



ESTIMATION OF GENETIC PARAMETERS FOR SOME AGRO MORPHOLOGICAL TRAITS AMONG NIGERIA EGUSI MELON GENOTYPES.

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ABSTRACT

In order to assess some genetic parameters among Nigerian Melon genotypes; the Melon genotypes were evaluated for their morphological and yield attributes at the Department of Biological sciences experimental garden, Federal University of Technology, Minna during 2015/2016 and 2016/2017 growing seasons, using a complete Randomized Block Design (CRBD) with three replicates. The agromorphological parameters were investigated using standard procedures. The results on the agromorphological parameters showed significant difference ($p \leq 0.05$) for most of the parameters studied. The study revealed that all of the agromorphological parameters were influenced by genetic factors such parameters are suitable for selection. Higher estimate for genotypic variances than environmental variances were observed for all the parameters which indicate good characters for selection and improvement of the crop. The highest genetic advance as percentage of mean (2924.2%) was obtained for weight of fruits ; whereas, number of seeds per fruit had the lowest (14.40%). High values of broad sense heritability estimates were observed for plant height at week 4 up to maturity, number of flowers per plant, number of flower buds per plant, days to germination and number of fruits per plant. Therefore, combination of high heritability estimates with genetic advance in the selection program is vital for selection of the crop in the future. Emphasis should be made on those agromorphological parameters that shows greater genetic importance for selection and improvement of the crop in Nigeria.

Keywords: Genotypic variance, Phenotypic variance Heritability, Egusimelon,

Introduction

Citrullus colocynthis (L.) is a variety of melon seeds, which is popularly called 'egusi' in West Africa. It belongs to a large family called Cucurbitaceae, which consist of 119 genera and about 925 species. It is one of the most important vegetable crops in the tropical, subtropical and Mediterranean zones of the world (Schippers, 2000). It is a native of Africa, which has perhaps been introduced to Asia, Iran and Ukraine (Schippers, 2000). Its common names include egusi in Yoruba, agushi in Hausa, epingi or paragi in Nupe and eashi in Gwari. Dialect names for this crop include egusi-itoo. It produces climbing vines up to 4 meters long, which are covered with stiff hairs. The heart-shaped or roughly palmate leaves are up to 12 centimeters long

and 14cm wide. It bears small yellow male and female flowers with petals less than a centimeter in length. The fruit is egg-shaped or an elongated ovate shape, up to about 19 centimeters long and 8cm wide, and cream in colour with green streaks. The plant is a creeping annual plant and an intercropping plant used in traditional farming practices; it grows well on light rich soil in the hot climatic regions of Africa. It has been known to tolerate low rainfall. In the Southeastern part of Nigeria, the crop is best cultivated after the first rainfall of the year (Akpambang *et al.*, 2008). Thirteen



weeks after planting the first fruits are harvested. The different species of Cucurbitaceae have served humans for over 10,000 years as important food and as source of many useful products (Ajuru and Okoli, 2013). In Nigeria, they are used for different purposes in different parts of the country. It is important to improve the productivity of the crop to satisfy the demands of dietary needs and raw materials for industrial processing to edible oil and livestock feedstuff through breeding programs. The success of increasing the productivity of any crop through breeding largely depends on the presence of variability among the breeding materials (Adeyemo and Ojo, 1991). Broad genetic variability is the basis for successful plant breeding and the successful development of adaptations to environmental conditions. Generally breeding programs depends on knowledge of the nature and magnitude of variations in the available materials, magnitude of association of characters with yield, extent to which these characters are heritable as well as extent of environmental influence on them (Aruah *et al.*, 2012; Ndukauba *et al.*, 2015). Various morphological and physiological characters contribute to yield. Each of these component characters has its own genetic systems. Further, these yield components are influenced by environmental fluctuations. Therefore, it is necessary to separate the total variations into heritable and non-heritable components with the help of genetic parameters such as genotypic and phenotypic coefficients of variation, heritability and genetic gain (Maniee *et al.*, 2009). Furthermore, knowledge of the association between yield and its components can improve the efficiency of selection in plant breeding (Izge *et al.*, 2001). This study was undertaken to estimate the genetic variability, heritability, character association among the different egusi-melon genotypes.

Materials and Methods

The morphological parameters were investigated using standard procedures after the techniques of Akinyele and Osekita (2006); Hegazi and Hamideldin (2010); Idehen *et al.* (2014). Specifically, the days to germination (DG) were determine as the interval between sowing of seeds and day a germinating seedling emerges above soil level. The number of leaves per plant (NL) at maturity was determined by counting the number of leaves attached to the plants. The length of vine of the plants at two weeks interval up to maturity was measured in centimetres (cm) using a metre rule. Sexual maturity (SM) was determined as the interval between emergence of seedling and appearance of flowers. For each of the morphological parameters mentioned above, mean value per plant was determined. The leaf colour and seed colour were determined using a Royal horticultural colour chart; leaf shape and seed shape were determined using a chart. Leaf texture was determined using fingertips (IPGRI, 2003).

The yields from the different accessions of Melon were determined using the following indices: number of fruits per plant (NF), number of seeds per pod (NSP), and weight of fruit (WF). For NSP and WF, ten fruits each were selected at random for all the accession and the values were recorded for further statistical analysis.

NF were determined by counting the total number of fruits a plant produced at the completion of the life cycle. NSP were determined by opening the fruit and counting the number of viable seeds which were determined by their relatively large size and firmness. WF were determined by measuring the pods on a weighing balance, mean values of yield parameters per fruit or plant were determined for the Melon plants.

Genetic Parameters Estimates

Broad Sense Heritability (h^2) was estimated according to Falconer (1989) using:

$$h^2 = \frac{\sigma^2_g}{\sigma^2_{ph}}$$

(equation1)

Where σ^2_g is the genotypic variance; σ^2_{ph} is the phenotypic variance. Phenotypic and



Phenotypic variances were obtained from the analysis of variance table using equations 2 and 3 as follows:

$$\sigma^2_g = \frac{MS1-MS2}{rXs}$$

$$\sigma^2_{ph} = \frac{MS1}{rXs}$$

3

(Where r: replication, s: season, MS1: Mean square for cultivar, MS2: Mean square for cultivar X season).

The mean values were used for genetic analyses to determine Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV), using equation 4 and 5 as follows:

$$GCV (\%) = \frac{\sqrt{\text{Genotypic Variance}}}{\text{Grand Mean}} \times 100$$

4

$$PCV (\%) = \frac{\sqrt{\text{Phenotypic Variance}}}{\text{Grand Mean}} \times 100$$

5

Genetic advance (GA) was calculated with the method suggested by Singh and Chaundry (1985) using equation 6 as follows: $GA = k. \sigma_{ph}. h^2$

6

Where K: constant = 2.06 at 5% selection intensity, σ_{ph} : square root of phenotypic variance, h^2 : Heritability

GA as percentage of mean (GAM) = $(GA/\text{Grand Mean}) \times 100$

7

Results and Discussion

Genotypic variance, phenotypic variance, Environmental variance, broad sense Heritability. Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV) and Genetic advance for eleven characters are presented in (Table 1) The result revealed considerable genotypic variances among the various accessions for the characters under consideration. The result revealed consistency in the environmental and genotypic variance. In all the eleven characters studied, the genotypic variance was quite higher than the environment variance.

Genotypic variance (GV) was higher than environmental variance (EV) for all the eleven (Table 1). However, the influence of the environmental factors on the expression of other characters as indicated by the magnitude of the EV was not evident. This indicates that the phenotypic variance (PV) was not caused by environmental influences of those characters. Consequently, such character possesses promising genetic variability; so, selection for them is very efficient and successes very high.

The higher GV (7916.65) was for plant height at maturity, this was followed by number of seed per fruit (6834.17), then number of flower buds per plant. The least GV (0.28) was recorded for weight of fruit per plant. Phenotypic variance (PV) was also highest in plant height at week 10 (10022.14) followed by number of seeds per fruit (8778.28), then number of flowers per plant (2973.55), and followed by plant height at maturity (7964.65); the lowest PV (0.40) was found in weight of fruit per plant (Table 1).

Genotypic coefficient of variation (GCV) was higher for number of fruits per plant (131.71%), then followed by number of branches per plant at maturity (86.77%), this was followed by number of flowers per plant (73.87%); the least GCV (17.54%) was found in fruit diameter. Genotypic coefficient of variation (GCV) ascertains the degree of genetic variability present in various quantitative traits. High GCV indicates the presence of exploitable genetic variability for these traits which may facilitate selection (Yandav, 2009). Polygenic variation may be phenotypic, genotypic or environmental and relative values of these three coefficients for a trait will give an idea about the magnitude of its variability (Nausherwan *et al*, 2008).

Genotypic coefficient of variation, which is the real indicator of the extent of genetic variability in a population, was high for all the characters, except for fruit diameter and days to flowering. For all the tested character, higher PCV than GCV values were obtained. The highest PCV (138.02%) was for number of fruits per plant, followed by number of branches per plant (97.41%), then followed by number of flowers per



plant (75.75%); the least PCV (20.50%) was found in fruit diameter (Table 1). High PCV is an indication of the presence of substantial horizon for selection of the trait under consideration which dependent on the amount of variability present. Thus, a greater potential is expected in the selection for number of fruits per plant, number of flowers per plant and number of branches per plant among the genotypes under study while there is a narrow scope for selection of fruit diameter and days to flowering on account of low amount of variability among genotypes studied. (Khan *et al*, 2009) reported that high PCV is an indication of the existence of greater scope for selection of the trait under consideration which is dependent on the amount of variability present.

The highest broad sense heritability (h^2) of (100%) was recorded for plant height at week 10 with an expected genetic advance over percentage of mean (GAM) of 46.10%. this was followed by plant height at maturity 99% with an expected GAM 17.58%, followed by plant height at week 6 (97%) with expected respective GAM of 103.37%. Number of leaves per plant at maturity produced the lowest heritability values (67%) and a corresponding lowest GAM values (54.09) (Table 1).

Heritability suggests the extent of genetic control for the expression of a particular trait and the reliability of phenotype in predicting its breeding value (Chopra, 2000). High heritability indicates less environmental influence in the observed variation (Mohanty, 2003; Eid, 2009). Heritability in the broad sense ($h^2_{b_s}$) indicates only whether there is sufficient genetic variation present in a population or not, which implies whether a population will respond to selection pressure or not (Milatovic *et al*, 2010).



Table 1: Estimation of Some Components of Genetic Parameters for some Agromorphological Characters among the Melon Accessions

Characters	Grand mean	Genotypic variance (σ^2g)	Phenotypic variance (σ^2p)	Environmental variance (e^2)	Broad sense heritability (h^2)/%	Genotypic coefficient of variation (GCV)/%	Phenotypic coefficient of variation (PCV)/%	Genetic advance (GA)	GA as a % of mean
Plant height at 4weeks (cm)	74.45	702.62	738.27	35.65	95	35.60	36.50	71.55	96.10
Plant height at 6 weeks after (cm)	81.86	1167.44	1200.55	33.10	97	41.74	42.33	84.79	103.57
Plant height at 8 weeks (cm)	137.98	1589.53	1695.73	106.20	94	28.89	29.84	57.63	41.76
Plant height at 10 weeks	211.23	995.94	10022.14	26.20	100	47.33	47.39	97.38	46.10
Plant height at Maturity	322.40	7916.65	7964.65	48.34	99	27.60	27.68	56.68	17.58
Days to germination	5.24	6.02	6.55	0.53	92	46.86	48.88	92.53	1765.83
Number of branches per plant at maturity	5.71	24.55	30.94	6.39	79	86.77	97.41	159.23	2784.58
Number of leaves per plant at maturity	100.49	1051.00	1570.99	519.99	67	32.26	39.44	54.36	54.09
Days to flowering	32.78	43.08	56.96	13.88	76	20.02	23.02	35.86	109.39
Number of flower bud per plant	82.52	3127.10	3292.86	165.76	95	67.77	69.54	136.04	1211.19
Number of flowers per plant	74.93	3063.65	3221.49	157.83	95	73.87	75.75	148.41	197.51



Number of fruits per plant	10.98	208.95	229.46	20.51	91	131.71	138.02	258.92	2358.1
Weight of fruit (g)	1.77	0.28	0.40	0.12	70	30.02	35.86	51.76	2924.2
Number of seeds per Fruit	322.91	6834.17	8778.28	1944.11	78	25.60	29.02	46.53	14.40
Fruit diameter	40.60	50.14	69.44	19.30	72	17.44	20.50	30.53	164.85



Conclusion

In conclusion, broad genetic variability was observed among the melon accessions that could be useful for future breeding purposes. The results of this study indicate that there is considerable genetic variation present in most of the traits to warrant selection for better genotypes. These traits can therefore be given special attention in selections aimed at melon improvement. In other to access the selection effect on trait more effectively, heritability accompanied with genetic advance is more useful than heritability alone.

References

- Ajuru, M. G. & Okoli, B. E. (2013). The Morphological Characterization of the Melon Species in the Family Cucurbitaceae Juss and their Utilization in Nigeria. *International Journal of Modern Botany*, 3(2), 15-19.
- Akinyele, B. O. & Osekita, O. S. (2006). Correlation and path coefficient analysis of seed yield attributes of okra [*Abelmoschus esculentus* (L.) Moench]. *African Journal of Biotechnology*, 5(14), 1330-1336.
- Akpambang, V. O. E., Amoo, I. A. & Izuagie, A. A. (2008). Comparative compositional analysis on two varieties of melon (*Coccythibis citrullus* and *Cucumeropsis edulis*) and a variety of almond (*Prunus amygdalus*). *Research Journal of Agricultural and Biological Science*, 4(1), 639-642.
- Aruah, B. C., Uguru, M. I. & Oyiga, B. C. (2012). Genetic variability and inter-relationship among some Nigerian Pumpkin Accessions (*Cucurbita* spp.). *International Journal of Plant Breeding*, 6(1), 34-41.
- Chopra, V. L. (2000). *Plant Breeding Theory and Practice* (2nd ed.). New Delhi: Oxford and IBH Publishers Pp14-20.
- Eid, M. H. (2009). Estimates of heritability and genetic advance of yield traits in wheat (*Triticum aestivum* L.) under drought conditions. *International Journal of Genetics and Molecular Biology*, 1(7), 115-120.
- Hegazi, A. Z. & Hamildeldin, N. (2010). The effect of gamma irradiation on the enhancement of the growth and seed yield of okro (*Abelmoschus esculentus*) and associated molecular changes. *Journal of Horticulture and Forestry*, 2(3), 38-51.
- Idehen, E. O., Kehinde, O. B., Wang, X. & Oyelakin, O. O. (2014). Discriminating Nigerian 'Egusi' Melon Accessions Using Agro-Morphological and Molecular Techniques. *Nigerian Journal of Biotechnology*, 28(1), 1-10.
- Izge, A. U., Kadams, A. M. & Gungula, D. T. (2006). Studies on character association and path analysis of certain quantitative character association among parental lines of pearl millet (*Pennisetum glaucum*) and their f₁ hybrids in a diallel cross. *African Journal of Agricultural Research* 1 (5), 194-198.
- Manice, M., Kahrizi, D & Mohammadi, R (2009). Genetic variability of some morpho-physiological traits in durum wheat (*Triticum durum* L.). *Journal of Applied Science* 9(7), 1383-1387.
- Milatovic, D., Nikolic, D. & Durovic, D. (2010). Variability, heritability and correlation of some factors affecting productivity in peach. *Horticultural Science*, 27(3), 79-87.
- Mohanty, B. K. (2003). Genetic Variability, heritability, correlation and path coefficient studies in tomato. *Indian Journal of Agricultural Research*, 37(1), 68 - 71.
- Nausherwan, N. N., Ghulam, M. S., Khali, M., Qamar, S. & Akhtar, S. (2008). Genetic variability, correlation, path analysis studies in garden pea (*Pisum sativum* L.). *Journal of Agricultural Research*, 36(1), 333-340.



- Ndukauba, J., Nwofia, G. E., Okocha, P. I. & Ene-Obong, E. E. (2015). Variability in Egusi- melon genotypes in Derived savannah Environment in southeastern Nigeria. *International Journal of Plant Research*, 5(1), 19-26.
- Schippers, R. R. (2000). *African Indigenous Vegetables: An Overview of the Cultivated Species*. Natural Resource Institute/ACP-EU. Chatham, UK: Technical Centre for Agricultural and Rural Cooperation.
- Yadav, Y. C., Sanjay Kumar, B. B. & Dixit, S. K. (2009). Genetic variability, heritability and genetic advance for some traits in Cucumber. *Indian Journal of Agricultural Research*, 8(1), 51-57.