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Research Article

Yield Attributes and Biochemical Compositions of Elites and Landraces of Pigeon Pea [*Cajanus cajan* (L.) Millsp]

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Abstract

Cajanus cajan (L.) Millsp (Pigeon pea) is an important leguminous crop grown mostly in the tropical regions of the world, Nigeria inclusive. The crop is still underutilised in Nigeria; the potentials of the crop in terms of yield traits and biochemical compositions, with ability of enhancing food security and preventing over-dependent on very expensive animal protein, is yet to be fully exploited. It was based on this premise that this study was designed. Twenty-five (25) accessions were obtained from International Institute of Tropical Agriculture, lbadan; National Centre for Genetic Resources and Biotechnology, Ibadan and Local farmers in Oyo state, Nigeria. The accessions were sown in the experimental farm in a Randomised Complete Block Design (RCBD) with three replicates. Standard procedures were followed for determination of yield parameters as well as biochemical compositions. It showed that NG/SA/11/08/108 produced the highest number of pods per plot (437.00) and the highest grain yield (2.6t/ha). Similarly, TCC-8126 produced the highest crude protein (22.53 %) while PG/OY/18/002 had the highest carbohydrate contents (52.22 %). TCC-8126 was the best elite genotype in terms of amino acid profile, containing glutamic acid (18.10 %), aspartic acid (11.4 %); arginine (7.41 %), alanine (5.90 %). The values produced for both nutritional compositions and amino acid profiles were within the recommended standard limits set by Food and Agriculture Organisation and United States Department of Agriculture. NG/SA/11/08/108, NG/AO/MAY/09/021/02, TCC-151, TCC-8126, TT-8129 and TCC-2 have been selected as promising genotypes that could serve as breeding lines for future breeding programme of *Cajanus cajan* in Nigeria.

Keywords: *Accessions, Yield traits, Food security, Crude proteins, Amino acids profiles*

Introduction

Pigeon pea [*Cajanus Cajan* (L). Millsp.] is one of the most important food legume crops of tropical regions of the world, including Italy, Australia, Hawaii, Uganda, Nigeria, the East and West Indies, India, the United States and Southeast Asia. It is a drought tolerant plant and exhibits a large variation for physiological maturity (FAOSTAT, 2015). Being an indigenous crop in Nigeria, it is called "Waken Kurawa" in Hausa, "Fio-Fio" or "Agbubu" in Igbo and Yoruba people call it "Otili" (Adebimpe *et al*., 2018). The seed of pigeon pea are rich in vitamin B, proteins, carotene and Vitamin C (ascorbic acid), and can be eaten fresh or dry. Present yield level which is very low could marginally be improved and stabilized through better crop management. It is a member of the Cajaninae sub-tribe of the cropland vital tribe Phaseoleae, which is part of the Papilionoideae sub-family of the Fabaceae relatives (Egbe, 2005).

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It is still grouped as part of underutilised crop species in Nigeria, and other the countries, whose production potential are yet to be exploited. In Nigeria, the crop is considered as the fifth cultivated legume following Soybean, cowpea, Groundnut and Bambara groundnut. Despite the importance of the crop in providing food rich in protein, its productivity in many parts of Africa remained low; when compared with the $2.5 - 13$ tha^{-1} average yield observed in India (Egbe, 2005).

Pigeon pea is cultivated in many other countries because of its multifaceted uses as food sources, feed for animals, fuel and fertiliser (Wilson *et al*., 2012). Lin-Qi *et al*. (2014) opined that the crop plays an important role in preventing nutritional food insecurity and poverty eradication among poor people in many countries of Asia and Africa. The nutritional composition of pigeon pea is evident from the high protein contents (21.5%) on a dry weight basis as well as its role as a major source of protein to almost 20% of the entire population of people (Odeny, 2007). It has very low Na and fat content (with no cholesterol) but it is high in fibre. The crop is also rich in carbohydrates and useful mineral elements, such as Ca, P and Mg (Amarteifio *et al*., 2002). The seeds can be prepared into various meals and served as substitute for cowpea, with mature seeds containing protein (21%), starch (53%), fat (2.3%), crude fibre (6.6%) and mineral (250.3 mg 100g-1) (Saxena *et al*., 2010).

Daudu *et al*. (2020) observed the existence of genetic variability among various accessions of pigeon pea in Nigeria. Adebimpe *et al*. (2018) suggested the need for biochemical characterisation of pigeon pea, other than phenotypic characterisation. Similarly, genetic bases of the long cooking time of the crop remains a mystery yet to be unravel. There is also an urgent requirement for a concerted effort towards exploring the hidden treasure conserved within these legume crops and to stimulate interest in their utilizations beyond the traditional localities. There is also the need to exploit plant protein sources rather than overdependence on animal protein sources in Nigeria (Upadhyaya *et al*., 2013; Davi and Saxena 2014). It was based on these premises that this research was designed to evaluate the yield attributes and biochemical compositions of elites and landraces of pigeon pea [*Cajanus cajan* (L.) Millsp].

Materials and Methods

Seed Collection: Twenty-five (25) pigeon pea accessions were collected; of which fifteen (15) elite seeds of pigeon pea were obtained from International Institute of Tropical Agriculture (IITA), Ibadan; five (5) landraces each were collected from National Centre for Genetic Resources and Biotechnology (NACGRAB) and local farmers in Kajola local Government Area Oyo state, Nigeria through direct contact to check yield and other agronomic characteristics.

Experimental Design and planting: Evaluation of the pigeon pea accessions (for agronomic) trait was carried out at the experimental garden of Department of Plant Biology, Federal University of Technology, Minna Nigeria. The seeds were sown in the field at the depth of 1-2cm in a Randomised Complete Block Design (RCBD) replicated three times. The seeds were sown at inter and intra – row spacing of 15cm by 15cm, plant-plant with five seeds per stand. At two weeks after emergence, the seedlings were thinned to two plants per stand. Weeding was done manually using hand hoe when necessary. No fertilizer was applied to the crop.

Determination of Yield Parameters: The yield parameters of the pigeon pea were investigation according to the method adopted by (Egbe and Vange, 2008) to determine length of pod, weight of pod, number of seeds per pod, weight of hundred seeds and grain yield per plant.

Determination of Biochemical Composition

Proximate Analyses: Standard procedures according to the procedures of Association of Official Analytical Chemists (AOAC, 2011) were used to determine crude protein, crude fat, crude fibre, crude ash, moisture and carbohydrates. The amino acid profile was determined by using Thin Layer Chromatography and modified Colorimetric Techniques as described by Schroeder *et al*. (1990).

Determination of Mineral Element: Mineral element was determined according to the method described by (AOAC, 2011), the sample were analyzed for selected metals (Ca, Cu, Fe, K, Mg, P, and Zn). Calcium and potassium were determined by the use of ash from each sample digested by adding 5ml of 2M HCl to the ash in the crucible and heat to dryness on a heating mantle.

Phosphorous was determined routinely by the vanado-molybdate colorimetric otherwise known as spectrophotometric method. The ash of sample obtained was treated 2M HCl solution and 10ml of the filtrate was pipette into 50 ml standard flask and 10 ml of vanadate yellow solution was added and the flask was made up to mark with distilled water, stopper and left for 10 minutes for full yellow colouration to develop. Concentration of the P was obtained by taking the optical density (OD) or absorbance of the solution on a Spectronic 20 spectrophotometer or colorimeter at a wavelength of 470 nm. The percentage phosphorous was calculated using formula;

$$\%\text{Phosphorus} = \frac{\text{Absorbance X Slope X Dilution factor}}{10{,}000}$$

Magnesium, Iron, Zinc, and Copper were determined using Buck 200 Atomic Absorption Spectrophotometer (AAS) through the suction tube. The digest of ash of each sample above was washed into 100ml volumetric flask with distilled water and made up to mark. This dilution was aspirated into the Buck 200 Atomic Absorption Spectrophotometer (AAS). Each of the mineral was read at respective wavelength with their respective hollow cathode lamps using appropriate fuel and oxidation combination.

Chromatographic analysis of amino acids (TLC Technique): Thin Layer Chromatography method was used to separate the amino acid contents in the samples. Aliquots of 50µl of the extracts were spotted on Avicel microcrystalline cellulose thin layer plate (Whatman analytical plates) along with 20µl of reference standard mixture. The reference mixture contained essential amino acids (lysine, histidine, phenylalanine, methionine, glycine, cysteine, proline, leucine, isoleucine, threonine, tyrosine, valine, arginine, tryptophan, and glutamic acid) each present at a concentration of 0.1% (w/v). One dimensional ascending chromatography was done, and the solvent system employed for the separation was n-butanol-glacial acetic acidic and water at a ratio 4:1:2 (v/v). After four hours of separation, the chromatograms were aired dried and the amino acids were located by spraying with locating reagent [0.2% (w/v) of ninhydrin in ethanol]. The sprayed chromatograms were allowed to air dry and later oven dried at 100^{o}C for 5minutes for the spots to be clearly identified. The separated amino acids were identified using the reference standard.

Data Analysis: Data obtained were pooled for analyses; Analysis of Variance (ANOVA) was used to compare the means among the genotypes for all the quantitative parameters. Duncan Multiple Range Test (DMRT) was used to separate the means where there was difference. All values were considered not significant at P>0.05. UPGMA Dendrogram was constructed for the Amino acid profile and other parameter to determine the diversity and similarities among the genotypes.

Results and Discussion

Number of seed per pod: Accession NG/SA/11/08/108 produced the highest number of seed per pod with (4.97) seed/pod while accession TCC-8127 and TCC-8129 had the least value (2.93) seed/pod. However, there was no significant difference among the other accessions (Table 1).

Pod length: As shown in Table 1, highest pod length (6.75 cm) was recorded in accession PG/OY/8/005, while the least value (4.23 cm) was obtained in TCC-1. These values were significantly different from each other. The results further showed that there was no significant difference among other accessions.

Pod weight: There was significant difference among the various accessions; NG/SA/11/08/108 produced the highest pod weight (71.60 g) while TCC-8104 had the least value (16.60 g). These values were significantly different from each other and from the values of all other accessions (Table 1).

100 seed weight: Highest value for 100 seed weight (78.00 g) was obtained in TCC-8127 while TCC-8126 had the least value (6.80 g). These highest and lowest values were significantly different from each other and from the value of all other accessions. Meanwhile, there are no significant difference between TB-72 (7.00 g) and TCC-8126 (7.00 g) (Table 1).
Grain yield per plant: For Grain yield per plant, there was significant difference among the accessions; NG/SA/11/08/108 produced the highest value (437.00 Yield/m^2) whereas TCC-8104 produced the least value (22.00); these values were significantly different from each other and from the value of all other accessions.

Crude protein and Crude fat content: The crude protein content among accessions ranged between 20.64% and 22.53%. The highest crude protein (22.53%) was obtained in TCC-8126 while the lowest 004 (20.64%) was obtained in PG/OY/2018/004.. As depicted in Table 2, the crude fat ranged from 1.22% to 1.45%. The highest crude fat was found in TCC-8129 (1.45%) and the least average content of fat was recorded in accession PG/OY/18/002 (1.22%).

*Crude fibre and Ash contents***:** The results revealed that the crude fibre content of pigeon pea ranged from 9.37% to 9.80%; the highest value (9.80%) was found in PG/OY/18/004 and the smallest (9.37%) was recorded in TCC-8126. Ash contents of pigeon pea ranged from 3.96% to 4.35%. Highest Ash content (4.35%) was found in TB-72 and lowest ash content (3.96%) was found in PG/OY/18/002.

Moisture and Carbohydrate contents: The result revealed that moisture contents ranged between 11.60% and 12.28% among the accessions. The highest moisture content (12.28%) was obtained in PG/OY/18/004 and the least (11.60%) in TCC-8126. The total carbohydrate content of pigeon pea under investigation ranged between 50.70% and 52.22%. The highest carbohydrate content (52.22%) was observed in accession PG/OY/18/002 while the least value (50.70%) was found in accession TCC-151.

Levels of Mineral content in the Pigeon Pea genotypes: As shown in Table 2, the potassium content ranged from 1.54 – 1.77 mg/Kg. The highest concentration (1.77 mg/Kg) was observed at NG/AO/MAY/09021/02 while the least mean concentration (1.54mg/Kg) was recorded at TB-72. The concentration of calcium in the pigeon pea seeds ranged from 0.17 to 0.38mg/Kg. The highest concentration of calcium (0.38mg/Kg) was observed in the accession TCC-2 whereas the least amount (0.17mg/Kg) was obtained in accession TB-72. A relatively higher concentration (0.31mg/Kg) of available phosphorous was observed in the genotype TCC-8129 and the lowest available phosphorus was found in accession TCC-151 (0.28mg/Kg). The mean concentration level of Mg varies from 0.11 to 0.14mg/Kg in dry weight pigeon pea samples. Significantly different magnesium concentrations were obtained in pigeon pea samples. The highest concentration was found in genotype PG/OY/18/004 (0.14mg/Kg) whereas the least amount obtained in genotype TCC-151.
The iron content of pigeon pea sample ranged from 3.25 to 5.90 mg/Kg dry weight. The mean concentration of iron was found to be highest in genotype TCC-2 (5.90 mg/Kg) and a low amount of iron was found in NG/AO/MAY/090/21/02(3.25 mg/Kg). Meanwhile, the concentration of zinc determined in pigeon pea genotype ranged from 6.80 to 8.80 mg/Kg dry weight. The highest level of zinc was observed in genotype TCC-8126 (8.80 mg/Kg) and the lowest level of zinc was determined in genotype PG/OY/18/002 (6.80 mg/Kg). The mean concentration of copper in this study ranged from 1.60 to 3.55 mg/Kg dry weights in Pigeon pea genotype, whereas, the relatively highest level of copper was found in genotype TCC-2 (3.55 mg/Kg) and the least was for that of PG/OY/18/002 (1.60 mg/Kg).

Amino acid composition of pigeon pea: The result of the amino acid composition of the pigeon pea accessions as presented in Table 3 and Table 4. Glutamic acid was the most abundant amino acid in all the genotype evaluated. The values ranged between 18.10 to 16.86% in TCC-8126 and CITA-3 respectively. The second most abundant amino acid in all the genotypes studied was Aspartic acid ranging from 11.40 to 10.77% in TCC-8126 and CITA-3 respectively. The highest value of Arginine was also recorded in TCC-8126 (7.14%) and least value (6.69%) from CITA-3; highest Glycine was recorded in TCC-8126 (5.84%) and the least (5.30%) was in CITA-3. Serine ranged from 5.25 to 4.87% while Alanine ranged between (5.90 to 4.51%). Tryosine ranged from 4.54 to 4.17% in both genotypes TCC-8126 and CITA-3 respectively. In Cystine the highest value recorded was from TCC-8126 (0.96%) while the lowest value recorded in CITA-3 (0.75%); for Orithine, the value ranged between 0.37 to 0.17% in both genotypes.

The highest essential amino acid in all the genotypes studied was leucine with values ranging from 7.86 to 8.30% in TCC-8126 and CITA-3; followed by Phenylalanine with the highest value recorded in TCC-8126 (8.10%) and least value (6.91%) in CITA-3. In Histidine, the value ranged between 3.80 to 4.14%. Methionine, Cystenine and Tryptophan are the limiting amino acids in most of the grain legumes including pigeon pea; methionine content of these studied ranged from 1.25 to 1.50%. The highest (1.50%) methionine was recorded in TCC-8126 followed by TCC-8129 (1.46%) and least value was found in CITA-3 (1.25%) as compared to other genotypes. The Tryptophan content in the seeds of pigeon pea genotypes ranged from 0.37 to 0.61%. The results revealed that comparatively higher Tryptophan content of 0.61% was observed in the genotype TCC-8126 and the lowest (0.37%) was observed in the CITA-3 genotype, respectively. The highest value of Cysteine was recorded in genotype TCC-8126 (1.46%) and the least was recorded in genotype CITA-3 (1.29%) Table 3.

Genetic similarity using amino acid profile: Cluster analysis of the 10 selected genotypes based on their similarity distance revealed high variability among the pigeon pea genotypes in term of amino acid composition, with the elites genotype were cluster together while the landrace were also cluster together with the exception of genotype TCC-15 (Figure I). At a genetic distance of 0.6, the genotypes were clustered into three major groups, with cluster I consist 20 % of genotypes TCC-2 and CITA-3 respectively. Cluster II consist 50 % of the genotypes with the exception of one elite genotype (TCC-151), while cluster III consist 30 % of the genotypes, i.e. TCC8129, TCC-8126 and TB-72.

Increase number of seeds per pod has been an important character in regions where pigeon pea is mainly grown for the domestic market and eaten as a green vegetable. The range (2.93 to 4.97) of seed per pod, estimated were lower than 5.52 by Kundy *et al*. (2015). However, this number was higher than those observed by Muniswamy *et al*. (2014) in Indian pigeon pea. Zavinon *et al*. (2019) also reported higher numbers of seeds per pod in the African germplasm than in the Indian germplasm of pigeon pea. Meanwhile, this was in conformity with what Omanga *et al*. (2015) and Shiferaw *et al*. (2005) observed; who reported that farmers preferred genotypes with high number of seeds per pod and seed weight (100-grain weight); Saxena *et al*. (2010) also buttressed a strong consumer preference for genotypes with many seeds per pod. The high number of seeds per pod observed in the current study confirmed with the findings of Silim *et al*. (2006); Upadhaya *et al*. (2007) and Manyasa *et al*. (2008) who reported higher numbers of seeds per pod in the African germplasm than in the Indian germplasm.

The highest 100-seed weight (78.00 g) obtained in TCC-8127and the smallest weight of 100-seed weight (6.80 g) in TCC-8126 were slightly similar to the report of Yu-Mi Cho *et al*. (2020) with a closer range (7.26-15.38) but different from the work of Upadhaya *et al*. (2007). A high grain yield per plant (437.00) obtained in accession NG/SA/11/08/108 was higher than those obtained in similar studies on pigeon pea (148.60) (Yu-Mi *et al*., 2020). This observation is similar to those observed by Ojwang *et al*. (2016); thereby, confirming the fact that pigeon pea grain yield can reach up to five tons/ha under optimum environmental conditions (Chalak *et al*., 2018). In all, the observations of the present study were comparable to those of previous reports (Uphadhyaya *et al*., 2007; Kumara *et al*., 2013; Zavinon *et al*., 2019).

Abiola *et al*. (2019) asserted that proteins are vital in the body for development of tissue as well as regeneration cell and also perform structural and catalytic roles in the body system Anjulo *et al*. (2021). Pawar *et al*. (2009) and Oke (2014) had reported crude protein constituent in pigeon pea leaf between 17.97% and 26.38%. These values were almost similar to those recorded in the present study. According to John (2005), the percent crude protein of commonly grown pigeon pea was in the range between 18% - 26%. Similarly, Sharma *et al*. (2011) and Kachare *et al*. (2017) reported the range of crude proteins of 20% - 26% and 17.62% - 25.45% respectively; these were all in conformity with the results obtained in the present study. The range of value for crude protein is within the permissible level of crude protein in pigeon pea (22.3%) recommended by FAO (2016).

Crude fat releases energy when oxidized and also enhances the delectableness of food (Adamu and Oyetunde, 2013). The range of crude fat from 1.22% to 1.45% this study was comparatively lower (3.68%) than those obtained by Olalekans and Abosede (2010); 2.77% recorded by Kunyanga *et al*. (2013); 2.74% recorded by Oke, 2014 and 4.78% obtained by Adamu and Oyetunde, 2013. However, Eltayeb *et al*. (2010) and Sharma *et al*. (2011) reported 1.2%, and 1.7% crude fat respectively while and John (2005) reported the crude fat content in ranges between 1.2% - 8.1%. USDA (2016) database reports put the permissible crude protein in pigeon pea at 1.49%. These were not dissimilar to the results of the present study. The similarity observed could be due to similarity in their core genetic makeup despite their variation in the seed sources.

Crude fibre contents in the present study was slightly higher than 6.98% reported by Kunyanga *et al*. (2013); 6.6% by Adamu and Oyentunde (2013). However, Oke (2014), and Eltayeb *et al*. (2010) reported the Crude fibre contents between 1.2% and 8.1% in pigeon pea, this was lower than 9.37% to 9.80% obtained in the study. Fibres aid in food digestion thereby enhancing optimal growth and purify the digestive tract by removing likely toxins from the body; it also inhibits the absorption of excess cholesterol (Abiola *et al*., 2019). The permissible level of crude fibre in pigeon pea recommended by FAO, (2012) was 1.5% which was lower compare to result of present study. This implies that pigeon pea could be an ideal food for people suffering from constipation.

Ash contents of the genotypes that ranged between 3.96% and 4.35% is lower than those of Oke (2014); Adamu and Oyetunde, (2013) reported 8.22% and 9.93% respectively. However, this study corroborate with the earlier finding of Kunyanga *et al*. (2013) (3.58%); Abiola *et al*. (2019) (4.58%) and Anjulo *et al*. (2021) (3.2%). The recommended permissible level of ash in pigeon pea by FAO (2012) was 3.8% which corroborate with the current investigation.

The moisture contents that ranged from 11.60% to 12.28% in the genotypes were close to those reported by Oke (2014) (11.2%) and Eltayeb *et al*. (2010) (11.7%). Olalekan and Bosede (2010) reported 8.45% moisture contents in pigeon pea; this was comparatively lower than the results obtained in this study. Similarly, Anjulo *et al*. (2021) had reported higher moisture content of 13.05%. High moisture content results in low shelf life and speedy deterioration of food products. The permissible level of moisture in pigeon pea recommended by FAO (2012) was 10.8%.

Westman (2002) expatiate that carbohydrates (CHO) are very important in the production of energy and maintenance of other metabolic processes in the body. Anjulo *et al*. (2021) had reported higher percentage CHO content (60.1%) than those obtained in the present study (50.7 to 52.22%). The difference may be due to the soil pH, and change in the agro-ecology of study areas. However, Saxena *et al*. (2010) reported 57.6%, Olalekan and Bosede (2010), Adamu and Oyetunde (2013), Kunyanga *et al*. (2013) and Oke (2014) had reported between 51.4% - 58.8% respectively. These were in good agreement with the results of this study. The permissible level of CHO in pigeon pea recommended by FAO was 60.4%; which was slightly more than those obtained in this study.

Generally, sulphur-rich amino acids (methionine, cystine and tryptophan) are limiting in legume crops including pigeon pea (Akande *et al*. 2010; Ade-Omowaye *et al*. 2015; Longvah *et al*. 2017). The methionine content which ranged from 1.25 to 1.50% obtained in this study was slightly higher when compare with those values reported by Oke (2014) 0.85 to0.88. However, it was in closer to1.16% obtained by Kachare *et al*. (2017) in pigeon pea. The recorded values of methionine content in the seeds of pigeon pea genotypes by Adamu and Oyetunde (2013) ranged from 0.730-1.22%. However, FAO (2016) recommended that methionine and cysteine contents should be 3.48%; hence all the genotypes were found to be deficit in these amino acids. Tryptophan contents in the seeds of pigeon pea genotypes ranged from 0.61 to 0.37%. These results corroborate with earlier values obtained by Kachare *et al*. (2017) i.e. 0.7% and Oke (2014) i.e. 0.42% in pigeon pea genotypes.

Glutamic acid was the most abundant amino acid in all the genotype evaluated; the values ranged between 16.86 to 18.10% respectively. Meanwhile, Akande *et al*. (2010) and Oke (2014) reported an average value of 19.7 and 12.02% respectively in glutamic acid; similarly, Ade-Omowaye *et al*. (2015) also reported 19.7% of glutamic acid in pigeon pea. The second most abundant amino acid among the genotypes was aspartic acid (ranging from 10.77 to 11.47%); Oke (2014) obtained a mean value of 7.46% of aspartic acid in cooked pigeon pea which is slightly lower when compare to other current study. This might be adduced to the fact that some of the aspartic acid had been lost during cooking due to the application of heat (Akande *et al*. 2010).

Ade-Omowaye *et al*. (2015) and Longvah *et al*. (2017) reported that pigeon pea seeds contain high amounts of arginine, aspartic acid, glutamic acid, leucine and lysine and could provide essential amino acids when consumed with cereals. Jukanti *et al*. (2012) opined that amino acid deficiencies in the little known legumes could be complemented by consuming cereals, which are rich in amino acids containing sulphur.

Pigeon pea is a good source of essential minerals like P, Mg, Fe, Ca, S and K but low in Na (Kunyanga *et al*. 2013). Copper is a trace essential element that plays a role in the formation of connective tissue and in the normal functioning of muscles, immune and nervous system. Jeremias (2006) reported that iron, together with copper plays a cogent role in the formation of red blood cells. The mean concentration of copper in this study ranged from 1.60 to 3.55 mg/Kg dry weights in Pigeon pea genotype; Rajni and Vikas (2016) reported just 0.12 mg/Kg of Cu, while Saxena *et al*. (2010) reported only 0.13 mg/Kg and Foodnet (2002) reported 0.13mg/Kg. These values were slightly lower when compared to the current investigation. Variation may be due to the difference in acidity and a texture of soil; however, the result obtained for Cu is within the permissible limit (1.2 mg/Kg) set by FAO (2012) in edible plants.

Calcium (Ca) was observed to be present in substantial amount in the genotypes; Ca is an important element that play important role in formation and development of bone and teeth. The value of Ca in the pigeon pea seeds was in the range of 0.17 to 0.38 mg/Kg; this was in agreement with that reported by Oke (2014) (0.32 mg/Kg). Singh *et al*. (2018) reported that the mean concentration of Ca in pigeon pea ranged from 0.895 mg/Kg – 1.19 mg/Kg while Kunyanga *et al*. (2013) reported (0.805 mg/Kg), these values were higher than those obtained in this study. The variations in concentration and order of accumulated metals in the samples could be partly due to variation in genetic makeup of the genotypes as well as soil pH. It is worthy of noting that the result obtained for Ca is lower than the permissible limit (1.3 mg/Kg) set by FAO (2012) in edible plants.

Birhanu (2015) opined that Magnesium (Mg) is a trace element that helps to maintain healthy nerves; it is also essential for proper iron metabolism as well as important for energy production. In human, prolong deficiency in Mg leads to chronic disease like diabetes, hypertension, coronary heart disease and Osteoporosis (Swaminathan, 2003). The mean concentration level of magnesium ranged between 0.11 and 0.14 mg/Kg dry weight pigeon pea genotypes. According to USDA (2016), the report level of Mg 18.3 mg/Kg, was higher than the results of the present study. The Permissible limit set by FAO (2012) was 1.8 mg/Kg which was also higher than the values obtained in the present study. This is an indication that Mg concentration is quite low in the pigeon pea genotypes used in this study.

Zinc (Zn) plays a role in immune function; it is a trace element which aid in wound healing, protein synthesis, DNA synthesis as well as cell division (Solomon, 1998). The concentration of zinc determined in pigeon pea genotype was from 6.80 to 8.80 mg/Kg dry weight. Kunyanga *et al*. (2013) had also reported value between 2.70 to 6.0 mg/Kg; also, imilarly, Sexena (2010), Patil *et al*. (2011) reported that the mean concentration of Zn was ranged from 0.08 mg/Kg to 0.36 mg/Kg. Abiola *et al*. (2019), however, observed an average of 0.48 mg/Kg of Zn in pigeon pea. The reason for these variations could be due to the higher leaching of base-forming cations and increasing acidity of the soil. The minimum limit of zinc in edible plants set by FAO (2012) and USDA (2016) was 0.274 mg/Kg and 0.276 mg/Kg respectively which were lower compare to the current study. This is an indication that the pigeon pea genotypes used in this study are rich in Zinc.

The iron (Fe) content of pigeon pea samples ranged from 3.25 to 5.95 mg/Kg dry weight; this was within the range of values reported by Kunyanga *et al*. (2013) (5.6 mg/100g); Anjulo *et al*. (2021) (5.97mg/Kg); and Singh *et al*. (2018) (5 mg/Kg). The reason behind this could be related to environmental differences such as increase in acidity of the soil in the study area. The result obtained for Cu is within the permissible limit (5.23 mg/Kg) set by FAO (2012) in edible plants.

Potassium (K) concentration was ranged between 1.56 – 1.77 mg/Kg. These results was in line with report of Nwokolo (2010) who reported the mean concentration of K in pigeon pea to be 1.25%; Rajni and Vikas (2016) also reported 1.14%. However, Oke (2014) reported higher value (4.6%) in K among pigeon peas. These could be attributed to different factors such as geographical and climatic variation, differences in physicochemical nature of the soil, and differences in the agricultural practices and inputs used for plant growth. The result obtained for K is within the permissible limit (1.10 mg/Kg) set by FAO (2012) in edible plants.

The available phosphorous content among the pigeon pea genotypes ranged from 2.8 to 3.1 mg/Kg; these values were comparatively lower when compare with the report of Anjulo *et al*. (2021) who reported the value of 6.82 mg/Kg. A relatively higher percentage of phosphorous may be due to previous fertilizer application to the soil, soil pH, organic matter, texture, and various soil management and agronomic practices in the study area. In a nutshell, P is highly sensitive to variation in environmental conditions, thus, could influence the variation. The result obtained for P is a bit lower than the minimum permissible limit (3.67 mg/Kg) set by USDA (2016) in edible plants.

Conclusion

The study revealed the existence of considerable variation among the elites and landraces of pigeon pea accessions with different accessions being favoured by different traits. Similarly, genetic relationships among accessions of pigeon pea show that some accessions are closely related to one another. In terms of yield performance, accessions NG/SA/11/08/108 and NG/AO/MAY/09/021/02 were similar, while accession TCC-151 was genetically distinct in terms of relatedness. These accessions can serve as source of gene transfer for hybridization of superior high yield cultivars.

Variation in proximate composition and amino acid profile show that genotype TCC-8126, TT-8129 and TCC-2 were found to be promising as they recorded considerable high values of nutritional contents and highest mineral content as well as good amino acid contents. These genotypes, considered as excellent breeding lines, could be valuable for future breeding program. The results of this study suggest that these legume crops are safe to be utilized as a staple food; since some of the concentrations of biochemical constituents are within the recommended limits of FAO and USDA limits. NG/SA/11/08/108, NG/AO/MAY/09/021/02, TCC-151, TCC-8126, TT-8129 and TCC-2 have been selected as promising genotypes that could serve as breeding lines for future breeding programme of *Cajanus cajan* in Nigeria.

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Table 1: Yield Parameters among the elite and landraces of pigeon pea in Oyo State

Parameter	NSPP	PODL (cm)	PW (g)	HSW (g)	No. of Pod/m^2	GYPP (t/ha)
PG/OY/18/001	3.17±0.19abc	5.16±0.09bc	32.80±0.86e	11.00±0.00f	140.00±0.00m	0.49
PG/OY/8/002	3.17±0.19abc	4.74±0.10ab	37.20±1.16fg	10.60±0.24f	152.80±0.20o	0.51
PG/OY/8/003	3.97±0.12g	4.95±0.10ab	36.40±1.36f	12.00±0.00g	118.00±0.00h	0.56
PG/OY/8/004	3.33±0.17bc	4.85±0.13abc	31.60±0.51de	10.80±0.2.00f	148.60±0.24n	0.53
PG/OY/8/005	3.40±0.19bc	6.75±1,32e	34.80±1.24ef	9.60±0.24e	69.80±0.20f	0.23
TCC-1	3.63±0.19c	4.23±0.09a	23.20±1.59ab	7.00±0.00a	128.00±0.00j	0.33
TCC-2	3.90±0.15f	4.76±0.08ab	30.80±1.59de	7.00±0.00a	265.00±0.00u	0.72
CITA-3	4.13±0.13gh	4.71±0.08ab	27.20±1.39c	8.00±0.00b	130.00±0.00k	0.43
TCC-6	3.37±0.11bc	4.45±0.09ab	24.60±1.86b	8.00±0.00b	121.00±0.00i	0.33
TCC-8	3.40±0.16bc	5.12±0.07bc	28.60±3.06cd	8.60±0.40c	43.80±0.20c	0.13
TB-72	3.40±0.16bc	4.51±0.09ab	25.80±1.02bc	7.00±0.00a	209.00±0.00r	0.50
TCC-151	3.13±0.22abc	4.85±0.14ab	42.00±1.84gh	11.00±0.00f	139.00±0.00l	0.48
TCC-8104	3.13±0.13abc	4.58±0.12a	16.60±1.03a	8.40±0.24bc	22.00±0.00a	0.06
TCC-8111	3.00±0.16ab	4.35±0.08ab	25.00±0.95bc	8.00±0.00b	47.00±0.00d	0.11
TCC-8125	3.63±0.13c	4.70±0.08ab	20.20±1.07a	7.00±0.00a	55.00±0.00e	0.14
TCC-8126	3.30±0.23abc	4.43±0.07ab	23.40±0.60ab	6.80±0.20a	229.00±0.00s	0.51
TCC-8127	2.93±0.18a	4.88±0.08ab	29.00±1.61d	7.8.00±0.00b	78.00±0.00g	0.18
TCC-8129	2.93±0.20a	4.88±0.10ab	29.20±1.16d	8.20±0.20b	152.00±0.00p	0.37
TCC-KPL-87	3.40±0.23bc	4.79±0.09ab	22.00±0.71ab	9.00±0.32d	33.00±0.00b	0.10
NG/SA/JAN/09/149	3.73±0.13d	5.23±0.09c	39.20±0.58g	10.60±0.24f	257.00±0.00t	1.02

NG/SA/JAN/09/179	3.43±0.17bc	6.42±0.12de	54.80±1.07i	13.00±0.00hf	312.00±0.00v	1.39
NG/SA/07/191	4.50±0.24h	4.76±0.10ab	32.80±1.56e	10.60±0.24f	188.00±0.00q	0.90
NG/AO/MAY/09/021/02	3.83±0.19e	5.21±0.11c	40.80±1.07g	11.00±0.32f	420.00±0.0x	1.77
NG/AO/MAY/09/021/01	3.60±0.17c	5.81±0.11d	42.00±0.71gh	11.60±0.24g	386.00±0.00w	1.61
NG/SA/11/08/108	4.97±0.23h	6.23±0.12de	71.60±2.06j	12.00±0.00g	437.00±0.00y	2.61

Values are Means±Standard Error of Mean; Values followed by different alphabet(s) on the column differ statistically at $P < 0.05$ tested by DMRT

NSPP= Number of seeds per pod; PODL= Pod length; PW= Pod weight; HSW= hundred Seed Weight; GYPP= Grain Yield per Plant

Table 2: Variation in Nutritional Composition among Elite and Landraces of Pigeon Pea Genotypes in Oyo State, Nigeria

PARAMETERS	CRUDE PROTEIN (%)	CRUDE FAT (%)	CRUDE FIBRE (%)	CRUDE ASH (%)	MOISTURE (%)	CARBOHYDRATE (%)	K mg/kg	Ca mg/kg	P mg/kg	Mg mg/kg	Fe mg/kg	Zn mg/kg	Cu mg/kg
CITA-3	21.09±0.02	1.37±0.01	9.64±0.02	4.22±0.01	11.95±0.03	51.74±0.02	1.58±0.02	0.20±0.02	2.9±0.00	0.12±0.00	4.00±0.20	7.70±0.10	2.40±0.10
TCC-8129	21.95±0.53	1.45±0.03	9.44±0.02	4.15±0.02	11.67±0.01	51.36±0.54	1.70±0.02	0.34±0.01	3.1±0.00	0.14±0.00	5.45±0.15	8.50±0.10	3.00±0.20
NG/SA/11/08/108	21.38±0.02	1.32±0.01	9.71±0.02	4.26±0.01	12.06±0.02	51.29±0.01	1.61±0.02	0.26±0.02	2.9±0.00	0.12±0.00	4.65±0.15	8.05±0.15	1.80±0.10
TB-72	21.26±0.02	1.29±0.01	9.67±0.01	4.35±0.01	11.84±0.01	51.63±0.02	1.54±0.02	0.17±0.02	2.8±0.00	0.12±0.00	3.60±0.10	7.35±0.15	2.05±0.15
PG/OY/2018/002	20.73±0.06	1.22±0.01	9.74±0.02	3.96±0.01	12.14±0.03	52.22±0.07	1.75±0.01	0.31±0.02	3.0±0.00	0.13±0.00	3.40±0.10	6.80±0.10	1.60±0.10
TCC-2	21.84±0.02	1.30±0.02	9.63±0.02	4.20±0.02	11.94±0.02	51.11±0.01	1.63±0.01	0.38±0.01	3.1±0.00	0.14±0.00	5.95±0.15	8.75±0.05	3.55±0.15
PG/OY/2018/004	20.64±0.04	1.24±0.01	9.80±0.02	4.31±0.02	12.28±0.01	51.75±0.04	1.72±0.01	0.27±0.01	3.0±0.00	0.14±0.00	5.20±0.10	8.30±0.10	2.70±0.10
NG/AO/MAY/09021/02	21.43±0.04	1.33±0.01	9.57±0.02	4.14±0.01	11.97±0.02	51.57±0.07	1.77±0.01	0.32±0.01	2.9±0.00	0.13±0.00	3.25±0.15	7.55±0.15	1.90±0.20
TCC-8126	22.53±0.04	1.41±0.01	9.37±0.02	4.30±0.01	11.60±0.01	50.78±0.08	1.68±0.02	0.36±0.01	3.1±0.00	0.13±0.00	5.60±0.10	8.80±0.10	3.30±0.10
TCC-15	21.73±0.05	1.35±0.01	9.78±0.01	4.35±0.01	12.10±0.01	50.70±0.08	1.56±0.01	0.18±0.01	2.8±0.00	0.11±0.00	3.75±0.15	7.05±0.15	2.20±0.10
FAO STD	**FAO, 2016**	**USDA, 2016**	**FAO, 2008**	**FAO, 2016**	**FAO, 2012**	**FAO, 2016**	**FAO, 2012**	**FAO, 2016**	**USDA,2016**	**USDA, 2016**	**FAO, 2012**	**USDA, 2016**	**FAO, 2012**
USDA STD	**22.3%**	**1.49%**	**1.5%**	**3.8%**	**10.8%**	**60%**	**1.10mg/kg**	**1.3 mg/kg**	**3.67 mg/kg**	**1.8 mg/kg**	**5.23 mg/kg**	**2.7mg/kg**	**1.2mg/kg**

Values are Means±Standard Error of Mean; Values followed by different alphabet(s) on the column differ statistically at $P < 0.05$ tested by DMRT

Table 3: Essential Amino Acid Profile among the Elite and Landraces of Pigeon Pea Genotypes in Oyo State, Nigeria

PARAMETER	HIS(%)	THR(%)	VAL(%)	LYS(%)	LEU(%)	ISO(%)	TRY(%)	MET(%)	PHE(%)	CYS(%)	PRO(%)
CITA-3	3.80±0.02^{a}	5.12±0.01^{a}	5.87±0.02^{a}	6.77±0.02^{a}	7.86±0.02^{a}	4.64±0.02a	0.37±0.02^{a}	1.25±0.02^{a}	6.91±0.02^{a}	1.29±0.01^{a}	4.76±0.01^{a}
TCC-15	4.02±0.01^{de}	5.26±0.01^{cd}	6.06±0.01^{ef}	6.97±0.01^{de}	8.08±0.01^{d}	4.96±0.01^{de}	0.48±0.02^{bc}	1.41±0.02^{d}	7.13±0.01^{d}	1.42±0.01^{de}	4.98±0.01^{cd}
TCC-8129	4.13±0.02^{g}	5.54±0.02^{f}	6.09±0.02^{f}	7.47±0.02^{gh}	8.28±0.01^{fg}	5.30±0.02^{g}	0.57±0.01^{ed}	1.46±0.01^{e}	8.08±0.01^{g}	1.43±0.02^{e}	5.38±0.01^{f}
NG/SA/11/08/108	3.97±0.01^{c}	5.21±0.02^{bc}	5.96±0.01^{b}	6.91±0.02^{c}	8.01±0.03^{c}	4.91±0.02^{c}	0.44±0.01^{b}	1.32±0.01^{bc}	7.07±0.02^{c}	1.36±0.01^{b}	4.91±0.02^{b}
TB-72	4.06±0.02^{def}	5.46±0.01^{e}	6.02±0.01^{de}	7.42±0.01^{g}	8.25±0.01^{f}	5.26±0.01^{g}	0.54±0.02^{de}	1.41±0.02^{d}	8.00±0.01^{f}	1.37±0.01^{bc}	5.31±0.02^{e}
PG/OY/2018/002	4.06±0.02^{ef}	5.26±0.01^{cd}	6.04±0.01^{de}	7.00±0.03^{f}	8.11±0.01^{de}	5.00±0.02^{e}	0.51±0.02^{cd}	1.37±0.01^{cd}	7.13±0.01^{d}	1.41±0.02^{cde}	4.99±0.02^{cd}
TCC-2	3.91±0.02^{b}	5.19±0.02^{b}	5.92±0.01^{b}	6.83±0.02^{b}	7.92±0.01^{b}	4.74±0.01^{b}	0.43±0.01^{b}	1.31±0.02^{b}	6.96±0.01^{b}	1.34±0.01^{b}	4.81±0.02^{a}
PG/OY/2018/004	4.10±0.01^{f}	5.30±0.01^{d}	6.13±0.01^{g}	7.06±0.01^{f}	8.14±0.01^{e}	5.05±0.01^{f}	0.54±0.02^{de}	1.41±0.02^{d}	7.20±0.02^{e}	1.46±0.02^{e}	5.03±0.01^{d}
NA/AO/MAY/09021/02	4.01±0.01^{cd}	5.24±0.02^{cd}	6.00±0.02^{cd}	6.94±0.02^{cd}	8.06±0.01^{d}	4.95±0.01^{d}	0.48±0.01^{bc}	1.37±0.01^{cd}	7.12±0.01^{d}	1.38±0.01^{bcd}	4.97±0.02^{c}
TCC-8126	4.14±0.00^{g}	5.54±0.01^{f}	6.11±0.02^{fg}	7.48±0.01^{h}	8.30±0.02^{g}	5.30±0.01^{g}	0.61±0.02^{f}	1.50±0.02^{e}	8.10±0.01^{g}	1.46±0.02^{e}	5.40±0.02^{f}

Values are Means±Standard Error of Mean; Values followed by different alphabet(s) on the column differ statistically at $P < 0.05$ tested by DMRT

HIS= Histidine, THR= Threonine, VAL= Valine, LYS= Lysine, LEU= Leucine, ISO= Isoleucine, TRY= Tryptophan, MET= Methionine, PHE= Phenylalanine, CYS= Cysteine, PRO= Proline

Table 4: Non Essential Amino Acid Profile among Elite and Landraces of Pigeon Pea Genotypes in Oyo State, Nigeria

PARAMETERS	TYR(%)	ALA(%)	ARG(%)	SER(%)	GLY(%)	ASP(%)	GLU(%)	CYS(%)	ORT(%)
CITA-3	4.17±0.01a	4.51±0.02a	6.69±0.02a	4.87±0.02a	5.30±0.01a	10.77±0.02a	16.86±0.02a	0.75±0.01a	0.17±0.02a
TCC-15	4.32±0.01de	4.66±0.02d	6.93±0.01de	5.03±0.01de	5.50±0.02d	10.95±0.01d	17.00±0.03c	0.86±0.01c	0.33±0.01de
TCC-8129	4.55±0.02f	5.88±0.01fg	7.37±0.02fg	5.25±0.01fg	5.81±0.02fg	11.35±0.02f	18.07±0.02f	0.91±0.02d	0.31±0.02d
NG/SA/11/08/108	4.26±0.01b	4.60±0.02bc	6.86±0.01c	4.95±0.02b	5.44±0.02c	10.88±0.02c	16.92±0.01b	0.80±0.01b	0.25±0.02b
TB-72	4.50±0.02f	5.84±0.01f	7.34±0.01f	5.20±0.02f	5.77±0.02f	11.33±0.01f	18.00±0.03e	0.86±0.01c	0.27±0.01bc
PG/OY/2018/002	4.31±0.02cd	4.65±0.01e	6.91±0.02cd	5.00±0.01bcd	5.53±0.01d	10.94±0.01d	17.00±0.02c	0.84±0.01bc	0.30±0.01cd
TCC-2	4.22±0.01b	4.58±0.01b	6.81±0.02b	4.97±0.01bc	5.37±0.02b	10.83±0.01b	16.92±0.01c	0.81±0.02b	0.23±0.01b
PG/OY/2018/004	4.37±0.02e	4.71±0.01d	6.96±0.01e	5.05±0.01e	5.60±0.02e	11.02±0.01e	17.05±0.01d	0.88±0.01cd	0.34±0.02de
NA/AO/MAY/09021/02	4.31±0.02cd	4.64±0.01cd	6.90±0.01cd	5.01±0.02cde	5.48±0.01cd	10.93±0.01d	16.97±0.01bc	0.84±0.01bc	0.32±0.01d
TCC-8126	4.54±0.02f	5.90±0.02g	7.41±0.02g	5.28±0.01g	5.84±0.01g	11.40±0.02g	18.10±0.02f	0.95±0.01e	0.37±0.01e

Values are Means±Standard Error of Mean; Values followed by different alphabet(s) on the column differ statistically at $P < 0.05$ tested by DMRT

TRY= Tryosine, ALA= Alanine, ARG= Arginine, SER= Serine, GLY= Glycine, ASP= Aspartic Acid, GLU= Glutamic Acid,CYS= Cystine, ORT= Orithine

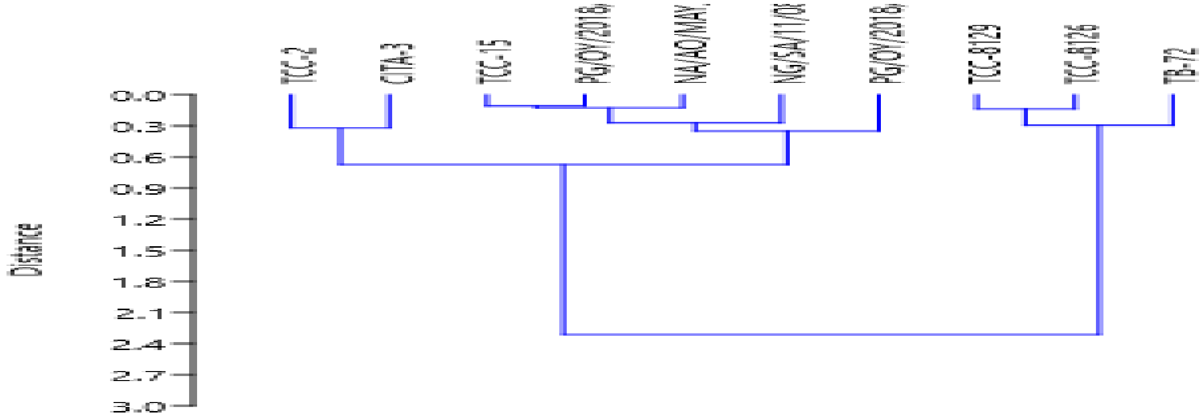

Figure 1: UPGMA Dendrogram of the Pigeon Pea Genotypes Using the Nutritional Compositions and Amino Acid Profile