00	19.46	-8.49	-366.7	-3.85	4.13
LCIC 9702 × Ex-Monguno	1.46	-0.70	-6.78	-223.9	6.15	1.24
SOSAT-C88 × Ex-Monguno	-1.88	-6.48	-6.20	157.2	-22.89	4.35
Ex-Borno × Ex-Monguno	-3.08	-44.84	-6.70	-152.6	-16.43	10.84
PEO 5684 × Ex-Baga	-0.53	-31.6	-11.09	-144.5	-9.11	3.12
Zango × Ex-Baga	-0.14	1.52	7.075	46.0	5.35	-2.06
LCIC9702 × Ex-Baga	-0.58	-19.31	-1.05	30.1	4.35	3.12
SOSAT C-88 × Ex-Baga	1.43	18.78	2.86	-1.6	-4.19	3.54
Ex-Borno × Ex-Baga	1.05	28.61	2.20	69.9	3.6	-7.72
PEO 5684 × Ex-Gubio	-0.97	-11.09	-10.09	-303.3	-18.78	10.43
Zango × Ex-Gubio	-0.30	-1.41	2.24	141.3	18.02	-1.75
LCIC 9702 × Ex-Gubio	-0.34	9.87	1.45	61.8	2.85	3.55
SOSAT C-88 × Ex-Gubio	0.66	-7.49	0.53	30.2	-3.69	-2.78
Ex-Borno × Ex-Gubio	0.95	10.12	5.86	69.9	1.60	-9.45
SE±	1.58	19.83	8.06	158.7	11.11	5.4

DFF=Days to 50% flowering, PH=Plant height, NPP=Number of panicles per plant, GYD=Grain yield, SCH=Striga count at harvest, DMI=Downy mildew incidence

EDIBLE OIL-BASED SWITCHABLE SOLVENT LIQUID-LIQUID MICROEXTRACTION FOR THE DETERMINATION OF LEAD USING FLAME-ATOMIC ABSORPTION SPECTROMETRY

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ABSTRACT
Edible oil-based switchable solvent liquid-liquid microextraction (EO-SS-LLME) was used prior to flame atomic absorption spectrometry (FAAS) for the determination of lead, complexed with ammonium pyrrolidine dithiocarbamate (APDC). Optimum extraction conditions were achieved using 500 µL edible oil as the extraction solvent, 10 mL of 2.0 M sodium hydroxide to form the salt of fatty acid and 150 µL of 8.0 M nitric acid for back extraction. Limits of detection and quantitation were found as 0.0453 and 0.1509 µg mL^{-1}, respectively. Good linearity was obtained with a coefficient of determination (R^2) value of 0.9954 with relative standard deviation of 3.4 and an enrichment factor above 45. Accuracy was checked by addition-recovery studies and percentage recoveries obtained were in the range of 97.2 and 105.8. The proposed method was applied for the determination of lead in cosmetic samples (i.e., lipstick, eye shadow, eye liner, face powder) where satisfactory results were achieved.

Keywords: Edible oil, Flame-atomic absorption spectrometry, Lead, Liquid-liquid microextraction, Switchable solvent

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INTRODUCTION
Dermal exposure is expected to be the most significant route for cosmetic products, because most of them are applied to the skin and leads to long-term exposure to different chemicals (Contado and Pagnoni, 2012). Lipstick and other cosmetic products are composed of several constituents such as oils, antioxidants, colorants, silica and titanium oxide (de la Calle *et al.*, 2017) that create different colors, properties and appearance to the finished product (Batista *et al.*, 2016; Gunduz and Akman, 2013). Lead, Pb, was described among the most dangerous contaminants (Smith and Flegal, 1995) that enter the body through ingestion, inhalation or skin absorption (Lilley *et al.*, 1988). It affects virtually all systems in the body causing a life-long adverse health effect which include reproductive, neurological, hematopoietic, hepatic and renal systems (Al-Saleh *et al.*, 2013; Piccinini *et al.*, 2013).

The World Health Organization (WHO) established the provisional tolerable weekly intake of Pb as 25 µg kg^{-1} body weight for all human groups the maximum allowable limit as 10 µgL^{-1} for Pb in drinking water (Cotruvo, 2017). Therefore, development of green and reliable analytical method for the determination of lead in cosmetics is indispensable for human health. Sample preparation is a critical step in quantitative analysis because it involves preconcentrating and cleaning the sample and to increase the sensitivity of instrumental techniques. Some methods such as, liquid-phase microextraction (LPME), deep eutectic solvent-based microextraction, solid phase microextraction (SPME), solidification of floating organic drop microextraction (SFODME) and dispersive liquid-liquid microextraction (DLLME) have been widely used for the preconcentration and separation of lead and other metal ions from different environmental, biological, water and cosmetic samples prior to their instrumental analysis. In recent years, switchable hydrophilicity solvents (SHSs) have gained a wide interest as alternative green solvents. They have ability to be reversibly switched from hydrophobic to hydrophilic (Jessop *et al.*, 2005) which allow the extraction of analytes without a disperser solvent (Wang *et al.*, 2019). However, edible oil based-switchable hydrophilicity solvent liquid phase microextraction (EO-SHS-LPME) provides a better and green alternative. These EO are non-

volatile, non-toxic, available, cheap, affordable, biodegradable and renewable.

The objective of the present work is to develop a novel and simple microextraction method that employ the use of EO as an alternative to conventional switchable solvent for the preconcentration and determination of lead in cosmetic samples prior to micro-injection flame atomic absorption spectrometry. The operation conditions and experimental parameters such as, volume and type of edible oil as switchable solvent, pH, concentration of ligand, type, concentration and volume of back extraction solvent were studied and optimized.

MATERIALS AND METHODS

Chemicals and reagents

All chemical and reagents used were of high purity analytical grades. During the experimental work, deionized (DI) water (18.2 MΩ.cm), treated with Purelab Ultra Analytic (ELGA LabWater, UK), was used for all preparations. Nitric acid, HNO_3 (65%, v/v) and ethanol (99%) were purchased from Reidel-de Haen (Germany), hydrochloric acid by Merck (Germany), sulfuric acid (95%), hydrogen peroxide and sodium hydroxide by Sigma-Aldrich (Germany). Stock solution of analyte 1000 mg L^{-1} lead (II) nitrate (Sigma-Aldrich, Germany) was diluted daily with 1.0 mol L^{-1} HNO_3 for working standards. A 1.0% (w/v) APDC (Sigma-Aldrich, Germany) was prepared in ethanol. The pH of the solutions was adjusted with buffer solution. Acetate buffer solution (CH_3COO^-/CH_3COOH) at pH 4.5 was prepared by dissolving sodium acetate trihydrate in DI water and adjusted with appropriate volume of acetic acid.

Apparatus

A Thermo scientific iCE 3000 series (USA) flame atomic absorption spectrometer (FAAS), equipped with air-acetylene flame as an atomizer, a lead hollow cathode lamp at 217.0 nm wavelength and a deuterium background correction. An electronic balance (Mettler-Toledo, Switzerland) was used for weighing the reagents. Vortex mixing was performed using an IKA MS 3 digital vortex (USA). Centrifugation was carried out using a Hettich Eba 20 centrifuge (Germany). All measurements were carried out with microinjection and peak heights were used for calculations.

EO-SHS-LPME procedure

The schematic procedure for the EO-SHS-LPME is described as follows: 500 µL of the optimized EO transferred into a falcon tube and 10 mL of 2.0 M NaOH was added for hydrolysis. This mixture is vortexed for 2 min and then centrifuged for 2 min to separate the excess glycerol in the aqueous solution with the viscous SFA. The SFA (switched-on form) formed was spiked with 100 µL of 100 mg L^{-1} Pb^{2+}, followed by 1 mL 10% NaCl, 2.0 mL acetate buffer (4.5) and completed to 10 mL with DI water before addition of 800 µL 0.1% w/v APDC. The mixture was vortexed for 5 min to achieve complexation and a stable emulsion completely miscible with no phase separation was obtained. This is followed by addition of 300 µL of 2.0 M H_2SO_4 to break the emulsion where the SFA is protonated back to an immiscible FA (switched-off form). Phase separation was induced upon centrifugation for 2 min. The FA layer collected was transferred into an eppendorf, followed by addition of 150 µL of 8.0 M HNO_3 for back extraction. The mixture was vortexed for 4 min to break the complex and release the analyte into the aqueous solution. The aqueous solution was collected using a HPLC syringe after centrifugation, followed by pH adjustment and then injected into the instrument.

RESULTS AND DISCUSSION

The operational conditions and experimental parameters such as, volume and type of edible oil as switchable solvent, pH, concentration of ligand, type, concentration and volume of back extraction solvent were studied and optimized based on one parameter at a time.

Different EO were tested for the extraction of the metal ion. The nature of the EO has a high impact towards extracting the analyte, as each contain a different R group in the FA. The interaction of the metal ion complex is attributed to the hydrophobic nature of the R group in the EO sample. Upon addition of a strong acid (e.g., H_2SO_4) causes the protonation of SFA into its hydrophobic form (FA), which results the extraction of the analyte complex into the floating FA layer when centrifuged.

The value of sample pH plays an important role in metal-ligand formation and also in the extraction. Studies revealed that, Pb^{2+} was generally extracted in acidic medium [10]. Therefore, the effect of pH was studied between the range of 1.5-7.5 in this method. The chelating agent, APDC could be unstable at low pH due to protonation, thus low recovery occurred because of little or no complexation. As pH increases

generally above 8.0, recovery decreases due to possible formation of insoluble hydroxides.
The APDC is an efficient chelating agent for preconcentrating Pb^{2+} due to its hydrophobic nature and formation of stable complex with the metal ion. The concentration was studied in the range of 0.05-0.175 % (w/v) for the recovery of Pb^{2+}. The maximum recovery was achieved at 0.1 % (w/v) of complexing agent, where further addition yielded an insignificant effect.

Also, among the important parameters that influence the extracted amount of analyte is the vortex time. The vortex time was studied between 1.0-7.0 min in order to increase the contact between the metal ion and the ligand for chelation. This in addition facilitate and increase the distribution of the SFA in the aqueous phase. The nature of the organometallic complex (Pb-APDC) is strongly hydrophobic, therefore strong acidic condition is needed to break the complex and release or free the metal ion into the aqueous solution. Different acids were used in order to back-extract Pb^{2+} from the extraction solvent. Highest recovery was obtained with HNO_3, whereas H_2SO_4 decompose the extraction solvent completely which is attributed to its high oxidizing ability, CH_3COOH forms a homogeneous mixture which is due to the weak nature of the organic acid. For this purpose, 2.0-14.0 M of HNO_3 was used and highest recovery was achieved at 8.0 M.

Application of EO-SHS-LLME-FAAS to cosmetic samples was carried out where satisfactory results were achieved through addition-recovery test. The percentage recovery (% R) was 97.7-104.0% which indicates the reliability of the method.

Conclusion

In this study, a novel and green switchable-hydrophilicity solvent liquid-liquid microextraction based on the use of edible oils prior to flame-atomic absorption spectrometry is proposed for the determination of lead in cosmetic samples. The advantages of replacing conventional organic solvents with edible oils include, but are not limited to, high biodegradability, low cost, renewability, sustainability, and high degree of greenness. The ability to switch them on and off through a simple, instantaneous reaction improves the extractability of the analytes due to the infinitely large surface of area of contact between the analytes and the extraction solvent in the sample solution, making them a good alternative to conventional switchable-hydrophilicity solvents. These advantages and compatibility with many detection techniques, make it possible to apply the proposed method to the extraction of a wide range of molecular and elemental analytes from different matrices.

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Table 1. Optimized parameters based on the proposed extraction procedure

S/No	Parameter	Range	Optimum
1	Volume of EO	300 - 700	500 μL
2	pH value	2.5 - 7.5	4.5
3	Conc. of APDC	0.05 - 0.2	0.1% (w/v)
4	Conc. of NaOH	0.5 - 3.5	2.0 M
5	Switching-off acid	0.5 - 3.5	2.0 M
6	Complexation time	1.0 - 7.0	5.0 min
7	Back-extraction	4.0 - 9.0	8.0 M

SILVER NANOPARTICLES SYNTHESIZED FROM *Azadirachta indica* LEAF EXTRACT ENHANCED CERTAIN AGROMORPHOLOGICAL AND YIELD TRAITS IN SOYBEAN LANDRACES IN NIGER STATE

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ABSTRACT

Soybean is a globally important legume crop that is a leading source of seed protein and oil. In an attempt to assess the effect of different concentrations of silver nanoparticle on the agro-morphological and yield traits of soybean, two different accessions of soybean (SOY-MNA-001 and SOY-MNA-002) were evaluated. The study was conducted at the experimental garden, federal university of technology, Minna, Niger State. The experiment was laid out in a complete randomized design arranged in 3 x 5 factorial combination with 4 replications. Different concentrations (0 ppm, 25 ppm, 50 ppm, 75 ppm and 100 ppm) of silver nanoparticle (AgNPs) were used in this study. The results revealed significant differences within the traits studied. The highest plant height (36.00 cm), number of pods per plant (152.20), weight of 100 seeds (10.61 g) and reduced number of days to 50% flowering (32.50 days) resulted from plants treated with 100 ppm of silver nanoparticle but highest number of leaves/plant (86.20) resulted from those treated with 25 ppm for SOY-MNA-001. For SOY-MNA-002, the highest weight of 100 seeds (11.00 g) as well as lowest number of days to 50% flowering (37.00 days) were obtained from plants treated with 100 ppm of silver nanoparticle. However, the highest plant height (29.42 cm) and number of leaves/plant (86.20) were recorded from plants treated with 75 ppm AgNPs and highest number of pods/plant (152.00) from those treated with 50 ppm AgNPs. It is therefore concluded that variation in concentrations of silver nanoparticle tend to influence certain morphological and yield attributes in soybean accessions.

Keywords: morphological attributes, silver nanoparticles, soybean, yield attributes

INTRODUCTION

Soybean (*Glycine max* L. Merr.) belongs to the family Fabaceae or Leguminosae and genus *Glycine* (Mukhtar *et al*., 2013). It is a globally important legume crop that is a leading source of dietary protein and oil in animal feed as well as a staple for human consumption (Hartman *et al*., 2011). According to the US Food and Drug Administration (2017), Soy is a good source of protein for vegetarians and for people who want to reduce the amount of meat they eat. Despite being an economically important crop, the yields of soybean continue to reduce due to lack of sufficient and suitable breeding programmes. In an attempt to improve the yield and efficiency to meet demand for the crop, different methods of crop improvement including nanotechnology has been employed. Nanotechnology involves the creation and manipulation of matter within the size of 1 -100 nm at the minimum of one dimension (Javed *et al*., 2019). Among all the nanoparticles, silver nanoparticles (AgNPs) have remarkable uses in crop production.

MATERIALS AND METHODS

10 ml of *Azadirachta indica* leaf extract was added to 1.5 mM aqueous solution of silver nitrate (AgNO3) for complete reduction of Ag^+ ions. The mixture was kept on magnetic stirrer at 30°C. Time and color change were recorded along with periodic sampling and scanning by UV-Visible (UV-Vis) spectrophotometer. The Complete reduction of Ag^+ ions was confirmed by the change in color from light or faint to yellowish colloidal brown. The colloidal solution was then kept aside for 24 hours for complete bio-reduction and saturation denoted by UV-Vis spectrophotometric scanning. The solution was sealed and stored properly for further use. The formation of silver nanoparticles was further confirmed by different spectrophotometric analysis (Niharika *et al.,* 2016). The synthesized silver nanoparticle was dissolved at different concentrations (0, 25, 50, 75 and 100 ppm) in de-ionized water. The soybean seeds were subjected to priming by soaking in the silver nanoparticle solutions of 1.00: 0.30 seed to solution ratio for about 4 hours. The treated seeds were allowed to dry under room temperature before planting. The planting bags containing soil were arranged in a complete randomized design of 3 x 5

factorial combination with 4 replications. The seeds of the two different accessions were sown in the bags at a depth of 1 – 2 cm.

Data analysis

Quantitative data obtained were pooled for analysis. Analysis of variance (ANOVA) was used to compare the various mean values. Duncan Multiple Range Test (DMRT) post hoc test was used to separate the means. All values were considered significant at $p \leq 0.05$.

RESULTS AND DISCUSSION

For morphological parameters, the results of the experiment revealed that the highest plant heights (36.00 cm and 29.42 cm) obtained for SOY-MNA-001 and SOY-MNA-002 resulted from plants treated with 100 ppm and 75 ppm AgNPs respectively. This is similar to the work of Nejatzadeh-Barandozi *et al.* (2014) who reported that 40, 60 and 100 ppm AgNPs caused improved plant height in basil. The highest number of leaves/plant (86.20) for SOY-MNA-001 was attained at 25 ppm while the highest number of leaves/plant (86.20) for SOY-MNA-002 was recorded at 75 ppm. This is similar to the work of Jasim *et al.* (2017) who reported significant enhancement in the leaf number after being treated with AgNPs.

For yield parameters, a significant increase was recorded in number of pods/plant (152.20), weight of 100 seeds (10.61 g) and a significant reduction in the days to 50 % flowering (32.50) at 100 ppm AgNPs for SOY-MNA-001. The highest weight of 100 seeds (11.00 g) and reduction in days to 50 % flowering (37.00) were recorded at 100 ppm but highest number of pods/plant (152.00) was recorded at 50 ppm AgNPs for SOY-MNA-002. These results are similar to the work of Jhanzab *et al.* (2019) but in contrast to the work of Piotr *et al.* (2019) who reported 50 ppm as optimum concentration to produce a reduction in number of days to flowering in comparison to control. Inconsistent plant responses to AgNPs may be due to the fact that nanoparticle actions depend on the plant species, AgNPs concentrations and application methods.

Conclusion

The results of the study revealed that the four silver nanoparticle treatments significantly enhanced the morphological and yields traits of soybean (*Glycine max*). However, 75 ppm and 100 ppm plants produced the highest number of pods per plant, weight of 100 seeds and also reduced the number of days to 50 % flowering. It is therefore concluded that silver nanoparticles cause optimum yield in soybean and can be used as an important tool in the improvement of the crop.

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Table 1. Agromorphological and Yield Traits of Selected Soybean Landraces Primed with Silver-Nanoparticles

Conc.	Plant Height (cm)	Number of leaves/plant	Number of pods per plant	100-seed weight	Days to 50% flowering
SOY-MNA-001					
0 ppm	26.34±1.32a	79.80±13.98a	75.80±16.42a	9.35±0.20a	36.00±1.00b
25 ppm	29.74±1.20a	86.20±10.01b	91.40±17.47a	9.87±0.21a	34.00±0.41ab
50 ppm	26.10±2.26a	73.00±18.37a	79.60±12.69a	10.58±0.24b	35.75±0.75ab
75 ppm	32.20±3.95a	77.20±9.19a	79.00±9.50a	9.77±0.25a	35.25±0.63ab
100 ppm	36.00±6.59b	66.60±11.00a	152.20±16.16b	10.61±0.20b	32.50±1.85a
SOY-MNA-002					
0 ppm	29.06±3.13a	67.00±5.70a	92.30±7.37b	10.08±0.28ab	39.00±1.08ab
25 ppm	28.14±1.91a	67.60±16.27a	102.90±11.64b	10.72±0.34b	40.25±0.85b
50 ppm	27.82±1.89a	82.40±0.93ab	152.00±11.00c	10.34±0.19ab	37.25±0.25a
75 ppm	29.42±2.30a	86.20±20.34b	127.00±18.01bc	9.19±0.48a	37.50±0.87a
100 ppm	28.04±0.22a	53.40±5.24a	53.00±6.29a	11.00±0.53b	37.00±0.82a

Values are means±standard error, values followed by the same superscript on the same column is not significantly different at $p > 0.05$

ENHANCING WINGED BEAN [*Psophocarpus tetragonolobus* L. (DC.)] GERMINABILITY THROUGH DIFFERENT PRE-SOWING SEED TREATMENT METHODS

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ABSTRACT
Winged bean adoption as an agricultural crop with nutritional and health benefits is often hampered by poor plant establishment when untreated seeds are planted. Seeds of three winged bean accessions (TPt2, TPt5, and TPt26) were subjected to different pre-sowing seed treatments. A trial consisting of 11 pre-sowing seed treatments including control was planted in a randomized complete block design with three replications at LAUTECH, Ogbomoso, Nigeria. Data were collected on germination counts at 2, 3, 4 and 5 weeks after sowing (WAS), and later converted to germination percentages. Treatments showed highly significant ($p < 0.0001$) differences for germinability. Germination percentages recorded for the treatments at 5 WAS varied from 18.1 to 80.0% and averaged 45.7%. Shaking seeds vigorously in a perforated tin had highest germination of 80% at 4 and 5 WAS. Mechanical scarification methods resulted in 124 - 176% germination advantage over the control (untreated seeds). Good field establishment may be achieved for winged bean when seeds are treated using mechanical scarification methods before planting.

Keywords: accessions, germination count, scarification, seed dormancy, winged bean

INTRODUCTION
Winged bean [*Psophocarpus tetragonolobus* (L.) DC. (Fam. Fabaceae)] is an under-exploited tropical legume with a remarkable nutritional value; all its parts – leaves, flowers, green pods, seeds (green and dried), and tuberous roots – are not only edible but high in protein content (Pavachoknagul *et al.*, 1989; Singh *et al.*, 2013; Mohanty *et al.*, 2013). The high protein content of 8 - 12% (in dry weight) of the tubers compared with 1 - 5% of cassava, potatoes, and other common tuberous crops, and the high oil content of the dried seeds make winged bean a potentially valued crop for addressing the nutritional and health needs of the poor and vulnerable populace especially in the developing countries (Koshy *et al.*, 2010; Mohanty *et al.*, 2013). It is also an excellent source of vitamins A, C, calcium and iron (Khalili *et al.*, 2013). The oil-rich dried winged bean seeds are well-endowed with certain pharmacologically beneficial anti-oxidants like trypsin and chymotrypsin inhibitors, haematoglutins and amylase inhibitors (Khalili *et al.*, 2013, Mohanty *et al.*, 2013).

In spite of the high nutritional and health values of this wonder crop, its production in West African countries like Nigeria remains marginal because farmers find the cultivation of the crop unattractive due to several factors that include the difficulties involved in achieving satisfactory and uniform plant stand establishment when untreated seeds are planted in the field (Koshy *et al.*, 2010). When untreated seeds of winged bean are planted, many failed to germinate because of seed hardness dormancy that confers impermeability on the seed coat thereby preventing water imbibition which is necessary for germination and development of embryos (Eira *et al.*, 2000). Impermeable seed coat dormancy that is partly associated with the adaptation mechanism for species' survival has been reported in several other crops like *Centrosema pubescens*, *Lupinus varius*, *Vigna ambacensis*, *Olea europaea*, *Medicago* spp., *Trifolium* spp., *Astragolus* spp., and *Acacia auriculiformis*. In order to achieve remarkable improvement in germinability of seeds for optimum plant populations of these crops, the hard seed coat must be broken through seed scarification.

Several seed scarification methods – chemical, physical and/or mechanical - have been adopted by earlier workers (Kimura and Islam, 2012; Olatunji *et al.*, 2013) to enhance germination of hard seeds of winged bean and other crop species. Kroshy *et al.* (2010) reported varying effects of water soaking and different levels of chemicals at varying temperatures on the germination of winged bean. Limited information is, however, available on using

different chemical and mechanical scarification methods as pre-sowing treatments for winged bean seeds. This study was, therefore, conducted to assess the effects of different chemical and mechanical pre-sowing seed treatment methods on the germination of winged bean seeds in the field.

MATERIALS AND METHODS

Seeds of three winged bean accessions stored at -20°C were obtained from Genetic Resources Centre (GRC), IITA, Ibadan. Random seed samples of the three accessions were subjected to pre-germination test to ascertain their viability. A batch of 100 seeds of each accession was thereafter subjected to 10 different pre-sowing treatments listed and described in Table 1.

A trial comprising 11 treatments including untreated seeds as control, each replicated three times, was planted in a randomized complete block design (RCBD) at the Teaching and Research Farm of Ladoke Akintola University of Agriculture (LAUTECH), Ogbomoso in 2016. Experimental plot comprised two 5 m rows spaced 1.0 m apart with 1.0 m spacing between plants within a row. Two seeds were planted per hill to obtain a maximum of 20 plants per plot.

Germination counts recorded on plot basis between two and five weeks after sowing (WAS) were expressed as percentages of the seeds planted (20 seeds per plot). Prior to conducting F-test, count data were square-root transformed to satisfy the condition of normality of the dataset. The transformed data were subjected to analysis of variance (ANOVA) using PROC GLM in SAS (SAS Institute, 2009).

RESULTS AND DISCUSSION

Results of ANOVA revealed that accessions, replications, and accessions × treatments interaction were not significant for the germination counts from 2 to 5 WAS (Table 2), suggesting that the three winged bean accessions did not vary significantly for germinability.

Highly significant ($p < 0.0001$) differences were detected among the pre-sowing treatments for germination counts at 2, 3, 4, and 5 WAS (Table 2), indicating that the pre-sowing seed treatments had varying effects on germinability. Hence, suitable methods for treating the winged bean seeds for the purpose of breaking seed dormancy and achieving enhanced germination before sowing can be identified among the studied treatment methods. This result corroborates earlier findings that treating winged bean seeds with different concentrations of certain chemicals prior to sowing enhanced their germination significantly (Koshy *et al.* 2010). Dormancy in winged bean has been attributed to seed hardness or impermeable seed coat (Eira *et al.* 2000). Therefore, any treatment, physical or chemical, that may be imposed on the seed before sowing to effectively break up the hard seed coat and open up the seed to water imbibition will definitely enhance winged bean seed germination, improve crop establishment, productivity, and ultimately make the cultivation of the crop attractive to farmers. Other mechanisms that cause seed dormancy in winged bean include environmental light conditions and immature embryos at the time of seed dispersal (Eira *et al.*, 2000). Mechanical scarification breaks up the seed strophiolar cleft of the seed coat thereby permitting water imbibition and germination while chemical scarification eliminates the hard or resistant portion of the hard seed for easy germination (Hamly, 1932; Pe *et al.*, 1975).

Means and other statistics for germination percentages recorded at 2, 3, 4, and 5 WAS and averaged across the three accessions are presented in Table 2. Mean germination percentages (based on the 20 seeds planted per plot) ranged between 9.8 and 76.1% with a mean of 35.3% at 2 WAS, and varied from 18.1 to 80.0% averaging 45.7% at 5 WAS (Table 3).

Germination percentages recorded at 3 WAS had the least coefficient of variation (CV) of 13.3% whereas the highest CV of 19.6% was observed at 2 WAS. One chemical treatment method, treatment 4 (seeds soaked in 80% H_2SO_4 for 1 min), and all the three mechanical treatment methods, namely treatments 8 (seeds scarified with a sharp scalpel), 9 (seeds scarified by shaking vigorously in a perforated tin), and 10 (seeds scarified by rubbing in between sand-papers), had significantly higher germination counts than the control (untreated seeds) on all the sampling dates (Table 3). Treatments 4, 8, 9, and 10 recorded 65.5, 124.1, 175.9, and 148.3% higher germination counts, respectively, when compared with treatment 11 (control or untreated seeds) at 5 WAS. Generally, the pre-sowing mechanical treatments 8, 9, and 10 using a sharp scalpel, shaking vigorously in a perforated tin, and rubbing in between sand-papers, respectively, gave higher germination

percentages than the chemical and water treatments, and the untreated seeds on all sampling dates. Pre-germination treatments of hard seeds with chemicals such as KNO_3 and H_2SO_4 have been previously reported with satisfactory results in different crop species (Pe *et al*., 1975; Fang *et al*., 2006; Olatunji *et al*., 2013). Findings from this study corroborated earlier reports by Koshy et al. (2010) that treating winged bean seeds with 80% H_2SO_4 enhanced germination significantly. Our results are also in agreement with several other workers who reported that the mechanical scarification methods gave more satisfactory results in terms of number of germinated seeds when compared with the other methods and untreated seeds (Karaguzel *et al*., 2004; Frederick *et al*., 2016). This was, however, contrary to the reports of Rostmani and Shasavar (2009) who observed that chemical scarification did better than mechanical scarification in Olive (*Olea europaea*).

Conclusion

The results of this study have further established that pre-sowing seed scarification is a prerequisite for achieving optimal field establishment of winged bean. Mechanical seed scarification when carefully done using sharp scalpel or razor blade, shaking in a perforated tin, or rubbing hard in between sand-papers, could probably be more preferred by farmers over the chemical treatments because they are relatively cheap pre-sowing seed treatment methods, though may be a little more tedious.

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Table 1. Mean squares of germination counts for three winged bean subjected to 11 pre-sowing seed treatments

Treatment	Description
1	Seeds soaked in water at 100 °C for 5 min
2	Seeds soaked in water at 50 °C for 5 min
3	Seeds soaked in water at room temperature for 5 min
4	Seeds soaked in 80% H_2SO_4 for 1 min
5	Seeds soaked in 50% H_2SO_4 for 1 min
6	Seeds soaked in 1% KNO_3 for 1 min
7	Seeds soaked in 0.5% KNO_3 for 1 min
8	Seeds scarified with a sharp scalpel
9	Seeds scarified by shaking vigorously in a perforated tin
10	Seeds scarified by rubbing in between sand papers
11	Untreated seeds as control

Table 2. Descriptions of the pre-sowing treatments imposed on 100 seeds each of three winged bean accessions

Source of variation	Df	Germination Count			
		2WAS	3 WAS	4 WAS	5 WAS
Accession (Acc)	2	0.19ns	0.23 ns	0.28 ns	0.21 ns
Treatment (Trt)	10	557.6***	412.8***	347.9***	348.2***
Block (treatment)	22	0.22 ns	0.21 ns	0.15 ns	0.13 ns
Acc x Trt	20	0.0ns	3.8ns	2.7ns	0.0 ns
Error	44	137.6	119.7	145.7	162.9

***Mean squares significant at $p < 0.0001$, ns=mean squares not significant; WAS=Weeks after sowing

Table 3. Treatment means for germination percentages recorded at 2 - 5 WAS and averaged across the three winged bean accessions

Treatment	Percent Germination			
	2WAS	3 WAS	4 WAS	5 WAS
Seeds soaked in water at 100 °C for 5 min	9.8	16.2	16.2	18.1
Seeds soaked in water at 50 °C for 5 min	24.2	36.5	36.5	39.2
Seeds soaked in water at room temperature for 5 min	18.1	28.8	31.3	31.3
Seeds soaked in 80% H_2SO_4 for 1 min	33.8	48.1	45.0	48.1
Seeds soaked in 50% H_2SO_4 for 1 min	28.8	39.2	42.1	42.1
Seeds soaked in 1% KNO_3 for 1 min	24.2	39.2	36.5	39.2
Seeds soaked in 0.5% KNO_3 for 1 min	22.1	36.5	36.5	39.2
Seeds scarified with a sharp scalpel	64.8	68.5	68.5	64.8
Seeds scarified by shaking vigorously in a perforated tin	76.1	76.1	80.0	80.0
Seeds scarified by rubbing in between sand papers	72.2	76.1	72.2	72.2
Untreated seeds as control	12.8	22.1	26.5	28.8
Mean ± SE	35.2 ± 7.3	44.3 ± 6.3	44.6 ± 6.1	45.7 ± 5.8
Coefficient of determination (R^2)	88.7	88.8	84.8	82.7
$LSD_{0.05}$	11.5	11.6	11.9	12.2
Coefficient of variance (CV%)	32.8	24.3	26.6	27.4

WAS = weeks after sowing

SILVER NANOPARTICLE SYNTHESIZED FROM HIISCUS SABDARIFFA LEAF EXTRACT ENHANCED CERTAIN AGROMORPHOLOGICAL AND YIELD TRAITS IN GROUNDNUT LANDRACES IN NIGER STATE

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ABSTRACT

The demand for groundnut production has been on the increase over the years due to rising demand for raw oil seeds. However, efforts have been made during the past decades by researchers to address this challenge with little success. Nanotechnology has offered a great promise in improvement of crops with little or no impact on the environment. Base on this premises, the effect of varying concentrations (0, 25, 50, 75 and 100 ppm) of silver nanoparticles from *Hibiscus sabdariffa* leaves on agro morphology and yield traits of three different groundnut accessions (GNT-MNA-001, GNT-MNA-002 and GNT-MNA-003) was evaluated. The experiment was laid out in a 3 by 5 factorial arrangement using complete randomized design in four replicates at the experimental garden, Federal University of Technology Minna, Nigeria. The highest plant height was recorded in genotype GNT-MNA-002 at 25 ppm with a mean value of 27.70 which is significantly higher than the value obtained from the other treatments. Highest number of pods per plant (13.8, 16.18 and 17.6) were recorded in 0 ppm treated plants within the three accessions; GNT-MNA-001, GNT-MNA-002 and GNT-MNA-003, respectively. Lowest width of pod per plant was found at 25 ppm in GNT-MNA-001 with the mean value of 1.55 which was significantly lower than the value recorded in the other treatments. Furthermore, there is a significant difference in hundred seeds weight recorded, with 75 ppm concentration having the lowest value of (42.11, 38.17 and 41.79) seeds weight in all the three accessions (GNT-MNA-001, GNT-MNA-002 and GNT-MNA-003, respectively). Hence, varying concentrations of biosynthesized nanoparticle have shown to possess the tendency to influence certain morphological and yield trait in groundnut accessions.

Keywords: biosynthesis, concentrations, groundnut, nanoparticles, variations

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is an annual legume belonging to the family Fabaceae and it is one of the fundamental edible oil seed crops in the world (Mukhtar *et al*., 2013). Groundnut is an important food crop worldwide with a production of over 47 million tons on near 28 million hectares annually (Food and Agricultural Organisation, 2017). Groundnut is ranked thirteenth in the world food crops position; fourth palatable oil generation after soybean, rapeseed, and cottonseed and third vegetable most important protein (FAO, 2017). Due to the growing demand for raw oilseeds and consumer preference for high quality edible oil, there is an increasing interest in groundnut production (Moumouni *et al.,* 2020). Several efforts have been made during the past decades by researchers to address a wide range of field problems.

Nanotechnology is a new exciting field of science which has numerous applications in the field of biotechnology as well as in agriculture. It offers a great promise in the improvement of crops with little or no impact on the environment. Nanotechnology focuses on the manipulation of matter with at least one dimension sized ranges from 1 to 100 nanometer (Pramod, 2018). Silver nanoparticles are the most studied and utilized NPs in the field of agricultural research to improve the efficiency, yield, and sustainability of crops (Chen and Schluesener 2008).

MATERIALS AND METHODS

The experiment was laid out in a 3 by 5 factorial arrangement using complete randomized design in four replicates at the Experimental Garden, Federal University of Technology Minna, Nigeria. Three groundnut accessions (GNT-MNA-001, GNT-MNA-002 and GNT-MNA-003) and leaves of *Hibiscus sabdariffa* was collected from local farmers.

Biosynthesized silver nanoparticles from the leaves of *Hibiscus sabdariffa* were dissolved at different concentrations (0, 25, 50, 75 and 100 ppm) in distilled water. Cleaned groundnut seeds

was subjected to priming by soaking in the silver nanoparticles solution for about 4 hours. The treated seeds were air dried before planting (Khalaki *et al.,* 2016).

Data analysis

Data collected on morphological and yield parameters was subjected to analysis of variance (ANOVA) to determine the significance differences and Duncan's Multiple Range Test (DMRT) was used to separate the means at $p \leq 0.05$ significant level.

RESULTS AND DISCUSSION

The table presented in table 1.0 declared that the treatment of groundnut seeds with silver nanoparticles at different concentrations resulted in variation in the plant height within the three accessions (GNT-MNA-001, GNT-MNA-002 and GNT-MNA-003) with the highest plant height (26.90, 27.70 and 27.26) at 50 ppm, 50 ppm, and 25 ppm respectively. In accession GNT-MNA-001 and GNT-MNA-002 there is a marked increment in the plant height at 50 ppm (27 cm, 27.70 cm) and 75 ppm (27.10 cm, 27.06 cm) respectively as compared to the value recorded at 0 ppm (26.74 cm, 25.98 cm). In accession GNT-MNA-003, a significant increase was observed in the plant height was at 25 ppm. At higher concentrations, inhibitory response of the nanoparticle was observed in the plant height. The decline in the plant height at higher concentration of Ag nanoparticles may be attributed to toxic level of nanoparticle. Hediat (2012) reported a stimulatory effect of small concentration of silver nanoparticle on the growth of Common bean (*Phaseolus vulgaris* L.) and corn (*Zea mays* L.), while increased concentrations induced an inhibitory effect. This is also in agreement Mahajan *et al.* (2011) and Seif *et al.* (2011).

Similarly, there was an increase in the yield parameters studied at 50 ppm concentration. Significant increase was observed in the number of pods per plant and width of pods per plant in all the three accessions at 50 ppm with the value of (16.00 cm, 1.79 cm), (16.18 cm, 2.01 cm) and (17.60 cm, 2.31 cm) respectively. Data also shows that the groundnut seeds treated with 50 ppm concentration produced the highest seed weight in all the three accessions. The role of Ag nanoparticle in the improvement of the yield might be due to enhancement of better absorption of nutrients for the production of photosynthetic pigment which result to considerable improvement in the growth and seed formation in plants (Piotr *et al.,* 2019). This is in conformation with Latif *et al.,* 2017.

Conclusion

The results of this present study suggested that varying concentrations silver nanoparticles have the tendency to improve the growth and yield parameters of groundnut. The maximum effect was found at 50 ppm concentration for the three accessions. Beyond this concentration, inhibitory response was observed. It is therefore concluded that application of silver nanoparticle on groundnut seeds has a remarkable promising potential in the production and improvement of groundnut.

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Table 1. Analysis of variance for morphological and yield traits

Factors	Plant height (cm)	Number of pods per plant	Width of pod per plant (cm)	100-seed weight (g)
GNT-MNA-001*Control	26.74^{abc}	13.80^{bcde}	1.78^{abcd}	42.02^{bc}
GNT-MNA-001*Conc. 1	24.64^{abc}	10.50^{ab}	1.55^{a}	42.29^{bcd}
GNT-MNA-001*Conc. 2	27.00^{abc}	16.00^{de}	1.79^{abcd}	42.52^{bcd}
GNT-MNA-001*Conc. 3	27.10^{abc}	11.10^{abc}	1.67^{ab}	42.11^{bc}
GNT-MNA-001*Conc. 4	26.90^{abc}	8.67^{a}	1.71^{abc}	40.23^{ab}
GNT-MNA-002*Control	25.98^{abc}	13.70^{bcde}	1.77^{abcd}	38.90^{a}
GNT-MNA-002*Conc. 1	26.8^{abc}	12.50^{abcd}	1.93^{bcde}	40.21^{ab}
GNT-MNA-002*Conc. 2	27.70^{c}	16.18^{de}	2.01^{cde}	40.26^{ab}
GNT-MNA-002*Conc. 3	27.06^{abc}	10.00^{ab}	1.92^{bcde}	38.17^{a}
GNT-MNA-002*Conc. 4	24.60^{abc}	9.91^{ab}	1.93^{bcde}	40.04^{ab}
GNT-MNA-003*Control	25.90^{abc}	17.00^{de}	2.14^{ef}	43.75^{cd}
GNT-MNA-003*Conc. 1	27.26^{abc}	15.73cde	2.05^{def}	43.66^{cd}
GNT-MNA-003*Conc. 2	23.68^{a}	17.60^{e}	2.31^{f}	44.66^{d}
GNT-MNA-003*Conc. 3	23.90^{ab}	17.33^{de}	2.21^{ef}	41.79^{bc}
GNT-MNA-003*Conc. 4	23.46^{a}	12.67^{abcde}	2.09^{ef}	43.60^{cd}
Standard Error of mean	0.78	1.57	0.09	0.77

ASSESSMENT ON END USERS PREFERRED TRAITS IN WATER YAM (*Dioscorea alata* L.) IN SOUTH-WEST NIGERIA

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ABSTRACT

Water yam is an important food and cash crop in Nigeria but has not gained much acceptability like white yam. One way to address this is through genetic improvement in collaboration with end users. Evaluation based on end users preferred traits is low and should be considered in breeding programme for better adoption. In this study, end users preferred traits in different accessions of water yam was assessed in south west Nigeria using structured questionnaire. The preferred traits evaluated are palatability, nutritional value, easy digestibility, time to cooking, texture, cultural acceptability, colour after cooking, food condiment suitability, flesh colour, water content and size. Out of these, palatability, nutritional value, easy digestibility and time to cooking were identified accordingly as the most preferred traits by the respondents. This information will provide insights into traits plant breeders could focus on while improving water yam for better adoption.

Keywords: end users, preferred traits, southwest Nigeria, water yam

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INTRODUCTION

Yam (*Dioscorea* spp.) is an annual stem tuber which serves as a major staple food in the tropics and subtropics of Africa. In Nigeria, yam is the second most important crop after cassava (FAO, 2019). Yam is mostly marketed as fresh tuber and can be utilized in different ways, ranging from boiled yam, fried yam, porridge, pounded yam among many others. It is a source of dietary calories and nutrients and it contributes to the income of most households (Liu *et al.*, 2007). There are over 600 species of yam, out of which six are socially and economically important in terms of food, cash and medicine (IITA, 2009). Some of these yam species are white yam (*Dioscorea rotundata*), yellow yam (*Dioscorea cayanensis*), water yam (*Dioscorea alata*), Chinese yam (*Dioscorea esculanta*) and trifoliate yams (*Dioscorea dumetorum*) (Zaknayiba and Tanko, 2013). In Africa, yam is extensively produced in the African yam belt region, a region including countries such as Nigeria, Ghana, Ivory Coast, Benin, Togo, and Cameroon (Alabi *et al.*, 2019). Nigeria is by far the world's largest producer of yams, accounting for over 70 – 76% of the world production (IITA, 2013). Nigeria produced 73.8% of total yam production in Africa (FAO, 2008). The world's second and third largest producers of yams are Ivory Coast and Ghana respectively.

Water yam, also known as winged yam, or greater yam, is one of the most widespread yam species in the tropical and subtropical areas of the world. It is produced mainly for its large, starchy underground tubers with fine edible fleshes (Adifon *et al.,* 2019). Water yam was introduced into Central and West African countries, from the Southeast Asia, during the 16th century (Mignouna *et al.*, 2015). *Dioscorea alata* plays an essential role in the nutrition, food security, income generation, and socio-cultural lives of more than 300 million people in the world (Alabi *et al.*, 2019).

In Nigeria, water yam is not as important as white yam because of its limited use caused by its high moisture content (Agwu and Avoaja, 2012). It therefore plays a minor role in both local and international yam trade. This have contributed to its declining popularity in the country despite its overwhelming nutritional and health benefits (Wireko-Manu *et al.,* 2013). Water yam contains high level of Total Dietary Fibre (TDF) which makes it suitable for management of pile, constipation and diabetes (Wireko-Manu *et al.,* 2013). It is also rich in Vitamin (B_6, C and E), beta carotene, calcium, potassium, magnesium, copper and antioxidants. These nutrients are known to play vital role in the general body upkeep as well as immune functioning, wound healing, reducing the risk of heart diseases, suppressing of blood sugar, bone growth and anti-ageing.

In Nigeria, water yam is utilized by end users in various forms depending on their end-use

suitability: for pounded yam, yam flour (amala), boiled yam, roasted yam, fried yam chips, porridge, grated water yams (ikokore) , yam balls (ojojo), starch, poundo flour, food condiment, feed for poultry and livestock among others (Zannou *et al.*, 2015). A crucial element in plant breeding is to ensure that farmers and others, such as processors and consumers will adopt and make use of new, improved varieties. This can be brought about through participatory plant breeding. This approach has helped in better adoption of crops like wheat, rice, millet, maize, and yam among others (Evenson and Gollin, 2003). Hence, the objective of this study was to assess end users preferred traits in different accessions of water yam in south west Nigeria using structured questionnaire.

MATERIALS AND METHODS

The main research instrument used to gather information for this study is questionnaire. The population of this study consisted of end users from age twenty (20) and above residing in southwest Nigeria. The target population sample was two hundred (200). A random sampling method was used in carrying out this study; the sampling of respondents was done among the six states in Southwest Nigeria. Questionnaires were administered to end users using Google forms and physical meeting for a time period of two (2) months. A total number of two hundred and seven (207) respondents were realized. Data collected were analyzed using the SPSS software version 20 while charts were plotted using Microsoft excel.

RESULTS AND DISCUSSION

The result from end users preferred traits is presented in Figure 1. Palatability was the most preferred trait by the respondents (176) followed by nutritional value (80), easy digestibility (76), time to cooking (75), texture (50), cultural acceptability (42), colour after cooking (40), food condiment suitability (39), flesh colour (30), water content (30), and tuber size (29). This is similar to the findings of Wireko-Manu *et al.* (2013) that most people consume water yam because of its palatability and nutritional value.

The forms of water yam utilization are presented in Figure 2. Water yam are utilized in various forms such boiled yam, fried yam chips, roasted yam, yam flour, pounded yam, poundo flour, starch, porridge, ikokore, ojojo, food condiments and feed. Consuming water yam as boiled yam (122), was the highest according to respondents followed by ikokore (73), ojojo (68), fried yam chips (61), roasted yam (60), pounded yam (52), yam flour (Amala) (41), porridge (39), food condiment (20), poundo flour (16), feed (16) and starch (13).

The result of respondents' frequency of water yam consumption is presented in Figure 3. White water yam is consumed very often by 75 respondents, often by 59 respondents, rarely by 63 respondents and 14 respondents have never eaten white water yam. For yellow water yam, 78 respondents rarely consume yellow water yam, 60 respondents have never eaten yellow water yam, 49 respondents often consume yellow water yam and 22 respondents consume yellow water yam very often. The respondents do not like purple water yam 135 respondents have never consumed it while 48 rarely consume it, those who consume purple water yam often are 16 and 10 consume very often.

Conclusion and Recommendation

In conclusion, end users are mostly interested in white and sweet taste (palatability) water yam and mostly prefer to consume it boiled. Therefore, it is recommended that plant breeders focus more on the sweet taste of white and water yam when improving or introducing new varieties.

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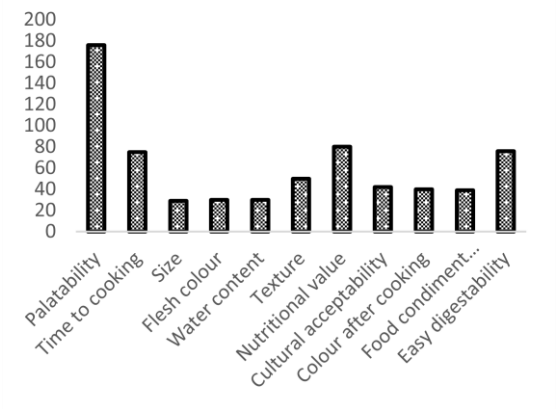

Figure 1. Bar chart showing end users preferred traits in water yam

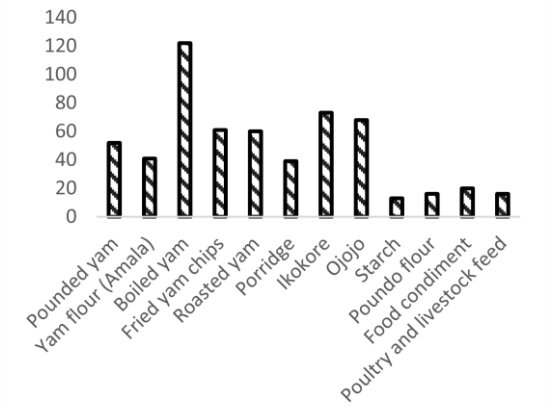

Figure 2. Bar chart showing the various forms of water yam utilization

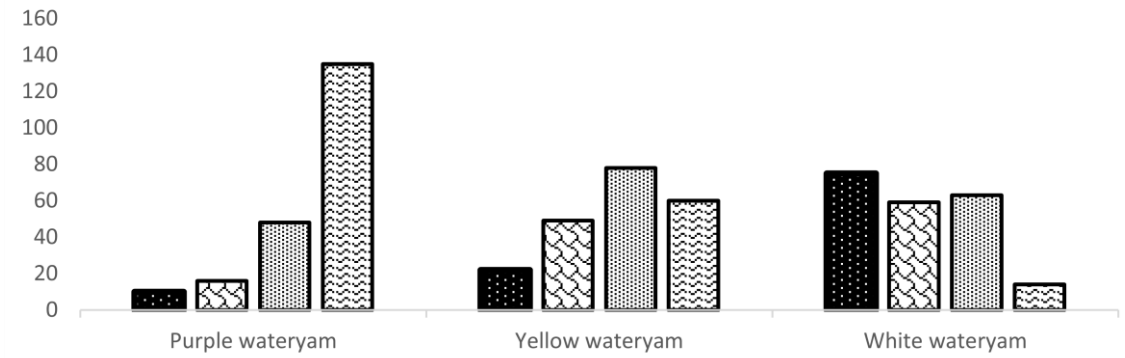

Figure 3. Bar chart showing the frequency of end users consumption of water yam

ENVIRONMENT RESPONSES OF RESISTANCE AND DISEASE PROGRESSION IN RICE (*Oryza sativa* L.) VARIETIES TO BLAST (*Magnaporthe grisea* (Hebert) Barr.) DISEASE

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ABSTRACT
This research is aimed at identifying the effects of environment on the disease progression and resistance of rice varieties to blast disease. Experiment one, was carried out during the dry season of 2016 at the screen house of National Cereals Research Institute (NCRI) Badeggi Nigeria, while experiment two was carried out during the rainy season of 2017 on the hydromorphic fields of NCRI. Experiment one was conducted in a completely randomized design in four replications. Experiment two was in a randomized complete block design in three replications. Twenty rice varieties were used for the experiment. The result showed that FARO 19 and ART16-16-11-29-1-B-1-11 had lowest disease progression rate and expressed consistent resistance to blast in both environments.

Keywords: Rice; Environment, Disease progression, Resistance; Blast disease

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INTRODUCTION
Rice is the world's leading food crop, cultivated over an area of about 155 million hectares with a production of about 596 million tonnes (paddy). In terms of area and production, it is second to wheat, providing about 22 % of the world's supply of calories and 17 % of the proteins. Maximum area under rice is in Asia (Farooq, 2011). Among the rice growing countries, India has the largest area (44.8 million hectares) followed by China and Indonesia. The leading countries producing rice crop are Japan, Brazil, China, India, Indonesia, Bangladesh, Vietnam, Thailand, Myanmar and Philippines (Bolajoko *et al.,* 2022). Rice production in Nigeria between 2001 and 2003 was estimated at 2.03 million tonnes while consumption was 3.90 million tonnes. The balance of 1.90 million tonnes was obtained by importation. In the last 30 years, production increased six folds with Nigeria producing 3.3 and 3.6 million tonnes of paddy rice between 2000 and 2005, respectively (WARDA, 2009).

Africa rice has been cultivated for 3,520 years, between 1,500 and 800 BC (Gana *et al*., 2013). O. *glaberrima* was propagated from its original center, the Niger delta river and extended to Senegal. However, it never developed far from its original region. Its cultivation even declined in favour of the Asian species, possibly brought to African continent by Arabs coming from the coast between seventh and eleventh centuries. In parts of Africa under Islam, rice was chiefly grown in southern Morocco. During the tenth century, Muslim traders also brought rice to east Africa. Although the diffusion of rice in most sub-Saharan Africa remains uncertain, Muslims brought it to the region stretching from Lake Chad to White Nile (Gana *et al*., 2009).

Statement of the Research Problem
The use of chemical fungicides to control disease has longed been viewed as a last resort for disease management (Bolajoko *et al.,* 2022). The two main diseases that affect rice production are rice blast and sheath blight (Otto, 2015). Outbreaks of these diseases are disastrous (NCRI, 2002). Disease control by materials with low environmental effects is most desired (El-Kazzaz *et al*., 2015). Both techniques have been used to manage rice blast, but neither of the two is considered to be highly successful. Culturally, rice blast is often severe in fields that are over-fertilised (Bolajoko *et al.,* 2022). The aim of this research is to identify the effect of environment on the disease progression rate and resistance in rice cultivars to blast disease.

MATERIALS AND METHODS
This research work was carried out in the screenhouse facility and on the hydromorphic rice fields of National Cereals Research Institute (NCRI) Badeggi, Nigeria. The two experiments

were located at an elevation of 118 meters above sea level between latitude 90^0 3′ North and 6^0 9′ East of the Southern Guinea Savanna region, with an annual rainfall of 400 – 600 mm and a mean temperature of 29.6^0 C as captured by Geographical Positioning System (GPS) equipment (GPS- 4300; Ethrex Garmin GPS, Taiwan).

Experimental material

The twenty rice varieties (FARO 52, NERICA 7, FARO 16, FARO 19, ART16-16-11-25-1-B-1-B-11, FARO 40, ART16-9-29-12-1-1-B-1, NERICA 4, ART16-9-6-21-1-2-2-B-B-1, FARO 38, FARO 31, ART15-21-2-4-1-B-1-B-1-1, ART16-4-24-4-4-2-1-B-5-2, ART15-16-12-3-1-B-1-B-3-1,ART16-13-11-1-2-B-2-B-2-1, FOFIFA 161, FARO 37, NERICA 1, ART16-9-122 and FARO 60) of rice used for the experiments were collected from NCRI Badeggi.

Experiment one; Screenhouse

Each pot of 25 cm diameter and 35 cm depth was filled with 8 kg silt-loam soil collected from the hydromorphic rice fields. The twenty varieties were replicated four times in a completely randomized design. Each pot was inoculated with blast isolates obtained from the infected blast leaves sourced from Badeggi rice fields.

Experiment two; Field

The experiment was laid out in a randomized complete block design with three replications. The experimental plot covered an area of 27 m x 10 m. The field was cleared and raked manually. Beds of 2 m x 1 m each were made at an inter-row spacing of 0.5 m, each carrying a different variety. Twenty beds were made in the same way for each of the three replications, at a spacing of 1 m x 1 m between replicates. The field was inoculated with blast isolates obtained from the infected blast leaves sourced from Badeggi rice fields.

Parameters observed

Parameters observed are; number of lesions, blast scoring, disease progression, emergence percentage, days to 50 % flowering, plant height, leaf area, days to maturity, tiller count, panicle number, panicle length,

Method of data analysis

Data collected were subjected to Analysis of Variance (ANOVA) using General Linear Model (GLM) procedure of SAS (SAS, 2008). Means were separated using Duncan Multiple Range Test at 5 % level of probability.

RESULTS

Screenhouse experiment

The mean morpho-agronomic parameters of the rice varieties grown under screenhouse are detailed in Table 1. Emergence percentage differed significantly between the varieties. Similar highest emergence percentage was recorded with FARO 38 (80.0%) and ART15-16-12-3-1-B-1-B-3-1 which was not significantly different from most of the other varieties except FARO 19, FARO 37 and ART16-9-29-12-1-1-1-B-1. Also, ART16-9-29-12-1-1-1-B-1 had the lowest emergence percentage of (30%) and is not significantly different from FARO 19. The number of days to 50% flowering varied significantly among the rice varieties. NERICA 8 and ART15-16-12-3-1-B-1-B-3-1 took longer days to 50% flowering, which were similar to most of the varieties except for that between FARO 16, FARO 49, ART16-9-29-12-1-1-1-B-1, FARO 38, FARO 31, ART15-21-2-4-1-B-1-B-1-1, ART16-4-24-4-4-2-1-B-5-2 and ART 16-9-122, respectively. Leaf area varied significantly between the varieties. ART 15-21-2-4-1-B-1-B-1-1(67.1cm^2) had the maximum leaf area compared to all the other varieties. FARO 49 recoded the least leaf area (44.1 cm^2) which was similar to most of the varieties except, ART16-9-29-12-1-1-1-B-1, ART 16-9-6-21-1-2-2-B-B-1 and NERICA 1, respectively. FARO52 had the highest height from (98.0 cm), which was not significantly different from all other varieties except from NERICA 1 with the lowest plant height of (63.5 cm). Result of tiller count showed that, ART 16-13-11-1-2-B-2-B-2-1 (22.3) had the highest tiller count with significant difference from FARO 52, NERICA 7, FARO 16, FARO 19, FARO 49, NERICA 4, FARO 31, ART 15-21-2-4-1-B-1-B-1-1, ART 15-16-12-3-1-B-1-B-3-1, FOFIFA 161, ART 16-9-122, FARO 60. ART 16-9-122 had the lowest tiller count of (14.8) with significant difference from ART 16-16-11-25-1-B-1-B-11, ART16-9-29-12-1-1-1-B-1, FARO 38, FARO 37 and NERICA 1.

Number of days to maturity differed significantly from 117.5 – 110.5. FARO 37 recorded the highest (117.5) days to maturity which differed significantly from other varieties except FARO 60. NERICA 4 had the highest (10.5) number of panicles without any significant difference from most varieties except for FOFIFA 161, and FARO 37.

Length of panicles showed significant differences among the rice varieties ranging from 22.4cm to 16.3cm. ART16-4-24-4-4-2-1-B-5-2 had the

highest length in panicles and was significantly different from most varieties except FARO 52, FARO 49 and FARO 31.

Result of the reaction of rice varieties to blast is presented in Table 2. The number of lesions on the leaves showed that NERICA 7 had the highest number (49), which is not significantly different from FARO 52 but significantly different from others. Disease progression was highest in NERICA 4 (29.1) and significantly different from others except ART16-9-6-21-1-2-2-B-B-1. There was no significant difference among the varieties in relations to leaf blast; however, NERICA 1 had the highest value of 6.7. There was significant difference among varieties for panicle blast with FARO 52 being significantly different from others and with the lowest value of 3.5.

Field experiment

The mean morpho-agronomic traits of twenty rice varieties grown on the field are shown in Table 3. Result of emergence percentage revealed that ART 16-16-11-25-1-B-1-B-11 had the highest emergence percentage of 86.1% and it was only significantly different from NERICA 4. FARO 60 had the lowest number of days to 50% flowering and it was significantly different from most varieties except ART16-16-11-25-1-B-1-B-11 and FARO 37. Leaf area result showed that FARO 60 had the largest leaf area (71.3 cm^2) and the smallest leaf area was from FARO 49. FARO 60 was significantly different from most varieties except ART-16-16-11-25-1-B-1-B-11, NERICA 4, ART 16-9-6-21-1-2-2-B-B-1, ART 16-13-11-1-2-B-2-B-2-1 and FARO 37. Result of plant height revealed that FARO 19 had the highest value (84.7 cm) while NERICA 1 was the least in plant height (41.5 cm).

FARO 19 showed significant difference from most varieties but was not significantly different from NERICA 7, NERICA 4, ART 16-4-24-4-4-2-1-B-52-2, ART 16-9-122 and FARO 60. On the other hand, NERICA1 was significantly different from most varieties which include NERICA 7, FARO 19, ART 16, 16-11-25-1-B-1-B-11, NERICA 4, ART 16-4-24-4-4-2-1-B-5-2, ART 16-9-122 and FARO 60. Result of tiller count revealed that NERICA 1 had the highest tiller count and was not significantly different from most varieties; however, it was significantly different from NERICA 4, FARO 31, ART 15-21-2-4-1-1-B-1-B-4, ART 16-4-24-4-4-2-1-B-5-2 and FOFIFA 161. On the other hand, NERICA 4 was only significantly different with NERICA 1, but was not significantly different with other varieties. Number of days to maturity varied from 123 days (NERICA 4) to 128 days (ART16-16-11-25-1-B-1-B-11, FARO 37 and FARO 60).

For days to maturity, ART 16-16-11-25-1-B-1-B-11, FARO 31, ART16-13-11-1-2-B-2-B-2-1, FOFIFA 161, FARO 37 and FARO 60 were significantly different from all other varieties. FARO 52 gave the highest panicle number (16) while FARO 31 had the lowest Panicle number (5.3). FARO 52 was significantly different from all varieties except ART 16-1-6-21-1-2-2-B-B-1. For panicle blast, FARO 19 had the highest panicle length of 22.9cm while FARO16 had the lowest panicle length of 16.8cm. FARO 19 was significantly different from FARO 16, ART16-9-29-12-1-1-1-B-1, FARO 37 and ART16-9-122 but was not significantly different from other varieties.

Result of disease infestation is presented in Table 4. There was significant difference among the varieties with respect to number of lesions. FARO 52 (9.1) had the highest while FARO 37 (2.2) gave the lowest. FARO 52 was significantly different from FARO 37 and FARO 16 but showed no significant difference from other varieties. The disease progression varied significantly from 60.3 (NERICA 7) to 6.5 (ART 16-16-11-25-1-B-11). NERICA 7 was significantly different from most varieties but was not significantly different from FARO 16, NERICA 4, FARO 31, ART 16-4-24-4-4-2-1-B-5-2, FARO 37 and FARO 60. Leaf blast ranged from 5-3. There was no significance difference among the rice varieties to leaf blast on the field experiment. Result of panicle blast showed that ART 16-9-29-12-1-1-B-1 was most affected (8.3). It was only significantly different from FARO 52. but was not significantly different from other varieties.

DISCUSSION

The research work showed that blast disease greatly affects the agronomic traits of the rice varieties across the two environments, which leads to variations in plant height, leaf area, tiller number, panicle length and panicle number. This agrees with the observations of Koutroubas *et al.* (2015). Who observed that inoculation of rice varieties with blast isolates affected immensely the overall agronomic traits of rice. Under the screenhouse, varieties with high above average grain yield were characterized with average

height, late flowering, wider leaves, fewer tillers and late maturity. This corroborates with the observations of Vange and Obi, (2006) who observed that agronomic traits and cultural practice affects blast disease effects on rice. Similarly, in the screenhouse environment, varieties with tiny leaves flowered earlier, had more tillers, average height, reached maturity earlier and expressed high rate of disease progression, which supports the works of Ishihara *et al.* (2014) who states that there is no significant difference between panicle and leaf blast. Tiller count in both the screenhouse and field environment had significant variation which could be as a result of nutrient level in the varieties. This supports the observation of Alan *et al.* (2009) statement that tiller productions were highly responsive to phosphorus levels in the varieties.

Similarly, the variation in emergence percentage between the varieties under the screenhouse and on the field is due to the differences in biological environment conditions. Rajarajan *et al.* (2016) work goes in agreement with this observation in his observation that variation in seedling emergence is as a result of differences in biological materials and environmental conditions. The research also showed significant variations in the number of days to 50 % flowering among the varieties across the environments, which could be as a result of genetic characteristics differences of the varieties to relative photoperiod sensitivity. Craufurd *et al.* (2000) and Hori *et al.* (2016) consents to this. They both suggested that early flowering duration target on plant breeding is based on their individual relative photoperiod sensitiveness.

Research results showed that on the field, some varieties had average rate of disease progression. This could be a reflection of wide leaves, fewer tillers, average height and delayed maturing qualities they possessed, which goes in line with the observations of Huang *et al.* (2010), who observed that phenotypic variance is evidence of resistance to rice blast disease. From the experimental results all the varieties did not show any significant difference in respect to leaf and panicle blast, they however varied in terms of disease progression with relations to the different environment. This is similar with the works of Ashraf *et al.* (2017), which states that mechanism of resistance to blast is influenced by environment.

Conclusion

It was concluded that seven varieties; ART16-13-11-1-2-B-2-B-2-1, ART16-4-24-4-4-2-1-B-5-2, FARO 31, NERICA 4, ART16-9-29-12-1-1-1-B-1, FOFIFA 161 and NERICA 1, gave the best resistance reaction to blast infection under the screenhouse and on the field. However, two varieties expressed slow disease progression rate effectively in both environments; FARO 19 and ART16-16-11-25-1-B-1-B-11. The research showed that environment and morpho-agronomic traits contributes to resistance in rice varieties to blast disease infection.

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Table 1. Morpho-agronomic parameters of rice varieties under the screenhouse environment

Variety	EP (%)	D50% F(days)	LA(cm2)	PH(cm)	TC	DTM(days)	PN	PL(cm)
FARO 52	60.0abc	69.5cdefgh	52.8cdef	98.0a	18bcdef	113defg	6ab	21.3abc
NERICA 7	65.0abc	65.8hi	53.3bcdef	81.7ab	16.5cdef	112.5efg	6.2ab	16.7d
FARO 16	75.0ab	72.0abcdef	58.63b	91.0a	17bcdef	112gh	6ab	17.4d
FARO 19	45.0cd	71.5bcdefg	55.2bcde	75.1ab	15.5ef	112.8defg	6.4ab	16.93d
ART 16-16-11-25-1-B-1-B-11	65.0abc	66.5ghi	57.3bcd	94.4a	20.3abc	114.3cde	7.3ab	16.3d
FARO 49	60.0abc	73.0abcd	44.1h	92.7a	15.3f	112.3fgh	7.7ab	21.3abc
ART16-9-29-12-1-1-1-B-1	30.0d	74.5abc	46.9gh	90.1a	19.4abcde	113defg	6.92ab	19.5bcd
NERICA 4	70.0ab	77.3a	58.8b	84.7ab	16.2def	110.5h	10.5a	18.8dc
ART 16-9-6-21-1-2-2-B-B-1	70.0ab	67.5efghi	49.0fgh	92.2a	18.6abcdef	113.3cdefg	9.1ab	19.1cd
FARO 38	80.0a	75.0ab	57.5bc	82.6ab	19.8abcd	112gh	6.5ab	19.4bcd
FARO 31	70.0ab	72.8abcde	56.2bcde	96.7a	18.1cdef	114.5bcd	6.7ab	23.5a
ART 15-21-2-4-1-B-1-B-1-1	70.0ab	75.5ab	67.1a	93.1a	18.3bcdef	113defg	5.8ab	17.7d
ART 16-4-24-4-4-2-1-B-5-2	75.0ab	72.3abcde	50.9efg	97.2a	18.5abcdef	112gh	7.7ab	22.4ab
ART 15-16-12-3-1-B-1-B-3-1	80.0a	77.3a	53.5bcdef	77.5ab	16.1def	113.8cdefg	8.3ab	18.6cd
ART 16-13-11-1-2-B-2-B-2-1	60.0abc	71.3bcdef	56.0bcde	82.4ab	22.3a	113defg	9ab	18.4cd
FOFIFA 161	75.0ab	69.0defghi	52.9cdef	92.7a	15.5ef	115bc	4.6b	19.4bcd
FARO 37	55.0bc	66.8fghi	52.1def	88.9a	20.8ab	117.5a	4.7b	16.3d
NERICA 1	70.0ab	68.5defghi	48.4fgh	79.6ab	20.3abc	114cdef	6.7ab	17.4d
ART 16-9-122	75.0ab	75.0ab	55.9bcde	63.5b	14.8f	115bc	8ab	16.9d
FARO 60	75.0ab	60.4i	51.9defg	90.4a	16.2def	116.3ab	6.5ab	18.7cd
Mean	66.3	71.2	53.9	87.2	17.87	113.48	7.02	18.8
±SE	7.2	1.6	1.6	7.1	1.2	0.57	1.39	0.98
p-value	0.0008	0.0001	0.0001	0.1104	0.0002	0.0001	0.3732	0.0001

Values are presented in mean of four replicates. Values with the same superscript alphabets within the column are not significantly different at ($p = 0.05$) by Duncan Multiple Range Test. KEY: EP: Emergence percentage, D50%F: Days to 50 % flowering, LA: Leaf area, PH: Plant height, TC: Tiller count, DTM: Days to maturity, PN: Panicle number, PL: Panicle length

Table 2. Reactions of rice varieties to blast disease in the screenhouse environment

Variety	NL	DPGN	LB	PB
FARO 52	36.4^{ab}	12.0^{cdef}	2.5^{a}	3.5^{c}
NERICA 7	49.0^{a}	18.9^{bc}	3.5^{a}	6.0^{ab}
FARO 16	18.9^{c}	6.6^{ef}	3.5^{a}	7.0^{ab}
FARO 19	23.0^{bc}	5.8^{ef}	4.0^{a}	7.0^{ab}
ART 16-16-11-25-1-B-1-B-11	20.5^{bc}	8.7^{def}	4.0^{a}	7.0^{ab}
FARO 49	15.8^{c}	8.0^{def}	4.0^{a}	7.0^{ab}
ART16-9-29-12-1-1-1-B-1	13.5^{c}	14.8^{cde}	3.0^{a}	8.0^{a}
NERICA 4	16.8^{c}	29.1^{a}	4.0^{a}	7.0^{ab}
ART 16-9-6-21-1-2-2-B-B-1	19.5^{c}	23.7^{ab}	4.0^{a}	7.0^{ab}
FARO 38	13.3^{c}	4.1^{f}	4.0^{a}	7.0^{ab}
FARO 31	21.6^{bc}	11.53^{cdef}	4.0^{a}	6.5^{ab}
ART 15-21-2-4-1-B-1-B-1-1	21.2^{b}	6.6^{ef}	3.0^{a}	5.0^{ab}
ART 16-4-24-4-4-2-1-B-5-2	14.1^{c}	18.7^{bc}	4.0^{a}	6.0^{ab}
ART 15-16-12-3-1-B-1-B-3-1	17.2^{c}	12.4^{cdef}	4.5^{a}	8.0^{ab}
ART 16-13-11-1-2-B-2-B-2-1	20.8^{bc}	10.1^{cdef}	4.0^{a}	7.0^{ab}
FOFIFA 161	15.1^{c}	13.2^{cdef}	4.0^{a}	6.0^{ab}
FARO 37	17.8^{c}	16.6^{bcd}	4.0^{a}	7.0^{ab}
NERICA 1	10.7^{c}	6.7^{ef}	6.0^{a}	8.5^{a}
ART 16-9-122	13.3^{c}	5.3^{f}	4.5^{a}	7.0^{ab}
FARO 60	15.3^{c}	11.5^{cdef}	3.5^{a}	7.5^{ab}
Mean	19.68	12.2	3.43	7.13
±SE	5.17	2.68	1.17	0.78
p-value	0.0009	<0.0001	0.9925	0.0224

Values are presented in mean of four replicates. Values with the same superscript alphabets within the column are not significantly different at (p = 0.05) by Duncan Multiple Range Test. KEY: NL: Number of lesions, DPGN: Disease progression, LB: Leaf blast, PB: Panicle blast

Table 3. Morpho-agronomic traits of rice varieties for field experiment

Variety	EP (%)	D50%F (days)	LA (cm^2)	PH (cm)	TC	DTM (days)	PN	PL (cm)
FARO 52	71.5ab	70.3cde	33.6cd	51.9def	14.7abc	125.0bc	16.0a	19.5ab
NERICA 7	49.1ab	72.7bcd	47.2bdc	80.6ab	14.3abc	125.0bc	9.2bc	22.8a
FARO 16	38.8ab	77.3ab	33.7cd	55.2cdef	15.9abc	124.0bc	10.3bc	16.8b
FARO 19	49.7ab	77.0abc	38.7cd	84.7a	14.0abc	124bc	9.6bc	22.9a
ART 16-16-11-25-1-B-1-B-11	86.1a	66.0ef	54.8abc	63.2bcde	15.8abc	128.0a	8.7bc	19.5ab
FARO 49	74.6ab	77.7ab	28.2d	60cdef	15.4abc	124.7bc	8.7bc	18.2ab
ART16-9-29-12-1-1-1-B-1	68.9ab	75.0abc	42.1bcd	42.3ef	14.9abc	125.3bc	9.2bc	17.3b
NERICA 4	42.4b	82.0a	52.3abc	69.4abcd	10.3c	123.0c	6.2bc	19.5ab
ART 16-9-6-21-1-2-2-B-B-1	75.2ab	77.0abc	54.6abc	52.7dcef	16.8ab	124.3bc	11.7ab	18.8ab
FARO 38	77.0ab	75.7abc	33.3cd	42.7ef	13.9abc	125.0bc	6.3bc	19.5ab
FARO 31	49.7ab	75.0abc	34.3cd	51.3def	12.3bc	125.7abc	5.3c	18.2ab
ART 15-21-2-4-1-B-1-B-1-1	68.6ab	82.0a	41.1bcd	45.0ef	10.9c	125.0bc	7.0bc	19.9ab
ART 16-4-24-4-4-2-1-B-5-2	49.1ab	77.7ab	37.1cd	81.3ab	11.13bc	124.0bc	6.3bc	19.7ab
ART 15-16-12-3-1-B-1-B-3-1	76.4ab	79.7ab	47.5bcd	61.3bcdef	14.5abc	124.3bc	8.1bc	19.5ab
ART 16-13-11-1-2-B-2-B-2-1	75.2ab	73.0bcd	51.4abc	54.5cdef	12.9abc	125.7abc	7.3bc	18.8ab
FOFIFA 161	54.0ab	76.0abc	43.7bde	62.6bcde	13.3abc	126.7abc	6.9bc	19.9ab
FARO 37	57.7ab	67.0def	26.4d	56.0cdef	12.1bc	128.0a	9.5bc	17.2b
NERICA 1	67.3ab	74.7bc	61.3ab	41.5f	18.1a	125.0bc	8.2bc	18.8ab
ART 16-9-122	78.2ab	79.3ab	45.3bcd	72.8abc	14.4abc	124.7bc	7.7bc	17.1b
FARO 60	49.1ab	62.3f	71.3a	73.5abc	13.0abc	128.0a	9.8bc	20.6ab
Mean	62.93	74.88	43.65	25.14	13.93	125.27	8.56	19.2
±SE	12.57	2.14	6.76	3.38	1.67	0.81	1.81	1.53
p-value	0.2629	0.0001	0.0019	0.3957	0.1702	0.0018	0.0724	0.3647

Values are presented in mean of three replicates. Values with the same superscript alphabets within the column are not significantly different at ($p = 0.05$) by Duncan Multiple Range Test. KEY: EP: Emergence percentage, D50%F: Days to 50 % flowering, LA: Leaf area, PH: Plant height, TC: Tiller count, DTM: Days to maturity, PN: Panicle number, PL: Panicle length

Table 4. Reaction of rice varieties to blast disease on the field environment

Variety	NL	DPGN	LB	PB
FARO 52	9.1a	15.7fgh	3.0a	4.3b
NERICA 7	7.2ab	60.3a	3.0a	6.3ab
FARO 16	3.9bc	49.1abc	3.7a	7.7a
FARO 19	4.8abc	9.1gh	3.7a	7.7a
ART 16-16-11-25-1-B-1-B-11	5.9abc	6.5h	3.0a	7.0ab
FARO 49	7.6ab	18.7efgh	3.7a	7.7a
ART16-9-29-12-1-1-1-B-1	8.0ab	26.9defgh	3.0a	8.3a
NERICA 4	5.2abc	52.0ab	3.0a	7.0ab
ART 16-9-6-21-1-2-2-B-B-1	7.2abc	33.2bcdef	3.0a	7.7a
FARO 38	8.0ab	26.9defgh	4.3a	7.7a
FARO 31	5.3abc	40.9abcd	3.0a	7.7a
ART 15-21-2-4-1-B-1-B-1-1	7.1abc	34.5bcdef	3.0a	5.7ab
ART 16-4-24-4-4-2-1-B-5-2	6.0abc	50.7ab	3.7a	6.3ab
ART 15-16-12-3-1-B-1-B-3-1	7.4ab	38.1bcde	5.0a	7.7a
ART 16-13-11-1-2-B-2-B-2-1	6.7abc	18.3efgh	3.0a	7.7a
FOFIFA 161	6.1abc	28.6cdefg	3.7a	7.0ab
FARO 37	2.2c	43.0abcd	3.0a	7.0ab
NERICA 1	5.8abc	33.4bcdef	4.3a	8.3a
ART 16-9-122	8.3ab	23.7defgh	3.0a	7.0ab
FARO 60	6.8abc	43.5abcd	3.0a	7.0ab
Mean	6.43	32.66	3.43	7.13
±SE	1.46	6.39	1.38	0.92
p-value	0.2838	0.0001	0.9999	0.4512

Values are presented in mean of three replicates. Values with the same superscript alphabets within the column are not significantly different at ($p = 0.05$) by Duncan Multiple Range Test. KEY: NL: Number of lesions, DPGN: Disease progression, LB: Leaf blast, PB: Panicle blast

EFFECTS OF FERTILIZER AND MOISTURE STRESS ON AGRONOMIC AND YIELD COMPONENTS OF CASSAVA GENOTYPES

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ABSTRACT
Nutrient and moisture-stress effects on cassava are often neglected because cassava is considered a 'hardy crop'. Information on the response of cassava to NPK fertilizer under moisture-stress is important. Two cassava genotypes (TME-419 and TME-581) were evaluated for agronomic and yield-related traits under irrigation-fertilizer and no-irrigation-no-fertilizer treatments. Irrigation effect was significant for yield-related traits, whereas, fertilizer effect was significant for agronomic traits. Genotypes differed for agronomic and yield-related traits. Irrigation × genotype and irrigation × genotype × fertilizer interactions had effects on dry matter (DMC) and number of primary branches (NPB), respectively. Irrigation increased fresh root yield (FRY), marketable yield (MKY), harvest index (HI), DMC and starch content (SC) by 64%, 71%, 23%, 12.6% and 21%, respectively, while fertilizer increased NPB and mass of fresh branches by 25.7% and 14%, respectively. TME-419 had more FRY, MKY, DMC and SC than TMS-581 by 20%, 19%, 10% and 17%, respectively. Irrigation and fertilizer were important for enhanced cassava performance.

Keywords: cassava root yield, drought, NPK fertilizer, starch content

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INTRODUCTION
Cassava (*Manihot esculenta* Crantz) is one of the main food and cash crops in the tropics serving as a major source of energy for most poor-resource farmers in sub-Saharan Africa (SSA), Asia and Latin America. The storage roots are utilized either fresh, or processed into products such as garri, fufu, flour, starch, animal feeds or biofuel. Nigeria is the highest producer of cassava in the world, but has not met production demand for domestic consumption and export potential. This is due to interplay of many factors including the cultivation of low yielding varieties, poor soil fertility and drought stress occasioned by erratic climatic conditions caused by climate change. Cassava's ability to produce in marginal environments and moisture deficit condition makes it the ideal food security crop in SSA, but has the potential to gives considerably higher yields with fertilizers and irrigation, especially in dry seasons (Okogbenin *et al.*, 2013). The use of chemical fertilizer can increase the yield of smallholder from 10 to 16 tonnes fresh roots per hectare (Hauser *et al.*, 2014). The mineralization of fertilizer and nutrient uptake is facilitated by optimum soil moisture content (Howeler, 2002). However, the reports on the performance of cassava genotypes under fertilization and moisture stress conditions are limited. Therefore, this study was conducted to obtain information on the performance of cassava genotypes under soil fertilization and moisture stress conditions.

MATERIALS AND METHODS
The experiment was conducted at IITA, Ibadan (7.34°N and 3.95°E, 273 m asl). The treatments included two levels of irrigations [irrigation (I_1) and no-irrigation (I_0)], two levels of fertilizers [fertilizer (F_1) and no-fertilizer (F_0)] and two cassava varieties (TME-419 and TMS-581). The six treatment combinations were laid out in a factorial experiment arranged in a randomized complete block design and replicated 4 times. Each plot consisted five rows, each of 4 m length. Twenty-five (25) centimeter cassava stakes were planted on intra- and inter-row spacing of 0.8 m x 1 m. Each plot was 20 m^2 comprising 25 plant stands. The trial consisted of two blocks (irrigated and non-irrigated), each comprising 24 plots. Water was supplied to the irrigated trial using drip irrigation system from planting to physiological maturity. Fertilizer treatment was as follows: 150 kg/ha of NPK 15: 15: 15 at 4 weeks after planting (WAP) and 8 WAP, respectively,

65.2 kg/ha of urea at 12 WAP, 52.6 kg/ha KCL, 12 WAP and 16 WAP, respectively. 4 L ha-1 Primextra Gold, a.i. 290 g/L S-Metolachlor plus 370 g/L Atrazine were used as pre-emergence herbicides and complemented by manual weeding. Data were recorded on number of primary branches, mass of fresh leaves, branches, stems and fresh roots and marketable yield. Harvest index (HI), Percentage dry matter content (DMC) and percentage starch content (SC) were estimated based on Fakuda *et al.* (2010). Prior to land clearing, soil samples were collected for the analysis of soil physical and chemical properties.

RESULTS

The soil of the experimental site was sandy loam, slightly acidic and had high depleted levels of organic carbon, N, P K (Table 1). The effect of fertilizer was significant for all the cassava agronomic traits measured, while irrigation effect was significant for all the yield-related traits (Table 2). Meanwhile, the varietal effect differed for most of the agronomic and yield-related traits. Irrigation × variety interaction effect was significant for mass of fresh branches (MFB) and dry matter content (DMC), while irrigation × variety × fertilizer effect was significant for number of primary branches (NPB) and MFB (Table 2).

Irrigation effect significantly increased fresh root yield (FRY), marketable yield (MKY), harvest index (HI), DMC and starch content by 63.89%, 71.08%, 23.26%, 12.63% and 20.89%, respectively, whereas fertilizer effect increased NPB, MFB and mass of fresh stems and branches (MFSB) by 25.74%, 14.05% and 47.52%, respectively (Table 3). Variety TMS-581 had better agronomic performance than TME-419, but TME-419 outperformed TMS-581 in all yield-related traits (Table 3). Irrigation effect significantly enhanced the DMC of TME-419 and MFB of TMS-581, but both genotypes were markedly increased for FRY, MKY and HI by the irrigation effect (Table 4). Irrigation × fertilizer interaction effect enhanced agronomic traits of the two cassava genotypes, but had no significant effect on yield-related traits (Table 4). Similarly, variety × fertilizer significantly increased the NPB of TMS-581, and MFB and MFSB of both genotypes, but not their yield-related traits (Table 4). The difference between the effects of no-irrigation × TME-419 × no-fertilizer treatment and irrigation × TME-419 × fertilizer was not significant for NPB and MFB, but the difference between no-irrigation × TMS-581× no-fertilizer treatment and irrigation × TMS-581× fertilizer was significant for both traits (Figure 1). The regression equations revealed that a unit increase in FRY increased starch content by 11.58%, whereas a unit increase in DMC decreased starch content by 6.18% (Figures 2a and b).

DISCUSSION

The significant effect of fertilizer on cassava agronomic traits signified that the nutrients (particularly nitrogen) actively stimulated the growth of stems, branches and leaves, consistent with Hauser *et al.* (2014) who reported that leaves and small stems utilize nitrogen nutrient 10 times than roots. The nonsignificant fertilizer effect on yield-related traits suggested that the fertilizer treatment did not significantly enhance root yield. This could be due to the low basal nutrient status of the soil and/or poor mineralization of the applied fertilizer. Nutrient absorption and distribution are closely related to plant growth rate, which depends on soil fertility and climate conditions as well as varietal characteristics (Howeler, 2002). However, studies (Hauser *et al* 2014; Adiele *et al.*, 2021) have shown that uptake of NPK are more concentrated in the leaves and stems of cassava than the storage roots. The significant effect of irrigation for FRY and other yield-related traits indicated that moisture was important for nutrient mineralization, absorption, translocation and cell maintenance for root formation and bulking in cassava, consistent with Howeler (2002) who reported that irrigation markedly increased cassava growth and cassava tuberous roots becomes the major sink of dry matter content 2-3 months after planting. The significant irrigation × variety interaction effect for DMC underscores the importance of irrigation for DM accumulation in cassava. Although TMS-581 had better agronomic performance than TME-419, it did not necessarily translate into better yield, suggesting that TME-419 had better nutrient utilization efficiency for FRY, MKY, DMC %SC. In addition, from the regression models, the significant positive relationship between FRY and SC indicated that a unit increase in FRY increased SC by 11.6%, indicating that both traits can be improved simultaneously, contrary to the

result of Njoku *et al.* (2020). On the other hand, the significant negative relationship between DMC and SC signified that a unit increase in root DMC decreased SC by 6%. This suggests that product such as garri that is dry matter-dependent would decrease starch yield in the cassava genotypes.

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Table 1. Physical and chemical properties of soil of the study site

Properties	Value	Critical level (Chude *et al.*, 2012)
Soil properties		
pH (1:1, H_20)	6.4	Neutral 6.6 – 7.2
Organic carbon (g/Kg)	5.7	10 – 14
Total nitrogen (g/Kg)	0.6	1.6 – 2.0
Available P (mg/Kg, ppm)	2.5	7.2
Exchangeable K (cmol/Kg)	0.1	0.3 – 0.6
Particle size distribution (g/Kg)		
Sand	775	
Silt	89	
Clay	136	
Textural class (USDA)	Sandy loam	

Table 2. Mean squares from the ANOVA of irrigation and fertilizer effects on the agronomic and yield traits of two cassava genotypes evaluated at IITA, Ibadan, Nigeria

Source	DF	No. of primary branches	Mass of fresh green branch	Mass of fresh stem & branch	Fresh root yield	Marketable yield	Dry matter content	Harvest index	% Starch content
REP	3	427.86	1.19**	25.04	65.60	73.39	25.49***	0.01	10.33
IR	1	42.78	0.21	3.63	1296.68***	1242.26***	130.13***	0.08**	135.88**
VAR	1	1875.78*	3.89***	15.13	213.31	140.28	81.12***	0.05*	97.23*
FERT	1	3341.53**	1.44*	583.28**	7.43	11.88	0.98	0.08**	13.55
IR × VAR	1	9.03	2.28**	11.76	0.15	0.84	14.06*	0.00	9.03
IR × FERT	1	19.53	0.03	1.49	3.60	2.55	2.14	0.00	0.29
VAR× FERT	1	1365.03	0.10	38.19	5.46	9.88	9.36	0.00	16.53
IR × VAR × FERT	1	2363.28*	0.97*	21.52	9.05	4.68	10.07	0.01	11.54
ERROR	21	373.10	0.22	47.37	73.81	67.27	2.88	0.01	12.72

*, **, *** $p \leq 0.05$, 0.01, and 0.001, IR: irrigation, VAR: variety, FERT: fertilizer

Table 3. The mean performance of two cassava genotypes evaluated for agronomic and yield-related traits under fertilizer and irrigation treatments at IITA, Ibadan, Nigeria

Treatment	No. of primary branches	Mass of fresh green branch (t/ha)	Mass of fresh stem & branch (t/ha)	Fresh root yield (t/ha)	Marketable yield (t/ha)	Harvest index	dry matter content (%)	Starch content (%)
Irrigation								
IR0	88.44	3.12	21.88	19.94	17.53	0.43	31.90	19.72
IR1	90.75	3.28	22.55	32.68	29.99	0.53	35.93	23.84
LSD (0.05)	14.20	0.35	5.06	6.32	6.03	0.07	1.25	2.62
% change	1.76	5.13	3.06	63.89	71.08	23.26	12.63	20.89
Fertilizer								
F0	79.38	2.99	17.95	26.79	24.37	0.53	33.74	22.43
F1	99.81	3.41	26.48	25.83	23.15	0.43	34.09	21.13
LSD (0.05)	14.20	0.35	5.06	6.32	6.03	0.07	1.25	2.62
% change	25.74	14.05	47.52	-3.58	-5.01	-18.87	1.04	-5.80
Variety								
TME-419	81.94	2.85	21.53	28.89	25.85	0.52	35.50	23.53
TMS-581	97.25	3.55	22.90	23.73	21.67	0.44	32.32	20.04
LSD (0.05)	14.20	0.35	5.06	6.32	6.03	0.07	1.25	2.62
% change	18.68	24.56	6.36	20.23	19.29	18.18	9.84	17.42

IR0: No-irrigation, IR1: Irrigation, F0: No-fertilizer, F1: Fertilizer

Table 4. The interaction effects of Irrigation, fertilizer and variety on the agronomic and yield traits of two cassava genotypes evaluated at IITA, Ibadan, Nigeria

Treatment interactions	No. of primary branches	Mass of fresh green branch (t/ha)	Mass of fresh stem & branch (t/ha)	Fresh root yield (t/ha)	Marketable yield (t/ha)	Harvest index	Dry matter content (%)	Starch content (%)
Irrigation × variety								
IR0 × TME-419	80.25	3.04	20.58	22.59	19.79	0.48	32.83	22.00
IR1 × TME-419	83.63	2.67	22.47	35.19	31.92	0.56	38.18	25.06
IR0 × TMS-581	96.63	3.20	23.17	17.29	15.27	0.38	30.97	17.45
IR1 × TMS-581	97.88	3.90	22.63	30.16	28.06	0.50	33.67	22.63
SE (0.05)	8.96	0.52	1.13	7.93	7.59	0.07	3.06	3.18
Irrigation × fertilizer								
IR0 × F0	79.00	2.94	17.82	20.76	18.42	0.48	31.46	20.47
IR0 × F1	97.88	3.30	25.93	19.13	16.64	0.38	32.33	18.98
IR1 × F0	79.75	3.04	18.07	32.82	30.32	0.59	36.01	24.40
IR1 × F1	101.75	3.53	27.04	32.53	29.66	0.48	35.85	23.29
SE (0.05)	11.91	0.26	4.95	7.38	7.24	0.08	2.36	2.50
Variety × fertilizer								
F0 × TME-419	78.25	2.59	18.35	29.79	27.02	0.57	34.79	24.90
F1 × TME-419	85.63	3.12	24.70	28.00	24.69	0.47	36.22	22.16
F0 × TMS-581	80.50	3.39	17.54	23.80	21.72	0.49	32.69	19.97
F1 × TMS-581	114.00	3.71	28.26	23.66	21.61	0.39	31.95	20.11
SE (0.05)	16.56	0.48	5.15	3.07	2.60	0.07	1.95	2.30

IR0: No-irrigation, IR1: Irrigation, F0: No-fertilizer, F1: Fertilizer, SE: Standard error

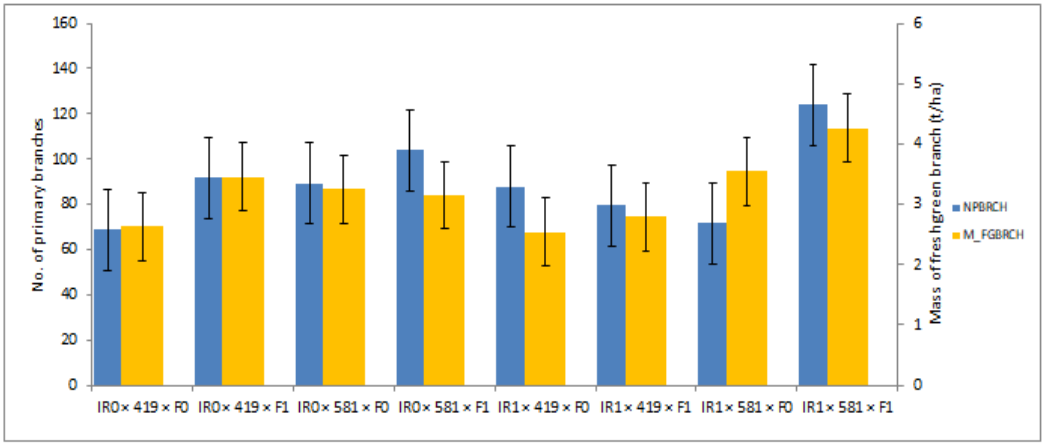

Figure 1: The effects of the interactions of irrigation, variety and fertilizer on the number of primary branches (NPBRCH) and mass of fresh green branches (MFGBRCH) of two cassava genotypes evaluated at IITA, Ibadan, Nigeria

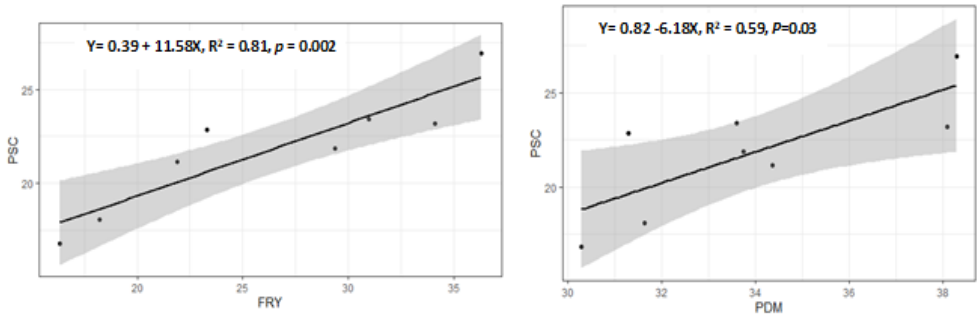

Figure 2: Scatter plots of the regression of percentage starch content (PSC) on the fresh root yield (FRY) and percentage dry matter content (PDM) of two cassava genotypes evalauated under irrigation and fertilizer treatment effects at IITA, Ibadan, Nigeria

EFFECTS OF PACKAGING MATERIALS ON PROXIMATE COMPOSITIONS OF CASTOR SEED (*Ricinus communis* L.)

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ABSTRACT

Despite the economic importance of castor seeds (*Ricinus communis L.*), there is little research attention on its storage. Therefore, this study investigated the effects of four different packaging materials (Jute, Polythene, polypropylene and Plastic bags) on proximate compositions of castor seeds. Proximate analysis was carried out following standard procedures. The pre storage proximate compositions obtained were: moisture content (2.71%), crude Fat (48.01%), crude Protein (13.16%) and Carbohydrate (30.69). After storage the %moisture content increased in jute bag (2.85%) and polythene (2.79%) but decreased in other containers from plastic (2.55%)> polypropylene (2.35%). However, there was increase in Crude fat and Protein but decrease in Carbohydrate. Jute bag has the highest fat (64.58%) and protein (23.16%) and least in carbohydrate (4.61%). Polythene was least in fat (58.08%) and plastic least in protein (15.67%). The result indicates that proximate compositions of the stored seed were affected by the packaging materials after three months.

Keyword: Castor seed, Packaging materials and Proximate

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INTRODUCTION

The Castor bean plant (*Ricinus communis* Linn) is a species of flowering plant in the family *Euphorbiaceae* (Oyewole *et al*., 2010). Castor beans contain 50 - 55 of non-edible oil and 26-30% protein due to the nature of the chemical composition. Similarly reported by Jayaraman *et al.* (2011) that, under a commercial grain storage, fungi were the primary cause of seeds deterioration which was depicted by loss of germinability, decreased in dry matter, increased fat acidity, grain heating, and ultimate sprouting. Anjorin *et al.* (2011) also added that seed-borne pathogens were major factors reducing seed vigor. Although seed quality is generally determined by genetic and physiological factors, and physical attributes of the seeds, harvesting and handling process, seed storage also should be considered. Simic *et al.* (2007) reported that pests and disease infection, seed oil content, seed moisture content, mechanical damage, seed longevity, packaging, pesticides, air temperature and relative humidity are responsible for quality decline in seed under storage. Some packaging materials are commonly used for storing seeds, but their suitability depends on the kind or type of seeds and their protection ability to the seed in storage.

MATERIALS AND METHODS

Two kilograms (2 kg) of freshly harvested castor seeds was collected from the NCRI and deshelled. Four packaging materials namely Jute bag, Polythene bag, Polypropylene bag and Plastic container were used for storage. Each packaging material was in three replicates. The experiment was set up in a Completely Randomized Design. Proximate analysis of the samples for moisture, total ash, crude fibre and fat was carried out in triplicate using methods described by Agboola *et al.* (2020) after three (3) months of storage.

Data analysis

Data generated was subjected to analysis of variance (ANOVA) using Statistical Package for social science (SPSS version 24). Duncan Multiple Range Test (DMRT) was used to separate the means and test for the level of significance at (5%).

RESULTS AND DISCUSSION

The pre storage proximate compositions obtained were: moisture content (2.71%), crude Fat (48.01%), crude Protein (13.16%) and Carbohydrate (30.69). After storage, highest moisture content was recorded in Jute bag (2.85%) and Polythene bag (2.79%). This may be due to the fact that jute bag is porous, thus allowing entrance of free air unlike other packaging materials. This was also reported by Santoso *et al*. (2015) No significant difference (p >0.05) was recorded in Ash content from all the packaging materials used. This is similar to the findings of Oso *et al.* (2011) who reported similar result. A significant increase in Fat was recorded in all the packaging materials with Jute bag

(64.58%) being the highest and the least in Polythene bag (58.08%). This is in contrast to the work of Mesele *et al.* (2022). Highest protein content was recorded in Jute bag (23.16%) and Plastic bag (15.67%) was the least. protein content recorded in this study agrees with the findings of Oso *et al.* (2011), Matos *et al.* (2011), Akande *et al.* (2012) who reported the range of 21–48% in their studies. No significant difference ($p < 0.05$) recorded in Fibre content of all samples stored which is in line with work of Matos *et al.* (2011), Akande *et al.* (2012) who reported the range of 1–3% in their studies. The carbohydrate content decreased in all packaging materials, the least was recorded in Jute bag (4.61%). Similar trend was reported by B. Melese *et al.* (2022) who reported emmer wheat stored in Grain pro bag had highest carbohydrate content after 3 months of storage.

Conclusion

The results obtained from this study revealed an increase in proximate compositions of castor seed in all packaging materials after three months of storage.

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Table 1. Effect of packaging material on proximate composition of castor oil seed

Treatments	Moisture	Ash	Fat	Protein	Fibre	Carbohydrate
Polythene	2.79±0.00c	3.28±0.68a	58.08±0.43b	23.09±0.11c	2.16±0.45a	10.60±1.67b
Plastic	2.55±0.00b	2.97±0.03a	62.36±0.37c	15.67±0.53b	1.96±0.02a	14.48±0.11c
Jute	2.85±0.00d	2.89±0.00a	64.58±0.60d	23.16±0.04c	1.91±0.00a	4.61±0.56a
Polypropylene	2.35±0.00a	2.66±0.00a	61.03±0.45c	22.55±0.22c	1.75±0.00a	9.67±0.66b
Pre-storage	2.71±0.25bc	3.28±0.34a	48.01±0.01a	13.16±0.10a	2.17±0.23a	30.69±0.73d

Values are mean ± standard error of mean. Values followed by different superscripts along the same column are significantly different at $p < 0.05$

PHYTOCHEMICAL SCREENING AND EFFECT OF *Balanites aegyptiaca* AQUEOUS LEAF EXTRACTS ON GERMINATION AND SOME SEEDLING GROWTH OF *Abelmoschus esculentus, Capsicum annuum* AND *Lycopersicon esculentum* (OKRA, SWEET PEPPER AND TOMATO)

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ABSTRACT

The Phytochemical Screening of Aqueous Leaf Extracts and Effect of *Balanite aegyptiaca* plant was carried out using standard method to investigate the presence of secondary metabolites and their potency against Germination and Seedling Growth of *A. esculentus* (Okra), *C. annuum* (Sweet pepper) and *L. esculentum* (Tomato). The main objective of this study is to determine the phytochemicals and effect of the aqueous leaf extracts of *B. aegyptiaca* plant parts. The aqueous leaf extract of *B. aegyptiaca* at varying concentrations of 2.5, 5.0, 10 and 20 mg/l were prepared using water as a solvent to screened phytochemicals constituents and tested against germination and seedling growth of three vegetable crops. The results of the phytochemical screening of *B. aegyptiaca* leaf extracts showed that the extract of the plant part revealed the presence of different secondary metabolites. Among the phytochemical compounds screened, saponins were found to be in excess. But, the present chosen solvent (water) was not able to extract resins out from the leaf. This indicated that the resins are not presence in the leaf of *B. aegyptiaca*, or may be the used solvent cannot extract it. Higher concentration (20 mg/l) of aqueous leaf extract exhibited inhibitory effect on the test crops, while lower concentrations (2.5 mg/l) showed stimulatory effect in some cases.

Keywords: *Balanite aegyptiaca*, germination, phytochemical screening, seedling growth

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INTRODUCTION

Many higher plants are capable of producing organic substances having autotoxic or antibiotic properties, when these substances function to inhibit the germination or growth of the plants nearby, the phenomenon is termed as allelopathy. The allelochemicals as well as the other phytochemicals present in plants have stimulatory or inhibitory influences on seed germination, seedling growth and yield of recipient plants. Plant parts have been found to produce and store various allelochemicals. Allelochemicals compounds released from different plant parts can either be released continuously, within specific periods or impulses when triggered by external factors such as precipitation (Rice, 1984). Leaves seem to be the most consistent source of inhibitors and most investigators have tested them, at least in combination of some other parts. However, commonly cited effects of allelochemicals include reduced seed germination and seedling growth. However, known sites effects for allelochemicals include cell division, pollen germination, nutrient uptake, photosynthesis, production of plant hormones and their balance, movement of stomata, pigment synthesis, respiration, amino acids, nitrogen fixation, specific enzymes activities and conduction tissues (Wink *et al*., 1998).

B. aegyptiaca (Delile), known as desert date, and *Aduwa* in Hausa northern part of Nigeria. It belongs to the family *Zygophyllaceae* (Daya *et al*., 2011). This tree is native to much of Africa and part of the Middle East. In Africa, it is particularly found in Sahel savanna and northern Sudan savannah zones of West Africa; in Nigeria the tree is more common in northern Nigeria. Literature has revealed antifidant, antidiabetic, mollusicidal, anthelmenthic and contraceptive activities in various *B. aegyptiaca* (Gupta *et al*., 2012). It is rich in carbohydrates, alkaloids, saponnins, flavonoids and vitamin C in particular (Daya *et al*., 2011). The seeds are particularly rich in oil and protein.

MATERIALS AND METHODS

Experimental Site

Laboratory and pot experiments were conducted at the Department of Biological Sciences and Agronomy, Bayero University, Kano. Kano State lies between longitude 9º30´N and 8º42´E in the Sudan Savannah Ecological Zone of Nigeria (Adamu, 2010). The area is characterized by Tropical wet and dry climate (Olofin, 1987).

Experimental design and treatment

The experiment was laid out in a complete randomized design and repeated three times. Each experiment consists of three vegetable crops (*A. esculentus, C. annuum and L. esculentum*) and four different concentrations (2.5, 5.0, 10.0 and 20.0 mg/l) of *B. aegyptiaca* aqueous leaf extracts.

Collection of plant parts

Fresh leaves of *B. aegyptiaca* were hand-picked from premises of Bayero University, Kano. Soon after collection, the collected plant parts were washed with tap water to remove soil, and air dried at room temperature in the laboratory for approximately three days. Exposure to sunlight was avoided to prevent the loss of active components. The dried samples were ground into fine powder using mortar and pestle and sieved with 0.5 mm sieve into fine powdered as described by Yusha'u *et al.* (2009) and Audu *et al.* (2018). The samples powdered were stored in airtight containers until extraction.

Extracts preparation

The grounded dried plant parts of *B. aegyptiaca* were extracted using the method described by Asa'adi *et al.* (2010) with slight modifications. About 50 g of grounded leaves and fruit powdered were measured using sensitive scale and then placed carefully into 500 ml cleaned and labeled conical flask of the respective extracting solvents. The mixtures were shaken properly, and then the flasks were covered and left for 3 days at room temperature. Thereafter the extracts were decanted and filtered through 2 mm mesh sieved to remove debris and finally filtered using Whatman No. 1 filter pepper. The filtrates were serially diluted by adding distilled water to get 2.5, 5.0, 10.0 and 20.0 mg/l concentrations. The extract was then transferred into cleaned labeled bottle containers and kept in the laboratory for later used.

Phytochemical screening of the extracts

Phytochemical analyses of the plant extracts were carried out using prepared extracts following standard procedure described by Kumar *et al.*, (2009), Yusha'u *et al.* (2009) Reena *et al.* (2010) Isam *et al.* (2016) and Audu *et al.*, (2018). The plant extracts were screened for the presence or absence of phytoconstituents, such as saponins, alkaloids, tanins, phenolics, reducing sugars, glycosides, flavonoids, resins and anthraquinones.

Seed germination test

Ten seeds of okra and thirty seeds of sweet pepper and tomato were placed separately in sterilized (9 cm diameter, 1.3 cm deep) Petri dishes contained two layers (90 mm diameter) What man filter paper (No. 1). The filter papers were moistened with 5 ml of respective aqueous leaf extract concentrations (2.5, 5.0, 10.0 and 20.0 mg/l) of the test plant part, and control plates were treated similarly with 5 ml of distilled water and repeated three times. The Petri dishes were covered with lid and labeled with the type of extract and test crops, and then kept on the table under laboratory condition. Plates were observed daily, and 5 ml of extract or distilled water was added to moisten the seeds and filter paper when required. Readings were taken, after 10 days of the complete germination period. Germination percentage (%) was calculated using the following formula.

Germination rate = germinated seed x 100 / Total number of seeds.

Pot experiment

Soil collection and pot preparation

Top soil for approximately (1 to 10 cm depth) was collected from Bayero University, Kano (New Campus) farm. The soil was mixed with manure in the ratio of 3:1. Seven kilogram (7 kg) of soil was measured and filled into 7 liters (19 cm diameter) perforated plastic pots (7 kg/pot) and arranged at the Agronomic Research Experimental unit. A total of 135 pots were used for the experiment. The pots were watered twice a day for two days before planting.

Sowing

Okra was sown at five seed per pot, while for Tomato and Sweet pepper two weeks seedlings were sourced from local farmers at Gadan village of BUK (New Campus), and transplanted two weeks after okra sowing. The seedlings were thinned to two per pot. Aqueous leaf extract of *B. aegyptiaca* were applied into the pots two weeks after sowing okra.

Treatment application

The aqueous leaf extract of *B. aegyptiaca* were applied to 4 pots of the experimental materials (test crops) as per treatment (concentrates) and the control pots were simply irrigated with tap water. The soil in the pots was kept moist

throughout the duration of experiment, for each treatment pot, 32.4 ml of the leaf extract concentration was used to irrigate the treatment pots, and the following day the pots were misted with water. New extracts were usually prepared after every 3 days.

Crop management practices

Cultural practices such as watering/irrigation, weeding and insect control were carried out following recommended practices for each crop. The crops were sprayed at weekly interval commencing from two weeks after sowing with cypermethrin at 1 L/ha.

Data collection

At two weeks interval after planting Okra, sweet pepper and Tomato, one plant was tagged in each pot to measure the growth parameter. Branches of the tagged plants were counted and the average number of branches per plant was recorded.

Statistical analysis

Statistical analysis was performed using the Gen stat (SAS 9.1.3 portable). The data were analyzed using one way analysis of variance (ANOVA) at a significant difference at $p < 0.05$ (Cochran *et al.*, 1967). Duncan's Multiple Range Test (DMRT, 1955) was used to evaluate for significant difference between control and treatment groups as described by (Duncan, 1955). The results are presented as mean ± SE mean. Percentage growth of inhibition or stimulation was calculated using the following equation described by (Sahoo *et al.*, 2010).

$I = 100 - \left(\frac{E1}{E2} x\, 100\right)$ where, I is % of inhibition or stimulation, E1 the response of control and E2 the response of treatment.

RESULTS AND DISCUSSION

The findings of this study revealed the presence of phytochemical compounds in different concentration of aqueous leaf extract of *B. aegyptiaca*. Altogether, eight phytoconstituents were analyzed presents in the *B. aegyptiaca* aqueous leaf extracts as presented in Table 1. The results showed the presence of common phytoconstituents like alkaloids, anthraquinones, tannins, phenolics, reducing sugar, glycosides, saponins and flavonoids in the test tree plant part. Among, the phytoconstituents identified, saponnins were found in excess quantity in *B. aegyptiaca* aqueous leaf extract. This is in line with the finding of Alhassan, *et al.* (2018) who reported that saponins were found in high concentration in *B. aegyptiaca* plant extracts. This results also agrees with Audu, *et al.* (2018) who reported similar result on *B. aegyptiaca* plant parts. El-rokiek *et al.* (2010), Khalaj *et al.* (2013), Einhiling, (2002) and Robert *et al.* (2009) reported that plant containing excess amount of such phytoconstituents tend to have inhibitory or stimulatory effects. In this study, the presence of phenolics in both the tested plant leaf extract might be related to their allelopathic activity as reported by Sahoo *et al.* (2010) which showed that phenolic compounds in the plant leaf extract inhibited the germination and growth of (sweet pepper, rice, soya beans, maize and okra).

The results showed that *B. aegyptiaca* aqueous leaf extract inhibited germination of seeds of all the three test crops, with the degree of inhibition being proportional to the concentration of the leaf extract. The lower seed germination of the test crops in the present study might be associated with the counteracting effect of phenolic, and saponnin in the leaf extract of the test tree species as observed by Ashafa *et al.* (2010) and Barakatullah *et al.* (2010) who reported that phenolic and saponnin compounds in the leaf extract of *M. indica* and *D. viscosa* reduced seed germination of the test crops. Furthermore, poor germination rate could be related with the inhibition of ion and water uptake (Rice, 1984), as well as the alteration of the activity of hormones (GA3) which regulate *de novo* amylase production or prevent the growth of the embryo during seed germination as reported by Sahoo *et al.* (2010).

Application of *B. aegyptiaca* aqueous leaf extract shows no significant effect on number of branches of the test crops at 2 WAS. But decrease in number of branches of the test crops were recorded at 4 and 6 WAS. In these findings leaf extract of lower concentration 5 mg/l exerted more inhibition than higher leaf extract concentration 10 and 20 mg/l, and was shown more on okra than tomato, perhaps due to their varied responses to the allelochemicals. This finding indicated that inhibition could occur even at lower concentration.

Although, these findings are laboratory and pot culture experiments, the aqueous extract from the matured leaves of *B. aegyptiaca* has the potency to reduce germination as well to suppress the seedling growth parameters (number of branches) of the test crops

Conclusion

The present study showed that *B. aegyptiaca* aqueous leaf extracts contained various phytochemical constituents which contribute to

their allelopathic effectiveness. Among, the phytoconstituents identified, saponnins were found in excess quantity. However, *B. aegyptiaca* was found to exhibits strong effects to suppress germination and number of branches of the test crops in the laboratory and pot culture experiments. The potency of the different concentration of *B. aegyptiaca* were >5 mg/l 10 mg/l >20 mg/l > 2.5 mg/l in most cases. Therefore, lower aqueous leaf extract concentration was more suppressive than the higher aqueous leaf extract in most cases.

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Table 1. Phytochemical Screening of *B. aegyptiaca* Aqueous Leaves and Fruits Extracts

Phytochemicals	Test	Colour	Inference
Alkaloids	Dragendroffs	Orange red	+
Anthraquinones	Hydolyzed	Rose pink	+
Flavanoids	Lead acetate	Pink tomato	+
Glycosides	Salkowkis	Brick red	+
Phenolics	Ferric Chloride	Precipitate	+
Reducing Sugar	Fehlings	Deep blue	+
Resins	Violet	Brick red	–
Saponins	Foam test	Violet	+ + +
Tanins	Ferric Chloride	Foothing deep bluish	+

high concentration (+++), low concentration (+), not detectable (-)

Table 2. Effects of different concentrations 2.5 to 20 mg/l of *B. aegyptiaca* aqueous leaf extract on germination of okra, sweet pepper and tomato

Treatments	Germination (%)		
	Okra	Sweet pepper	Tomato
B. aegyptiaca (mg/l)			
0	56.7a	77.8a	55.5a
2.5	53.3a (-5.9)	71.1a (-8.6)	55.3a (-0.4)
5.0	53.3a (-5.9)	66.6a (-14.4)	53.9a (-2.9)
10.0	50.0a (-11.8)	55.6a (-28.5)	51.1a (-7.9)
20.0	46.7a (-17.6)	47.8a (-38.6)	50.0a (-9.9)
SE±	8.30	4.60	8.91
f–prob	0.927	0.530	0.986

Means followed by the same letter(s) within the same treatment group are not significantly different at 5% level of probability using DMRT. Values in the parenthesis indicates inhibitory (-) or stimulatory (+) effects in comparison to control (0).

Table 3. Effect of different concentrations of aqueous leaf extracts of *B. aegyptiaca* on number of branches of okra, sweet pepper and tomato

Treatments	Number of branches at 4 WAS		
	Okra	Sweet pepper	Tomato
B. aegyptiaca (mg/l)			
0	0.7a	0.0a	0.7a
2.5	0.7a (0)	2.0a (0)	1.0a (+42.9)
5.0	0.0a (+100)	0.3a (0)	0.7a (0)
10.0	0.7a (0)	0.0a (0)	1.7a (+142.9)
20.0	0.3a (-57.1)	0.0a (0)	0.7a (0)
SE±	0.29	0.27	0.79
F–prob	0.452	0.30	0.868

Means followed by the same letter(s) within the same treatment group are not significantly different at 5% level of probability using DMRT. Values in parenthesis indicate inhibitory (-) or stimulatory (+) compared control

Table 4. Effect of different concentrations of *B. aegyptiaca* aqueous leaf extracts on number of branches of okra, sweet pepper and tomato.

Treatments	Number of branches at 6 WAS		
	Okra	Sweet pepper	Tomato
B. aegyptiaca (mg/l)			
0	0.7a	0.0a	1.7a
2.5	0.7a (0)	2.0a(0)	1.7a (0)
5.0	0.0a (+100)	3.0a (0)	0.7a (-58.8)
10.0	0.7a (0)	2.0a (0)	2.7a (+58.8)
20.0	0.3a (-57)	0.3a (0)	0.7a (-58.8)
SE±	0.29	0.18	0.72
F–prob	0.452	0.212	0.230

Means followed by the same letter(s) within the same treatment group are not significantly different at 5% level of probability using DMRT. Values in parenthesis indicate inhibitory (-) or stimulatory (+) compared control

PHYTOCHEMICAL SCREENING AND ANTHELMINTIC ACTIVITY OF LEAVE'S EXTRACTS OF *Withania somnifera*

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ABSTRACT

Medicinal plants have been used in the treatment of various diseases because they possess pharmacological activities. Withania Somnifera is among the most widely used medicinal plant in Ayurveda and it has been used as an important herb in the traditional Indian medicinal system. Phytochemical screening and anthelminthic activity of leaves extracts of Withania Somnifera were studied using different solvents of varying polarity. Maceration method was used for the extraction of phytochemicals and an in-vitro anthelminthic study was conducted on the extracts in a dose dependent manner by using Indian adult Earthworm (*Pheretima posthuma*) as test organism. The highest extraction was observed in methanol solvent with percentage yield of 27.5%. The phytochemical screening revealed the presence of alkaloids, flavonoids, saponins, tannins, terpenoids, quinines, glycosides, steroids, phenols, and proteins. All the leaf extracts of *Withania somnifera* showed anthelminthic activity against the test organism (Earthworms). Aqueous leaf extracts at 50 μg/ml concentration showed the highest anthelmintic activity at the shortest time of 5 ± 0.2 and 9 ± 0.1 minutes of paralysis and death respectively, relative to the positive control Albendazole at 10 μg/ml concentration where the paralysis and death occurred at 4 and 10 minutes respectively. From the findings of this study, it revealed that the leaves extracts of *Withania somnifera* contain phytochemicals that have anthelmintic activity. Further work is recommended to evaluate the in vivo anthelmintic activity of the plant and toxicity of the extracts.

Keywords: anthelmintics, leaf extracts phytochemical, *Withania somnifera*

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INTRODUCTION

Plant materials which are derived from plant parts such as stem, bark, leaves, fruits and seeds have been used in phytomedicine that produce a definite physiological action on human body, and the most important of these natural bioactive constituents of plants are alkaloids, tannins, flavonoids and phenolic compounds (Susheel Gulati *et al.*, 2017). World health organization (WHO) have recognized medicinal plants as the important part in the health care of about 80% of the world population in developing countries (Moghal *et al.*, 2016). Withania somnifera which is usually called Ashwagandha, Indian ginseng or winter cherry in Hindi is belong to the family of Solanaceae and it is commonly located in hot and dry climates countries such as Pakistan, India, and Iran (Munir *et al.*, 2022). The plant is one of the most valuable plants in the traditional Indian medicinal systems (Susheel Gulati *et al.*, 2017). Withania somnifera is considered as a good natural source of potent and chemotherapeutic agent (Dwivedi *et al.*, 2015). Its various parts such as leaf, root have been used to treat various diseases including cancer, diabetes, sexual and nervous disorders, ulcer, stress, arthritis and immunological disorders (Thanwar Mayuri *et al.*, 2018).

Helminthiasis is a parasitic infection which can easily be spread among humans and animals and it is caused by helminthes, and it is mostly occurred in developing countries due to inadequate sanitary conditions and poor management practices (Zeb and Alya, 2013). Therefore, in this study, we reported the phytochemical evaluation of leaves extracts of *Withania somnifera* using different solvents and their application as anthelmintic agents for curing Helminthiasis.

MATERIAL AND METHODS

The fresh leaves of the plant were collected from Botanical Garden, Jodhpur National University

Rajasthan India with the help of university horticulturist. It was authenticated by prof. N.L Vyas from the Botany department J.N.U. The plant materials were washed thoroughly with normal tap water followed by sterile distilled water and then dried under shaded condition at room temperature. The leaves were crushed to powder using grinding machine and sieved to obtain very fine particles and then stored at 4°C in light air container bottle prior its use.

Preparation of crude extracts

20 g of the powdered leaves of Withania somnifera was macerated in 60 ml of methanol for 3 days at room temperature and the resulting extract was filtered with filter paper (Whatman No. 1). The residue was further extracted using the same procedure. The filtrates obtained were combined and evaporated to dryness. The same procedure was carried out using water as the extracting solvent. The percentage yield of the extracts was determined using the following formula.

$$\% \text{ yield} = \frac{\text{Weight of the crude extract}}{\text{Initital weight of powdered plant}} \text{ x } 100$$

Preliminary Phytochemical analysis of the extracts

Preliminary phytochemical analysis of leaf of *Withania somnifera* was performed using standard methods with some modifications as reported previously in (Evans, 2009).

In-vitro Anthelmintic activity of the leaf extracts of Withania somnifera

The anthelmintic assay was conducted according to the method of Ajaiyeoba *et al.* (2001) with some modifications. Indian adult earthworms *Pheretima posthuma*, 10 - 12 cm in length and 0.2-0.3 cm in width were used as test organisms due to its anatomical and physiological similarity with the intestinal roundworm parasites of human beings, and they were obtained from water logged area of moist soil and washed with normal saline to remove all faecal matter. The methanol and aqueous leaf extracts of *Withania somnifera* were suspended in normal saline to prepare 5, 10, and 50 μg/ml concentrations. Albendazole (10 mg/ml) was used as standard test control and distilled water as control. The earthworms were divided into five groups, each containing three worms (N = 3) and were placed in Petri dishes containing 50 mL of desired formulation. The observations were made for paralysis and death time for each earthworm. The paralysis time was said to occur when there is no movement except when vigorously shaken. The time of death was recorded after ascertaining that worm neither moved when even dipped in warm water (50°C) (Pandu, 2013). The results of this study were expressed as mean ± SEM (Standard Error of mean), and compared with the standard group. The $p < 0.05$ was considered to be statistically significant.

RESULTS AND DISCUSSIONS

The percentage yield obtained from both methanol and aqueous extracts of the leaf of *Withania somnifera* are shown in Table 1. The highest percentage yield was observed in methanol solvent with 27.5%. The results showed that, methanol solvent present a significant extraction ability of the phytochemical present in the plant materials. Aqueous and alcoholic extracts were found to contain high yield of Secondary metabolites as compared with other solvents (Vinotha *et al.*, (2015). The preliminary phytochemical analysis of leaf extracts of *Withania somnifera* revealed the presence of Alkaloid, Flavonoid, Glycoside, Steroid, phenol, terpenoid, saponins, coumarin, quinine and protein in both methanol and aqueous extracts. The results are nearly similar with the study conducted by Mayuwuri Thanwa *et al.* (2013) which indicated the presence of alkaloids, flavonoids, phenolic compounds, proteins, carbohydrate and glycosides aqueous, ethanolic and acetone extracts of leaves of *Withania somnifera* (Thanwar Mayuri *et al.*, 2018).

Anthelmintic activity of the leaf extracts of Withania somnifera

The in vitro anthelmintic activity leaf extracts of *Withania somnifera* is presented in Table 3. All the methanol and aqueous extracts displayed anthelmintic activity in a dose-dependent manner where Aqueous leaf extract of *Withania somnifera* at the concentration of 50 μg/ml showed the highest anthelmintic activity at the shortest time of 5 ± 0.9 and 9 ± 0.1 minutes of paralysis and death respectively relative to the positive control Albendazole at 10 μg/ml in which the paralysis and death occurred at 4 and 10 minutes respectively. The findings of this study suggest that the plant possesses potent anthelmintic activity and can be used as an alternative to the synthetic drugs. The Anthelmintic activity of *Withania somnifera* may be due to the presence of phenolic and alkaloid phytochemicals (Pandu, 2013).

Conclusion

The present study assessed the phytochemicals present and in vitro anthelmintic activity of methanol and aqueous leaf extracts of *Withania somnifera*. From the results of the study, it

indicated that the leaf of the plant contains some important phytochemicals that can act as anthelmintic. However, further study for in vivo is recommended to determine the bioactive metabolites responsible for the anthelmintic activity of the plant, mechanisms of action and potential toxicity of the extracts.

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Table 1. Percentage yields of the leaf extracts

Solvents used	Weight (g)	% yield	Texture	colour
Methanol	5.5	27.5	sticky	Yellowish green
Water	4.8	24	Non-sticky	Light green

Table 2. Preliminary phytochemical analysis of leaf extracts of *Withania somnifera*

Phytochemical	Methanol extract	Aqueous Extract
Flavonoid	+	+
Alkaloids	+	+
Glycosides	+	+
Steroids	+	+
Phenols	+	+
Terpenoids	+	+
Tannins	+	+
Saponins	+	+
Resins	+	+
Coumarins	-	+
Quinines	+	+
Proteins	+	+

Present (+), absent (-)

Table 3. Anthelmintic activity of leaf extracts of *Withania somnifera*

Treatment groups	Concentration (µg/mL)	Time for paralysis (min)	Time for death (min)
Distilled water	0	0	0
Albendazole	10	4	10
Methanol extract	5	22±0.8	28±0.3
	10	15±0.5	19±0.1
	50	8±0.3	11±0.4
Aqueous extract	5	12±0.8	20±0.4
	10	8±0.6	12±0.7
	50	5±0.2	9±0.1

PHYSIO-AGRONOMIC RESPONSES AND SEED YIELD OF RHIZOBIA INOCULATED SOYBEAN (*Glycine max* (L.) Merrill) VARIETIES SOWN AT DIFFERENT DATES IN THE GUINEA SAVANNA AGRO-ECOLOGY OF NIGERIA

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ABSTRACT
Field trials were conducted to determine the growth response and yield of soybean varieties to rhizobia inoculation at two (2) different sowing dates during 2018 rainy season at the Research Field of IITA, Ahmadu Bello University, Zaria-Samaru in the Northern Guinea Savanna and IITA Research farm, Kubwa Abuja in the Southern Guinea Savanna of Nigeria. Four varieties of soybean (TGx 1904-6F, TGx 1951-3F, TGx 1955-4F and Sambaiba) were studied and the treatments were laid out in a Randomized Complete Block Design (RCBD) with three replicates. Results indicated that inoculation, sowing date and variety significantly ($P< 0.05$) influenced growth and yield components. Sambaiba, an exotic variety had the highest CGR, RGR and IPAR and it outperformed the other varieties in yield at Samaru while all other varieties performed better than Sambaiba at Kubwa. Late-June sowing date was significantly the best planting time. Significant interaction between variety and inoculation treatments was observed on CGR, number of pods per plant and seed yield per hectare where inoculated Sambaiba variety recorded the highest values while the significant interaction between variety and sowing date on LAI indicated higher values for varieties TGx1904-6F and TGx1955-4F at late June and early July respectively. had the highest LAI value.

Keywords: Soybean; CGR, Inoculation; TGx1951-3F; physio-agronomic; Sambaiba.

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INTRODUCTION
Soybean, (*Glycine max* (L.) Merrill) though classified as an oilseed, contains significant amount of all the essential amino acids, minerals and vitamins for human nutrition. With an average of 40% protein content, 30% carbohydrate and 20% oil (Adu - Dapaah *et al.*, 2004; MoFA and CSIR, 2005), the crop can serve as a sufficient plant-based protein source—protein yield on dry matter basis is about twice that of meat and most beans and nuts and four times that of milk (Dalley *et al.,* 2004)—for human consumption using less energy, water and land (Aiking, 2011). The crop is also an excellent source of vegetable oil in the international market. Globally, soybean is produced to a tone of 352.64 million metric tons (FAO, 2017) with USA, Brazil, Argentina and China as leading producers with average outputs of 119.5,114.5, 54.9 and 13.1 million metric tons respectively (FAO, 2017). Soybean growth is influenced by climate and soil characteristics. It is a short-day plant with a wide range of environmental adaptability but high moisture requirement is critical at the time of germination, flowering and pod forming stages and dry weather is necessary for ripening (Krishna and Sachdev, 2014) and the overall growth of the crop is significantly influenced by the presence of rhizobia strains which facilitate biological nitrogen (N) fixation through symbiosis to partially or fully meet the crop's N requirement (Hungria and Kaschuk, 2014) and consequently its physiological growth requirement. Though soybean is easily introduced in places where it is not native, its production in such places (especially in Africa) is challenged by the lack of these rhizobia strains i.e. *Bradyrhizobium japonicum* and *Sinorhizobium fredii* (Unkovich *et al.,* 2008). Noticeably, soybean is more adapted to the Southern and Northern Guinea Savannas of Nigeria where it was successfully introduced in 1928 after initial failed attempts at Moore plantation, Ibadan in 1908 (Iwe, 2003)—a derived ecology. However, several improved varieties that are high yielding, non-shattering, diseases resistant and well adapted to different regions have been developed but unfortunately these varieties are yet to be fully explored by farmers whose output of about 973.3 kg ha^{-1} (FAO, 2017) falls far below the

yields of 3 t ha^{-1} achieved on research stations in Nigeria (Tefera, 2011) and this could be attributed to the fact that most of the indigenous rhizobia cannot meet all the N requirements of the legume even when promiscuous soybeans are planted (Sanginga *et al.,* 1996). Co-inoculation of Bacillus strains in soybean plants with *Bradyrhizobium japonicum* could provide large increases in nodule number, nodule weight, shoot weight, root weight, total biomass, total nitrogen, and seed yield (Bai *et al.* 2003). Rhizobial inoculation proved to be a cheap way to increase soybean yields; improving nutrient uptake, plant growth and seed quality, with low financial risks. Despite the strong agronomic and economic case for the use of inoculants, the local availability and use of good quality inoculants in Nigeria is problematic at present (Ronner *et al.,* 2015).

In addition to the rhizobium strain nodulating the legume, other interacting factors for soybean growth improvement, enhanced nutrient uptake and superior seed quality, are genotypes and bio-physical environment (Giller *et al.,* 2013). Genotypes respond differently to different strains rhizobium (Nsengiyumva, 2017). Conducive bio-physical environment for optimum growth is a function of time of sowing. If sown too early, soybean may have poor emergence or limited growth because of high temperature and exposure to days shorter than critical length resulting in rapid progress to maturity and consequently stunted growth and low yields (Boquet and Clawson, 2007). Environmental conditions associated with late sowing affect crop features related to the capture of radiation and portioning of crop resources. These include less vegetative growth (Board *et al*., 1992), shorter stems (Boquet, 1990); lower reproductive nodes (Board *et al*., 1999), and shortening of the reproductive phases (Kantolic and Slafer, 2001). Delayed sowing generally shifts reproductive growth into less favorable conditions with shorter days and lower radiation and temperature (Egli and Bruening, 2000). Considering the role of *Bradyrhizobium japonicum* in enhancing water and nutrients absorptions and promoting the general growth performance of many soybean genotypes, it is hypothesized that co-innoculation with *Bradyrhizobium japonicum* may favor the development of four soybean varieties (TGx 1904-6F, TGx 1951-3F, TGx 1955-4F and Sambaiba) and therefore this study evaluates the growth response of these soybean varieties to inoculation and determines the prime sowing date to avail the soybean varieties with favorable environmental conditions for optimum growth and seed yield in the Guinea Savanna of Nigeria.

MATERIALS AND METHODS

Field trials were conducted during the 2018 Rainy Season at the Research Field of International Institute of Tropical Agriculture, University farm of Ahmadu Bello University, Zaria at Samaru in the Northern Guinea Savanna and International Institute of Tropical Agriculture Research farm, Kubwa Abuja in the Southern Guinea Savanna of Nigeria. Soil samples were randomly collected from nine (9) locations on the field within each of the experimental site at 0 – 30 cm depth using hand-held soil auger and composite soil sample was taken after bulking. The composite sample was air dried, sieved through 2 mm sieve and subjected to laboratory analysis according to Walkley-Black procedures at the Department of Agronomy, Ahmadu Bello University Zaria and analytical laboratory of International Institute of Tropical Agriculture, Ibadan.

The treatments consisted of four varieties of soybean (TGx 1904-6F, TGx 1951-3F, TGx 1955-4F and Sambaiba), two sowing dates (late June and early July) and two levels of inoculation (inoculation and without inoculation). The treatments were laid out in a randomized complete block design and replicated three times. Sites were harrowed to fine tilth and ridged. Plots were prepared in ridges with gross plot size of 5.0 x 3.0 m (15 m^2) and a 5 x 1.5m (7.5 m^2) net plot. The inter and intra row spacing was at 75 x 10 cm respectively. Ten kg of the soybean seed was measured and placed in a container. Gum Arabic was dissolved in 100 mls of warm water. The gum Arabic solution was allowed to settle down before use. The seeds were moistened with the gum Arabic solution and mixed thoroughly. 100 g of the inoculant was sprinkled on the moistened seeds and also mixed thoroughly, ensuring that all the seeds were effectively covered with the inoculant. The moistened inoculated seeds were spread on a dry clean tarpaulin and kept away from direct sunlight for 7 minutes before sowing. Six seeds were sown per hole and later thinned to four plants per stand at 14 days after sowing. Sowing was done on the 23rd of June 2018 and 30th of June 2018 for the Samaru location; and 27th of June 2018 and 4th of July 2018 for the Kubwa. The plots were treated with Pendimenthalin as pre-emergence herbicide at the rate of 1.6 kg a.i/ha and complimented with hoe weeding at

4WAS. Fertilizer at the recommended rate of 40 kg P_2O_5 and 40 kg K_2O per hectare was broadcast and incorporated into the soil.

Five (5) plants tagged within each net plot were ear-marked for the periodic (6, 9 and 12 WAS) evaluation of crop's growth, these were used to monitor the studied growth parameters on per plants basis. Crop growth rate (CGR), Relative growth rate (RGR), Leaf area index (LAI), Absolute growth rate (AGR), leaf area duration (LAD) and photosynthetic active radiation (PAR) were the physio-agronomic dynamics studied. CGR was estimated as described by Radford, (1967); thus;

$$CGR = \frac{W_2 - W_1}{T_2 - T_1} \text{ (g m}^{-2} \text{ wk}^{-1})$$

Where W_2 and W_1 are dry weight in plant at time T_2 and T_1 in weeks, respectively. The RGR is expressed in g $g^{-1}wk^{-1}$ and was estimated as suggested by Radford (1967);

$$RGR = \frac{\text{In } W_2 - \text{In } W_1}{t_2 - t_1} \text{ g g}^{-1}\text{wk}^{-1}$$

Where ln = Natural log Where W_2 and W_1 are dry weight in plant at time T_2 and T_1 in weeks, respectively. LAI of each plot was recorded according to Fehr and Caviness (1977) using AccuPAR model ceptometer (Model LP-80). The sensor was placed diagonally across the two inner rows on the soil surface below the soybean canopy so that the two ends of the sensor were in line with the soybean rows. Five measurements were also taken and the displayed average recorded. Measurements were made under cloud-free conditions between 1200 and 1400 h. AGR is the function of amount of growing material present and is influenced by the environment. It gives Absolute values of biomass between two intervals and it was computed as;

$$AGR = \frac{h_2 - h_1}{T_2 - T_1} \text{ (c m wk}^{-1}\text{)}$$ Where, h_1 and h_2 are the plant height at t_1 and t_2 times respectively.

The LAD was estimated as described by Power et al. (1967);

LAD = (L1 + L2) X (t2 – t1)

Where L1 LAI at first stage, L2 = LAI at second stage and t2-t1 = time interval in days. The PAR of plant leaves in each plot was obtained according to Fehr and Caviness (1977) using AccuPAR model ceptometer (Model LP-80). The sensor was placed diagonally across the two inner rows on the soil surface below the soybean canopy so that the two ends of the sensor were in line with the soybean rows. Five measurements were also taken and the displayed average recorded. Measurements were made under cloud-free conditions between 1200 and 1400 h. The percentage of PAR intercepted by the soybean canopy was calculated as:

IPAR = [1.0 – (PARb/PARa)] × 100

Where: IPAR = intercepted PAR, PARa = PAR, µmol m^2 s^{-1}, measured above soybean canopy, PARb = PAR measured below soybean canopy.

Number of pods per plant, number of seeds per pod, total number of nodules per plant, total number of effective nodules, 100-Seed weight (g), grain yield per hectare and harvest Index (H I). The pods from the tagged plants per net plot were harvested at maturity Harvesting was done at physiological maturity. At harvest, the number of pods per plant of five sampled plants from each net plot were counted and average recorded. Number of nodules per plant from the sampled plants were counted and the average recorded. Effective nodules of the sampled plants were separated from non-effective nodules of the sampled plants. Then the number of effective nodules were counted and recorded. This was achieved using garden fork to dig out the plant gently, washed the root together with nodules of the plant thoroughly with enough water. A razor blade was used to dissect the nodules into two halves. When dissected, reddish, brownish or pinkish color indicated effective nodule while greenish color indicated ineffective nodule.

Harvested pods were threshed and winnowed to obtain clean grain, thereafter the number of grains per pod were counted using seed counter (DC-3 model) and the average number of seeds per pod was recorded. 100-seed weight was determined by weighing five sets each of 100 seeds obtained from threshed, winnowed harvested pods from each net plot and averaged out and recorded using a Mettler balance (Toledo 16001). Weight of the seeds was recorded using Mettler balance (Toledo 16001) on the basis of seed yield per net plot. Thereafter, seed yield per hectare was extrapolated and expressed in tonnes per hectare. HI was obtained using the ratio of the weight of grains to total dry plant material.

$$\text{H I} = \frac{\text{Grain weight}}{\text{Total dry matter}}$$

The data collected were subjected to statistical analysis of variance (ANOVA) using SAS software (Version 9.2) to test treatment effects for significance. The differences between treatments means were compared using Duncan Multiple Range Test (DMRT).

RESULTS

Soil and chemical properties of the experimental sites at 0-30 cm depth are shown in Table 1. The

analysis showed that soil in Kubwa site had a sandy loam texture, acidic and moderate in available phosphorus content (15.7 mg kg^{-1}) while the soil in Samaru is loamy, moderately acidic and also moderate in available phosphorus content (19.2 mg kg^{-1}). The percentage of organic carbon was low in Kubwa whereas in Samaru was high and total nitrogen from both sites were low. The exchangeable bases Ca, Mg, and K were low except for Na which was slightly high at both locations while the cation exchange capacity was also low at both sites.

Crop growth rate (g m^{-2} wk^{-1}) and relative growth rate (g g^{-1} wk^{-1})

The influence of inoculation, sowing date and soybean varieties on crop growth rate (CGR) during 2018 Rainy Season is shown in table 2. Inoculation and sowing date had no significant effect throughout the sampling stages at both locations except at later growth of 9 – 12 WAS when early July sown plants had the significantly highest CGR. Varieties did not differ in CGR at early growth stages (6-9WAS) but at 9-12 WAS varieties TGx 1904-6f and Sambaiba had significantly highest CGR at Kubwa and Samaru respectively. Interaction between variety and inoculation on crop growth rate was significant at 6-9 WAS at Samaru and shown in Table 5. Sambaiba variety with or without inoculation gave the highest CGR value but was still statistically similar with the other three varieties.

The same trend of CGR was observed on the RGR (Table 2) of soybean varieties as influenced by inoculation and sowing date at all sampling periods and at both locations. But in addition, variety TGx1904-6f also had the significantly highest RGR while other varieties were at par at 9-12WAS at Kubwa. None of the interactions was significant.

Absolute Growth Rate (AGR) and Leaf Area Duration (LAD)

The influence of inoculation, sowing date and soybean varieties on AGR in 2018 Rainy Season is presented in Table 4. The result indicated that inoculation had no significant effect on AGR at both locations and all sampling stages. So also sowing date at Kubwa. But Early-July sown soybean plants consistently and significantly had the highest AGR at Samaru. Inconsistent varietal response was observed on AGR of soybean but at later growth stage of 9-12 WAS Sambaiba and TGx1951-3f had the significantly highest AGR at Kubwa and Samaru respectively. None of the treatments effects interactions was significant.

Table 4 also shows the leaf area duration (LAD) as influenced by inoculation, sowing date and soybean varieties in 2018 Rainy Season. Inoculation did not significantly affect LAD at all the sampling periods at locations. Also, sowing date did significantly affect LAD of soybean plants at 6 -9 WAS at Samaru and 9-12 WAS at Kubwa. However, late-June sown plants at 6 – 9 WAS and early-July at 9 – 12 WAS had the significantly highest LAD at Kubwa and Samaru respectively. TGx 1904-6f, TGx1951-3f and TGx1955-4f consistently had statistically similar LAD significantly higher than Sambaiba at all sampling stage at both locations except at 6 – 9 WAS at Samaru when all the varieties recorded statistically similar LAD.

Leaf Area Index (LAI) and Intercepted Photosynthetic Active Radiation (IPAR µmol$m^{-2}s^{-1}$)

Table 5 show LAI and IPAR as influenced by inoculation, sowing date and soybean varieties in 2018 Rainy Season. Inoculation did not significantly affect LAI and IPAR at all the sampling periods at both locations. Effect of sowing date on LAI of soybean was not significant at 6 - 9 WAS at Samaru. But at 6-9 WAS, Late-June sown plants had the significantly highest LAI at Kubwa while Early-July sown plants had the significantly highest LAI at 12 WAS at both locations. Sowing date did not significantly influence IPAR of soybean at 6 WAS and 6-to-12 WAS at Kubwa and Samaru respectively. At Kubwa, Late June sowing resulted in significantly higher interception of PAR at 9 WAS while Early July sown plants significantly intercepted the highest PAR at 12 WAS.

At 6 and 9 WAS, Sambaiba variety had the significantly lowest LAI than other varieties which had statistically similar LAI at both locations. At 12 WAS, TGx 1955-4f had the significantly lowest LAI than Sambaiba at Kubwa while no significant difference was observed on LAI at Samaru. The same varietal response was observed on IPAR at all sampling periods at both locations. At Samaru, a significant interaction was recorded between variety and sowing date at 6 WAS on LAI.

Number of Pods per Plant (NPP)

Table 7 shows number of pods per plant as influenced by inoculation, sowing date and soybean varieties in 2018 Rainy Season. At Kubwa, inoculated soybean produced significantly highest NPP. More pods per plant were recorded for late June sowing than for early

July sowing. At Kubwa, TGx 1904-6F variety produced significantly highest NPP comparable with TGx 1951-3F while Sambaiba produced the significantly lowest NPP which was statistically similar to TGx 1955-4F. However, at Samaru, Sambaiba had NPP that was significantly higher than that of TGx 1951-3F and TGx 1955-4F. TGx 1951-3F and TGx 1955-4F had statistically similar and the lowest NPP. Interactions between varieties and inoculation on number of pods per plant was significant at Samaru in Table 8. Noteworthy is that both inoculation and sowing date did not significantly influence NPP at Samaru.

Number of Seeds per Pod (NSP)

Results showed that inoculation and sowing date did not show any significant difference for number of seeds per pod at both locations (Table 7). However, variation in number of seeds per pod among the four varieties was significant at both locations. At both locations, Sambaiba produced statistically more grains per pod than the other varieties while TGx 1904-6F and TGx 1951-3F produced the lowest number of grains per pod. None of the interaction is significant.

Number of Nodules per Plant (NNP)

Table 7 shows number of nodules per plant as influenced by inoculation, sowing date and soybean varieties in 2018 Rainy Season. It was observed that inoculation did not significantly affect number of nodules per plant at both locations. Sowing date had significant effect at Samaru only where late June sowing recorded significantly higher number of nodules per plant compared to early July sowing. The varieties did not differ significantly on number of nodules per plant at both trial locations. None of the treatment interactions on number of nodules per plant was significant at both locations.

Effective Nodules per Plant (%) (ENP)

Table 7 shows effective nodules per plant (%) as influenced by inoculation, sowing date and soybean varieties in 2018 Rainy Season. The result shows that only inoculation significantly influenced effective nodules per plant at both locations. The inoculated soybean gave significantly higher percentage of effective nodules per plant than non-inoculated soybean at both locations. None of the interaction was significant on percentage of effective nodules per plant.

100-Seed Weight (g) (100SW)

Inoculation and variety significantly influenced 100-seed weight at Samaru only (Table 7). The result shows that inoculated soybean gave the highest 100-seed weight than the seed weight of non-inoculated soybean. The significant differences among the four varieties on the 100-seed weight showed that TGx 1955-4F produced heavier 100-seed that was statistically similar with TGx 1951-3F while Sambaiba had the lowest 100-seed weight that was similar to that of TGx 1904-6F. The interactions among the treatments also did not show any significant difference on 100-seed weight at both trial locations.

Grain Yield (Kg ha-1) (GY)

The effect of inoculation and sowing date on soybean grain yield at Kubwa and Samaru is presented in Table 7. At both locations, inoculated soybean resulted in grain yield that was significantly higher than that of non-inoculated plants. Sowing date was significant at Samaru only where sowing in late June gave higher grain yield compared to early July. At Kubwa, the three adapted varieties (TGx 1951-3F, TGx 1955-4F and TGx 1906-6F) produced statistically similar and higher grain yield than the exotic variety (Sambaiba). However, at Samaru, highest yield was obtained from Sambaiba followed by TGx 1951-3F and the lowest yield was obtained from TGx 1904-6F and TGx 1955-4F. There was significant interaction between variety and inoculation on grain yield at Samaru (Table 9). The result shows that with or without inoculation Sambaiba variety gave the highest grain yield. However, TGx 1955-4F when not inoculated produced the lowest grain yield that was comparable with TGx 1904-6F.

Harvest Index (HI)

Table 7 shows Harvest index as influenced by inoculation, sowing date and soybean varieties in 2018 Rainy Season. The result indicated that Inoculation and sowing date did not have significant effect on HI at both locations. However, there was a significant difference among varieties on HI at both locations. At Kubwa, TGx 1951-3F variety had the highest HI than the other varieties, followed by TGx 1904-6F and TGx 1955-4F which were statistically similar while Sambaiba had the lowest HI. At Samaru, the variety Sambaiba turns out to have higher HI. Difference among other varieties on HI was not significant. None of the interaction among the treatments on HI was significant.

DISCUSSIONS

The sufficient amount of rainfall (500-850 mm) received during the trial and the relatively stable air temperature ranges of 21.1^{0}C - 32. ^{0}C at Kubwa and 18.8^{0}C – 32.3^{0}C at Samaru during the

growth stages of the crop might have contributed to the better establishment of the crop. Also, the relatively higher available soil phosphorus content (15.7 mg kg^{-1} and 19.2 mg kg^{-1}) at both locations might have stimulated seed germination, development of roots, stalks and stems strength (Malhotra *et al.,* 2018) and influenced the performance of the soybean. Soil factor accompanied with weather differences such as more sunshine hours, temperature and moisture could be responsible for the general better performance of the soybean varieties in growth and yields as similarly observed by Krishna and Sachdev (2014) and thus their adaptability to the savanna.

The significant increase observed on CGR and AGR with inoculation at vegetative stages of 6 – 9 WAS respectively, could be due to prevalence of conducive environment for rhizobia-host plant symbiosis.in fixing N which enhanced nutrient uptake warranting the accumulation of assimilates for robust vegetative growth. A trend similar to Solomon *et al.* (2012) on significant influence of inoculation on dry matter production at mid-flowering. The statistical parity observed growth (RGR, CGR, AGR), photosynthetic (LAI, IPAR and LAD) and yield (NSP, ENP and HI) components despite the application of inoculant suggests the possibility of the presence of indigenous competitive rhizobia in the soils and this is supported by the findings of Sanginga and Okogun (2003). Application of inoculant significantly improved NPP, ENP, 100SW and Seed yield and this could be due to complementary effect of inoculant in improving symbiotic N fixation, directly inducing plant growth through IAA production, ammonia production and P solubilization—which plays an important role in an array of cellular processes, including maintenance of membrane structure, synthesis of bimolecules and formation of high energy molecules, sugar metabolism, energy storage and transfer, stimulation of flower and seed formation (Malhotra *et al.,* 2018)—and indirectly by inhibiting the pathogenic fungi. In conformity, Abdel-Fattah *et al.* (2011) reported that inoculating soybean and mug bean with *Bradhyrizobium* significantly increased pod and seed number. The increase in ENP with application of inoculant is contrary to the findings of Ramos *et al*, (2003) while the increased seed yield with inoculation agrees with the work of Choudhry (2012).

Crop growth rate, relative growth rate, absolute growth rate, intercepted photosynthetic active radiation, number of pods per plant, number of nodules per plant and seed yield were found better across sampling periods and locations in Late-June sowing date. It could be that Early-July sowing does not favor good crop establishment and it has been attributed to climatic variables by Kassam *et al.* (1975) shifting reproductive growth into less favorable conditions with shorter days and lower radiation and temperature. These include less vegetative growth (Board *et al.*, 1992), shorter stems (Boquet, 1990) and lower reproductive nodes (Board *et al.*, 1999). More so, Egli and Bruening (2000) found that reduced radiation and temperature accounted for most of the reduction in yield associated with late sowing.

The response of variety was significant for CGR, RGR and AGR with advancement of growth from 6 to 9WAS and for IPAR, LAI and LAD at later growth stage of 12WAS. This variation could be attributed to the inherent genetic makeup of these varieties that phenotypically translate into formation of large canopy which enhanced their ability to intercept solar radiation for higher assimilate production. Similarly, Joshi *et al.* (2013) leaned the significant differences that existed in growth characters among soybean cultivars to genomic compositions which were highlighted in their phenotypic variations. Yield characters, number of pods per plant, number of seeds per pod, 100-seed weight, harvest index and seed yield responded significantly. These phenomena could be as a result of variation in genotype x environment (moisture, abundant sunshine, temperature) interaction and contribution of the prevailing soil factors that ultimately affected the yield characters. Koti *et al.* (2005) confirmed this fact that soybean genotypes had differences in sensitivity and response to various environmental factors.

The interaction between variety and sowing date on leaf area index at 6WAS. This could be due to the timeliness of sowing and early canopy spread which enhanced the crop ability to utilize the edaphic and climatic growth factors especially at the vegetative stage. This is in line with the findings of Singh *et al.* (2000) who stated that early sown soybean crop (June) exhibited extended vegetative and reproductive phases that exerted favorable effect on LAI compared to late sown crop (July). The interaction between variety and inoculation of soybean resulted to an increase in some growth and yield attributes. The highest number of pods per plant (54.73) and

grain yield (2385.63 kg ha^{-1}) were obtained from the interaction of variety Sambaiba with inoculant application. This could be as a result of positive response the variety had to inoculant compared to the local indigenous varieties (TGx 1904-6F, TGx 1951-3F and TGx 1955-4F) which maybe promiscuous.

Conclusion

Late June sowing and application of inoculants resulted in better growth and seed yield of soybean in the guinea agro-ecology of Nigeria. Sambaiba, which is an exotic variety, has the best performance at Samaru and hence is recommended for adoption for soybean grain production in the area while indigenous varieties; TGx 1951-3F, TGx 1955-4F and TGx outperformed the ecotic variety (Sambaiba) in seed yield per hectare at Kubwa implying that they adapt well to Southern Guinea Savanna.

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Table 1. Physical and chemical properties of soil of the experimental sites at 0 – 30 cm depth for 2018 rainy season

Location/Soil depth (cm)	KUBWA 0 - 30	SAMARU 0 - 30
Soil characteristics		
Textural class	Sandy loam	loam
Chemical composition		
pH in H_2O (1:2.5)	4.9	5.6
Organic carbon (g kg^{-1})	2.2	13.6
Available phosphorus (mg kg^{-1})	15.7	19.2
Total nitrogen (g kg^{-1})	0.15	0.95
Exchangeable bases (c mol kg^{-1})		
Calcium	0.44	2.13
Magnesium	0.06	0.31
Potassium	0.01	0.13
Sodium	0.10	0.21
Exchangeable acidity	0.45	0.29
ECEC	1.07	3.07

Soil analyzed in the Analytical laboratory of agronomy, International Institute of Tropical Agriculture (IITA) Ibadan for Kubwa location and Analytical Laboratory of Agronomy Department, Ahmadu Bello University, Samaru Zaria for Samaru location (2019)

Table 2. Crop growth rate (gm^{-2} wk^{-1}) and relative growth rate of soybean varieties as influence by inoculation and sowing date in 2018 rainy season at Kubwa and Samaru

Treatment	CGR				RGR			
	KUBWA		SAMARU		KUBWA		SAMARU	
	6 - 9 WAS	9 - 12 WAS	6-9 WAS	9-12 WAS	6-9 WAS	9-12 WAS	6-9 WAS	9-12 WAS
Inoculation (I)								
Inoculated	1.35	8.07	2.20a	8.43	0.21	0.41	0.17	0.33
Non-inoculated	1.40	6.43	1.84b	8.29	0.22	0.37	0.19	0.30
SE±	0.168	0.782	0.099	0.937	0.024	0.037	0.010	0.020
Sowing date (S)								
Late June	1.35	7.39	1.96	4.92b	0.21	0.39	0.18	0.22b
Early July	1.40	7.11	2.08	11.80a	0.22	0.39	0.18	0.41a
SE±	0.168	0.782	0.099	0.937	0.024	0.037	0.010	0.020
Variety (V)								
Sambaiba	1.20	5.09b	2.21	11.58a	0.20	0.28b	0.21a	0.39a
TGx 1904-6F	1.25	9.55a	1.93	6.41b	0.20	0.50a	0.19ab	0.30b
TGx 1951-3F	1.54	7.95ab	1.97	8.43ab	0.23	0.43ab	0.16b	0.29b
TGx 1955-4F	1.51	6.41ab	1.98	7.03b	0.23	0.35ab	0.17b	0.27b
SE±	0.238	1.106	0.140	1.325	0.033	0.052	0.014	0.028
Interaction								
S x I	NS	NS	NS	NS	NS	NS	NS	NS
V x I	NS	NS	*	NS	NS	NS	NS	NS
V x S	NS	NS	NS	NS	NS	NS	NS	NS
V x S x I	NS	NS	NS	NS	NS	NS	NS	NS

Means followed by the same letter (s) within a treatment group in a column are statistically similar at 5% level of probability using DMRT. WAS= Week after sowing, NS= Not significant, SE± = Standard Error and *= Significant.

Table 3. Interactions between variety and inoculation on crop growth rate (gm^{-2} wk^{-1}) at 6 - 9 WAS in Samaru

Variety	Inoculation	
	With	without
Sambaiba	2.18ab	2.23ab
TGx 1904-6F	1.67b	2.20ab
TGx 1951-3F	1.50b	2.43a
TGx 1955-4F	2.02ab	1.93ab
SE±	0.199	

Means followed by the same letter (s) within a treatment group in a column or row are statistically similar at 5% level of probability using DMRT. WAS= Week after sowing

Table 6. Interactions between variety and sowing date on Leaf Area Index (LAI) at 6 WAS at Samaru

Variety	Sowing Date	
	Late June	Early July
Sambaiba	1.98d	2.88c
TGx 1904-6F	6.18a	5.60ab
TGx 1951-3F	5.75a	4.85b
TGx 1955-4F	6.08a	5.80a
SE±	0.271	

Means followed by the same letter (s) within a treatment group in a column or row are statistically similar at 5% level of probability using DMRT. WAS= Week after sowing

Table 8. Interactions between Variety and Inoculation on Number of Pods per Plant at Samaru

Variety	Inoculation	
	With	without
Sambaiba	54.73a	44.27ab
TGx 1904-6F	49.02ab	36.97b
TGx 1951-3F	40.15b	38.08b
TGx 1955-4F	31.58bc	29.93bc
SE±	4.138	

Means followed by the same letter (s) within a treatment group in a column are statistically similar at 5% level of probability using DMRT

Table 9: Interactions between Variety and Inoculation on Grain Yield (Kg ha^{-1}) at Samaru

Variety	Inoculation	
	With	without
Sambaiba	2385.63a	2095.05b
TGx 1904-6F	1800.18cd	1775.28d
TGx 1951-3F	2089.05b	1979.43bc
TGx 1955-4F	1979.85bc	1626.93d
SE±	67.165	

Means followed by the same letter (s) within a treatment group in a column or row are statistically similar at 5% level of probability using DMRT

Table 4. Absolute growth rate (cm wk^{-1}) and leaf area duration of soybean varieties as influence by inoculation and sowing date in 2018 rainy season at Kubwa and Samaru

Treatment	AGR				LAD			
	KUBWA		SAMARU		KUBWA		SAMARU	
	6-9 WAS	9-12 WAS	6-9 WAS	9-12 WAS	6-9 WAS	9-12 WAS	6-9 WAS	9-12 WAS
Inoculation (I)								
Inoculated	5.40	4.80	4.68	3.20	109.62	116.55	218.61	229.32
Non-inoculated	4.94	4.42	4.37	3.06	105.84	115.08	206.43	210.63
SE±	0.168	0.782	0.667	0.0567	7.014	5.334	6.762	7.455
Sowing date (S)								
Late June	4.16b	3.69	3.31b	2.78b	121.38a	115.71	216.93	208.74b
Early July	6.18a	7.53	5.75a	3.49a	94.08b	115.92	207.9	231.42a
SE±	0.168	0.782	0.0537	0.00567	7.014	5.334	6.762	7.455
Variety (V)								
Sambaiba	4.36b	5.98a	5.22a	3.22b	52.71b	87.15b	149.73b	216.72
TGx 1904-6F	4.49b	4.17c	3.83d	3.19b	117.81a	128.52a	233.1a	221.97
TGx 1951-3F	4.8b	4.03c	4.13c	3.63a	132.09a	126.21a	230.16a	225.96
TGx 1955-4F	7.02a	4.28b	4.93b	2.50c	128.52a	121.8a	236.67a	215.46
SE±	0.238	0.106	0.0760	0.0767	9.933	7.518	9.576	10.542
Interaction								
S x I	NS	NS	NS	NS	NS	NS	NS	NS
V x I	NS	NS	NS	NS	NS	NS	NS	NS
V x S	NS	NS	NS	NS	NS	NS	NS	NS
V x S x I	NS	NS	NS	NS	NS	NS	NS	NS

Means followed by the same letter (s) within a treatment group in a column are statistically similar at 5% level of probability using DMRT. WAS= Week after sowing, NS= Not significant, SE± = Standard Error and *= Significant.

Table 5. Leaf area index and Intercepted photosynthetic active radiation of Soybean Varieties as influence by Inoculation and Sowing Date in 2018 Rainy Season at Kubwa and Samaru

Treatment	LAI						IPAR					
	KUBWA			SAMARU			KUBWA			SAMARU		
	6WAS	9 WAS	12WAS	6WAS	9WAS	12WAS	6WAS	9WAS	12WAS	6WAS	9WAS	12WAS
Inoculation (I)												
Inoculated	2.07	3.15	2.40	4.98	5.43	5.49	56.91	81.85	85.06	87.38	94.78	92.86
Non-inoculated	1.88	3.16	2.32	4.81	5.02	5.01	51.88	81.35	82.31	86.33	94.96	91.30
SE±	0.174	0.160	0.094	0.135	0.187	0.168	3.464	2.051	1.282	1.468	1.061	0.924
Sowing date (S)												
Late June	2.32a	3.46a	2.05b	5.00	5.33	4.61b	58.99	88.98a	80.10b	85.53	94.47	92.93
Early July	1.63b	2.85b	2.67a	4.78	5.12	5.90a	49.80	74.23b	87.28a	88.18	95.27	91.22
SE±	0.174	0.160	0.094	0.135	0.187	0.168	3.464	2.051	1.282	1.468	1.061	0.924
Variety (V)												
Sambaiba	0.93b	1.58b	2.57a	2.43c	4.70b	5.62	35.87b	58.58b	89.85a	67.33c	92.03b	92.45
TGx 1904-6F	2.02a	3.59a	2.53ab	5.89a	5.21ab	5.36	57.72a	86.75a	84.90ab	96.19a	94.52ab	92.53
TGx 1951-3F	2.47a	3.82a	2.19ab	5.30b	5.66a	5.10	61.08a	90.81a	80.72bc	87.38b	97.06a	92.40
TGx 1955-4F	2.48a	3.64a	2.16b	5.94a	5.33ab	4.93	62.92a	90.28a	79.28c	96.51a	95.88ab	90.93
SE±	0.247	0.226	0.132	0.192	0.264	0.238	4.899	2.900	1.813	2.076	1.500	1.306
Interaction												
S x I	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
V x I	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
V x S	NS	NS	NS	*	NS	NS	NS	NS	NS	NS	NS	NS
V x S x I	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS

Means followed by the same letter (s) within a treatment group in a column are statistically similar at 5% level of probability using DMRT. WAS= Week after sowing, NS= Not significant, SE± = Standard Error and *= Significant.

Table 7. Yield and yield components of soybean varieties as influenced by inoculation and sowing date during 2018 rainy season at Samaru and Kubwa

Treatment	NPP		NSP		NNP		ENP		100SW		GY		HI	
	Kubwa	Samaru	Kubwa	Samaru	Kubwa	Samaru	Kubwa	Samaru	Kubwa	Samaru	Kubwa	Samaru	Kubwa	Samaru
Inoculation (I)														
Inoculated	33.83a	40.34	2.09	1.36	29	50.49	69.59a	72.51a	14.06	16.55a	2145.51a	2063.68a	0.37	0.28
Non-inoculated	24.88b	40.84	2.16	1.24	28.07	36.22	64.43b	58.16b	13.86	15.59b	1789.93b	1869.18b	0.36	0.27
SE±	1.099	2.069	0.061	0.05	3.265	4.956	1.613	1.715	0.231	0.31	42.502	33.583	0.007	0.01
Sowing date (S)														
Late June	31.06a	42.82	2.17	1.28	28.48	52.93a	67.3	63.83	14.28	15.96	2022.78	2035.74a	0.37	0.27
Early July	27.65b	38.36	2.08	1.32	28.59	33.78b	66.72	66.84	13.65	16.18	1912.65	1897.11b	0.36	0.28
SE±	1.099	2.069	0.061	0.05	3.265	4.956	1.613	1.715	0.231	0.31	42.502	33.583	0.007	0.01
Variety (V)														
Sambaiba	24.04c	49.50a	3.03a	1.59a	22.73	44.13	68.53	64.25	13.75	15.79bc	1607.90b	2240.34a	0.31c	0.32a
TGx 1904-6F	34.36a	42.99ab	1.55c	1.10c	30.27	40.21	64.96	66.96	14.53	14.72c	2005.71a	1787.73c	0.37b	0.24b
TGx 1951-3F	30.98ab	39.12bc	1.68c	1.15c	29.79	47.81	65.5	65.09	13.98	16.51ab	2172.18a	2034.24b	0.43a	0.27b
TGx 1955-4F	28.04bc	30.76c	2.25b	1.36b	31.35	41.27	69.05	65.04	13.6	17.27a	2085.08a	1803.39c	0.35b	0.27b
SE±	1.554	2.926	0.086	0.071	4.617	7.009	2.281	2.426	0.327	0.438	60.107	47.493	0.01	0.014
Interaction														
S x I	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
V x I	NS	*	NS	NS	NS	NS	NS	NS	NS	NS	NS	*	NS	NS
V x S	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
V x S x I	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS

ROOT AND GRAIN YIELD TRAITS OF RICE ON TOPOSEQUENCE SOILS OF A DERIVED SAVANNAH ECOLOGY

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ABSTRACT

Twelve upland rice varieties comprising interspecific NERICA and OFADA varieties were raised in potted toposequence soils obtained from the crest, middle slope and valley bottom in an open field experiment. Pots were supplemented with manual watering. The genotypes were assessed for root and grain yield traits. Analysis of data on vegetative and yield components generated variances and heritability estimates of plant traits and the influence of toposequence soils. Varietal effect was significant for grain weight per plant ($p < 0.01$), panicle length and primary branching (($p < 0.05$). Across the toposequence soils, root length, root weight and grain weight per plant had significant ($p < 0.01$) mean squares (MS) while root branching was significant at $p > 0.05$. The interaction between variety and toposequence soils was significant for root weight and grain weight per panicle. Grain weight per plant and root branching recorded the highest value for GCV (47.69, 28.30), PCV (51.52, 34.41) and broad sense heritability (44.59, 35.22) respectively. Out of the three toposequence soils, the highest means were recorded by the valley bottom for root branching score, root weight, grain weight per panicle, panicle number and primary branching while grain weight per plant and root length were highest in the middle slope. Correlations among root and grain yield traits give promise of advantageous joint selection.

Keywords: correlations, heritability, toposequence, upland rice, variation

INTRODUCTION

Rice is a cereal crop that belongs to the family *Poaceae* which was (formerly *Gramineae*) and genus Oryza. Rice grains are the most important crop that is widely consumed by humans' population, including Asia and parts of Africa. It ranks second after maize in the worldwide cereal production with a global figure of 480.3 mt. Rice is an increasingly important crop in Nigeria. Indeed, rice paddy production of Nigeria increased from 3.7 million tonnes in 2017 to 4 million tonnes in 2018 but yield still remain poor at 2.0 – 3.0 t/ha Kamai, *et al*, 2020.

The cultivation of rice, especially along the toposequence of the upland paddy is often confronted with variable moisture limitations due to cessation of or significantly inadequate rainfall. The concomitant co-occurrence of drought at any stage of growth affects the plant but moisture stress between maximum tillering and panicle filling is usually unstable. Boling *et al* (2008) had reported substantial variability in soil nutrient and moisture conditions and its complex effect on yield.

In recent times, many NERICA varieties that were selected from *Oryza sativa* and *Oryza glabberima* crosses were released for cultivation. These varieties are expected to combine the genetic versatility of grain production in *Oryza sativa* with drought tolerance features of *Oryza glabberima*. Nonetheless, the yield of rice in Nigeria is fairly below the global average. There is, thereby, need to assess the NERICA varieties along the upland soil toposequence to provide guide on further selection steps toward having genotypes that combines root traits with grain yield traits under toposequence soil conditions which represent the cultivation continuum. Hence, this study is aimed at assessing the performance of rice varieties through some root and grain yield traits to guide research direction for further genetic development of available varieties.

MATERIALS AND METHOD

Twelve rice varieties, *viz*., NERICA 1-8, NERICA 12, NERICA 15, NERICA 18 and OFADA were established in the nursery and transplanted at three weeks into polythene pots with 28 cm in diameter and 28 cm in depth. The pots were filled with 5 kg of soil obtained from the upper crest, mid-slope and valley bottom of a toposequence. The experiment was carried out in Ayetoro (derived savannah ecology) and the pots were arranged following the Completely Randomized Design (CRD) and replicated three times. Standard agronomic practices were carried out in the nursery and after transplanting.

Data collection and analyses

Data were collected on root and grain yield traits after harvesting. Means of each treatment for each replicate were computed and subjected to the analysis of variance and correlation analysis using the GENSTAT software (Version 12). PCV and GCV were determined as a percent ratio of the phenotypic variance and genotypic variance respectively to the mean of each trait. Heritability estimates were obtained as a ratio of genotypic variance to total variance.

RESULTS AND DISCUSSION

There were significant differences among the rice varieties for grain weight per plant at ($p < 0.01$) and panicle length and primary branching ($p < 0.05$) (Table 1). The significant mean squares indicate presence of variation that can be exploited for further advancement through hybridization among the rice varieties and selection for enhanced grain yield.

Across toposequence soils, root length, root weight, grain weight per plant, panicle number, primary branching and secondary branching showed significant differences at ($p<0.01$), while root branching was significant at ($p<0.05$). The significant toposequence soils x variety interaction for root weight and grain weight per panicle implies that there may not be consistency in the grain production by the varieties possibly through differing ability to gather nutrients and water resulting in variable yield in different soils (Nassir and Adewusi, 2015). The PCV and GCV were generally low indicating limited variability and that the improvement of the yield traits within these genotypes may have reached the highest level, suggesting the involvement of other rice populations in subsequent breeding efforts for higher grain yield and better root performance across toposequence soils (Nassir *et al.*, 2017). The equally low heritability further compounds subsequent selection based on the NERICA population alone.

The valley bottom recorded significantly higher mean for root branching score (1.94), root weight (7.69g), panicle number (11.19) and primary branching (13.61) (Table 2). These however did not translate to highest grain weight per panicle. With adequate moisture, root development may slow down, thereby channeling more product of photosynthesis into grain production. In contrast, the middle slope recorded the highest root length (36.44) and grain weight per plant (23.28). Olagunju et al (2018) had earlier reported higher grain weight per plant for valley bottom soils. The longest panicles and secondary branching of panicles were obtained in the upper crest. The diffused nature of expression of traits in the different soils is a pointer to environmental influence on trait expression in rice and requires that the traits be studied separately rather than just using grain yield as the only consideration for performance.

The results also give insight on the trait to be focused on for ecology specific improvement for grain yield. The lower grain weigh per plant relative to other locations gives indication that the upland and middle slope would give good yield where moisture is not limiting. Significant correlations were obtained between some root and grain yield traits. Panicle length had significant positive correlation with root length (0.341) and root weight (0.351). Root branching was additionally correlated to root length, root weight and primary branching. Grain weight per panicle had positive correlation with all grain traits except panicle number. The significant positive correlation of most of the root and yield related traits to panicle characters indicate some usefulness of the traits for further concurrent selection for grain yield increases.

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Table 1. Mean squares of root and grain yield traits, PCV, GCV and H^2 of rice varieties on a toposequence

Source of variation	df	RL	RB	RW	GWP	GWPL	PL	PN	PB	SB
Variety (V)	11	42.72	1.24	4.63	1.81	151.87**	19.51*	10.82	9.78*	0.49
Toposequence soils (TS)	2	485.86**	1.51*	97.60**	0.82	1054.93**	4.11	362.79**	42.75**	6.58**
V x TS	22	43.93	0.61	8.70*	2.28**	68.64	10.37	9.95	5.75	0.76
Error	72	49.51	0.47	4.41	1.00	43.77	7.74	11.75	4.94	0.69
Mean		34.04	1.79	6.17	3.14	17.39	25.14	8.59	12.36	2.28
PCV		20.07	47.69	34.68	31.90	48.60	13.10	40.40	20.30	36.50
GCV		0.00	28.30	2.84	0.00	30.30	6.90	6.30	9.40	0.00
H2		0.00	35.22	0.51	0.00	28.00	22.00	2.30	17.60	0.00

** Significant at $p < 0.01$, * Significant at $p < 0.05$, RL- Root length, RB- Root branching, RW-Root weight, GWP- Grain weight per panicle, GWPL- Grain weight per plant, PL- Panicle length, PN- Panicle number, PB-Primary branching, SB- Secondary branching

Table 2. Mean performance for nine traits of rice on the toposequence soils

Characters	Upper crest	Middle slope	Valley bottom
Root length (cm)	29.81b	36.44ab	35.88ab
Root branching (s)	1.86ab	1.56c	1.94a
Root weight (g)	4.42c	6.39b	7.69a
Grain weight per panicle (g)	3.07a	2.91a	3.22a
Grain weight per plant (g)	15.97b	23.28a	12.71c
Panicle number (No)	5.06c	9.53b	11.19a
Panicle length (cm)	25.53a	24.97a	24.92a
Primary branching (No)	11.61b	11.86b	13.61a
Secondary branching (s)	2.64a	2.39a	1.81b

Score (s)

Table 3. Correlation coefficient for nine traits of rice varieties across toposequence

Trait	RL	RB	RW	GWP	GWPL	PL	PB	SB
RB	0.34**							
RW	0.24*	0.43**						
GWP	-0.01	-0.03	-0.09					
GWPL	0.13	-0.01	0.00	0.27**				
PL	-0.07	-0.04	0.03	0.32**	0.13			
PB	0.18	0.29**	0.11	0.35**	0.01	0.12		
SB	-0.05	-0.10	-0.14	0.26**	0.35**	0.32**	-0.06	
PN	0.25**	0.03	0.35**	0.02	0.47**	0.03	0.05	0.12

*, **: significant at $p < 0.05$ and $p < 0.01$, respectively, RL- Root length, RB- Root branching, RW-Root weight, GWP- Grain weight per panicle, GWPL- Grain weight per plant, PL- Panicle length, PN- Panicle number, PB-Primary branching, SB- Secondary branching.

CONTRIBUTION OF NITROGEN FIXATION BY INDIGENOUS RHIZOBIAL ISOLATES TO A SUCCEEDING MAIZE CROP IN THE RAINFOREST OF NIGERIA

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ABSTRACT

Nitrogen (N) accrued in soil and residual beneficial effect of indigenous rhizobial isolates IDC8, TRC2 and OIa6 (c3a) and check rhizobial-strains R25B+IRj2180A inoculated to soybean-varieties: TGx1448-2E, TGx1908-1F and TGx1910-2F; cowpea-varieties IT89KD-288 and IT97K-568-18 and the control were evaluated in three locations namely: Idi-Ayunre, Orile-Ilugun and University of Ibadan Research Farm (UITRF) in rainforest-savanna transition zone of Nigeria. Following the harvesting of inoculated legumes, maize variety-TZEComp4C2 was planted in all the fields to assess the N accrued. Plantings were carried out in a Randomized Complete Block Design with three replicates. Data were collected on fresh and dry weights of cobs, grain yield/ha, %N in grain. Results revealed that in UITRF, all inoculated plots of cowpea variety IT89KD-28–maize sequence had significantly ($p<0.05$) higher yield compared to their corresponding treatments under maize-maize sequence plots and approximately 36.6% increase in legume-maize sequence compared to maize-maize sequence. Biological Nitrogen Fixation should be a core component of a sustainable agro-ecosystems

Keywords: legume, maize, nitrogen, rhizobia,

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INTRODUCTION

Nitrogen is needed for crop production especially for cereals such as maize wheat, sorghum etc. to ensure food security for the ever-growing world population (Lahda *et al.*, 2005). However, there are many important processes through which nitrogen is made available to plants in the soil; among these various processes is Biological Nitrogen Fixation (BNF) (Dommergues and Dien, 1986), one of the ways by which BNF takes place in this soil is by cultivation of legumes. Legumes are grown for different purposes, but the ultimate benefit lies in their ability to fix atmospheric N_2 in order to reduce the cost of manufactured N-fertilizer (Hardarson and Atkins, 2003). Therefore, BNF of an effectively nodulated legume is a vital and indispensable aspect of sustainable agriculture (Graham and Vance, 2000; Sessitch *et al.*, 2001). And considering the high cost of synthetic N fertilizer through Haber-Bosch process, its indiscriminate use without soil testing and its escalating environmental damage, there is the need to look for another means by which nitrogen can be made available to plants in the soil; this study was carried out to assess how efficient and effective indigenous rhizobial strain inoculated to legumes are in contributing to soil N to support maize production in the rain forest of Nigeria

MATERIAL AND METHODS

The trials were conducted in three different locations namely: Idi-Ayunre (latitude 7°26´N and longitude 3°54´E), Orile-Ilugun (latitude 7°13´N and longitude 3°31´E), and the University of Ibadan Teaching and Research Farm (UITRF) (latitude 7°30´N and longitude 3°45´) within the rainforest-savanna transition zone of Nigeria. Routine soil analysis was carried out, Somasegaran and Hoben (1994) method was used to estimate the rhizobial population of the soils of the three locations

First field trial

The first field trial was carried out to compare the check rhizobial strains and indigenous rhizobial isolates for nitrogen fixing efficiency and to measure N accrued in the soil by the inoculated legumes. A total land area of 2,184 m² marked out for this trial in each location was cleared, marked and pegged into plots measuring 4 m x 4 m (16 m²). The experiment was a factorial combination of five 5 levels of rhizobial strains (the control -- no inoculation, indigenous Isolate 1– OIa6(c3a), Isolate 2 – IDC8, Isolate 3 – TRC2, Exotic strain – R25B + IRj2180A), five legumes- three soybean varieties (TGx 1448-2E, TGx 1908 – IF and TGx 1910-2F), two cowpea varieties (IT89KD – 288 and IT97K– 568 – 18) as well as one maize variety (TZE COMP4C2) laid in completely randomized design.

Second field trial

Following the harvesting of the planted inoculated legumes, the fields were planted to an early maturing maize variety (TZE COMP4C2) as a follow up crop to assess the residual effect of N-fixed by the legume on the cereal crop. The planting distance was at 75 cm x 25 cm using 2 seeds/hole sown 4 – 5 cm deep and later thinned to 1 plant/stand resulting in 53,333 plants/hectare. The sequences are as follows: IT89KD – 288-Maize (288-M), IT97K– 568 – 18- Maize (568-M), TGx 1448-2E- Maize (1448-M), TGx 1908 – IF- Maize (1908-M), TGx 1910-2F- Maize (1910-M), and a maize variety TZE COMP4C2 (M-M)

Data collection

Data were collected on number of cobs, fresh and dry weights of stovers (g) and cobs, grain yield (kg/ha), %N in grain.

Statistical analysis

Data were analyzed using analysis of variance (ANOVA) using PROC GLM of statistical analysis system (SAS 2003). Standard error of means and Least Significant Different (LSD) were used to separate the means.

RESULTS AND DISCUSSION

The stover dry weight of all treatments in cowpea variety IT97K-568-18-maize sequence plot and all treatments excluding control under soybean variety TGx1910-2F maize plots were significantly ($p < 0.05$) higher when compared to their corresponding treatment under maize-maize sequence plot. Cowpea varieties (IT89KD-288 inoculated with IDC8 produced the highest stover dry weight in IA (Table 1). The stover dry weights of maize-maize sequence plots under all the inoculation treatments in all the locations were significantly ($p < 0.05$) lower compared to their corresponding treatments of legume-maize sequence. The maize grain yield of soybean variety TGx1910-2F-maize sequence plots inoculated with exotic strain R25B+IRj2180A and soybean variety TGx1448-2E-maize sequence plots inoculated with OIa6(c3a) were significantly different at $p<0.05$ when compared across locations (Figs 1&3). Where maize was grown after legume, maize yield increase was comparatively higher than where maize was grown after maize. Similar observations have been reported by Alves *et al* (2003) and Sanginga (2003) that maize planted after soybean had a significant yield increase compared to maize planted after maize Different legume species planted appeared to be one of the major factors responsible for different N accrued in the soil which resulted to differences in maize yield obtained. It was observed that maize planted on plots previously planted to TGx1910-2F a soybean variety, in two locations, IT89KD-288 a cowpea variety, in all locations produced the highest maize grain yields. This is likely to be due to the fact that soybean variety TGx1910-2F and cowpea variety IT89KD-288 were able to establish a functional symbiosis with the inoculated strains which was responsible for their high biomass production. These legume varieties may also have genetic potential for high biomass production which might have led to high N accrual in the soil for optimal maize yield production.

Conclusion

In assessing the residual benefit of different legumes planted with and without inoculation in a crop rotation where maize was grown after legume (legume – maize sequence) and maize grown after maize (maize – maize sequence) the N benefit of the symbiotic association between the inoculated strain and the legume planted were clearly seen. Therefore, BNF of an effectively nodulated legume should be a vital and indispensable aspect of sustainable agriculture. The indigenous rhizobial isolates were less efficient compared to the exotic strains. However, identifying effective indigenous rhizobial strains can be used to improve soil N in the absence of exotic strains.

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Table 1. Maize Stover dry weights (t/ha) of the three locations

Crop sequence (Cs)	Strains (S)	UITR & F SDW	IA SDW	OI SDW
M-M	6(c3a)	8.9	10.2	11.6
	IDC8	6.2	14.4	11.7
	TRC2	8.2	11.2	10.6
	R25B+	8.2	12.3	10.9
	control	6.4	7.2	10.1
288-M	6(c3a)	15.8	19.6	15.3
	IDC8	12.1	25	15.6
	TRC2	14	23.3	20.1
	R25B+	14.6	18.7	23.8
	control	9.3	11.4	15.6
568-M	6(c3a)	10.3	13.6	18.4
	IDC8	12.4	18.2	20.6
	TRC2	11.2	15.7	18
	R25B+	10.7	20.2	19.9
	control	8.3	13	18.6
1448-M-	6(c3a)	11.9	21.1	16.6
	IDC8	13.7	20.1	18
	TRC2	10.7	14.7	17.6
	R25B+	18.7	18.7	23.2
	control	8.89	12.9	11.3
1908-M	6(c3a)	10.9	13.9	18.2
	IDC8	10.8	18.1	15.9
	TRC2	10.4	15.6	16
	R25B+	10.7	18.6	15.7
	control	8.7	11.3	20.7
1910-M	6(c3a)	11.8	23.9	22.4
	IDC8	10.3	22.6	22.7
	TRC2	12.1	17.9	21.2
	R25+	11.8	22.9	21.8
	control	8.7	14.3	14.3
SE				..
(Cs)		0.7	1.2	0.9
Strain(S)		0.6	1.1	0.8
Cs×S		1.5	2.8	2.1
ANOVA				
(Cs)		*	***	***
(S)		ns	ns	ns
Cs×S		*	*	*

Error degree of freedom = 60, SE = Standard Error; ns = not significant; ***, ** and * = $p < 0.001$, 0.01 and 0.05 respectively. SDW-Stover Dry Weight, ID- Idi-ayunre, IO- Orile-Ilugun, UITR &F- Univ. of Ibadan Teaching and Research Farm

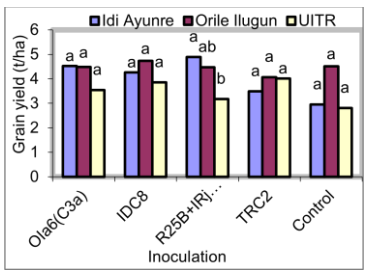

Figure 1: Maize grain yield of TGx1910-2F - maize sequence plots across locations

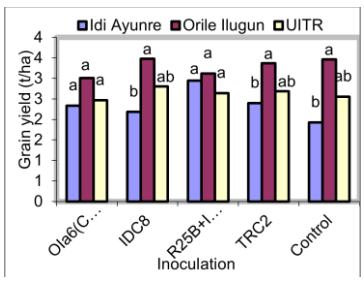

Figure 2: Maize grain yield of maize - maize sequence plots across locations

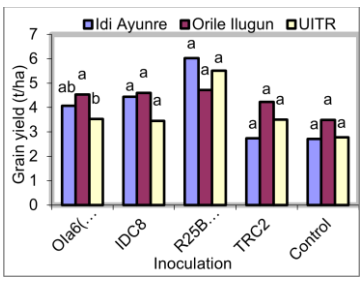

Figure 3: Maize grain yield of TGx1448-2E - maize sequence plots across locations

*Bars with the same letter are not significantly from each other

NITROGEN FIXING EFFICIENCY OF INDIGENOUS RHIZOBIAL STRAINS ON BIOLOGICAL NITROGEN FIXATION OF THREE SOYBEAN (*Glycine max* (L.) Merill) VARIETIES IN RAIN FOREST NIGERIA

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ABSTRACT

Field and pot experiments were carried out at University of Ibadan Research Farm (UITRF), Idi-Ayunre (IA) and Orile-Ilugun (OI) to study the effectiveness of indigenous rhizobial isolates: TRC2, IDC8, OISa-6e, R25B, IRj2180A on Biological Nitrogen Fixation of soybean varieties TGx1448-2E, TGx1908-1F and TGx1910-2F. The pot experiment was arranged in a 2 × 3 × 6 factorial in completely randomized design and the field experiment laid in randomized complete block design in three replicates. Data were collected on number of nodules, N-fixed and yield. Results revealed that low rhizobial count (<14 cell g-1 soil) of the study locations favored competitiveness of the inoculated strains against resident rhizobial population for nodule formation of the soybean varieties. In IA location, TGx1908-1F and TGx1910-2F had significantly ($p < 0.05$) higher numbers of nodules, N-fixed and grain yield with IDC8 and OISa-6e than with the resident strains. The study showed that soybean production can be improved with indigenous rhizobial strains inoculation

Keywords: biological nitrogen fixation, indigenous rhizobia, nodulation, soybean

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INTRODUCTION

Cultivation of soybean is not limited to its dietary benefit alone but it also helps in soil productivity and it plays a key role in agricultural systems that help to improve soil fertility through biological nitrogen fixation in the sub-Saharan Africa (Sanginga *et al*., 2000b). Rhizobia are soil free living bacteria that have the ability to infect the root of leguminous plants and form nodules which help to fix N in the soil. Many research findings have revealed that there is variation in the nitrogen fixation of soybean when associated with different *Rhizobium japonicum* strains. This variation in total nitrogen fixed (ranging from 26 – 199 kg N ha^{-1}) has been partly attributed to variation in genetic traits, yield maturity and environmental constraints. Houngnandan *et al.* (2000) also affirmed that response to inoculated treatment depends on the field and the population or number of rhizobia in the soil Chairman and Ballard (2004), however, observed that indigenous or resident rhizobial strain that has strong ability to compete for nodule occupancy than the introduced inoculant strain has the tendency to form an ineffective symbiosis. Studies on indigenous rhizobia for N fixing efficiency in soybean in the forest transition zone of Nigeria are at best scanty. Ojo *et al.* (2015) selected three indigenous rhizobial strains that are highly infective on soybean in the forest transition zone of Nigeria but information on their N fixation efficacy was lacking. To increase soybean nodulation, N fixation and production in the zone, it is imperative to search for efficient indigenous rhizobial strain. Therefore, the aim of the study was to evaluate the performance of three indigenous rhizobial isolates for N fixation in soybean in the forest transition zone of Nigeria.

MATERIALS AND METHODS

The trials were conducted in three different locations namely: Idi-Ayunre, (AI), Orile-Ilugun (IO) and the University of Ibadan Teaching and Research Farm (UITRF) within the rainforest-savanna transition zone of Nigeria

Pot experiment.

Soil sampling and preparation

Top soil (0 – 15 cm) samples from the three selected locations were separately collected, air-dried, passed through 2 mm sieve and sterilized using direct flaming method with the aid of a Terraforce sterilizing machine (IITA fabricated sterilizing machine). Two kilograms soil was weighed into each pot for the planting.

Soil analyses

Routine soil analysis was carried out, Somasegaran and Hoben (1994) method was used to estimate the rhizobial population of the soils.

Planting and Inoculation

Seeds of three soybean varieties (TGx1448– 2E, TGx1908–1F and TGx1910–2F) were separately

planted in all the pots containing sterile and non-sterile soils from each selected location. Four seeds were planted per pot and thinned to two plants per pot at five days after planting (DAP). Two (2) ml broth culture of the rhizobial strains, Isolate - OISa-6e, Isolate– IDC8, Isolate– TRC2, Exotic strain 1 – R25B, Exotic strain 2 – IRj2180A separately prepared were inoculated to the two plants in each pot one week after planting.

Experimental design

The experiment was a factorial combination of two (2) soil treatments (partially-sterile and non-sterile), three (3) soybean varieties, five rhizobial strains and the control, laid in completely randomized design. Each treatment was replicated three times.

Field Experiment

The field experiments were carried out in the three selected locations mentioned above and set up in a two-factorial arrangement with rhizobial strain and soybean variety implemented in a split block design with three replicates of 4 m × 4 m each. The rhizobial strains were IDC8, TRC2, OISa-6e, R25B+IRj2180A and the control. Strains R25B and IRj2180A were exotic strains used separately in the greenhouse experiments but combined together for the field experiment. One kilogramme of seeds of each soybean variety was inoculated with 10 grams peat culture of each rhizobial strain, procedure followed was as outlined by Somasegaran and Hoben (1994).

Data

Data collected include number of nodules, shoot dried weight, and grain yield

Statistical analysis

Data were analysed using analysis of variance (ANOVA) using PROC GLM of statistical analysis system (SAS 2003). Standard error of means and LSD were used to separate the means.

RESULTS AND DISCUSSION

The rhizobial count of the three locations in our study was generally low with the highest of 13 cells per gram soil found at UITRF. Population of indigenous rhizobia in most tropical soils are low (Ahmad, 1981) and response of crops to inoculation is likely to occur when rhizobial count is less than 10 cells per gram of soil (Okogun and Sanginga, 2003). The nodules formed in UITR&F soil was significantly ($p < 0.05$) reduced in sterile soil when compared with nodules formed in non-sterile soil (Fig. 1). Nodulation in IA soil was very low, less than 10 nodules per pot, and more nodules were significantly ($p < 0.05$) formed in sterile soil than in non-sterile soil unlike UITRF and OI soils. In IA location, soybean variety TGx1908-1F inoculated with TRC2 in sterile soil produced the highest number of nodules and in non-sterile soil, isolate OISa-6e did not form nodules in any of the varieties. No nodulation was observed in TGx1908-10F inoculated with indigenous strains IDC8 and TGx1910-2F inoculated with R25B. The interaction of TGx1908-1F and rhizobial strain R25B+IRj2180A at UITRF led to significantly higher grain yield when compared to other varieties with no inoculation (Table 1). The variety TGx1908-1F inoculated with R25B+IRj2180A is the only treatment with grain yield more than 3 t/ha in UITRF. (Table 1). While the average grain yield for the un-inoculated plants was approximately 1.5 t/ha, the average grain yield for plants inoculated with the indigenous isolates was 1.9 t/ha at UITRF. The R25B+IRj2180A inoculated plants had significantly higher grain yield and shoot dry weight than other plants at IA. The average grain yield for R25B+IRj2180A inoculated plants at IA was 3.6 t/ha compared to other inoculated plants, 2.0 t/ha, and un-inoculated plants 1.3 t/ha. The highest grain yield (> 4.0 t/ha) in this study was observed in soybean variety TGx1908-1F inoculated with R25B+IRj2180A at IA (Table 1). The grain yield of soybean ranged between 0.7 – 1.8 t/ha at OI, values that were generally lower to those of UITRF and IA. Grain yield of TGx1908-1F was significantly lower compared to the other varieties. Orile-Ilugun was the only study site with grain yield not above 2 t/ha (Table 1). In our study, soybean response to inoculation varied across locations. Compatibility of strains with legume varieties and genotypes is an important factor that can affect effectiveness of legume symbioses (Bulland *et al.*, 2005). It is important to note the effectiveness of inoculation of R25B+IRj2180A on TGx1908-1F which produced the highest grain yields in IA and UITRF. This exotic strain had outstanding adaptation across the locations with their influence on nodulation, total N fixed and uptake and grain yield. Vanlauwe *et al.* (2019) reported that most exotic strains used in inoculants have broad adaptability with outstanding performance in broad range of soil

Conclusion

The indigenous rhizobial isolates OISa-6e, IDC8 and TRC2 had potentials for use as inoculant to increase soybean production in the rainforest of Nigeria. Their ability to compete with the resident rhizobial population for nodule

occupancy and improve grain yield and N fixation of some of the soybean varieties is evident. Further studies on the performance of co-inoculation of the indigenous isolates in soil with low and high rhizobial count is suggested.

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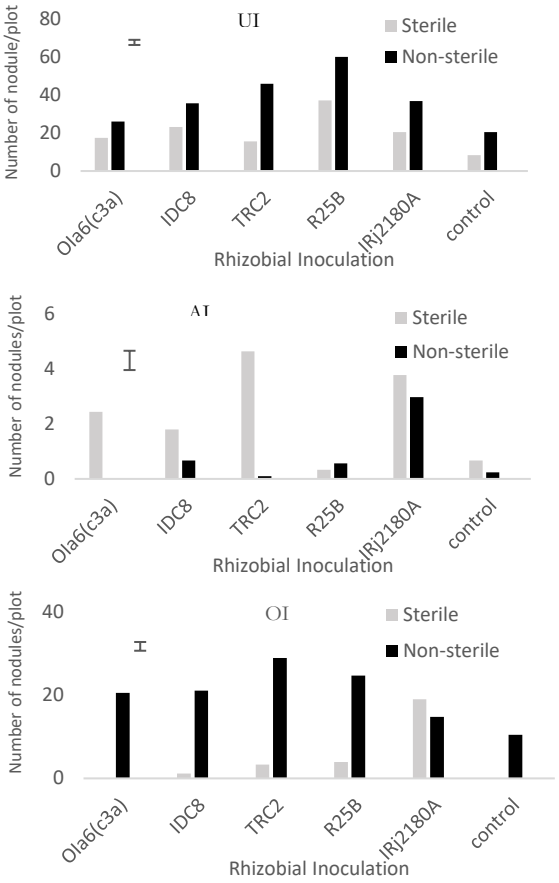

Figure 1. Number of nodules as affected by rhizobial inoculation and soil sterilization on three soybean varieties at University of Ibadan (UI), Idi-Ayunre (IA) and Orile-Ilugun (OI) in pot experiment. Bars represent SE of mean

Table 1. Grain yield of three soybean varieties as affected by rhizobial inoculation in three locations

Variety	Strain	UITR	IA	OI
TGx1448-2E	OISa-6e	2	1.9	1
	IDC8	2.2	2.1	1.5
	TRC2	2	1.8	1.3
	R25B+IRj2180A	1.6	3.6	1.5
	control	1.5	1.5	1.5
TGx1908-1F	OISa-6e	1.7	2.8	1.3
	IDC8	1.8	1.5	0.9
	TRC2	1.5	1.4	0.7
	R25B+IRj2180A	3.1	4.1	1.1
	control	1.6	1.2	0.9
TGx1910-2F	OISa-6e	2.1	1.9	1.4
	IDC8	1.6	2.6	1.5
	TRC2	2.2	1.6	1.8
	R25B+IRj2180A	1.9	3.1	1.5
	control	1.5	1.3	1.7
SE	Variety (V)	0.2	0.2	0.1
	Strain (R)	0.2	0.2	0.1
	V × R	0.3	0.4	0.2
ANOVA	Variety (V	ns	Ns	***
	Strain (R)	ns	***	Ns
	V × R	*	**	Ns

†Error degree of freedom =16
SE = Standard Error; ns = not significant; ***, ** and * = p<0.001, 0.01 and 0.05 respectively.

EFFECT OF STORAGE CONTAINERS ON SEED VIABILITY AND SEEDLING VIGOUR OF JUTE MALLOW (*Corchorus olitorius* L.) ACCESSIONS

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ABSTRACT
Seed conservation of Jute mallow (*Corchorus olitorius*) in gene banks is essential for success of their use in breeding programmes. The objective of this study was to assess the germination and seedling vigour performance of jute mallow seeds after short term storage using three different storage containers (plastic container, aluminium can and aluminium foil). Seeds of eight accessions of jute mallow were stored under short term storage conditions for twenty months and thereafter evaluated for germination and germination index. The experiment was conducted in a 8 x 3 factorial arrangement using completely randomized design in three replications. The results of analysis of variance revealed that effect of storage containers was highly significant ($p < 0.01$) on germination and seedling vigour of Jute mallow. Seeds stored in aluminium foil had the highest germination (72.58%) and lowest emergence index (4 days) hence recommended for storing seeds of this crop under short term conditions.

Keyword: Germination, jute mallow, seed, vigour

INTRODUCTION
Jute mallow (*Corchorus olitorius*) is an important African leafy vegetable hence true potential of this vegetable need to be exploited by breeders in breeding programmes. The conservation of jute mallow seeds in gene banks is essential for success of their use in breeding programmes however, seed storage has been shown to affect seed quality (Coolbear, 1995) hence seed storage and retention of viability therefore form essential aspects in seed gene bank management. Seeds are hygroscopic in nature which means they pick up and release moisture from and to the surrounding air until the vapour pressures of seed moisture and air reach equilibrium which can lead to rapid seed deterioration especially where humid conditions prevail hence choice of packaging material becomes a major concern for seed conservationist. The objective of this study therefore was to investigate the effect of different storage containers on germination and seedling vigour of jute mallow seeds.

MATERIALS AND METHODS
Eight accessions of jute mallow seeds, regenerated in isolation at the experimental field of National Center for Genetic Resources and Biotechnology (NACGRAB), Ibadan, Nigeria during the late growing season of 2019 was used for the study. Fifty grammes of each of the processed seed samples were subdivided into three and packed separately using three packing containers (plastic container, aluminium can and aluminium foil) and thereafter stored under short-term storage conditions in January 2020.

Laboratory seed quality tests
The laboratory seed quality tests (standard germination and seedling vigour) were carried out on seed samples in March 2022. The experiment was conducted in 8 x 3 factorial arrangement using completely randomized design in three replications with 100 seeds per replication. Each sample of *C. olitorius* seeds were steeped in hot water at about 90°C for five minutes to break dormancy. They were subsequently spread on some layers of absorbent paper and dried under shade. Standard germination test was carried out on seed samples using tissue paper method by placing 100 seeds on moist tissue paper in Petri dish (11 cm in diameter). The Petri dishes were kept at room temperature of about 25 ± 2°C for 7 days. Germination counts were carried out and percentages were calculated by expressing the number of seedlings in a replicate that emerged 7 days after planting as a percentage of the number of seeds planted according to ISTA (1993) rules. Germination Index (GI) was calculated by taking the germination counts at 5, 7 and 9 days after planting and the data were substituted into the following formulae: $\sum(Gt/Dt)$ where Gt =

number of germinated seeds on day t and Dt = time corresponding to Gt in days.

Statistical analysis

Data obtained from laboratory experiments were subjected to analysis of variance (ANOVA), using Generalized Linear Model Procedure (PROC GLM) of Statistical Analysis System (SAS, 1990) package. Treatment means were thereafter separated by use of the least significant difference (LSD) at 0.05 level of probability.

RESULTS AND DISCUSSION

Influence of accessions was significant ($p < 0.01$) for germination test as well as emergence index of jute mallow seeds (Table 1). Similarly, the effect of storage container was significant ($P<0.01$) for germination test as well as emergence index of jute mallow seeds however, the interactive effect of accession and storage container was only significant ($p < 0.01$) on emergence index of jute mallow seeds (Table 1). The mean germination for accession ranged from 18.22 to 92.67% while emergence index also ranged from 4 to 7 days (Table 2). This agrees with the report of Dombos (1995) who reported that genetic differences exist among cultivars for the ability to acquire and maintain good seed quality. Jute mallow seeds stored in aluminium foil container had highest germination (72.58%) and lowest germination index (4 days).

Conclusion

This study concludes that aluminium foil was the superior among the three containers with highest germination and lowest emergence index hence recommended for storing jute mallow seeds under short term conditions.

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Table 1. Mean squares, means, coefficient of determination (R^2) and coefficient of variation (CV) from the analysis of variance for germination and germination index of jute mallow

Source of variation	Degree of freedom	Germination (%)	Germination index (days)
Replication	2	37.56ns	0. 42ns
Accession (ACC)	7	4790.98**	9.39**
Storage container (STC)	2	856.06**	8.26**
ACC X STC	14	90.02ns	1.64**
Error	46	48.92	
Total	71	546.97	1.7
R2 (%)		0.14	0.88
CV		10.62	11.85
Mean		65.8	4.7

*****, ******, Significant at probability level of 0.05 and 0.01, respectively; ns = not significant

Table 2. Effects of accessions and storage containers on seed germination and emergence index of Jute mallow

Treatment	Germination (%)	Germination index (days)
Accessions		
NGB00651	89.11a	3.5f
NGB00205	92.67a	4.1ed
NGB00221	69.77b	4.62c
NGB00213	68.89b	4.0ef
NGB00231	60.89c	5.2b
NGB00226	18.22d	6.9a
NGB00217	72.00b	4.6cd
NGB00225	55.33c	4.8cb
LSD	6.64	0.53
Storage containers		
Plastic	61.18b	4.9a
Aluminium can	63.83b	5.2a
Aluminium foil	72.58a	4.0b
LSD	4.06	0.32

Means with different letters within the column of the same factor are significantly different at $p < 0.05$

INFLUENCE OF SEED PRODUCTION ENVIRONMENT ON GERMINATION AND SEEDLING VIGOUR OF SORGHUM ACCESSIONS IN SHORT TERM STORAGE

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ABSTRACT:
Seed production environment plays a significant role in determining the quality of seeds. The objective of this study was to investigate the influence of seed production environment on germination and seedling vigour of sorghum accessions in a short-term storage. Seeds of seventeen accessions of sorghum produced at two agroecological environments of Nigeria: Kishi, Oyo State and Badeggi, Niger State, processed in December, 2021 and stored for twenty months in short-term storage conditions were used for this study. The seeds were evaluated for germination and germination index before and after storage using 17 x 2 x 2 factorial arrangement in three replications. The results of analysis of variance (ANOVA) revealed that accession, storage period, and seed production location interactive effect was highly significant on germination percentage and emergence index. The germination of seeds produced at Badeggi was significantly higher (93.35%) than that of Kishi (81.04%) suggesting that Badeggi location would be better for seed production of Sorghum.

Keywords: emergence index, germination, location, sorghum

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INTRODUCTION

Sorghum (*Sorghum bicolor* (L) Moench) is an important cereal for its contribution both human and animal nutrition however, the quality of seed sown has a great influence on farmer's success. Seed production environment plays a significant role in determining the quality of seeds in storage. The maximum expression of physiological quality of seed is dependent on the genetic make-up and external factors during seed development on mother plant. (Bewley and Black, 1994; Dornbos, 1995). Adequate knowledge of the relative contributions of different factors that influence seed quality will therefore be important in ensuring proper conservation of seed quality for utilization in breeding programmes. Germination capacity and vigour are crucial aspects of seed quality. Standard germination test is used worldwide to determine the maximum germination potential of a seed batch under optimum conditions. However, this test has its drawbacks as it can only predict field emergence under favourable environmental conditions. Seed vigour is an indication of ability of seed to emerge under a wide range of environmental conditions and it is therefore the most indicator of physiological quality. Due to the importance of seed production environment on the quality of seeds produced, it is therefore necessary to investigate the effect of production environment of sorghum on its quality. The objective of this study was to investigate the influence of seed production environment on germination and seedling vigour of sorghum accessions under short term storage.

MATERIALS AND METHODS

Seventeen accessions of sorghum seeds produced at two agro-ecological environments of Nigeria: Kishi, Oyo State and Badeggi, Niger State, processed in December, 2021 were used for this study. The processed materials were stored for twenty months under short term storage conditions (18 ± 2°C, 30% RH) in January, 2021. The seeds were evaluated for germination and germination index before storage in January, 2021 and after storage in August, 2022. The experiment was conducted in 17 x 2 x 2 factorial arrangement using completely randomized design in three replications with 100 seeds per replication.

Laboratory seed quality tests

Standard germination test was carried out on seed samples using tissue paper method by placing 100 seeds on moist tissue paper in Petri dish (11 cm in diameter). The Petri dishes were

kept at room temperature of about 25 ± 2ºC for 7 days. Germination counts were taken and percentages were calculated by expressing the number of seedlings in a replicate that emerged 7 days after planting as a percentage of the number of seeds planted according to ISTA (1993) rules.

Germination percentage = $\frac{Number\ of\ emerged\ seedling\ 7th\ day\ after\ planting}{Number\ of\ seeds\ planted} \times 100$

Germination Index (GI) was calculated by taking the germination counts at 5, 7 and 9 days after planting and the data were substituted into the following formulae:

$$GI = \sum(Gt/Dt)$$

where Gt= number of germinated seeds on day t and Dt= time corresponding to Gt in days.

Data analysis

Data obtained from the laboratory experiments were subjected to analysis of variance (ANOVA), using Generalized Linear Model Procedure (PROC GLM) of Statistical Analysis System (SAS, 1990) package. Treatment means were thereafter separated by use of the least significant difference (LSD) at 0.05 level of probability.

RESULTS AND DISCUSSION

The results of analysis of variance (ANOVA) revealed that accession, storage period and seed production location interactive effect was significant ($p < 0.01$) on germination percentage and emergence index of sorghum seeds. This suggests that there is need to identify locations at which seed quality of specific accession are highest. The germination of seeds produced at Badeggi was significantly higher (93.35%) than that of Kishi (81.04%) suggesting that Badeggi location would be better for seed production of Sorghum (Table 1). Furthermore, the results imply that seed production location should be given a higher priority when taking seed production decisions. This agrees with the report of Dombos (1995) who reported that among .

various factors affecting seed quality, the genetic effect is minimal in comparison with environmental effect. However, the germination index for Badeggi and Khisi are approximately four days (Table 2). The significant effect of accessions on germination percentage and germination index also agrees with the report of Dombos (1995) who reported that genetic differences exist among cultivars for the ability to acquire and maintain good seed quality.

Conclusion

This study shows that production location should be given a higher priority when taking seed production decisions. This study led to the conclusion that Badeggi location would be better for sorghum seed production in comparison with Khisi.

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Table 1. Mean squares, means, coefficient of determination (R^2) and coefficient of variation (CV) from the analysis of variance for germination (G%) and germination index (GI) of Sorghum

Source of Variation	Degree of freedom	G%	GI
Replication	2	0.96ns	0.01ns
Location (LOC)	1	7733.02**	3.53**
Accession (ACC)	16	665.93**	0.93**
Storage period (STP)	1	678.35**	181.40**
ACC × LOC	16	320.85**	0.72**
ACC × STP	16	227.01**	0.78**
STP × LOC	1	7.84ns	0.47**
ACC × STP × LOC	16	132.59**	0.60**
Error	134	36.42	0.06
Total	203	171.65	1.19
R^2		0.86	0.96
CV		6.92	6.17
Mean		87.2	4.08

*, **, Significant at probability level of 0.05 and 0.01, respectively; ns = not significant

Table 2. Effect of production location on seed germination (G%) and (GI) index of sorghum

Location	G%	GI
Badeggi	93.35a	4.21a
Khisi	81.03b	3.94b
LSD	1.67	0.07

Means with different letters within the column of the same factor are significantly different at P=0.05

COMPARATIVE ASSESSMENT OF GERMINATION CHARACTERISTICS BETWEEN *Solanum melongena* AND *Solanum aethiopicum* SEEDS AFTER SHORT TERM STORAGE

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ABSTRACT
Germination capacity and vigour are crucial aspects of seed quality. The objective of this study was to compare germination characteristics of two Solanaceae species (*Solanum melongena and Solanum aethiopicum*) seeds. Three accessions each of *S. melongena* (NGB00251, NGB02318, NGB07696) and *S. aethiopicum* (NGB02660, NGB02670 and NGB02669) were used in this experiment. Standard germination test was carried out on seed samples in in December, 2021 and September, 2022 using Complete Randomization Design (CRD), replicated three times with 100 seeds per replication. The results of combined analysis of variance (ANOVA) revealed that mean germination of *Solanum melongena* seeds was significantly higher (79.67-90.67%) than *S. aethiopicum* seeds (35.33-67.67%) suggesting that species of Solanaceae family should be given prime consideration while evaluating for germination in order to avoid wrong conclusion.

Keywords: accession, germination, Solanaceae, species

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INTRODUCTION
Solanum macrocarpon (eggplant) and *Solanum aethiopicum* (garden egg) are common vegetables in southern part of Nigeria. *S. macrocarpon* is an important leaf vegetable for some people of southern part of Nigeria especially for the rural dwellers while *S. aethiopicum* also serves as an important fruit vegetable for large population of rural and urban dwellers of Nigeria however, the germination response of the cultivated species of general *Solanum* is a major constraint to its production. The reports from earlier studies revealed that different germination rates have been described in different species including some accessions of *Solanum melongena* and related species (Demir *et al.*, 2005; Ibrahim *et al.*, 2001). The germination capacity and vigour are crucial aspects of seed quality hence study of germination pattern in these species would be of interest for their conservation and utilization in breeding programs. The objective of this study therefore was to investigate the germination pattern of *S. macrocarpon and S. aethiopicum* in a short-term storage

MATERIAL AND METHODS
Seeds of three accessions of each of the *Solanum* species: *S. macrocarpon* and *S. aethiopicum produced* during late growing season of 2020 were used in this study. The samples were kept in the short-term storage environment (18±2ºC) located at the National Centre for Genetic Resources and Biotechnology (NACGRAB) Ibadan, Nigeria in January 2021. The laboratory experiment was conducted at Seed Testing Laboratory of NACGRAB using completely randomized design in three replications. The stored seed samples were tested for germination in January, 2021 and after storage in August, 2022 by placing one hundred seeds in a germination plastic container lined with four layers of tissue paper moistened with 15 ml of distilled water. The containers were covered and placed in a germinating chamber at 25 ± 2ºC. The seeds were kept moist every day for seven days thereafter germination percentages were determined at seven days after planting according to International Seed Testing Association ISTA (1993) rules.

Germination Index (GI) was calculated by taking the germination counts at 5, 7 and 9 days after planting and the data were substituted into the following formulae: $\sum(Gt/Dt)$ where Gt= number of germinated seeds on day t and Dt= time corresponding to Gt in days. Data obtained from laboratory experiments were subjected to analysis of variance (ANOVA), using Generalized Linear Model Procedure (PROC GLM) of Statistical Analysis System (SAS, 1990)

package. Treatment means were thereafter separated by use of the least significant difference (LSD) at 0.05 level of probability.

RESULTS AND DISCUSSION

Influence of accessions was significant ($p < 0.01$) for germination test on seeds of *Solanum* species (Table 1). Similarly, the interactive effect of accession and storage time was also highly significant ($p < 0.01$) on germination of *Solanum* species seeds (Table 1) indicating that germination performance of species of solanum seeds depends on storage time in the storage environment. The results of the data analysis revealed that mean germination of *Solanum melongena* seeds was significantly higher (79.67 - 90.67%) than *S. aethiopicum* seeds (35.33 - 67.67%) suggesting that species of Solanaceae family should be given prime consideration while evaluating for germination (Table 2). This agrees with the report of Dombos (1995) who reported that genetic differences exist among cultivars for the ability to acquire and maintain good seed quality.

Conclusion

This study concludes that *Solanum melongena* seeds has better germination performance than *S. aethiopicum* seeds after storage under short term conditions.

Table 1. Mean Squares, Means, Coefficient of Determination (R^2) and Coefficient of Variation (CV) from the analysis of variance on germination of *solanum melongena* and *solanum aethiopicum*

Source of variation	Degree of freedom	Germination (%)
Replication	2	82.33ns
Accession (ACC)	5	2834.67**
Storage time (STR)	1	215.11ns
ACC X STR	5	1088.44**
Error	22	120.39
Total	35	646.97
R2 (%)		0.88
CV		16.37
Mean		67

*, **, Significant at probability level of 0.05 and 0.01, respectively; ns = not significant

Table 2. Effect of accession and storage time on germination of *Solanum melongena* and *Solanum aethiopicum*

Factor	Germination (%)
Accessions	
NGB07696	90.67a
NGB00251	82.00a
NGB02318	79.67ab
NGB02669	67.67b
NGB02670	47.67c
NGB02660	35.33c
LSD	13.84
Storage time (STR)	
Before storage	64.56a
After storage	69.44a
LSD	7.59

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GENETIC VARIATION OF THREE YAM (*Dioscorea rotundata* POIR) LANDRACES AND RESPONSE TO *Meliodogyne incognita* AND *Scutellonema bradys* USING SINGLE NODE VINE ROOTING TECHNOLOGY

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ABSTRACT

Yam is an important staple in West Africa, but its production is constrained by nematodes such as *Meliodogyne incognita* and *Scutellonema bradys*. Crop rotation and nematicides are used to reduce yield losses caused by nematodes. Use of tolerant yam varieties is an efficient control measure with unknown negative environmental effects. Response of yam landraces to nematodes, using single node vine rooting technology were investigated. Zygotic seedlings from 500 accessions of three landraces [*Pepa* (n=144), *Amula* (n=248) and *Hembakwase* (n=108)] were evaluated for Morphological Diversity-MD: Sixteen accessions selected based on MD were planted in pots arranged in a completely randomised design with three replicates. Inoculation was done eight weeks after vine planting at rate of 500 and 250 nematode eggs/juvenile per plant of *M. incognita* and *S. bradys*, respectively. Root Gall (RG) and Nematode Population Density (NPD) were assessed and analysed using ANOVA at $\alpha_{0.05.}$ Significant difference was observed among the accessions. RG ranged from 1.5±0.15 (P172-*Hembakwase*) to 1.7±0.6 (P301-*Amula*) and NPD ranged from 235 (P172-*Hembakwase*) to 38,605 (P190-*Hembakwase*) for *M. incognita* and 0 (P181-*Hembakwase*) to 12,005 (P483-*Amula*) for *S. bradys*. Five accessions: P172 (*Hembakwase)*, P53 (*Pepa)* and P283, P446, P410 (*Amula)* were tolerant of *M. incognita*, while 11 accessions P524, P486, P273, P365, P301 (*Amula),* P128, P131, P43, P85 (*Pepa)* and P173, P181 (*Hembakwase)* were tolerant of *S. bradys.*

Keywords: nematode, vine rooting, tolerant, *M. incognita* and *S. bradys*

INTRODUCTION

Yam serves as major source of income, food and nutrition for many Africa homes, over 60 million producers, processors, marketers, transporters, traders and consumers are in West Africa (Asiedu and Maroya 2011). In West Africa, particularly in Nigeria, yams have high cultural value. It is part of the bride price in marriage ceremony and annual festivals are held, to celebrate its harvest. Demand for yam consumption is generally very high and yam production is very profitable despite high cost of production (Mignouna *et al.,* 2014). Constraints of yam cultivation include high cost of planting material, high labour demand and cost for most of the cultural operations, high cost of labour and other inputs, unreliable sources of credit, pests, mainly the effect of nematode and other yam diseases, low soil fertility and erratic weather conditions are among the problems (Mignouna *et al.,* 2014). To overcome these challenges, yam-breeding scientist will need to focus on development of new breeding methods and strategies, for better utilization of existing genetic diversity, the discovery of new traits, development of new varieties, incorporating consumer-preferred characters, including control of nematode infestation in yam fields.

Nematodes have been reported as one of the greatest enemies of yam producing farmers (Yao *et al.,* 2017), the problem of nematode attack account for about 35% loss in yam production (Adesiyan and Odihirin, 1977). For yam to become an export crop in Nigeria and in other West Africa countries and to increase the food and income level of the yam farming families, the challenge of plant-parasitic nematode has to be overcome. Effect of nematode on yam poses a significant threat to yam production in term of quality and quantity in almost all the yam-growing regions in the world (Yao *et al.,* 2017). Mainly because of the variation existing among zygotic seeds due to genetic recombination and they can be used to search for resistant genotypes. Botanical seeds are used for propagation in breeding programs, only because the progenies are different from the parents due to out-crossing. Therefore, genetic variation is needed to achieve development of nematode resistant varieties through identification of genotypes that can tolerate or resist the attack by

nematode. Genetic diversity will be used to select and breed for nematode tolerance. Traditionally, yam propagation has been by the use of whole or cut tubers, but used recently, are High Ratio Propagation Technologies (HRPT) like adapted miniset technique, Single Node Vine Rooting (SNVR), Temporary Immersion Bioreactor System (TIBS) and Aeroponics and Hydroponics System (AS) were developed for yam propagation to increase seed yam availability and production.

MATERIALS AND METHODS

Four clusters were obtained based on the morphological evaluation of the genotypes. Four plants were selected at a random from each of the four clusters (2, 4, 5 & 6) for inoculation and screening for nematode, replicated three times. A total of 144 bags were filled with 8 litres of sterilized topsoil, and planted with ten vine cuttings from each mother plant. The mother plants were 24 weeks old when the vines were cut. The bags were hanged vertically with plastic saucers at the bottom. The plants were inoculated at eight weeks after planting, with root-knot nematode (*M. incognita*) and dry rot nematode (*Scutellonema bradys*) at rate of 500 and 250 nematode eggs/juvenile per plant. The experimental design was CRD, and data were collected before and at harvesting:

Statistical analyses

Data were analysed with the Statistical Analysis System (SAS 9.3) software using descriptive statistics and analysis of variance at p=0.05.

RESULTS AND DISCUSSION

Nematode infestation on the plants varied significantly in term of root gull, tuber cracking and population density. The traits like tuber gull, dry rot, crazy root and tuber root gull were not significant (Table 1). But the level of tolerance among the genotypes varied significantly. Wehner *et al.,* 2005, stated that the host will be susceptible if RF > 1 and Gi > 40), moderately resistant/Tolerant when RF ≤ 1 and Gi ≤ 40 and resistant when RF < 1 and Gi < 40. While Cladius-Cole *et al* (2017), also stated that, resistance mean when RF ≤ 1 and GI ≤ 2. Based on these, accessions like; P210, P128 and P85 are resistant to *M. incognita*, while accessions like; P524, P483, P128, P131, P43, P520, P273, P85, P173, P365, P181 and P301 are resistant to *S. bradys*.

However, the total population of *S. bradys* in soil and root, are significant. Whereas only the total population of the *M. incognita* in root was significant (Table 2). Measure on economical threshold, the results show that plant were resistance to both (*M. incognita* and *S. bradys).* According to Tylka 2009, the tolerance and resistance is measure when number of nematode were ranged from 50 – 100 eggs/100 cc of soil or 200 eggs/100cc of soil. According to Weber G. *et al.,* (1995), the population density is correlated to the amount of damage by nematodes in the yam environment. In this study, there were significant difference in the tolerance level among the cultivars. With high level of nematode populations at harvest with mean values ranging from 350 to 6000 per 100 cc of soil, without significant damage by the nematodes. The lowest population of nematodes were recorded in some of the accessions, which also ranged from 10 to 500 eggs.

Conclusion

The response to nematode infection or the resistance ability of plant is measured by absence or reduction in the population of the nematode in the environment of host plant. This study establishes out that there was significant variation among the yam screened for nematodes resistance (*M. incognita* and *S. bradys*). This were expressed by non-visible signs of infection, the low rate of survival by nematodes or the low population density of nematodes after inoculation and the low level of damage caused by the nematodes on the various parts of the plant (roots and tubers of yam). From the observed phenotypic reaction of the plant to the nematode, it shows that genetic variance is important in identifying and selecting yam cultivar for nematode resistance/tolerance. The result show that plants grown from zygotic seed could be used to develop yam variety that are tolerance to nematode because; it is fast, save and cost-effective to use the vine cutting technology to carry out the screening exercise. Also, for the Nigerian government to meet the need for yam exportation, this finding is needed to solve the problem of nematodes. The method is useful for studying plant-parasitic nematodes on yam and for investigating the response of yam clones to nematode infections.

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Table 1. Descriptive statistic and Analysis of variance for various nematode traits measured.

Trait	Mean	CV %	Mean squares		LS.
			Between Clone df =2	Error df = 515	
Root gall	1.5± 0.7	34.7	0.43	0.28	***
Tuber gall	1.1± 0.1	26.9	0.18	0.09	Ns
Tuber cracking	1.2±0.2	23.5	0.47	0.04	*
PD	618.7±69.1	376	1615	2449	**
Dry rot	1 ± 0.0	0	0	0	Ns
RF (*S. bradys*)	0.61±2.9	48.5	29.8	7.9	*
RF (*M. incognita*)	1.2±2.6	94.7	13.12	5.86	NS

*, and *** indicate 0.05 and 0.001 level of significance and Ns mean not significance, PD= Population Density

Table 2: Nematode population among yam cultivars evaluated in the study

Trait	Cv%	Means	Std Dev.	Means Square between Clone df =44	Error df= 42	LS
P.M. i. in soil	192.6	2583	119	3098	2475	NS
P. S. b. in soil	382.3	500	124	1851	3653	*
P.M. i. in root	164.1	530.3	135	2580	1575	***
P.S. b. in root	218.5	34.7	5.4	845	5736	**
P S. b. in tuber	614.3	1.4	0.4	22.5	10.4	Ns
P. M. i. in tuber	685	62.7	30.2	1298	1245	NS
RF M. inc.	194.7	1.2	2.6	13.1	5.9	NS
RF S. bradys	448.5	0.61	2.9	9.8	7.9	*

*, **, and *** indicate 0.05, 0.01 and 0.001 level of significance and Ns mean not significance.

IMMUNE RESPONSES OF TWO GENOTYPES OF YORUBA ECOTYPE NIGERIAN INDIGENOUS CHICKEN TO NEWCASTLE DISEASE

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ABSTRACT

The study assessed the effects of Newcastle disease on the Immune responses of Yoruba Ecotype Nigerian Indigenous Chicken. The Yoruba Ecotype is a native of the forest zone of the country. They are light chickens found in the swamp, Rainforest and Derived Savannah agro-ecological zones. The genetic resources base of the indigenous chickens in the tropics is rich and form the basis for genetic improvement and diversification to produce a breed adapted to the tropics. A total of forty (40) indigenous chickens made up of twenty (20) each of Yoruba Frizzled feathered and Yoruba Naked Neck were infected with New Castle Disease through physical contact. Newcastle infected chickens were introduced into their different compartments. Clinical signs, mortality and hemagglutination Inhibition (HI) Titre evaluation were used to assess the immune responses. The experimental chickens developed clinical signs of Newcastle disease from day 10. Mortality was recorded from day 11 after infection, with 35% in Frizzled feathered and 30% in Naked Neck. The chickens were bled on day 0, 11 and 28 post infection for HI titre determination. On day 0, HI Titre of the two Genotypes were below 3log2 of 1.0. on day 21 there was significant differences within each HI Titre ($p < 0.05$) with the Naked Neck having the highest mean HI Titre value of 8.0 while the Frizzled feathered had titre value of 6.5. There was decrease in the mean HI titre in the two genotypes on day 28 with Naked Neck having the least reduction. It could therefore be concluded that, the naked neck was more resistant to Newcastle disease than the frizzled feathered. Thus, it is recommended that Naked Neck should be selected and crossed with other Genotypes within the Yoruba Ecotype to increase resistance to Newcastle disease.

Keywords: chicken, hemagglutination inhibition, genotype, indigenous newcastle disease

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INTRODUCTION

The Yoruba Ecotype is a native of the forest zone of the country. They are light chickens found in the swamp, Rainforest and Derived Savannah agro-ecological zones whose mature body weight ranges between 0.68-1.5kg. Yoruba ecotypes have a higher level of adaptation to its environment than the Fulani Chickens (Oluwumi *et al*.,2006; Abdu-rahman, 1987; Horst, 1988). The genetic resources base of the indigenous chickens in the tropics is rich and should form the basis for genetic improvement and diversification to produce a breed adapted to the tropics (Horst, 1988). Horst (1988) described nine major genes of the indigenous chicken that can be used in genetic improvement programme. There is little information on the genetic makeup of the indigenous chickens of Africa. However, information on the FAO Domestic Animal Diversity Information System (DADIS) shows that these genes are prevalent in the local populations across the countries of Africa.

A number of major genes has been identified in the genome of the Nigerian Indigenous chicken population among which is the feather distribution (peter *et al*.,2003). Among the major genes of interest is the Frizzled feathered, Frizzling is caused by an incomplete dominant gene., known as F gene. The homozygote may look bane, there are modifying genes that make the extent of curling less extreme (Hutt, 1949) Heterozygote have less extreme effects (Some,1988) Haaren-Kiso *et al*, (1992) also reported that the f gene as heterozygote caused a 40% reduction of feather weight at slaughter and an increase in comb weight. Another major genes of interest is the naked neck. The Naked Neck gene is incompletely dominant with Na/Na birds showing an isolated tuff of feathers on the ventral side of the neck above the crop (Merat, 1986). The bare skin becomes reddish particularly in male as they approach sexual maturity (Somes, 1990). Merat (1990) reported that in high temperatures near 300 c or higher, Naked Neck birds had a better laying rate World

poultry science (2009) reported that Naked Neck is highly resistance to disease.

Disease resistance is a trait often controlled by multiple genes as well as interactions between several factors (Hartmann, 1997). The chicken Major Histocompatibility complex (MHC) is one genetic system which control disease resistance (Bacon, 1987). In chickens the MHC is called the B complex; it was originally described as a system controlling blood group antigen (Briles *et al.*, 1950). One of the most interesting features of the chicken MHC is the strong influence it exerts on resistance to a variety of viral, parasitic, and bacterial diseases (Bacon, 1987; Lamont, 1998). MHC control of disease resistance has been established for Marek's disease (MD) (Briles *et al.*, 1983) with very little information on the possible disease resistance associated with Nigerian indigenous chicken.

Newcastle disease is the most important limiting factor in rural chicken farming in most developing countries of the world and a serious threat to intensively reared chickens (Echeonwu *et al.*, 2008). The disease is endemic in Nigeria and continues to be responsible for high mortality and morbidity among village and exotics poultry (Saidu *et al.*, 1998; Baba *et al.*, 1998). It is currently been ranked as the most economically important disease of chickens in Nigeria and elsewhere and currently controlled by routine vaccination (Ezeokoli, 1984). The outbreaks of this disease were more common in layers (Abdu *et al.*, 2005b) and during the dry harmattan (November March) (Saidu *et al.*, 1994; Halle *et al.*, 1999; Abdu *et al.*, 2005a). Clinical signs associated include: sudden drop in egg production often accompanied by production of abnormal eggs, loss of appetite, fever, weakness; nervous signs, which include loss of balance, circling, backward progression and convulsive, stiff and wry neck, wing and leg paralysis.

Testing of disease resistance potential can be direct by infecting the host with the virulent pathogen (Okoye and Abu-Adulugba 1998, *et al.*, 2002), and response of the host towards the pathogen is evaluated. Few scientific researches have been conducted to establish the disease resistance within the Nigerian indigenous chicken especially the varieties within the Ecotype. Therefore, there is need to determine the Immune Responses of Two Genotypes within the Yoruba Ecotype Nigerian Indigenous Chicken to Newcastle disease.

MATERIALS AND METHODS

Experimental site

The experiment was carried out at the Teaching and Research Farm, University of Ibadan, Ibadan, Nigeria. The site is located on latitude 7°20'N, 3°50'E, 200m above sea level.

Experimental chicken

Twenty indigenous chickens each from YFF and YNN were used for the experiment. On arrival, the chickens were given a dose of antibiotics and anticoccidial in accordance with the manufacturer recommendation. The chickens were put on deep litter and fed commercial layers mash containing 16% crude protein and 2600MEKcal/kg with water ad libitum.

Experimental design

Completely randomized designed was used. The chickens were allocated into two treatments of YFF and YNN, having four replicates each of five birds.

Inoculation

Each bird was naturally exposed to Newcastle disease by coming in contact with already infected chickens which were mixed with them in their different compartments. Clinical Signs and Mortality: The birds were observed twice daily for clinical signs and mortality up to 28 days post-infection. (-) was assigned for no clinical signs noticed, (+) was assigned for depression, ruffled feather, loss of appetite and weakness, (++) was assigned for nervous signs, which include loss of balance, circling, backward progression and convulsive, stiff and wry neck, wing and leg paralysis. Percentage mortality was calculated using:

$$\% \text{ Mortality} = \frac{\text{Number of dead birds}}{\text{Total number of birds}} \times 100$$

Blood Sampling and determination of Newcastle Disease Antibody Titres: Before infection and on days 21, 28 post infection, blood samples were collected from randomly selected birds and Newcastle disease antibodies titre were determined. Haemagglutination Inhibition (HI) test was used to determine specific antibodies against Newcastle disease virus by the method described by Allan and Gough (1974).

Statistical Analysis: All data collected from the experiment were analysed using one way analysis of variance procedure of Statistical Analytical System (SAS, 1990).

$Yij = \mu + \acute{a}i + eij$

Where Yij = Individual observation assumed to be random elements

μ = Population means fixed and unknown,

a_i= Treatment effect, effect of ecotype i : varieties assumed fixed

e = error associated with each record ij assumed random and normally distributed.

RESULTS

Clinical Signs: The clinical signs observed in each variety are presented in Table 1, on day nine the two varieties did not show any clinical sign. On day ten, clinical signs were observed in the two varieties in which seven out of twenty chickens from YNN showed clinical signs of depression, ruffled feathers and nine out of twenty chickens from YFF showed the same signs mentioned. On day eleven PI, on day twelve and thirteen PI, two from YNN, five from YFF showed clinical signs; nervous signs which include loss of balance, circling and backward progression respectively. Signs were observed in YNN and YFF till seventeenth day post-infection. No clinical sign was observed in the two varieties from day eighteen till the end of the experiment

Mortalit

Table 1 shows mortality pattern of the experimental chickens, mortality started on day ten post-infection, there was one from YNN while there was none in YFF. On day eleven there were two in YNN and four in YFF. Mortality then continued up to 13th day post-infection in YFF but there was none in YNN. The % mortality in YNN was the least (30%) and YFF (40%). All the dead chickens were examined and positive to lung consolidation, enteric haemorrhage, proventricular haemorrhage and follicular atresia.

Antibody titre

Table 3 shows the mean HI titres 10 (expressed as $\log_2$). In the two genotypes, it was observed that on day zero before inoculation, there was similarity in the mean HI titres and they were below $3\log_2$. The YNN had the highest mean HI titre (7.5) but differed significantly $p < 0.05$ from YFF mean HI titre (6.25) On day 28 post infection there was slight decrease in the antibody titre of the two genotypes

DISCUSSION

The presence of clinical signs and mortality recorded further showed that indigenous chicken including the various varieties within the Ecotype are susceptible to ND which corroborates the report of Okoye and Aba Adulugba (1998) that this group of chicken do experience fulminating ND. In this experiment, the clinical signs were observed in all the two groups of chicken from day ten up to eighteen post infection It also showed that comingling infected chicken with uninfected can result to infection, this observation further showed the possible means of transmission of the virus through contact. Twelve of the YFF chickens, fourteen of the YNN chickens, some of which showed nervous signs survived the infection, which is in agreement with the literature that birds showing nervous signs have a tendency to recover and there is variation in immune responses within the ecotype (Yongolo 1990; Bell 1992).

From this study, YNN recovered faster than the YFF and mortality was 40% to 30%. This could be attributed to major gene effect which could have helped the chicken to recover faster and combat the virus. The findings corroborated the work of Auerez *et al.* (2003) who reported that Mexican indigenous naked chicken showed higher survival rate than the commercial line. Based on the major gene effect, it could therefore be reasonably assumed that Naked Neck gene contributed to the resistance to disease than the Frizzle gene. The mean HI titres for the two genotypes on day zero before infection were below 3log 2 which had been reported to be protective (Allan and Gough, 1974, Musa *et al.* 2009) which showed that local chickens are also susceptible to Newcastle disease, the number one killer of the free range local chickens in Africa (Minga *et al.*, 1989; Bell 1992; Yongolo 1996). The mean HI titre on day 21 post-infection (Table3) shows that the two genotypes had mean HI titre >3log2, this indicates that the survived chickens seroconverted and had attained the protective level. This observation corroborated the reports of Mtambo *et al.* (1999) and Waihenga *et al.* (2002) that high levels of HI titre contributed towards the recovery of the infected birds. The significant difference in the HI titres ($P<0.05$) at day 21 between YFF and YNN is evidence that the different major genes within Yoruba Ecotype differ in their humoral response to the viral challenge which in turn account for the differing disease resistance capability. Although there have been differences in the opinion as to whether there is correlation between disease resistance and major genes, this investigation further showed that there is variation in disease resistance of major genes.

Conclusion

The current study revealed that variation in immune responses to Newcastle disease exists among major genes within Yoruba Ecotype of

the Nigerian indigenous chicken with YNN chickens having the least mortality rate and highest mean HI titre hence are superior in terms of resistance to Newcastle disease. Hence it will be advantageous if these major genes that are gradually going into extinction can be conserved for future breeding programme. A cross-breeding between YNN chicken and YFF chicken may give better performance in terms of resistance to Newcastle disease. Further work is required in order to ascertain the basis and mechanisms of this observed resistance using genetic method of characterisation such as Major Histocompatibility Complex (MHC) Typing and identification of Quantitative Trait Loci (QTLs)

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Table 1. Clinical signs of the infected chickens

Days post infection	Genotype	
	YFF	YNN
01-Aug	-	-
9	-	-
10	9	7
11	11	8
12	11	9
13	15	10
14	11	6
15	8	5
16	5	4
17	2	1
18	-	-
19	-	-
20	-	-
21	-	-

(-): no clinical signs noticed, (+): respiratory signs (depression, ruffled feathers, loss of appetite and weakness), (+ +): nervous signs (twisting of head and neck, circling and loss of balance, YFF= Yoruba Frizzled Feathered chicken, YNN=Yoruba Naked neck chicken

Table 2. Daily mortality of the infected chickens

Days post infection	Genotype	
	YFF	YNN
1-9	0	0
10	0	1
11	4	2
12	3	3
13	1	0
14 to 21	0	0
% mortality	40%	30%

Table 3. Daily mortality of the infected chickens

Days post infection	Genotype	
	YFF	YNN
0	1.50	0.17
21	6.25ab	0.52
28	5.73b	0.53

Means in the same row with different superscripts are significantly ($p < 0.05$) different from each other

DIFFERENT POLLINATION METHODS FOR HYBRID SEED PRODUCTION IN *Capsicum fructescens*

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ABSTRACT

Capsicum fructescens are very important vegetable crops. The production is influenced by the season, weather conditions, flowering pattern and management practices. Pollination is among the major factors influencing its production. There is need to make cross pollination to have all season high quality pepper. The experiment was carried out in pots containing loamy soil in the nethouse. It was arranged in a randomized block design with two replicates. The objective was to develop quality hybrid seed production. The three different pollination methods were I Removal of petals of developed bud before pollination, ii Emasculation and bagging with second parent plant, iii Pollination of Fresh opened flowers. The total number of flowers pollinated for each of the different method was 200. The fruit weight of Genotypes CfOLA5a was 3.3 gm while genotype CfOLA5b gave 10.1 gm. The hybrid mean fruit weight was 12.9 gm. The pollinate on success percentage was between 20 - 50%. The number of crossed fruits was more in I and ii than in iii. The hybrid variety produced when planted gave seven number of petals instead of the normal five.

Keywords: cross pollination, genetic variation, *Capsicum,*

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INTRODUCTION

Pepper is one of the most important vegetables widely cultivated in Nigeria and other parts of the world. It is commonly used as condiments to many foods, spicy in hot sauce. It can be served in many fish, chicken and goat recipes. It can also be added to other foods as spicy flavour. Most African stew and soups are seasoned with pepper due to its culinary properties. The fruit colour can be green, yellow, orange, red and black. The most common is green when in mature and red when mature. This is essential for the flavour and taste as the green colour becomes red the flavour becomes sweeter. The price of pepper vary greatly depending on the colour. Capsicum frutescens are generally diverse and economically important, they are eaten fresh or processed as the fruits provide vitamin C, carotenoids, vitamin E, flavonoids and capsaicinoids. To increase the cultivation area and yield of *C. frustescens* we must develop the techniques to increase fruit formation from flowers.

MATERIALS AND METHOD

Germplasm of local pepper cultivars were collected from the different agro-ecological zones of the country. The germplasm *C. frutescence* - slim fruit shape was selected for this work. Experiment in the glass house was carried out to determine the pollination techniques and their effect on flower and fruit set. The seed of the two parents were planted in the soil. The evaluation of the characters conducted on the field using a randomised complete block design with each plot replicated three times at the experimental site of the National Horticultural Research Institute, Ibadan, Nigeria. All the recommended cultural practices for pepper production were carried out.

RESULTS AND DISCUSSIONS

The hybrid obtained with the parents were evaluated in a randomised complete block design with three replications. There was no significant difference in the Plant height and the number of days to harvesting (Fig. 1). The earliest number of days to flowering was observed on the hybrid Cf OLA_{ab}. The fruit weight of Cf $OLAa_b$ was 12.9 gm due to its large size. The hybrid Cf OLA_b fruit weight was 10.1 gm. The highest number of flowers/plant was found Cf OLA_a followed by Cf OLA_{ab} and Cf OLA_b (fig1)

Fig. 2 shows the variation in the number of petals in Cf OLAab. The percentage occurrence for flowers having five number of petals was fifty. The percentage of occurrence for flowers having

six number of petals was ten while the flowers with seven numbers of petals had forty percentage.

Adetula and Olakojo 2006 revealed the potentials of Nigerian *Capsicum frustescens* accessions with higher yield and fruit quality. The global pepper production recorded by FAO for 3,737, 635ha was 36,415.621 tons in 2016. The low yield was due to low productivity and the production of pepper. The techniques of pollination of i and ii performed better than iii. The percentage success for the different techniques in Fig. 3. Plate a,b and c show flower with five, six and seven petals. Increase in the number of petals in the flower increase the size of the flower and the fruit weight.

Conclusion

The removal of petal of developed bud before pollination and Emasculation and bagging with second parent plant gave the best hybrid seed production.

The management and technique of flower pollination will accelerate the pepper's performance in terms of high quality fruit and yield.

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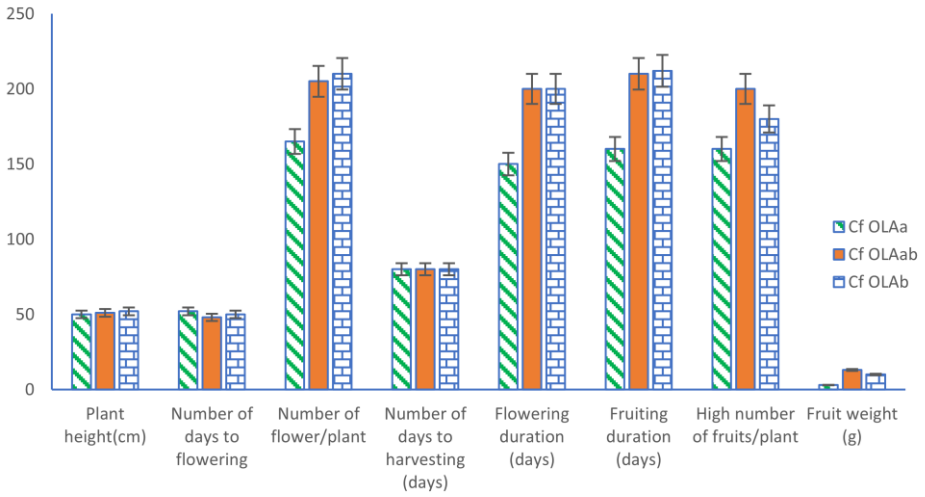

Fig 1: Performance of the Characters of Parents and the hybrid

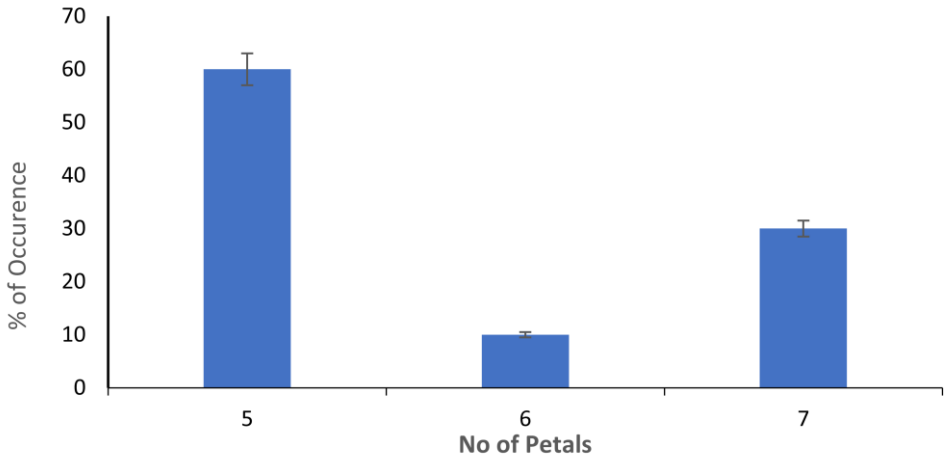

Fig 2: Variation in the number of Petals of Hybrid CfOLAab

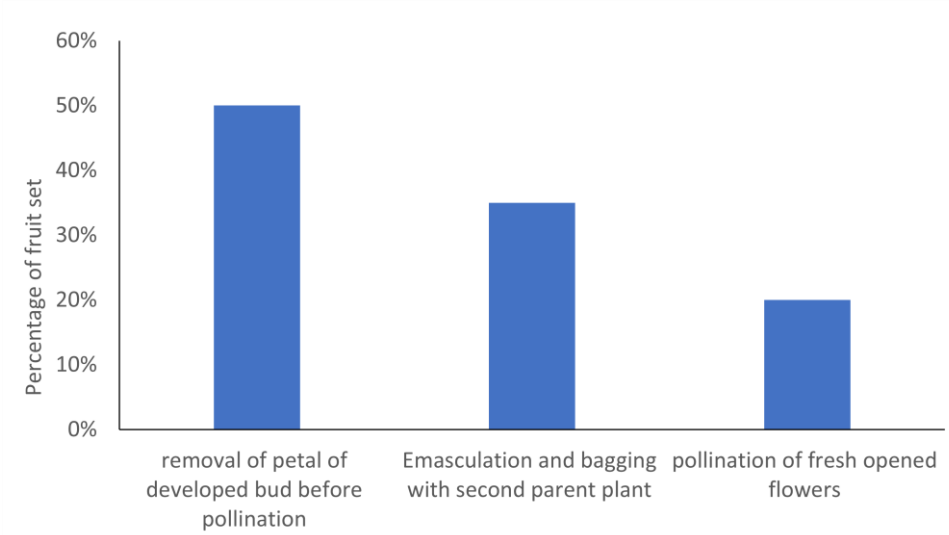

Fig.3. Percentage success of pollination in C.frutescence

Plate a. Flower with five petals

Plate b. Flower with six petals

Plate c. Flower with seven petals

SYNTHESIS OF DITOPIC LIGANDS FOR THE CONSTRUCTION OF PHOTOACTIVE COORDINATION POLYMERS FOR THE REDUCTION OF CO_2.

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ABSTRACT

A new type of polymer materials, developed by the complexation of metal ions with ditopic organic ligands are receiving much attentions these days due to their widespread applications particularly in energy storage and photocatalytic reduction of CO_2. However, the most efficient photocatalytic systems consist of 2nd or 3rd row transition metal complexes, usually those of d^6 ruthenium (II) or iridium (III). Although, these complexes are characterized by long-lived MLCT state and have a very negative reduction potential, the construction of catalysts based on these rare transition metals presents a critical economic limitation to their widespread usage. Here, we alternatively think of synthesizing complexes which utilize cheaper and, more abundant metals which are comparable with or even surpass in terms of some remarkable features to develop a bi–metallic and bi–functional coordination polymer which will in alternation contain photosensitive and electron accepting site such that the good distribution of the metal centers would be controlled by the synthesis of a ditopic polypyridine ligands containing different coordination sites and allowing selective complexation of the metal cations. Precisely transition metals of the first row series in particular chromium and copper are utilized in this synthesis.

Keywords: ditopic, MLCT photocatalytic, polypyridine

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INTRODUCTION

Recent development in the field of energy conversion and storage has necessitated the investigation of the photophysical and photochemical properties of varieties of metal complexes, especially those of Cu(I)phenanthroline $[Cu(NN)_2]^+$ owing to the possibility of practical application of these complexes in various field, particularly in the photocatalytic reduction of CO_2, design of photosensitizers and lots more. Majority of systems developed consist of a combination of separated photosensitizing and catalytic units, while the close association (linking) of these two units are less frequent. The bi-metallic and bi-functional coordination polymers, synthesized by the complexation of metal ions with organic ditopic ligands, can be regarded as a novel type of polymer materials, especially in terms of the significant dependence of the electronic properties on the combination of metal ions and ligands. Such polymers have received much attention due to a potentially wide spectrum of applications including energy and information storage, photoluminescent devices and electrochromic displays.

MATERIALS AND METHODS

Reactions were monitored by thin layer chromatography (TLC) using commercial aluminum-backed silica gel plates. TLC spots were viewed under ultraviolet light and by heating the plate after treatment with phosphomolybdic acid or potassium permanganate. Chromatography purifications were performed by column chromatography using Silica Gel 60 (40-60 mesh). ^{1} H NMR Spectra (400 MHz and 500 MHz) and ^{13}C NMR spectra (75 MHz) were recorded on Avance III 400 Bruker spectrometers; Chemical shifts for ^{1}H spectra are values from tetramethylsilane in $CDCl_3$ (δ 0.00 ppm). Chemical shifts for ^{13}C spectra are values from $CDCl_3$ (δ 77.16 ppm). ^{1}H NMR spectra are reported as follows: chemical shift (ppm), multiplicity (br: broad; s: singlet; d: doublet; t: triplet; q: quadruplet; m: multiplet), coupling constant (Hz), integration and assignment.

Materials

4-bromo-2,5-dimethylbenzaldehyde was prepared using a prescribed procedure. 1,4-dibromo-2,5-dimethylbenzene, nitrophenanthroline, bis(pinacolato)diboron, $PdCl_2$(dppf), KOAC, DMF, NH_4OAC and BuLi were procured from commercial suppliers and used as supplied. All other compounds were prepared using a prescribed procedure.

Synthesis of 4 –bromo-2,5-dimethylbenzaldehyde (13)

To a solution of 1,4-dibromo-2,5-dimethylbenzene (2.64 g, 10 mmol) in THF (5 mL) was slowly added n-BuLi (4.4 mL, 10.5 mmol, 2.4 M in hexane) at -78^{0}C. The reaction mixture was continuously stirred at -78^{0}C for 10 min. After 10 min, a complete conversion to the corresponding lithium reagent as indicated by TLC. *N,N*-Dimethylformamide (1.6 mL, 20 mmol) was added and the reaction mixture was warmed to room temperature and stirred again for 1 hour before the addition of aq. NH_4Cl (20 mL). The aqueous phase was extracted with ether (2 x 50 mL). The organic layers were washed and dried with $MgSO_4$ concentrated in vacuo to give the pure product as a white powder. ^{1}H NMR (400 MHz, $CDCl_3$) δ 10.19 (s, *J* = 1.2 Hz, 1H), 7.63 (s, 1H), 7.46 (s, 1H), 2.60 (s, 3H), 2.43 (s, 3H) (Liu and Knochel, 2007).

Synthesis of 4'(4-bromo-2,5-dimethylphenyl)-2,2':6',2"-terpyridine (23)

2-acetylpyridine (1.7 g, 14.8 mmol), 4 –bromo-2,5-dimethylbenzaldehyde (1.5 g, 7.9 mmol) and KOH (830 mg, 14.8 mmol) were refluxed in a mixture of NH_4OH (50 ml) and EtOH (30 ml) for 1 day. The beige precipitate was filtered was filtered off (1.3 g, 3.17 mmol, 45%). [9] ^{1}H NMR (400 MHz $CDCl_3$) δ 8.75 – 8.64 (m, 4H), 8.44 (s, 2H), 7.90 (td, *J* = 7.8, 1.6 Hz, 2H), 7.49 (s, 1H), 7.36 (dd, *J* = 6.5, 5.0 Hz, 2H), 7.24 (s, 1H), 2.41 (s, 3H), 2.31 (s, 3H) (Afsar *et al.*, 2013).

Synthesis of 4'(4-pinacolatoboron-2,5-dimethylphenyl)-2,2':6',2"-terpyridine (24)

Compound (2) (200 mg, 0.4 8mmol), bis(pinacolato)diboron (270 mg, 1.05 mmol), [1,1'-bis(diphosphino)ferrocene] dichloropalladium ([Pd(dppf)Cl_2]) (24mg, 0.03 mmol) and KOAc (283 mg, 2.88 mmol) were heated at 80^{0}C in 8 mL of dioxane under argon. The reaction was quenched with H_2O (10 mL) and extracted with toluene (2 x 20 mL). The organic phase was evaporated yielding to brown oil. Pentane is added and the formed brown solid was filtered off. The filtrate was concentrated under vacuum to yield about 12% of a yellow oil which solidifies with time (Afsar *et al.*, 2013). ^{1}H NMR (400 MHz, $CDCl_3$) δ 8.72 – 8.64 (m, 4H), 8.46 (s, 2H), 7.87 (dd, *J* = 7.8, 1.7 Hz, 2H), 7.68 (s, 1H), 7.36 – 7.29 (m, 2H), 7.18 (s, *J* = 11.3 Hz, 1H), 3.81 (s, 4H), 2.53 (s, *J* = 13.0 Hz, 3H), 2.34 (s, *J* = 14.4 Hz, 3H), 1.07 (d, *J* = 7.2 Hz, 6H). ^{13}C NMR (101 MHz, $CDCl_3$) δ 156.51, 155.37, 152.26, 149.30, 141.66, 141.23, 137.27, 136.94, 131.14, 131.11, 123.82, 121.66, 121.48, 77.16, 72.44, 31.80, 22.06, 21.89, 19.90 (C-B is a broad line, not detected) 11 B NMR (128 MHz, $CDCl_3$) δ 27.65.

Synthesis of 5-Amino-1,10-phenanthroline (phen-NH$_2$) (25)

Hydrazine monohydrate (1 mL, 0.031mol, excess) was added to a suspension of 5-nitro-1,10-phenanthroline (250 mg, 1.11 mmol) and Pd/C (10%, 25 mg catalyst) in degassed ethanol (15 mL) under nitrogen. The reaction mixture was sonicated for 1 hour at room temperature, refluxed for 24 hours, cooled to room temperature. It is then extracted with 120 mL of DCM, filtered to remove Pd/C, evaporated to dryness and dried under vacuum to yield product as a yellow solid in 84% yield [11]. ^{1}H NMR (400 MHz, $CDCl_3$) δ 9.21 (dd, *J* = 4.3, 1.5 Hz, 2H), 8.98 (dd, *J* = 4.3, 1.6 Hz, 2H), 8.30 (dd, *J* = 8.4, 1.6 Hz, 2H), 8.02 (dd, *J* = 8.1, 1.5 Hz, 2H), 7.67 (dd, *J* = 8.4, 4.3 Hz, 2H), 7.53 (dd, *J* = 8.1, 4.3 Hz, 2H), 6.97 (s, 2H), 1.25 (s, 4H) (Sazanovich *et al.*, 2008).

RESULTS AND DISCUSSIONS

The result revealed as presented in Scheme 2, that the ditopic ligand could be synthesized by a Suzuki coupling of a bromo substituted phenantroline 10 with a boronic terpyridine unit 11. The phenantroline part could be accessed from commercially available 5-nitrophenantroline 15 by sequential alkylation, reduction of the nitro followed a diazotization/bromination step. And the terpyridine would be obtained from commercially 4-bromo-2,5-dialkylbenzaldehyde 13 and acetylpyridine 14.The first ligand we started to prepare is the one were R1/R2 = butyl and R3/R = methyl.

Preparation of the starting aldehyde (4-bromo-2,5-dimethylbenzaldehyde)

Through a successful metal halogen exchange with nBuLi followed by treatment with DMF, 1,4-dibromo-2,5-dimethylbenzene was transformed to the corresponding aldehyde which is the starting material for the subsequent preparation of bromoterpyridine. Detail desption of the transformation is given in Scheme 3.

Preparation of bromoterpyridine 23

The attempt to prepare bromoterpyridine **23** was successful and was realized in 7 steps (scheme 4), starting from the commercially available acetyl pyridine 14 which was condensed with 4-bromo-2,5-dimethylbenzaldehyde 13 in KOH to obtain the corresponding aldol product 17 in a reasonable yield of about 81%. Compound 17 was then dehydrated to give rise to alpha-beta unsaturated product 18 which was then transformed through Michael addition to obtain an intermediate ketone that was utilized in the formation of an imine bearing compound **20** on

treatment with ammonia. Subsequent rearrangement of 20 followed by a ring closure resulted in the compound 22 which was finally oxidized by atmospheric oxygen to obtain the bromoterpyridine 23 in 88% overall yield.

Preparation of the boronic ester

Different palladium catalyst was proposed in order to search for a condition that will give a reasonable borylation yield from the synthesized bromoterpyridine. $Pd(dppf)Cl_2$ was found to be suitable and facilitate the smooth borylation. A Miyaura–Ishiyama borylation reaction between **23** and bis(pinacolato)diboron (molar ratio: 1:1) was carried out in the presence of catalytic $PdCl_2(dppf)$ in dioxane to provide boronic ester 2 as a light yellow solid in 12% yield (Scheme 5)

Preparation of bromophenanthroline

The synthesis of bromophenanthroline 30 was planned in six steps. It begins with the reduction of 5-nitro-1,10-phenanthroline with hydrazine using Pd/Cs as catalyst to obtain the corresponding 5-amino-1,10-phenanthroline **25** in 84% yield. It was followed by a deprotonation/nucleophilic addition of the resulting product using BuLi, producing an intermediate ion **26** which upon treatment with water give rise to **27** in 19% yield. Aminophenanthroline **28** would be obtain as the product of the oxidation of **27** with MnO_2. This will be followed by the formation of a diazonium salt 29 on reacting compound **28** with $NaNO_2$. Finally, the transformation of the diazonium salt into the corresponding bromide using CuBr as shown in scheme 6.

Formation of the planned ligand

A suzuki coupling reaction between the bromophenanthroline 30 and the synthesized boronic ester 24 was planned to be conducted according to the method previously described in order to obtain the target ligand 31 (Scheme 7)

Formation of the coordination polymer

Finally, the planned coordination polymer will be formed from the synthesized bridging ligand 13 by the alternating installation of the two different transition metals (Cu & Cr) along the specific coordination sites of the ligand.

Conclusion

The stepwise synthesis of the starting aldehyde (4-bromo-2,5-dimethylbenzaldehyde) proceeded well and was obtained in good yield. Likewise, the synthesis of bromoterpyridine and boronic ester was equally successful.

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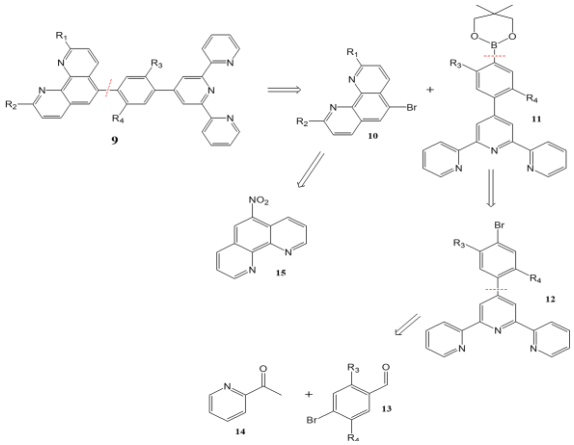
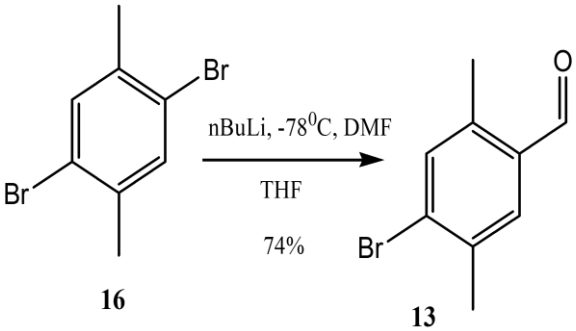
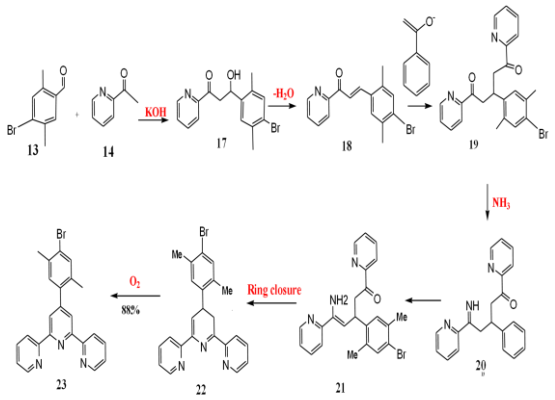


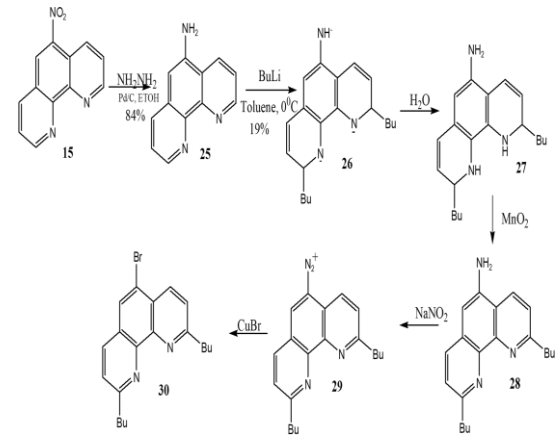
Scheme 2 Retrosynthetic analysis of the planned ligand



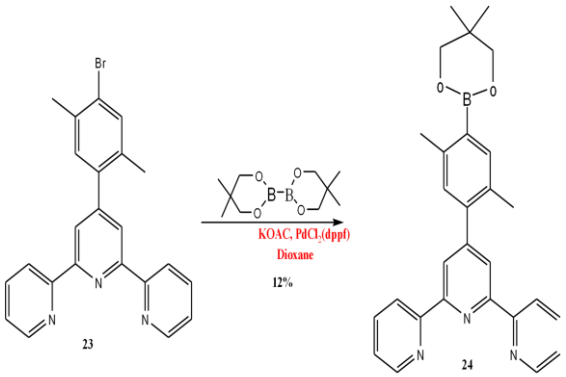
Scheme 3. Preparation of the starting aldehyde



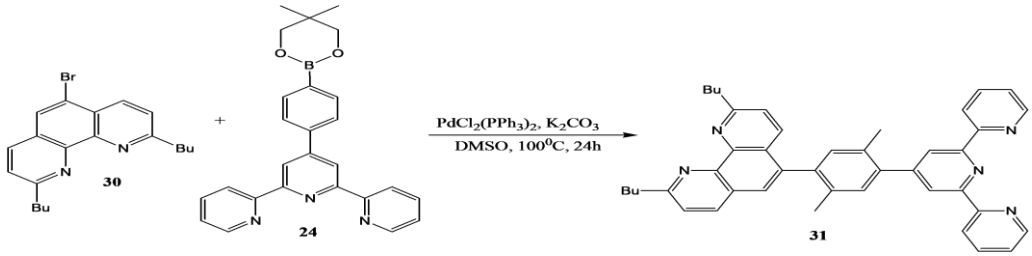
Scheme 4. Best route to access bromoterpyridine



Scheme 6. Best route to access bromophenanthroline



Scheme 5: Palladium catalysis in the borylation of bromoterpyridine



Scheme 7. Suzuki Miyaura cross coupling

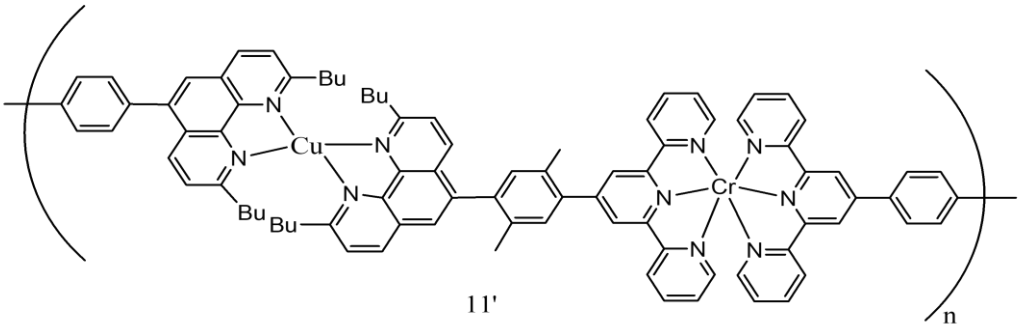


Fig 7: Structure of the coordination polymer

COMPARATIVE PERFORMANCE AND REACTION TO FALL ARMYWORM INFESTATION ON IMPROVED VARIETIES OF MAIZE (ZEA MAYS L.) UNDER RAINFOREST AGRO-ECOLOGY OF NIGERIA

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ABSTRACT

In 2016, there was outbreak of insect pest called Fall armyworm (*Spodoptera frugiperda).* The most affected crops were and are still cereals. The pest is a threat to food security in Nigeria and sub-Saharan Africa as a whole. It has been suggested that the most feasible control option for this pest is Integrated Pest Management and one of the most important components for resource constrained African farmers is the use of pest resistant or tolerant variety. The aim is to evaluate 25 varieties of maize for fall armyworm resistance/tolerance and come up with resistant/tolerant variety or varieties that can be used by farmers directly or used as breeding material. Twenty-five improved varieties of maize (*Zea mays* L.) were evaluated at the experimental field of NACGRAB during the early season of 2021 to compare their performance and reaction to fall armyworm infestation under natural conditions. The experiment was laid out as randomized complete block design with three replications. Data recorded were days to anthesis and silking, Anthesis-silking interval, plant height, ear height, plant count at harvest, fall armyworm leaf feeding at week four, six, and eight; and leaf feeding score at week four, six, and eight. The results of analysis of variance revealed highly significant ($p < 0.01$) mean squares for all the traits evaluated except for anthesis- silking interval, fall army worm feeding at week 8 and leaf feeding score at week 8 suggesting that these improved varieties have potential to serve as breeding materials for these traits.

Keywords: fall armyworm, anthesis, silking, varieties

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INTRODUCTION

Cereals productions are important as food and cash crops in Nigeria. Cereals serve as food for humans and as feed for livestock (Ajiboye *et al.*, 2021). Cereals commonly cultivated in Nigeria include maize, sorghum, pearl millets, rice, and finger millet. These cereals have been central to the food security of Nigeria. Maize production has enjoyed renewed interest over the years. Maize (*Zea mays* L.) belongs to the grass family Poaceae (formerly Gramineae). All the cereals belong to this family. Maize has been totally domesticated, therefore maize needs farmers care for its survival. Among the cereals, maize has highest grain production potential and highly efficient in transforming sun energy into food energy. This is the reason why the longer the gestation period of maize the higher the yield due to higher production of photosynthate, hence extra-early maize produces lower yield while late maize produces higher yield due to higher production of photosynthate.

Among the world's cereal crops, maize is the third in rank while wheat and rice rank first and second respectively. However, in Nigeria and in Africa as a whole and in Latin America, Maize rank first while it ranks third after rice and wheat in Asia. Maize is used in more ways than any other cereal. It is used as human food, livestock feed and for industrial purposes. Every part of maize has economic value; the grain, leaves, stalk, tassel and even the cobs are used to produce hundreds of food and non-food products depending on Countries of the world and the locality where the maize is produced. In Nigeria, prior to 2016, there have been different biotic factors (pests) and abiotic factors limiting the maize production. Among the biotic factors include witch weed (*Striga sp*) and various lepidoptera pests like stem borers such as *Sesamia calamistis, Busseola fusca, Eldana saccharina* etc. However, in early 2016 there was outbreak of Fall armyworm in Southern parts of Nigeria (Akinbode et al., 2016a). Thousands of hectares were devoured by this pest. The worst hit cereals

are Maize and Sorghum. Within a year or two, the pest has spread to various parts of Nigeria. Fall armyworm (*Spodoptera frugiperda*) is native to Tropical and Sub -tropical regions of Americas. *Spodoptera frugiperda* defoliates, destroy, and turn leaves of maize to rag looking mass thus reducing photosynthetic ability of the cereals. The adult is a moth. It has complete metamorphosis, and it is the larva stage that is damaging. The damage becomes severe in the drought period when rain temporarily ceases for a period. The adult Fall armyworm is a moth. It is a nocturnal pest and highly migratory and therefore it is transboundary pest. The pest is a threat to food security of the nation Nigeria and Sub-Saharan Africa. The insect is a polyphagous pest and therefore can change the host to alternative host. It is a threat to agro and agro-allied industries. In the area surveyed in Nigeria, average of 395.05 hectares of land area affected per state. Average crop loss of 68.2% has been recorded per state affected by Fall armyworm. An average of $52.7m was lost per State so far since 2016 in States affected by Fall armyworm. Despite that there have been efforts in 12 States in Nigeria as at 2018, many farmers have abandoned maize planting in those parts of the Country while sale of green maize during time of harvest have reduced drastically (Ajiboye et al., 2021).

MATERIALS AND METHODS

Twenty-five improved varieties of maize (*Zea mays* L.) were evaluated at the experimental field of NACGRAB during the early season of 2021 to compare their performance and reaction to fall armyworm infestation under natural conditions. The experiment was laid out as randomized complete block design with three replications. Data recorded were days to anthesis and silking, Anthesis-silking interval, plant height, ear height, plant count at harvest, fall armyworm leaf feeding at week four, six, and eight; and leaf feeding score at week four, six, and eight.

RESULTS AND DISCUSSION

From Table 1, varieties were highly significantly different ($p < 0.01$) for fall armyworm leaf feeding (FAWLF4) 4 weeks after planting. This shows that varieties evaluated show degree of difference in their reaction to fall armyworm leaf feeding at 4 weeks after planting. Some varieties show resistance/tolerance to fall armyworm at 4 weeks old. This was contrary to report of Akinbode et al., (2016b) who submitted that severity of fall armyworm varies with locations but did not vary with maize varies. Also from Table 1, Varieties were highly significantly different ($p < 0.01$) for leaf feeding score 4 weeks after planting. This is in agreement with Guthrie (1989) who submitted that resistance to leaf feeding by first generation European corn borer was easy to find. European corn borer is a Lepidoptera just like fall armyworm.

From Table 2, varieties were highly significantly different ($p < 0.01$) for Fall armyworm leaf feeding at 6 weeks after planting and also significantly different for leaf feeding score at 6 weeks after planting.

From Table 3, varieties were not significantly different for fall armyworm leaf feeding eight (8) weeks after planting (FAWLF8) and for leaf feeding score 8 weeks after planting. This is probably due to the fact that the maize varieties have reached maturity stage at this period which makes leaf feeding not significantly different to determine susceptibility/tolerance of maize.

Conclusion

The results of analysis of variance revealed highly significant ($p < 0.01$) mean squares for all the traits evaluated except for, fall army worm feeding at week 8 and leaf feeding at week 8 suggesting that these improved varieties have potential to serve as breeding materials for these traits. Despite these varieties showed some potential to serve as breeding materials, the non-significant effect fall army worm leaf feeding at week 8 and leaf feeding score at week 8 indicates that the destructive effect of fall army worm is less severe at this stage. Nevertheless, more investigation will be carried out.

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Table 1. Mean squares, means and coefficient of variation of Fall armyworm leaf feeding and leaf feeding score at 4 weeks after planting

Source of Variation	DF	FAWLF4	LFS4
Rep	2	882.61**	5.16**
Varieties	24	667.78**	1.63**
Error	48	139.28	0.47
Total	74	334.02	0.97
CV (%)		31.24	24.72
Mean		37.77	2.76

Table 2. Means squares, means and coefficient of variation fall armyworm leaf feeding and leaf feeding score at 6 weeks after planting

Source of variation	DF	FAWLF6	LFS6
Rep	2	544.36**	7.45**
Varieties	24	474.10**	2.90*
Error	48	90.75	1.02
Total	74	227.34	1.83
CV (%)		25.26	32.55
Means		37.72	3.11

Table 3. Means squares, means and coefficient of variation fall armyworm leaf feeding and leaf feeding score at 8 weeks after planting

Source of Variation	df	FAWLF8	LFS8
Rep	2	5070.52**	0.33^{ns}
Varieties	24	1292.37^{ns}	2.86^{ns}
Error	48	939.24	1.76
Total	74	1165.43	2.08
CV (%)		61.20	40.16
Means		50.08	3.31

*, **, Significant at probability level of 0.05 and 0.01, respectively; ns = not significant, DF= degree of freedom, FAWLF4= Fall Arnyworm leaf feeding at week four, LFS4= Leaf feeding score at week four, FAWLF6= Fall Arnyworm leaf feeding at week six, LFS6= Leaf feeding score at week six, FAWLF8= Fall Arnyworm leaf feeding at week eight , LFS8= Leaf feeding score at week e

ASSESSMENT OF CADMIUM, CHROMIUM AND LEAD CONTENTS OF SOME VEGETABLES AND FODDER PLANTS IRRIGATED WITH WASTE WATER ALONG KWAKWACHI-ZUNGERU WASTE WATER CHANNEL

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ABSTRACT
This study evaluated the level of three different heavy metals namely (viz; Cadmium, Chromium and Lead) pollution in some vegetables (*Amarathus hybridus, Beetroot valguris, Corchorus olitorius, Mentha piperita, Petroselium crispum, Solanum molengena,* and *Talinum triangulari*) and fodder plants (*Albizia lebbeck, Echinochloa pyramidalis* and *Ficus thonnigii*) irrigated with wastewater along kwakwachi-zingeru waste water channel in Kano metropolitan. Atomic absorption spectrophotometeric (AAS) technique was used to analyze the concentrations of these metals. The results obtained showed that the range of Cd was [0.76 to 3.83 mg/kg]; Cr [2.32 to 8.77 mg/kg] and Pb [0.55 to 17.63 mg/kg]. The results obtained were compared with the maximum permissible limits and were found to exceed World Health permissible limits. The results suggested that waste water irrigation has negative impact on the vegetables irrigated along Kwakwachi –Zungeru wastewater channel.

Keywords: fodder, heavy metals, vegetables, waste water

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INTRODUCTION
Vegetables are rich sources of vitamins, minerals, and fibers, also have beneficial antioxidative effects, however, intake of heavy metal-contaminated vegetables may pose a risk to the human health (Ali and Al-qahtani, 2012). They are the primary source of mineral nutrients, vitamins, secondary plant metabolites, and other compounds that support human health and nutrition (Tangahu *et.al*., 2011). Assessment of metal contamination in food items is one of the most important aspects of food quality assurance (Charles *et.al.,* 2018). Vegetables take up heavy metals and accumulate them in their edible and non-edible parts at quantities high enough to cause clinical problems to both animals and human beings. As an example, the consumption of contaminated food can seriously deplete some essential nutrients in the body causing a decrease of immunological defenses, disabilities associated with malnutrition and a high prevalence of upper gastrointestinal cancer (Guerra *et al.,* 2012). Vegetables absorb toxic elements and gather them in proportion to elevate amounts that are enough bases for causing medical complications both in human beings and animals on consuming these contaminated plants (Randhawa *et al.,* 2014). Fodder plants serve as source of essential metals for grazing animals and the mineral status of these forages is a function of multiple factors, which interact with one another to produce varied effects and one of such factors is the differences caused by climatic changes. It is important to know the micro-nutrient concentrations of fodder plants because livestock performance is based largely on nutrition in terms of both quality and quantity (Amune and kakulu, 2012). It has been said that Forages increasing in polluted environment can congregate heavy metals at elevated concentrations, posing grave danger to animals and human physical state (Ahmad *et al.,* 2013). Robinson,(2010) suggested that forage plants absorb most of the minerals and heavy metals from the soil and polluted air and most of the heavy metals have a great concern for livestock due to their toxic effects. The nutrition of grazing animals is a complicated interaction of soil, plant and animal whereas plants are the main source of food for the animals (Ahmad *et al.,* 2013).

MATERIALS AND METHODS
In the preparation of reagents, chemicals of analytical grade purity and deionised water were used. All glasswares were washed with liquid detergent and rinsed with distilled water before drying in an oven at 105°C. All weighing were done using analytical weighing balance model FA2004 and analysis of the metals was done using Agilent Atomic Absorption Spectrophotometer (AAS) model 200 series 240FS.

Sample collection

The seven different vegetable samples (viz:*Amarathus hybridus,AH, Beetroot valguris BV, Corchorus olitorius CO, Mentha piperita MP, Petroselium crispum PC, Solanum molengena SM,* and *Talinum triangulari TT*) and three different fodder plants(viz :*Albizia lebbeck AL, Echinochloa pyramidalis EP* and *Ficus thonnigii FT*) were collected from kwakwachi/zungeru irrigation sites and all samples were washed with deionized water to remove any adhered materials and soil and stored in polyethylene bags and coded.

Sample pre-treatment

Vegetable**s** and fodder plants samples were cut into small pieces, dried at 105°C for 2 hours in an oven and were pounded using pestle and mortar until a powder was produced which was stored in an air-tight plastic container.

Preparation of Reagents

All reagents were analar grade and used without further purification. Glass wares were washed with warm detergent solutions, rinsed with deionized water and oven dried at 50°C. 2.103 g of cadmium nitrate $Cd(NO_3)_2$ was dissolved in 100 cm^3 of deionized water, the solution was later diluted to 1000 cm^3 mark of volumetric flask with deionized water, the standard working solutions were prepared by diluting different portions of the stock solution to give the standards with concentration ranges from 0.2 1.0 ppm. 7.696g of chromium nitrate $(Cr(NO_3)_3.9H_2O)$was dissolved in 100 $cm^3$of deionized water, the solution was later diluted to 1000cm^3 mark of volumetric flask with deionized water, the standard working solutions were prepared by diluting different portions of the stock solution to give the standards with concentration ranges from 0.2 – 1.0 ppm. 1.59 8g of lead (II) nitrate $Pb(NO_3)_2$ was dissolved in 100 cm^3 of deionized water, the solution was later diluted to 1000 cm^3 mark of volumetric flask with deionized water, the standard working solutions were prepared by diluting different portions of the stock solution to give the standards with concentration ranges from 0.2 1.0 ppm.

Digestions of vegetables/plants Samples

1.0 g portion of each finely ground vegetable and fodder samples were weighed separately into a pyrex beaker of 250 cm^3 and 10 cm^3 of 1:3 ratio of HNO_3 and HCl was added. The mixture was digested on hot plate until a clear solution was obtained, the beaker was then allowed to cooled and content was then diluted with 20 cm^3 distilled water in 50 cm^3 volumetric flask (Funtua *et al*., 2008). This was done in triplicate, blank solution was also made. The solution was analyzed for Cadmium, Chromium and Lead using Agilant Atomic Absorption Spectrophotometer (AAS). A calibration plot of absorbance against concentration of each element under investigation was plotted from which the concentrations of the elements were obtained by extrapolation (Musa, 2011)

Data analysis

The statistical analysis of all data was conducted using SPSS software (version 20.0). One way ANOVA was used to determine the significance difference of the elements in the samples at $p < 0.05$ of significance level.

RESULTS AND DISCUSSION

The results of the analysis of these metals concentration in vegetables and fodder plants irrigated with wastewater along Zungeru (a) and Kwakwachi (b) are presented in Figures 1a,b - 3a, b

DISCUSSION

A total of ten samples obtained from kwakwachi and zungeru irrigation sites were analyzed for, Cd, Cr and Pb. Figures 1a and 1b showed the distribution pattern of cadmium (Cd) average concentration in vegetables samples analyzed ranged from 0.76 mg/kg to 3.83 mg/kg. The highest content was found in *B. valgurus* (3.83 mg/kg). According to FAO/WHO (2002) the permissible safe limit of cadmium is 0.3 mg/kg but all the samples analyzed were above the permissible limit, the accumulated levels of cadmium in all the plants is as a result of the use of wastewater and solid waste (Guerra *et al.,* 2012). Bigdeli and Seilsepour (2008) investigated the accumulation of heavy metals in some vegetables irrigated with waste water reported the concentration of cadmium in Eggplant, Mint leaves and Coriander as 0.12, 0.09 and 0.13 mg/kg respectively which are lower than the findings of this work. Results of statistical analysis, has shown the variation in cadmium concentration across all the plants at ($p < 0.05$).

The average concentration of chromium in all the samples analyzed range from 2.32 mg/kg to 8.77mg/kg; (Figures 2a and 2b). *E. pyramidalis* was found to be the highest and *B.valgurus* has the least concentration, statistically *E. pyramidalis* shows significant different to *S. molegena*, *M. piperita*, *A. hybridus, T. triangulare*, *B. valgurus*, While *T. triangulare* and *B. valgurus* shows no significant to all the plants ($p < 0.05$), (Tables 1 and 2). Deribachew *et al.,* (2010) reported the concentration of chromium in Cabbage and

Potato as 4.8 and 5.1 mg/kg, which are comparable to our findings and are above the recommended limit of 2.30 mg/kg (FAO/WHO 2002). The level of heavy metals in plants depends mainly on the levels of soil contamination and plant species (Askira *et al*., 2014).

The average mean concentration of Lead in this study range from 0.00 mg/kg (not detected) to 17.63 mg/kg as it is clearly seen from figures 3a and 3b. Statistically, *E.pyramidalis* shows significant different to all the plants followed by *P. crispum* and *B. valgurus* showed no significant different to all the plants ($p < 0.05$). The levels of lead found in this work were several folds higher than the recommended safe limit of 0.3 mg/kg (FAO/WHO, 2001), except for *T. triangulari* and *B. valgurus*. The high level of Lead in these plants samples analyzed may possibly be as a results of a solid waste from different angle into the waste water channel and is used to irrigate the plants. Oluwole, *et al*., (2013) reported the elevated concentration of Lead in some plants could be as results of pollutants from waste water, farm soil or due to pollution from the highways traffic, which is similar to the findings of this work.

Conclusion

This study presents the concentrations of three heavy metals pollutants in some vegetables and fodder plants consumed by populace in Kano metropolitan. The study revealed the concentrations of Cd, Cr and Pb determined in levels found to be above the tolerable limit for human consumption. The results found showed that waste water irrigation has negative impact on the vegetables irrigated along Kwakwachi Zungeru wastewater channel. Maleki and Zarasvand (2008) reported that too much content of these metals in food is linked with a number of diseases, especially of the cardiovascular, renal, nervous and skeletal system. Foodstuffs grown on contaminated soil or irrigated with wastewater can accumulate toxic metals and ingestion of such foods could be detrimental to animal and humans health. (Aslam *et.al*.,2010).

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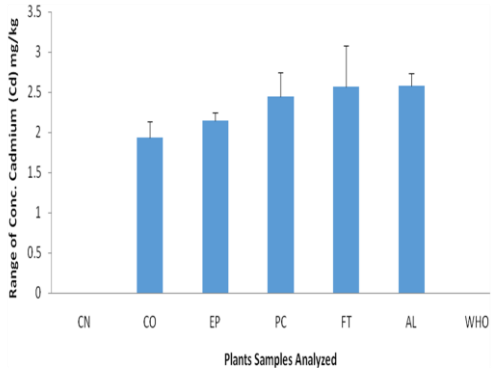

Figure 1a. Mean concentration of cadmium in the plants samples analyzed (mg/kg)

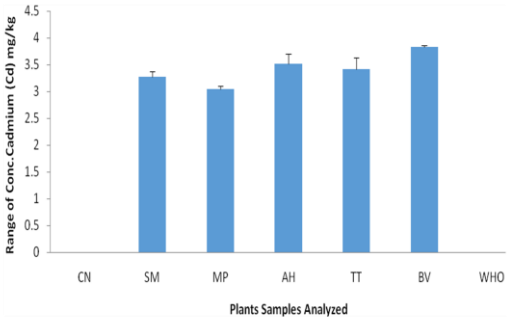

Figure 1b. Mean concentration of cadmium in the plants samples analyzed (mg/kg)

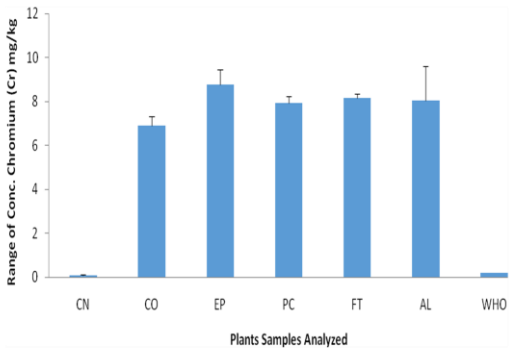

Figure 2a Mean concentration of chromium in the plants samples analyzed (mg/kg)

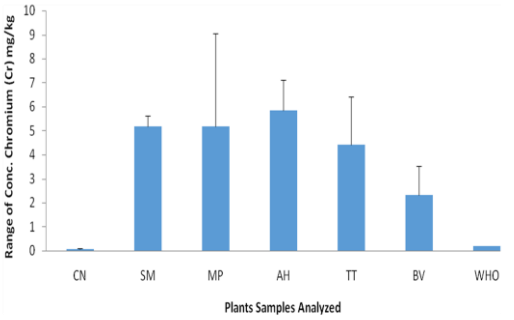

Figure 2b. Mean concentration of chromium in the plants samples analyzed (mg/kg)

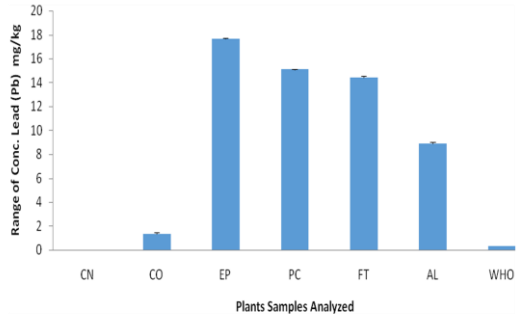

Figure 3a. Mean concentration of lead in the plants samples analyzed (mg/kg)

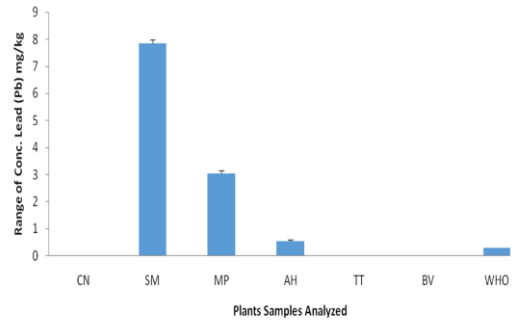

Figure 3b. Mean concentration of lead in the plants samples analyzed (mg/kg)

Table 4.1. Shows the mean concentration (mg/kg) of essentials and non-essential metals in soil samples from the sampling sites and control

Sites	Cd	Cr	Pb
KW	0.01±0.01	ND	0.05±0.04
ZW	0.01±0.01	ND	0.12±0.00
CW	0.05±0.01	0.02±0.01	0.02±0.01
NESREA/WHO	0.2	0.05	0.05

Table 4.2. Shows the mean concentration (mg/L) of essential and non-essential metals in waste water samples used for irrigation from the sampling sites and control

Sites	Cd	Cr	Pb
KS	ND	ND	18.00±6.08
ZS	ND	3.47±0.12	30.67±9.29
CS	3.93±1.24	0.20±0.35	0.25±0.31
NESREA/WHO	03-Jun	0.1	85

PERFORMANCE EVALUATION OF CASTOR SEED OIL ALKYD PAINT

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ABSTRACT

The performance characteristics of alkyd paint film derived from castor seed oil were determined in terms of chemical resistance, drying schedules and light fastness. The films were prepared by applying a thin spread of the alkyd paint on a clear glass panel and dried at room temperature. The drying process was monitored in terms of time-set-touch, surface-dry and dry-through. The chemical resistance was determined using ASTM (D 1308-67) standard test method at room temperature, the resistance of the paint film to different solvent media (Water, KOH, H_2SO_4, NaCl) were determined. The result obtained showed that Castor Seed Oil Alkyd Paint Film exhibits good performance characteristics.

Keywords: chemical resistance, drying schedule, light fastness, set-to-touch, dry- through

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INTRODUCTION

Castor bean is cultivated for the seeds which yield viscous, pale-yellow, non-volatile and non-drying oil. It has been used for industrial and medicinal purposes. However, medicinally, it is widely used as a human laxative cathartic agent. Particularly, in cases of certain radiological examinations, which require prompt and through evacuation of the small intestine (Stubiger *et al.*, 2003). Its botanical name is *recinus communis L* of the family *Eurphobiaceas*a plant indigenous to many parts of the world. Castor oil is one of the few naturally occurring glycerides with high purity. Since the fatty acid portion is nearly 90% of recinoleic. The oil is not only a naturally occurring resource, it is also inexpensive and environmentally friendly (Salimon *et al.,* 2010). Castor oil has been valued as non-drying oil for its lubricating and hydraulic properties. However, it has been reported that its modification by severe dehydration resulted in an oil with excellent drying properties for use in the production of alkyd resin (Onukwli *et al.,* 2008). The extracted castor oil inhibited the growth of all the test organisms. Among the gram-positive bacteria *staphloccucus aureus* was the most sensitive and micro *coccus luteus* was the least sensitive. Generally, the oil was found to be more effective on bacteria than fungi (Momoh *et al.,* 2012).

Vegetable oils are triglycerides which typically consist of glycerol and saturated and/or unsaturated fatty acids. The composition of the fatty acids contained in oil will determine its industrial use. The general structure of triglycerides is shown in Fig. 1.1 (H_2C-O-CO-R, HC-O-CO-R', H_2C-O-CO-R"). Fig1.1 General structure of triglycrides. From a chemical point of view, triglycerides offer two reactive sites, the double bond in the unsaturated fatty acid chain and the carboxylic acid group of the fatty acid chain (Odetoye *et al.*, 2008). The oils that are mostly employed for alkyd resin synthesis are linseed, soybean and tall oils. These oils are largely imported to Nigeria for the formulation of coatings for metal cans used in packaging beverages, foods, drugs, etc. However, vegetable oils are available locally, which remained untapped. These include mahogany seed oil, castor seed oil, tobacco seed oil, etc. These vegetable oils owe their values as raw materials for decorative and protective coatings to their ability to polymerise or dry after they have been applied to surface forming tough, adherent, impervious, and abrasion resistance films (Momodu *et al.,* 2011).

The pharmacological study and physico-chemical characterization of Khaya senegalensis seed oil found that, the seed oil resembled the simple linoliec-oleic-palmitic type. And the oil showed anti-inflammatory and a minimal antibacterial activity (Karigal *et al.*, 2010). The percentage oil yield and physiological properties of different ground nut species (*Arachis hypogea*) showed that, the crude ground nut oil contained higher level of all the physiological properties tested than the refined oils. But in the contrast the crude oil is more liable to rancidity (Nkafamiya, *et al.*, 2010). The fatty acid composition and physico-

chemical properties of Malaysian castor bean, Resinus communis L. seed oil, showed that the oil contains relatively high lipid contents (Salimon *et al.*, 2010). The synthesis and evaluation characteristics of walnut seed oil-modified alkyd resin, revealed that, the oil gave alkyd resin whose coating properties are comparable to those of commercial resins J57 (Momodu *et a*l., 2011). Industrial utilization of castor oil for alkyd synthesis and evaluation studies found that, dehydrated castor oil can be transformed to a resinous material capable of being used as a potential binder for paint and varnishes (Ogunniyi, *et al.*, 1998). The utilization of alkyd-epoxy blends as a multi-purpose coating showed good performance of the blends with respect to drying time, hardness, flexibility, gloss, thermal stability and chemical resistance, in particular against alkalis (Dutta, *et al.*, 2006).

Vegetable Oils as Polymeric Coatings

Alkyd Resins

Alkyds are oil modified polyesters consisting of a polyol (usually glycerol, trimethalol propane or pentaerythritol), a multi-functional acid (phthalic acid or trimellitic acid) and an unsaturated fatty acid formed by poly-condensation reaction. They find important application as binders in surface coatings. They are classified as short (30 – 42%), medium (43 – 54%), long (55 – 68%) and very long (≥ 68%), based on the percent weight fraction of vegetable oil in the resin (Manawwer *et al.,* 2014). Alkyds resins are the reaction products of polybasic acids, polyhydric alcohols and monobasic fatty acids or oils. It is a chemical combination between oil or oil derived fatty acids and polyester polymer, thus enhancing the mechanical properties, drying speed durability of these oleoresinous vehicles formed over and above those compared with the oil themselves. These resins, today comprises about half of all resins used in the surface coating industry. In spite of a large number of other synthetic resins being available for use in paint formulations, the alkyd resins surpassed all of them in versatility and low cost together with a broad spectrum of performance properties (Shaker *et al.,* 2012). The structure of a typical alkyd resin is given in Fig 1.1 About 60 – 70% of an alkyd resin comprises of biologically derived or degradable raw materials; fatty acids, glycerol, pentaerythritol and the rest as non-biodegradable (phyhalic acid). Alkyds are available in two forms i.e. 'drying" or "non-drying" alkyds; the former refers to alkyds with drying vegetable oils, containing polyunsaturated fatty acids while the latter refers to alkyds obtained from non-drying vegetable fatty acids. They show a good gloss retention, durability, and weathering resistance while poor chemical resistance, particularly in alkaline media due to the presence of higher number of ester groups (Dutta *et al.*, 2006).

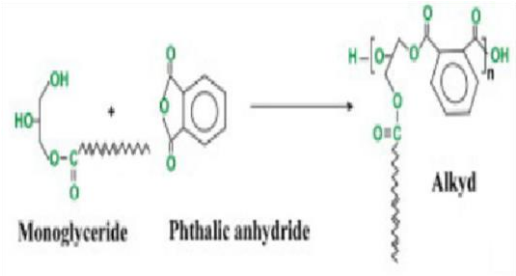

Fig. 1.2. Chemical transformation of VO to alkyd (Manaweer, *et al.*, 2014)

Paints

Paints are described as a colloidal mixture of chemical substances which when spread over a surface in a thin layer, form a solid, cohesive and adherent film. They are used in our daily life for decorative purposes as well as for protecting surfaces against environmental effects like UV-radiation, chemical inversion and mechanical stresses. A conventional paint consists of binder, pigment, solvent and additives. The polymer-binding material (alkyd resin) with a large extent of variations is responsible for the formation of continous film that adhere to the substrate and hold other sub-substances together (Ogunbisi *et al.,* 2014).

Composition of Paints

A coating can only preserve an article if it is durable itself. Furthermore, the coating film must not become detached from the substrate to be protected if lasting protection is to be achieved. Since the coating always has to adhere closely to the substrate, the coated area may be regarded as a composite material. Careful coordination of the coating and the substrate is equally as important as appropriate preparation of the surface prior to application. Contamination of the interface between the work piece and coating with foreign substances may cause failure of the material under mechanical loads or under attack by environmental influences (Clausen, 1980).

The basic components of paint include:

- **The film forming substances** can either be macromolecular products or low molecular mass compounds that react to form macromolecules on curing eg. rsesins, plasticisers, pigments, extenders.
- **Additives** this denotes auxiliary products that, even in small concentrations, significantly improve the mechanical properties of paints or films. They are classified according to their effects. eg driers, antiskinning agents, curing, leveling agent, wetting, antifloating and antiflooding agents, dispersion agents, flattening (matting) agents.
- **Solvents** are volatile fluids that evaporate from the coatings during the film-forming processes. They are very important components of liquid paint formulations. E.g. mineral spirit, xylene, or butyl acetate (Clausen, 1980)

MATERIALS AND METHODS

Materials

Castor and seed oil was purchased from Kasuwar Kurmi market in Kano city, Kano Nigeria. All chemicals and solvents used were of analytical grade and were used without further purification. The glasswares used were washed with detergent, rinsed with distilled water and dried before used. All weighings were carried out on an electric Mettler balance model H30AR, iodine value, saponification number, acid value, percentage free fatty acid, specific gravity was carried out using burrette, standard laboratory apparatus. FTIR spectral analysis of the castor and mahogany seed oils and alkyd resin samples were recorded in the range of 4000 – 650 cm^{-1} using CAREY630 machine, viscosity measurements of alkyd resins and formulated paint samples were carried out using BrookField DV-E Viscometer with spindle size-61. Antimicrobial activity studies were carried using petridishes in an incubator.

Methods

Formulations of the Alkyd Paints

Three different formulations containing 0 g, 10 g, and 20 g of the alkyd resin from castor seed oil were produced. In each formulation, red ferric oxide was mixed with white spirit before adding to the alkyd resins. Also paint additives such as extenders, thickeners and driers were added and stirred to obtain a homogeneous mixture. Table 4.1.9 and 4.2.0 show the various formulations of the alkyd paints prepared.

Performance Evaluations of the CSO Alkyd Paint Films

The performance characteristics of the films were determined in terms of chemical resistance, drying schedules, and light fastness. Films of both castor and mahogany seed oil alkyd paints were prepared by applying a thin spread of the resin on clear glass panel and dried at room temperature. The drying processes were monitored in terms of the time of set-to-touch, surface-dry and dry-through (Momodu *et al.*, 2011). The chemical resistance was determined using ASTM (D 1308 – 67). Standard test method at room temperature, the resistance of the films to different solvent media (water, KOH, H_2SO_4, NaCl) was determined. Table 4.1.2, 4.2.3, and 4.2.3 show detailed accounts of the chemical resistance, drying schedules and light fastness tests respectively.

RESULTS AND DISCUSSION

Table 3.1.0 shows the physico-chemical properties of the alkyd resin prepared from the reactions between the castor and mahogany seed oils with glycerol and phthalic anhydride. The colour of the alkyds are black and dark brown for the castor and mahogany seed oils respectively as compares to their corresponding precursor oils. The darkening in the colour of the alkyds could be attributed to the high temperature of the reaction, oxidation and the catalyst (MacDonald, *et al.*, 1994). The acid values and viscosities of the alkyd are lower compared to the commercial standards C-AKD and L-AKD (Shaker *et al.,* 2012).

Table 3.2.0 shows the constituents of the formulations of the castor seed oil modified alkyd resin paints. From the table, three different formulations containing 0 g, 10 g and 20 g of the castor seed oil modified alkyd resin were produced. They were coded CSO-R_1 for the first formulation containing 0 g resin and CSO-R_2, for the second formulation containing 10 g resin and the CSO-R_3 containing 20 g resin.

Table 3.3. shows the chemical resistance characteristics of the different alkyd resin paint formulations of both castor and mahogany seed oil. The performance characteristics of the films were determined in terms of chemical resistance, drying schedule and light fastness. From the table, the films of the different formulations of the alkyd paints prepared were subjected to alkali resistance test where they showed poor resistance. But for acid resistance

both alkyd films proved to be resistant, so also, for brine and water. However, poor resistance to alkali may be explained on the basis that they consist essentially of ester group, which are known to be susceptible to hydrolysis by alkali (Momodu *et al.*, 2011).

Table 3.4. shows the drying schedule of the different formulations of oil the alkyd resin paints at an ambient temperature. The drying times of coating are significant in determining when a freshly painted room, floor or stair may be put back to use or a coated article handled or packaged. Slow drying may result in dirt pick-up or on an exterior surface, moisture may cause non-uniform appearance. The set to touch condition is reached when the film has solidified sufficiently, by evaporation or chemical reaction or both, that it no longer flows nor sticks to a finger that lightly touches it. In this test method, the set-to-touch time is reached when a pear – shaped depression appears in the film when it stops flowing. The surface dry condition is reached when the film surface has cured, so that the film does not adhere to very light objects on it (ASTM, 2003).

For the set-to-touch drying test the result was 15, 28, 40, min. for the blank, CSO-R_1, CSO-R_2 respectively for the surface dry test the results are: 30, 120, 140 minutes for blank, CSO-R_1, CSO-R_2. From the above deductions it shows that for the castor seed oil alkyd resin paints generally have a good drying property.

Table 3.5. shows the light fastness test for the different alkyd resins paint formulations, using artificial light for 96 hours. The applied colour is checked for light fastness using blue wool standards which consist of eight strips of wool fabrics, each dyed using different dye with different light fastness properties, with a scale of 1 to 8. The samples were placed in a special light fastness cabinet (Microscal Fastness Tester MK1) fitted with mercury-tungsten (MBTF) 500-watt lamp, whose spectral composition is similar to that of sunlight. Part of test strips and the sample are exposed to the light and part of them are covered to be used as a reference. This standardized test is run until the most lightfast test strip level 8 has begun to fade slightly. The colour sample are then compared to the test strips and given light fastness rating. The rating consists of the level of the blue scale whose colour most closely corresponds to the change in the coloured samples (Schminke, 2010). The light fastness of all the samples range between 6 and 7 as shown in table 3.5. hence, the ratings of the samples were assigned by comparing the samples to that of blue wool standard. The sample is given a scale rating which most closely corresponds to the change in colour as that of the sample. Therefore, in general all the samples have a good to very good light fastness.

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Table 3.1. The Physico-Chemical Properties of Alkyd Resins

Properties	CSO-resin	C-AKD	L-AKD
Colour	Black	Brown	Brown
Acidvalue(mg/g)	11.00	25.80	35.60
Viscosity (cp)	3.84	10.00	12.80

Table 3.2. The constituents of formulations of the alkyd resin paint films derived from castor seed oil

Components	CSO-R_1	CSO-R_2	$CSOR_3$
Solvent	42	42	42
Resin	0	10	20
Pigment	15	15	15
Extender	5	5	5
Thickner	2	2	2
Drier	0.3	0.3	0.3

CSO-R_1 = castor seed oil resin paint containing 0 g Resin, CSO-R_2 = castor seed oil resin paint containing 10 g Resin, CSO-R3 = castor seed oil resin paint containing 20 g Resin

Table 3.3. Chemical resistance of castor and alkyd paints films

Test	Blank	CSO Paint	
		10(g)	20(g)
Alkali (0.1 M KOH)	2	2	2
Acid (0.1 M H_2SO_4)	2	1	1
Brine (5% w/w)	2	1	1
Distilled water	1	1	1

1 = Film not removed 2 = Film removed

3.3. Drying schedules tests for the alkyd paints films

Characteristics	Blank	CSO-R_1	CSO-R_2
Set to touch (mins)	15	28	40
Surface dry (mins)	30	120	140
Dry through (hour)	2	24	30

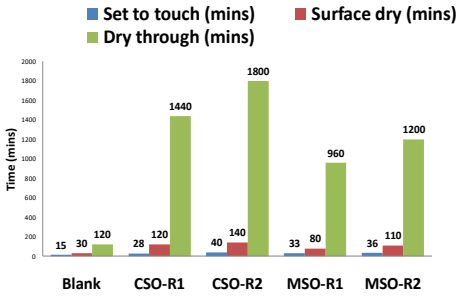

Fig. 4.3: Drying time of different CSO and MSO Alkyd Resin Paints

3.4. Light fastness tests for the alkyd paint films

Samples	Grade	Degree of fading	Lig
CSO R_2	7	Very slight fading	Ex
CSO R_1	6	Slight fading	Ve
Blank	4	Appreciable fading	Mo

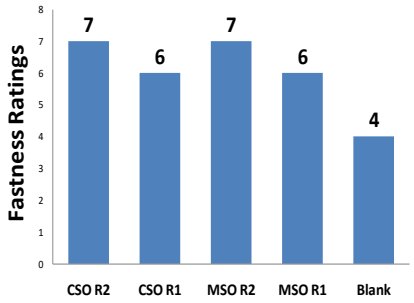

Fig.4.4: Light fastness test MSO and CSO Alkyd Resin Paints

OPTICAL SENSING APPLICATION OF NI-SUBSTITUTED BARIUM TITANATE/POLYANILINE NANOCOMPOSITES

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ABSTRACT

Ni^{2+} substituted $BaTiO_3$ tetragonal perovskite ceramics with composition formula $Ba_{1-X}NixTiO_3$ were synthesized by sol-gel method route, the synthesized ceramics were ground, pre-calcinated at 800°C and calcinated at 950°C to get nano-sized particle. Polyaniline (PANI) was prepared by oxidative polymerization of aniline monomer using ammonium persulphate. Barium nickel titanate polyaniline composite were made by mixing the duo in 1:1ratio after which they were ground thoroughly to make the homogeneous mixture for analyses. The composites were characterized using X-ray diffraction (XRD), Fourier transforms infrared (FTIR), UV-vis spectroscopy, field emission scanning electron microscopy (FE-SEM). The band gaps are 2.63, 2.49 and 2.02 for $BaTiO_3$/polyaniline, $Ba_{0.9}Ni_{0.1}TiO_3$/polyaniline, and $Ba_{0.8}Ni_{0.2}TiO_3$/polyaniline respectively. The band gap values are much lower than that of normal barium titanate (3.2eV) as observed from the literature and this is due to the presence of polyaniline which is conducting material minimizing the Fermi level between valance and conductive band. The nanocomposites may useful as optical sensor.

Keywords: barium titanate, band gap, optical sensing, polyaniline,

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INTRODUCTION

An insulating property of ferroelectric materials have attracted much attention due to the possibility of application to various electronic devices such as memory cell capacitors, high-density random-access memories (ferroelectric RAMs), and dynamic RAMs. It is well known that perovskite ABO_3-type $BaTiO_3$ (BTO) is an excellent ferroelectric crystal with the band gap about 3.8 eV and the ferroelectric–paraelectric transition temperature above 400 K and it is extensively used as dielectric in multilayer ceramic capacitor (MLCC) because of its high permittivity and low loss. Their applications do not stop there, $BaTiO_3$ can be used in devices like sensor, transducer, microwave filter, infrared detector, heater and dynamic random-access memory (Buscaglia *et al.*, 200). In recent years, fruitful researches are being conducted on the doped barium titanate materials, that is the impact incorporation of impurities on ferroelectricity, dielectric constant, capacitance, optical properties and phase transition nature of $BaTiO_3$ ceramics (Gou *et al.*, 2012). A large number of works focused on how to modify those properties, this can be achieved introducing the impurities by doping with some transition or rare earth metals or composites with some conductive polymers such as polyaniline. Polyaniline (PANI) is homopolymer having benzenoid, quinonoid or both molecular formulas that exist in different proportions. Polyaniline has been known as conducting polymer since 1862 discovered by D. H. Letheby (Ezzati *et al.*, 2018; Bhandari, 2018; Ran *et al.*, 2018). It drawn greater attention of scientists due to its' high electrical conductivity, rich chemistry and attractive processing properties. Polyaniline can be easily prepared either chemically or eletrochemically from acidic aqueous solutions. The chemical method has a large significance because it is very reasonable method for the mass production of PANI. The most common preparation method is by oxidative polymerization with ammonium peroxodisulfate as an oxidant. PANI composites with metals, metalloids and nonmetals were studied and recorded a considerable progress. Polyaniline

composites with inorganic materials like BaTiO3, and other inorganic salts were investigated for their optical properties.

MATERIALS AND METHODS

$Ba_{1-x}Ni_xTiO_3$ (x=0.0, 0.1, 0.2) powder of pure and doped $BaTiO_3$ ware prepared by sol–gel method. This chemical method has the advantage that it is relatively simple, easy, stoichiometric composition control and low cost. Weighted amounts of the appropriate proportions of high purity barium nitrate, nickel nitrate, titanium dioxide and citric acid precursors, were dissolved in 100 ml of distilled–H_2O contain 500 ml beaker. The solution was heated on magnetic stirrer at 100°C stirred by magnetic bit until the solution turned into gel and finally into ceramic. The ceramic was ground, pre-calcined at 800^0C and calcined at 950^0C in muffle furnace. This is how Doped nickel barium titanate in the form of powder was produced. Polyaniline was synthesized via oxidative polymerization method. In this method 23.28 gm of aniline monomer was gradually poured into 91.15 ml of hydrochloric acid at 0^0C in a chilled ice bath followed by addition of 40.47 gm ammonium persulphate dissolved in distilled water. The polymer was confirmed to be formed as the solution turned into dark green precipitate. The solution was continuously stirred for an hour after which distilled water was added. The solution was filtered and washed with distilled water and methanol until the clear filtrate was obtained. The sample was dried in an oven at 60°C for 48 hours.

RESULT AND DISCUSSION

XRD analysis

Fig. 1 shows the XRD pattern of Ni doped $BaTiO_3$/PANI nanocomposite. According the JCPDS card no (050625), single phase $BaTiO_3$ with presence of traces of barium carbonate as secondary phase formed during the synthesis was observed at undoped (0.0) and first doping (0.1) peaks at 950°C.Crystal peaks appeared in all patterns but increases as the Ni contents increases. Shoulder at the peak with hkl (002) 45.5-45°C appeared at the first doping which indicates changing from cubic to tetragonal phase. Splitting of this peak, (002) and (200) indicated clearly the presence of tetragonal phase of $BaTiO_3$ in these powders. As the concentration of Ni in $BaTiO_3$ increases, the (002) intensity at 45°C is increasing. The analyses showed that $Ba_{1-x}Ni_xTiO_3$ Ceramics are tetragonal symmetry in the space group P4 mm.In the same fig small broad peak at 2θ = 25° show the presence of PANI and also show some degree of crystallinity in undoped and first doping of nickel in barium titanate.

FTIR analysis

Fig. 2 shows the FTIR pattern for synthesized $Ba_xNi_{1-x}TiO_3$ which pre-calcinated at 800°C and calcinated at 950°C for 6 hours and the spectra showed the peak around 300-500 cm^{-1} which is due to Ti-O vibration and carbonate peaks (CO_3^{-2}) at 851.71, 1051.15, 1425.45, 164766 and 2337.07 cm^{-1}. The carbonates peaks realized are due to the presence of $BaCO_3$ secondary phase. The Ti-O absorption peak got narrower and sharper which shows the crystallinity of the material as the number of vibrational molecules decreases and amorphous TiO_2 transform into octahedrally TiO_6 as confirmed by XRD in Fig 5 (Mo *et al.*, 2008). The intensity of carbonate peaks diminishes as the nickel doping increases, which shows the decreasing of impurities. The bands present in the TiO_6 octahedral are O-Ti-O bending (390 cm^{-1}) and Ti-O stretching (538 and 630 cm^{-1}) (Jin *et al.*, 2009). In addition to the peaks of T-O, CO_3^{-2} , various peaks are observed which indicates the presence of polyaniline in the composite. These peaks include C-C, C=C, C-N, C-H, N-H and 1-4 disubstituted aromatic ring (benzenoid) at 1141, 1588, 1330.75, 2948.23, 3464 and 814.45 cm^{-1} respectively. The carbonate peaks around 2380 cm^{-1} increased at the first nickel doping (0.1) and then dramatically decreased at the second doping of nickel (0.2) to show the a little or absence of carbonates impurity from barium carbonate ($BaCO_3$). The spectra also show the peak at 1500 cm^{-1} and 1550 cm^{-1} may be due to quinanoid and benzenoid rings respectively.

FESEM/EDX/mapping analysis

Fig. 3 (a) and (b) presents the FESEM, EDX spectra and elemental mapping of barium titanate/PANI for nanocomposites $BaTiO_3$/polyaniline and $Ba_{0.9}Ni_{0.1}TiO_3$/polyaniline respectively. Both nanocomposites show different morphologies with agglomeration of the nanoparticles of barium titanate and polyaniline. The barium titanate nanoparticles are well embedded in the polyaniline. Two possible scenario results in the current morphology, the first being the surface amorphous structures of the polyaniline crystallized in situ and the small nanoparticles of barium titanate merged into larger ones. The second is that the surface amorphous structure of polyaniline nanoparticles diffused quickly to the

surface of the barium titanate particles and then crystallized. The EDX spectra and elemental mapping shows all the substituted elements for polyaniline and barium titanate. Hence, the stoichiometry of the prepared nanocomposites is maintained.

Optical properties

The optical band gap energy (E_{gap}) was determined by using the method proposed by Wood and Tauc formula. Thus, the value of band gap (E_{gap}) of barium nickel titanate/polyaniline composite was obtained by extrapolating (tangent) the linear portion of the curve or tail (y=0) in the UV-Vis Absorbance spectrum. The Wood and Tauc formula are given as

$$\alpha h\upsilon = A\left(h\upsilon - E_g\right)^n \quad (1)$$

Where E_g is band gap energy, A is constant, h is plank's constant, υ is frequency and α is absorption. From the Fig. 4 the band gap spectra values are much lower than that of normal barium titanate (3.2 eV) as observed from the literature and this is due to the presence of polyaniline which is conducting material minimizing the Fermi level between valance and conductive band. The band gap for $BaTiO_3$/polyaniline, $Ba_{0.9}Ni_{0.1}TiO_3$/polyaniline, and $Ba_{0.8}Ni_{0.2}TiO_3$/polyaniline are 2.63, 2.49 and 2.02 respectively.

Conclusion

BNT/PANI composites were successfully synthesized by thorough mixing of barium nickel titanate and polyaniline in 1:1 ratio. Nanoparticles formations in the composites were confirmed by XRD, FTIR, FE-SEM and ultraviolet (UV) visible spectroscopy. The XRD spectra pattern shows the intensity of the peak transforming from cubic to tetragonal as the nickel concentration increases. FTIR pattern shows the formation of Ti-O stretching, C=C, N-H, disubstituted benzenoid functional groups confirming the formation of polyaniline and traces of carbonates impurities which disappear as nickel concentration increases. FE-SEM.UV analyses gives the ban gap which is decreases drastically as compare with BNT as the nickel concentration increases, the drastic falling of band gap may be due conducting property of polyaniline. Polyaniline is good for reducing the Fermi level which also decreases the energy gap from valence bond and conducting band.

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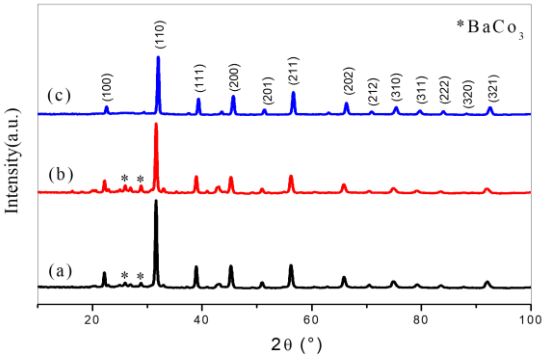

Fig. 1. XRD spectra of barium titanate/polyaniline nanocomposites (a) $BaTiO_3$/polyaniline, (b) $Ba_{0.9}Ni_{0.1}TiO_3$/polyaniline, and (c) $Ba_{0.8}Ni_{0.2}TiO_3$/polyaniline

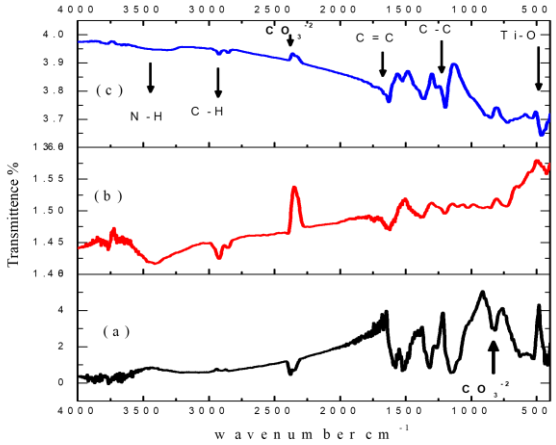

Fig. 2. FTIR spectra of barium titanate/polyaniline nanocomposites (a) $BaTiO_3$/polyaniline, (b) $Ba_{0.9}Ni_{0.1}TiO_3$/polyaniline, and (c) $Ba_{0.8}Ni_{0.2}TiO_3$/polyaniline

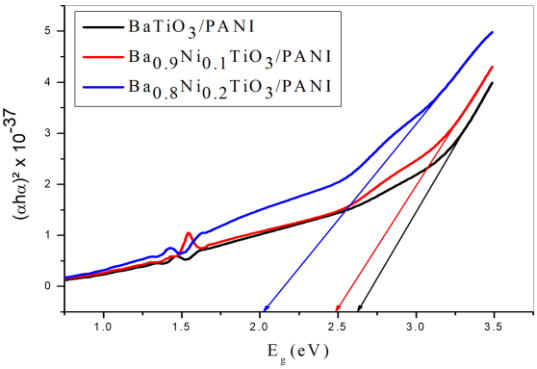

Fig. 4 Band gap of barium titanate/PANI nanocomposites

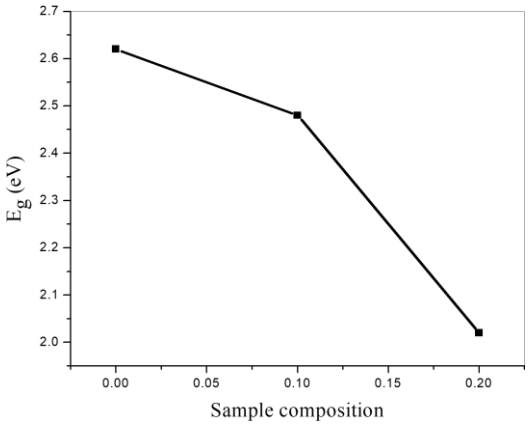

Fig. 5. Variation of band gap with composition of barium titanate/PANI nanocomposites

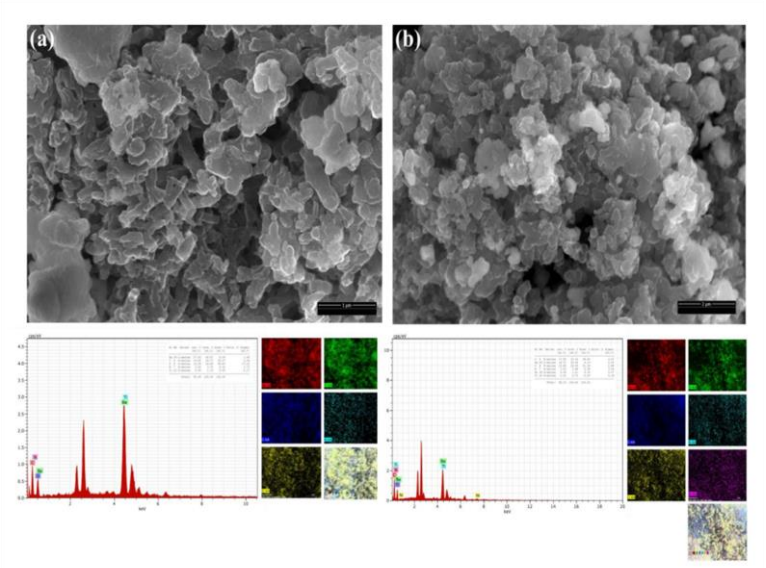

Fig. 3 FESEM, EDX spectra and elemental mapping of barium titanate/PANI nanocomposites (a) $BaTiO_3$/polyaniline and (b) $Ba_{0.9}Ni_{0.1}TiO_3$/polyaniline

EFFECTS OF GAMMA IRRADIATION ON THE AGRO-MORPHOLOGICAL TRAIT OF SELECTED NIGERIAN SPINACH (*Amaranthus hybridus* L.) ACCESSION

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ABSTRACT

The mutagenic effects of gamma irradiation on the agro-morphological traits of spinach accessions were investigated to induce useful genetic variability for further breeding programme. Seeds of two spinach (*Amaranthus hybridus* L) accessions (GWM-002 and GWM-003) were collected from the Plant Biology Departmental Seed gene bank, Federal University of Technology Minna, Niger State. The seeds were exposed to five different gamma irradiation doses (0 Gy, 50 Gy, 100 Gy, 150 Gy, 200 Gy) at Centre for Energy and Research Training (CERT), Ahmadu Bello University, Zaria, Nigeria. The irradiated and the control seeds were planted at Department of Plant Biology Garden in a randomized complete block design with three replicates each. The results obtained showed significant differences ($p \leq 0.05$) on the agro-morphological traits with the highest number of leaves per plant (35.00), plant height (41.48), length of spike (33.16) and leave surface area (48.40) in GWM-002 and highest number of leaves per plant (38.60), plant height (52.50), length of spike (37.50) and surface area (80.40) in GWM-003. Therefore, 150 Gy and 200 Gy doses of gamma irradiation were obtained to be appropriate in creating beneficial traits in Spinach (*Amaranthus hybridus* L.) accessions.

Keywords: accession, agro-morphological, spinach, gamma irradiation

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INTRODUCTION

Amaranthus hybridus L. (2n =32) is popularly (called smooth Amaranthus or amaranth or pig weed) is cultivated in several areas of the world including south America, Africa, India, China and the United States (He and Corke, 2010). It is among the first generation of food crops in the world (Gigliola and Vera, 2012), and one of the most promising plant genera, and it consists of approximately 70 species of which 40 originated from the Americans, 17 are mainly vegetable species, three are grain while others are weedy (Andreas *et al.,* 2011). In Nigeria especially Yoruba community all species are referred to as "tete" even though they may add a second name to indicate a particular variety or species. The Hausas refers to them as "alaiyaho" while Igbos call them "imne". Spinach is a multipurpose crop whose leaves and grains are tasty and of high nutritional value, additionally, it can be cultivated as an ornamental plant (Venskutonis and Kraujalis, 2013). Amaranth is considered one of the most commonly produced and consumed indigenous vegetables on the African continent (Grubben, 2004). Spinach is mostly annual fast growing herbs that are mostly cultivated on lowlands especially the leafy species. Cultivation is not restricted to distant farms, Riverside, and home gardens as some families maintain some plants in small pots inside the house. Generally, spinach is fast growing and can be ready for harvest within weeks.

Mutation breeding by gamma rays is one of the most powerful methods for introducing a wide genetic variability in crops, as well as developing new varieties (Animasaun *et al.,* 2014). They are effective in improving growth and quality of plants, through their high mutation frequency; and can interact with atoms and molecules, thus producing free radicals in cells that affect the morphology, anatomy, biochemistry and physiology of the plants (El-Khateeb *et al.,* 2016). Large number of plant mutant varieties with desirable agro-morphological traits has been developed in closely related species by various authors using irradiation (Chopra, 2005 and Falusi *et al*., 2012). This can also be of great value and benefit for the improvement of spinach (*Amaranthus hybridus* L.) which is an important food crop in Nigeria. The improvement of the crop through creation of variability would give room for selection of high yielding variety with improved agro-morphological characters and increase its agricultural productivity. Therefore, this study was carried out to determine the effects of the gamma irradiation doses on the agro-morphological parameters of selected Nigerian spinach (*Amaranthus hybridus* L.) accessions

MATERIAL AND METHODS

Seeds of two accessions of *Amaranthus hybridus* viz; GWM-002 and GWM-003 were collected from the Plant Biology Departmental Seed gene bank, Federal University of Technology Minna, Niger State. The viability of the seeds was tested before and after gamma irradiation according to the method described by (Maity *et al.*, 2009). Viable seeds of the accessions were irradiated at Centre for Energy and Research Training (CERT), Ahmadu Bello University, Zaria, Nigeria. The doses include; 50 Gy, 100 Gy, 150 Gy and 200 Gy, with un-irradiated seeds (0 Gy) as the control. The irradiated seeds with the control were planted in experimental pots, filled with sandy-loamy soil. Each treatment was replicated three times and arranged in a randomized complete block design, at the botanical garden of the Department of Plant Biology, Federal University of Technology Minna, Nigeria. All agronomic practices were carried out when necessary and the plants were monitored for morphological parameters.

Statistical analyses

The agro-morphological parameters collected for the experiment plant height, number of leaves per plant, length of spike, number of spikelets per plant, leaves surface area, and seed weight (100 seed). The data generated were subjected to statistical analysis using Analysis of variance (ANOVA) to test for significant differences and Duncan's multiple range test (DMRT) was used to separate the means.

RESULTS AND DISCUSSION

The effects of gamma irradiation on morphological parameters are presented in table 1 below. The result showed that gamma irradiation significantly ($p \leq 0.05$) influenced the highest plant height of 10.58 cm obtained in 50 Gy at week 2 while 30.22 cm and 41.46 cm were obtained in 150 Gy at week 4 and harvest respectively in accession GWM-002 were not significantly different from the height of other doses and lowest plant height of 6.48 cm, 23.68 cm and 34.92 cm were obtained in control and 50 Gy at week 4 and harvest respectively in accession GWM-002. Similarly, in accession GWM-003 highest plant height of 34.42 cm and 52.50 cm were obtained in 200 Gy at week 4 and harvest respectively. The highest plant height (34.42) obtained in 200 Gy at week 4 in accession GWM-003 were not significantly different ($p > 0.05$) from the height of other doses (Table 1).

A pronounced variation was observed in the number of leaves of mutant spinach at the different doses of gamma irradiation. In accession GWM-002 (35.00), the highest number of leaves (35.00) was recorded in 200 Gy which was not significantly different from other doses. Similarly, no significant ($p > 0.05$) highest number of leaves per plant (38.60) were obtained in plants exposed to 200 Gy gamma ray in accession GWM-003. The result reveals that gamma irradiation at high doses (200 Gy) increase the number of leaves in spinach. This result is however contrary to the findings of (Tshilenge *et al.*, 2013) who observed variations in the number of leaves of gamma irradiated groundnut (*Arachis hypogaea* L.) with 100 Gy having the highest number of leaves per plant. These differences could be attributed to difference in the biochemical and physiological constituents of the plants. As reported by Lockhart *et al.*, (1996), the increased in leaf number and area provides an increase in the surface area for gaseous ex-change which considerable affect the process of photosynthesis. Therefore, higher number of leaves will definitely give room for more photosynthetic processes, hence increase the plant production (Table 1).

Similarly, a significant variation was observed in most of the yield parameters such as number of spikelets per spike, length of spike, weight of 100 seeds and surface area in all the doses. The highest weight of 100 seeds (0.18 g), length of spike (33.16), number of spikelets per spike (106.4) and surface area (48.40) was obtained in plants exposed to 200 Gy gamma ray in accession GWM-002. In accession GWM-003, the highest weight of 100 seeds (0.20 g) was obtained in 200 Gy while the highest number of spikelets per spike (153.8), length of spike (37.50) and surface area (80.40) was also obtained in plants exposed to 200 Gy gamma ray (Table 2).

This could be attributed to the increase in the number of leaf and leaf area obtained in the doses which increase the photosynthetic rate of the plants and result in high yield. Khan and Wani, (2005) reported a decrease of pod number at 0.4 kGy (400Gy) treatments and an increase at 50 kGy (500 Gy) without a change in the number of seed per pod of chickpea. These differences could be due to the fact that gamma rays produce radicals that can damage and affect differentially plant morphology, anatomy, biochemistry, and physiology depending on the irradiation level and species of plants.

Conclusion

This study has demonstrated that 150 Gy and 200 Gy significantly influenced the agro-morphological traits such as plant height, number of leaves per plant, length of spike, number of spikelet per spike and surface area. Therefore, for effective induction of useful genetic variability in spinach (*Amaranthus hybridus* L.) accessions, moderate doses of gamma irradiation of 150Gy and 200 Gy should be employed for its improvement and selection of desirable mutants for breeding purpose.

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Table 1. Effects of gamma irradiation on the agro-morphology of spinach (*Amaranthus hybridus* L.) accessions

Irradiation Dose (Gy)	Plant height @ 2 WAG	Plant height @ 4 WAG	Plant height @ harvest	No. of leaves
GWM-002				
0	8.90±0.62ab	23.68±1.93a	40.20±3.16a	27.60±5.39a
50	10.58±1.11b	27.22±2.00a	34.92±1.79a	26.40±1.44a
100	8.58±1.59ab	26.60±2.23a	38.74±2.17a	29.80±3.02a
150	9.90±0.99ab	30.22±3.26a	41.46±3.36a	32.20±3.79a
200	6.48±0.97a	24.98±1.97a	37.62±1.43a	35.00±5.27a
GWM-003				
0	11.10±1.37a	30.44±2.14a	42.26±3.35a	35.40±2.52a
50	12.96±0.72a	33.14±2.72a	44.40±3.27a	30.80±2.50a
100	14.12±1.35a	30.74±2.64a	42.08±1.83a	29.00±1.48a
150	14.08±0.73a	33.28±0.28a	43.90±0.61a	28.40±1.29a
200	10.18±1.71a	34.42±3.12a	52.50±3.05b	38.60±6.49a

Values are Means ± Standard Error, followed by the same superscript(s) along the column are not significantly different at $p > 0.05$ as tested by DMRT., weeks after germination (WAG)

Table 2. Effects of gamma irradiation on the yield of spinach (*Amaranthus hybridus* L.) accessions

Irradiation Dose (Gy)	Length of spike	No. of spikelet per spike	100-seed weight	Surface area
GWM-002				
0	19.98±3.45s	46.20±10.24a	0.14±0.01ab	30.00±0.55a
50	27.84±3.76ab	69.00±5.25a	0.14±0.01ab	33.00±1.14a
100	31.40±1.03b	68.20±5.71a	0.18±0.02b	31.20±0.80a
150	30.54±2.90b	63.20±11.89a	0.13±0.01a	47.80±1.24b
200	33.16±1.41b	106.4±53.71a	0.15±0.01ab	48.40±1.21b
GWM-003				
0	32.80±3.10ab	93.40±21.17	0.16±0.02a	33.20±1.28b
50	32.86±3.71ab	113.0±18.26a	0.20±0.01a	30.20±1.28b
100	27.92±2.15a	74.80±12.54a	0.16±0.01a	39.40±1.78c
150	31.80±2.26ab	73.20±14.01a	0.19±0.03a	23.60±1.17a
200	37.50±2.99s	153.8±58.42a	0.19±0.03a	80.40±1.91d

Values are Means ± Standard Error, followed by the same superscript(s) along the column are not significantly different at $p > 0.05$ as tested by DMRT

EFFECT OF SYNTHESIZED SILVER NANOPARTICLES FROM *Catharanthus roseus* LEAF EXTRACTS ON AGROMORPHOLOGICAL TRAITS OF SOME COWPEA GENOTYPES IN NIGER STATE, NIGERIA

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ABSTRACT

Cowpea is one of the most widely adaptable and salubrious grain legumes grown in moderately hot regions of Africa, Asia and America. A six weeks study was conducted to evaluate the effect of synthesized silver nano-particles (AgNPs) from *Catharanthus roseus* leaf extracts on agro-morphological traits of some cowpea genotypes (NGC-KT-19 and NGC-ZG-24) in Niger State. Seeds were soaked in different concentrations (0, 25, 50, 75 and 100 ppm) of silver nanoparticles for 4 hours, sowed in planting bags laid out in a complete randomized design (CRD). The results revealed some significant differences within the traits studied. NGC-KT-19 recorded its highest plant height (112.24 cm) and leaf length (15.68 cm) with plants treated with 50 ppm concentration of AgNPs, number of leaves (63.80) and number of branches (23.40) with 25 ppm, leaf width (8.74 cm) with 100 ppm concentration of AgNPs. For NGC-ZG-24, the highest plant height (28.82 cm) was recorded in plants treated with 75 ppm, leaf length (11.88 cm) and leaf width (7.34 cm) with 50 ppm, number of leaves with 25 ppm and number of branches (15.40) with 100 ppm of AgNPs. These variations could be attributed to some environmental factors and varying concentrations of AgNPs which revealed that the traits are independent of the various concentrations used.

Keywords: cowpea, silver nanoparticles, *Catharanthus roseus*, concentrations

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INTRODUCTION

Cowpea is a globally important legume crop that contains high protein, carbohydrate and vitamins (Gabriel *et al.*, 2021). In addition, it has low fat content, which is important in the prevention of diverse metabolic and cardiovascular diseases. Nigeria is the largest producer and consumer of cowpea which accounts for 61% of the production total Africa, 58% worldwide and fifty-two percent of Africa's production of cowpeas is used for food, 13% as animal feed, 10% for seeds, 9% for other uses, and 16% is wasted (Baysah, 2013). Islam *et al.* (2017) emphasized that all parts of the plant used as food are nutritious providing protein and vitamins. Cowpea has high level of folic acid and low levels of anti-nutritional and flatulence producing factors (Tony *et al.,* 2014). In spite of Cowpea been a very important crop in Africa, its production has been hampered by several biotic and abiotic factors (Da Silva *et al.*, 2018). Among this fungal attack it has been reported to be the most devastating biotic factor contributing to the reduction of cowpea yield potential in sub-Saharan Africa. Various synthetic fungicides, insecticide, herbicide used on control of the disease have led to some adverse effects such as toxic residue, development of resistant strain, high cost and toxicity to both the environment and animals due to high presence of heavy metals in them (Kareem *et al.*, 2018). The growing concern over this environmental impact of agrochemicals stimulates a transition to a sustainable agriculture, which undoubtedly requires the development of alternatives to agrochemicals. One such possibility is the utilization nano-technology to curtail the harmful effects of these chemicals on the crop, environment as well as human. However, thorough understanding of the role of nano-sized engineered materials on plant physiology, phenotypic traits and bio-chemical properties is still lacking (Khodakovskaya *et al.*, 2011).

MATERIALS AND METHODS

Fresh leaves of *C. roseus* broth solution was prepared by taking 10 g of thoroughly washed and finely cut leaves in a 300 mL Erlenmeyer flask along with 100 mL of sterilized double distilled water and then boil the mixture for 5 min before decanting, extract was filtered through Whatman filter paper stored at -15 °C. Filtrate were treated with aqueous 1 mM AgN03 solution and incubated at room temperature. As a result,

a brown-yellow solution was formed, indicating the formation of silver nanoparticles. It showed that aqueous silver ions could be reduced by aqueous extract of plant parts to generate extremely stable silver nanoparticles in water (Ponarulselvam *et al*., 2012). Seeds were soaked in different concentrations (0, 25, 50 75 and 100 ppm) for 4 hours, sowed in planting bags laid out in complete randomized design arranged in 4 x 5 factorial combination replicated 4 times and agro-morphological parameters were assessed using the standard procedures of Falusi *et al.* (2014).

Statistical analysis

Quantitative data obtained were pooled for analysis. Analysis of variance (ANOVA) was used to compare the various mean values. Duncan Multiple Range Test (DMRT) was used to separate the means. All values were considered significant at $p < 0.05$.

RESULTS AND DISCUSSIONS

The results observed for agro-morphological traits at six weeks after germination revealed that the highest plant height obtained (112.24±13.21 cm and 28.82±5.64 cm) from NGC-KT-19 and NGC-ZG-24 cowpea genotype recorded in plant treated with 50 and 75 ppm respectively. This is in contrast with the work of Nejatzadeh-Barandozi *et al.* (2014) who reported that 40, 60 and 100 ppm AgNPs caused improved plant height in basil. A significant higher number of leaves 63.80±8.66 for NGC-KT-19 and 74.20±18.38 for NGC-ZG-24 were observed in 25 ppm respectively. This is similar to the work of Jasim *et al.* (2017) who reported significant enhancement in the leaf number after being treated with AgNPs. For number of branches 25 ppm recorded 23.40±3.70 as the highest for genotype NGC-KT-19 and 100 ppm has the value of 15.40±0.55 for NGC-ZG-24 as the highest. In Leaflet length plant treated with 50 ppm is having 15.68±0.37 cm for NGC-KT-19 and 11.88±0.89 cm for NGC-ZG-24 as the highest mean value in 50 ppm of AgNPs. Lastly, within the leaflet width results NGC-KT-19 is having a significantly higher value of 8.74±0.43 cm in 100 ppm and NGC-ZG-24 genotype has 7.34±0.66 cm attained in 50 ppm. Similarly, Tung *et al. (*2018) repoted a positive effect of high-concentration on Chrysanthemum morifolium with 75 ppm AgNPs applied to tissue cultures significantly improved length and width of leaves. The inconsistency in the plant's response to AgNPs may be due to the fact that nanoparticle actions depend on plant genotype, AgNP concentration, and application method. In another study, Piotr *et a*l. (2019) stated that different plant response to different AgNP doses may be due to the effect of hormesis.

Conclusion

The results showed that the agro-morphological traits treated were significantly enhanced It could be assumed that seeds treated with AgNPs prior to planting stimulated more growth and development which was more vigorous from the beginning of the cultivation.

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Table 1. Agromorphological traits of genotype NGC-K-19 treated with different concentration of silver nanoparticles (AgNPs) from *Catharanthus roseus* at 6 weeks after germination (mean values)

Concentration	Plant height (cm)	Number of leaves	Number of branches	Leaflet length (cm)	Leaflet width (cm)
0 ppm	26.77±7.10a	53.00±31.49a	11.80±4.44a	8.62±0.72a	5.88±0.49a
25 ppm	24.08±8.15a	74.20±18.38a	14.60±1.34ab	11.64±0.67b	6.96±0.22ab
50 ppm	27.08±11.04a	71.20±33.16a	14.60±1.34ab	11.88±0.89b	7.34±0.66b
75 ppm	28.82±5.64a	57.60±7.16a	14.20±1.09ab	10.38±0.38ab	6.80±0.14ab
100 ppm	26.64±4.17a	71.80±18.99a	15.40±0.55b	10.38±0.38a	7.10±0.44ab

Values are presented in mean ± standard error of mean. Value followed by the same superscript (s) within the same column are not significantly different at the 5% level tested by DMRT

Table 2. Agromorphological traits of genotype NGC-ZG-24 treated with different concentration of silver nanoparticle (AgNPs) from *Catharanthus roseus* at 6 weeks after germinate (mean values)

Conc	Plant height (cm)	Number of Leaves	Number of Branches	Leaflet Length (cm)	Leaflet Width (cm)
0 ppm	84.08±24.80ab	46.20±7.26ab	16.80±2.35a	12.94±0.80a	7.48±0.50a
25 ppm	69.92±19.83ab	63.80±8.66b	23.40±3.70a	12.86±0.83a	7.50±0.53a
50 ppm	112.24±13.21b	38.80±2.80a	16.20±0.20a	15.68±0.37b	8.72±0.44a
75 ppm	39.64±11.64a	38.40±3.74a	16.20±2.29a	14.64±0.74ab	7.90±0.22a
100 ppm	54.00±0.00a	46.60±3.89ab	20.00±1.30a	15.20±0.61b	8.74±0.43a

Values are presented in mean ± standard error of mean. Value followed by the same superscript (s) within the same column are not significantly different at the 5% level tested by DMRT

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