



PHENOTYPIC CHARACTERISATION OF SEEDS OF SOME NIGERIAN PIGEON PEA (*Cajanus cajan* (L.) Millsp.) ACCESIONS

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Abstract

Pigeon pea (*Cajanus cajan* (L.) Millsp.) is a multipurpose legume crop that provides food, fodder and fuel wood for small-scale farmers. However, the crop is face with the challenge of genetic erosion, with limited attention from the research community. Hence, the need to assess the diversity among the crop for its improvement and exploration. A total of twenty (20) accessions, consisting of fifteen (15) improved genotypes collected from International Institute of Tropical Agriculture (IITA) Ibadan and Five (5) local genotypes collected from local farmer in Okeho, Kajola Local Government Area, Oyo State Nigeria were used for the study. The accessions were evaluated, using a standard descriptor of pigeon pea, for seed characters such as: Seed Colour Pattern (SCP), Base Seed Colour (BSC), Seed Eye Colour (SEC), Seed Eye Width (SEW) and Seed Shape (SS). Results showed that 42.5% of these accessions are plain, 32.5% are speckled, while 15% are mottled and speckled, only 10% are ringed in their colour pattern. On the base colour, only 5% are white, 10% are cream, and 37.5% have light-brown, while 47.5% have reddish-brown. Also, in their eye colour 22.5% accessions having light-brown, 25% are reddish-brown while 52.5% possessed dark purple colour. On the seed eye width, only 30% of the accessions are narrow, while both medium and wide are 35%. Pigeon pea seed possess various shapes of which only 10% are oval in shape among accessions collected, while 25% are globular in shape, 30% are square (angular) and 35% are elongate in shape. Euclidean hierarchical Cluster diagram on the bases of these 5 qualitative character, clustered the accessions into 5 different groups at genetic distance of 40.0 with accession PG/OY/2018/004 been clustered as a distinct group. However, morphological as well as molecular characterisations are required to arrange these accessions into more distinct genotypes; this will eventually provide the raw materials needed for the pigeon pea improvement programme in Nigeria.

Keywords: Genetic diversity, *Cajanus cajan*, phenotypic characterisation, improvement.

INTRODUCTION

Pigeon pea (*Cajanus cajan* (L.) Millsp.) is one of the major food legume crops of both tropics and subtropics. Pigeon pea is a drought tolerant plant and exhibits a large variation for physiological maturity (FAOSTAT, 2015). Pigeon pea is one of the most important crops cultivated in India and is currently the sixth most important legume food crop in the world (Varshney *et al.*, 2011). The crop is mostly grown in India, Nepal, and African countries including; Kenya, Malawi, Uganda, Tanzania, south African and Nigeria (Høgh-Jensen *et al.*, 2007; Lin-Qi *et al.*, 2014), and originated from Barbados where the seeds were considered as an important pigeon-feed (Gowda *et al.*, 2011). Pigeon pea is an important crops in the whole of Africa with the production reported in more than 33 countries, including, Nigeria, Mali, Niger, Kenya, Mozambique, Malawi, Ethiopia and southern Tanzania (Odeny, 2007; Høgh-Jensen *et al.*, 2007). Egbe (2005) reported that the pigeon pea-producing states in Nigeria include: Kogi, Taraba, Benue, Plateau, Kaduna, Adamawa, Enugu, Ebonyi, and Oyo, with the total area subjected to its cultivation is estimated to be over 190,000 hectares of land.



This plant is grown in many regions across the world and is known by different names, such as the Tropical green pea, Red gram, Congo pea. Pigeon pea grows in many other countries because of its multiple uses as a source of food, feed, fuel and fertiliser (Wilson *et al.*, 2012). This legume crop plays a significant role in ensuring nutritional food security and elimination of poverty among poor people in many countries of Asia and Africa (Lin-Qi *et al.*, 2014). It has been cultivated for more than 3,500 years in semi-arid and arid areas. It has been regarded as one of the most important grain legumes due to its ability to withstand biotic and abiotic stresses (Singh, 2005). Despite having widely cultivated in Africa, little seems to be known about its level of production in Nigeria, but surveys conducted by Remanandan and Asiegbe (1993) and Egbe and Kalu (2006) indicated that pigeon pea is widely cultivated in Nigeria and it appears that the intensity of pigeon pea cultivation is influenced by the culture and food habits of its people. It is still considered as underutilised crop species in the country whose production potential has not been exploited. In Nigeria, in terms of cultivation, the crop is the fifth legume after cowpea (*Vigna unguiculata*), Bambara groundnut (*Vigna subterranea*), Soybean (*Glycine max*) and Groundnut (*Arachis hypogaea*). Despite the significance of pigeon pea in providing protein rich food in vegetarian diet, its productivity in many producing areas in Africa remained low, when compared with the average yield potential of between 2.5 t ha⁻¹ to 3 t ha⁻¹ observed in India (Snapp, 2003). This is mainly due to several biotic and abiotic constraints the crop is exposed to in environments of Africa (Varshney *et al.*, 2011).

Pigeon pea yields in Nigeria and other African countries are very low, ranging from 0.40 to 0.70 t ha⁻¹ as it reported in Kenya and South African respectively (Egbe and Vange 2008; Khakhi 2014). Pigeon pea also integrates in the cropping systems mainly in alley cropping for soil fertility restoration (Aihou *et al.*, 2006). It is intercropped with other crops such as maize and yam. Egbe and Adeyemo (2006), reported that Pigeon pea can be intercropped with maize without negative effects on the yield and yield components of maize.

The nutritive value of the species is evident from the high protein content on a dry weight basis (21.5%), and its role as a major protein source to about 20% of the world's population (Mathews and Saxena 2003; Odeny 2006). Pigeon pea has very low fat and sodium content with no cholesterol and is high in fibre. The crop is also rich in carbohydrates and useful mineral elements, such as calcium, phosphorus and magnesium (Amarteifio *et al.*, 2002). The seeds can be prepared into various meals and served as substitute for cowpea, with mature seeds containing 21% protein, 53% starch, 2.3% fat, 6.6% crude fiber and 250.3 mg 100g⁻¹ mineral (Saxena *et al.*, 2010).

As a perennial shrub, pigeon pea has many advantages over annual legumes is that, several harvests are possible and its capacity to enhance soil fertility is much higher (Høgh-jensen, 2011). The effects of the crop on soil protection against erosion are well known (Upadhyaya *et al.*, 2013). Moreover, pigeon pea has a huge untapped potential for improvement both in quantity and quality of production in Africa (Odeny, 2007).

In the cropping systems, farmers grow traditional long-duration landraces, which take 9–10 months to mature with grain yields of 0.4 ton/ ha⁻¹. The problem of low yield in the region affects smallholder farmers who grow the crop to produce food with limited resources (Saxena *et al.*, 2010). Pigeon pea research in terms of crop improvement is still at a low level in Nigeria compared to other grain legumes such as cowpea; farmers still cultivate traditional varieties. Determination of genetic diversity of any given crop species is necessary for improvement of the crop because it generates baseline data to guide selection of parental lines and design of breeding scheme.



MATERIALS AND METHODS

A total of twenty (20) accessions; consisting of fifteen (15) improved genotypes TCC-1, TCC-2, CITA-3, FCC-6, TCC-8, TB-72, TCC-151, TCC-8104, TCC-8111, TCC-8125, TCC-8126, TCC-8127, TCC-8156, TCC-KPL-87 collected from International Institute of Tropical Agriculture (IITA) Ibadan and Five (5) local genotypes PG/OY/2018/001, PG/OY/2018/002, PG/OY/2018/003, PG/OY/2018/004, and PG/OY/2018/005 collected from local farmer in Okeho, Kajola Local Government Area, Oyo State Nigeria were used for the study. The accessions were evaluated for qualitative parameters such as; Seed Colour Pattern (SCP), Base Seed Colour, (BSC), Seed Eye Colour (SEC), Seed Eye Width (SEW) and Seed Shape (SS) using a standard descriptor of pigeon pea. A total of 30 seeds from each accession were randomly selected, observed and score for the qualitative parameters.

Data analysis

The result obtained were pooled for analysis, simple bar chart were used to represent the percentage of the qualitative parameters. The data obtained were used for the construction of Euclidean hierarchical Cluster dendrogram using statistical software.

RESULTS

Results showed that 42.5% of these accessions were plain, 32.5% are speckled, 15% are mottled and speckled, and 10% are ringed in their colour pattern (Figure 1). The seed base colour showed that 5% are white, 10% are cream, 37.5% light-brown, and 47.5% are reddish-brown (Figure 2). Also, in their eye colour 22.5% accessions are light-brown, 25% are reddish-brown while 52.5% possessed dark purple colour (Figure 3). On the seed eye width, 30% accessions are narrow, while both medium and wide are 35% respectively (Figure 4). Pigeon pea seed possess various shapes of which 10% are oval in shape among accessions collected, 25% is globular in shape, 30% is square (angular) and 35% are elongate in shape (Figure 5).

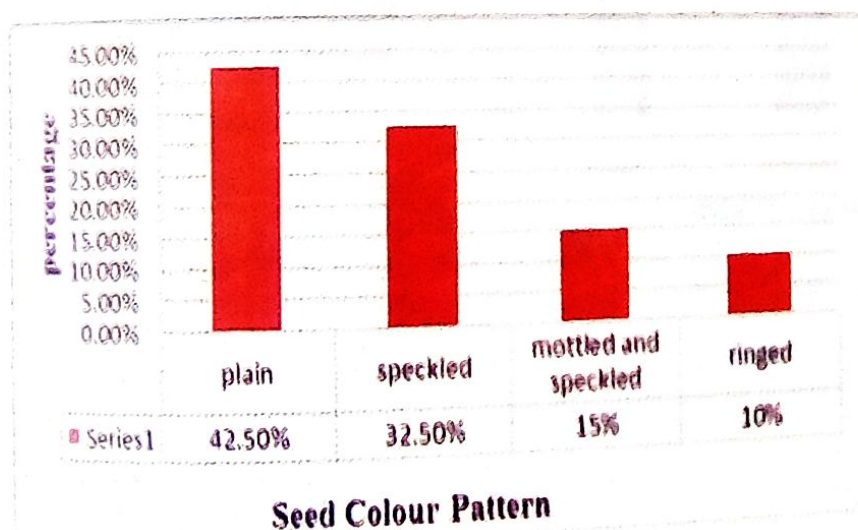


Figure 1: Percentage of Seed Colour Pattern

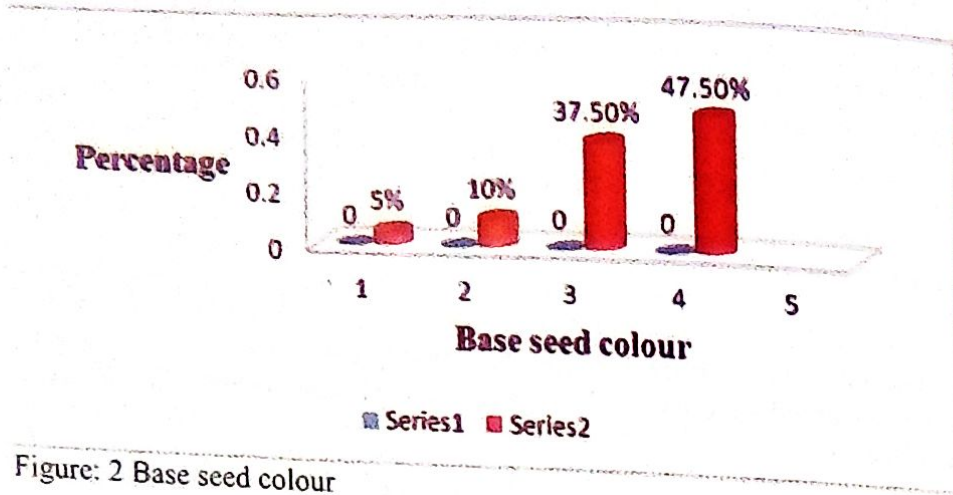


Figure 2 Base seed colour

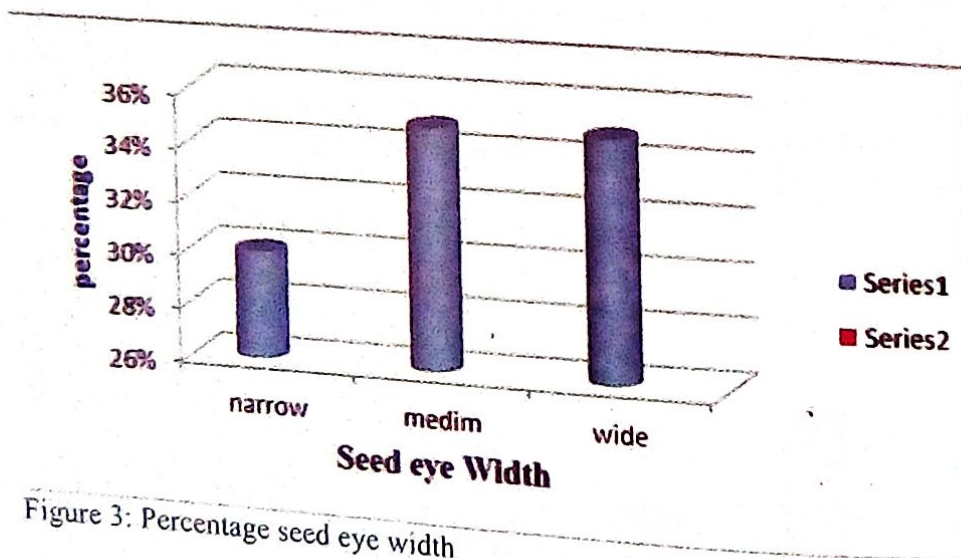


Figure 3: Percentage seed eye width

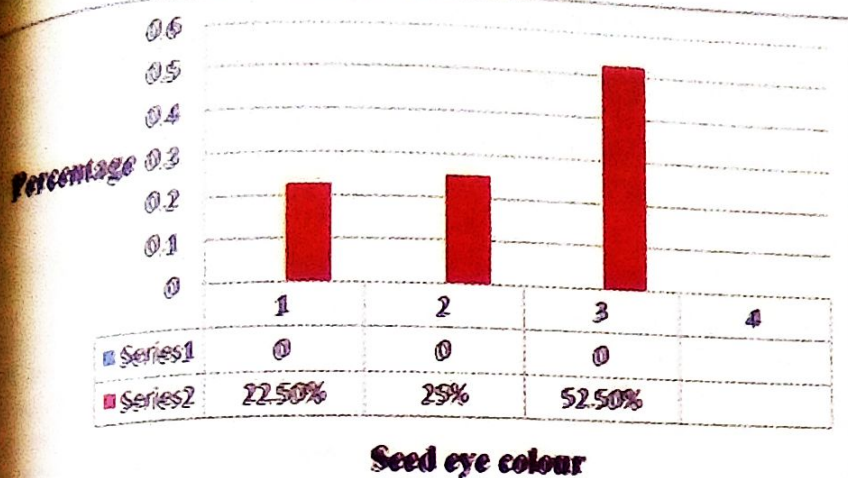


Figure 4: Percentage Seed eye colour

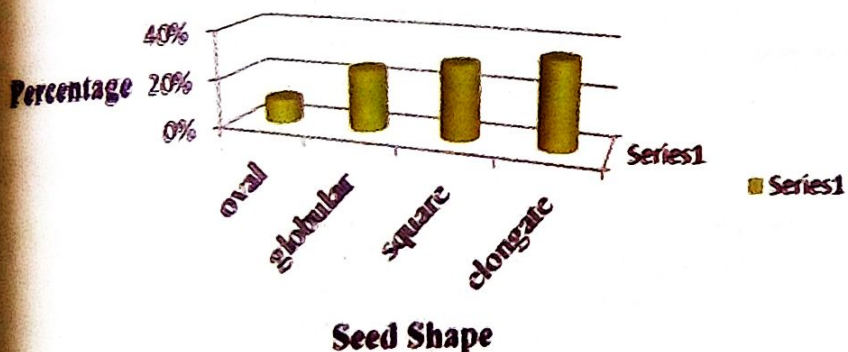


Figure 5: Percentage Seed Shape.

The Euclidean hierarchical Cluster dendrogram clustered the 20 genotypes into 5 cluster groups at 40.0 genetic distance (Figure 6). Cluster I comprised of four genotypes (TCC-1, TCC-2, TCC-8125, CITA-3, and TCC-8). With the exception of TCC-1 accession that has different seed colour pattern, all the accessions clustered in group I have the same seed eye colour. Cluster II comprised of seven genotypes (TCC-8104, TCC-8126, TB-72, TCC-8156, TCC-8111, TCC-8127 and TCC-151). Genotype TCC-8126 and TB-72 are shown to be the most closely related accession while TCC-8156 and TCC-8111 are clustered together indicating the same genotype. Cluster III consist of a single and distinct genotypes (PG/OY/2018/005, PG/OY/2018/001, TCC-8129, TCC-2, and TCC-8129) which all have the same seed eye width except accession TCC-2. Genotype PG/OY/2018/002, PG/OY/2018/003 and TCC-6 are cluster in group V, of which all three genotypes possessed the same seed eye colour. Among the accession clustered in group V, genotype PG/OY/2018/002 and TCC-6 have the same seed shape and seed eye width, with the exemption of accession PG/OY/2018/003.

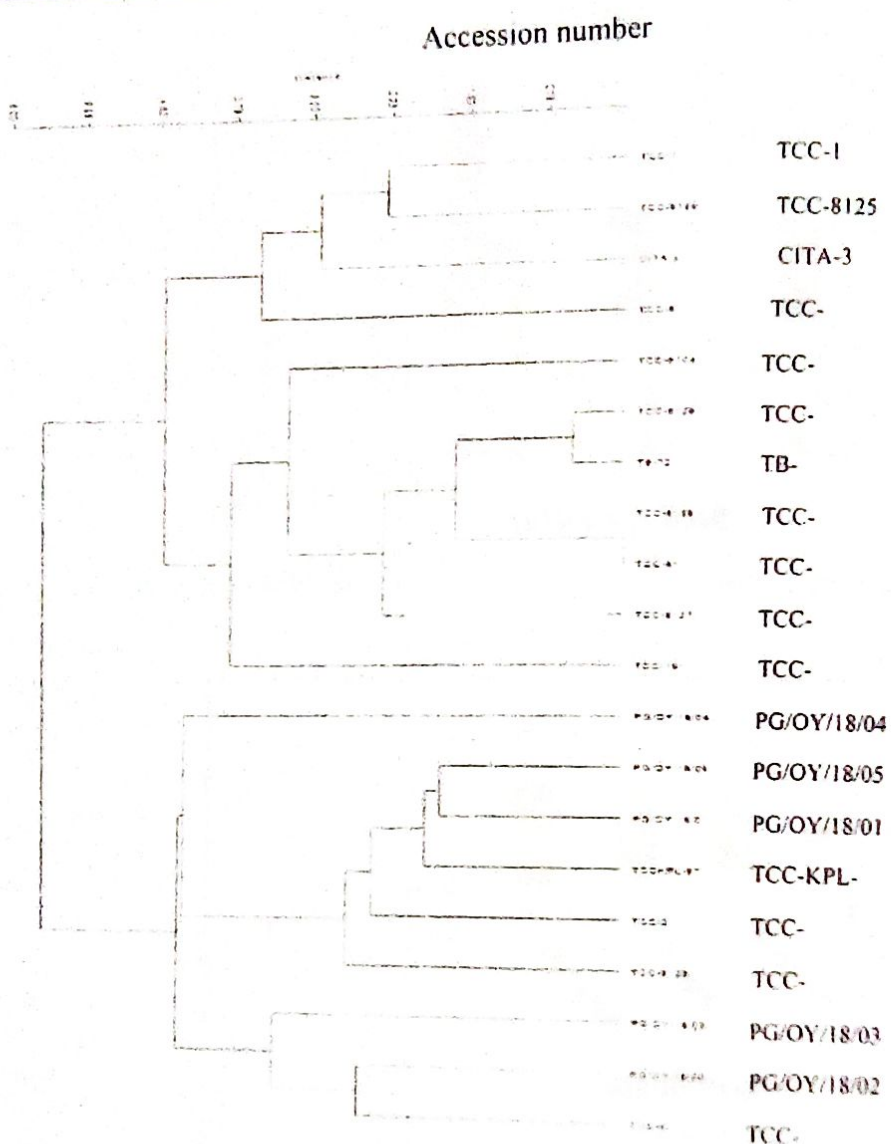


Figure 6: Euclidean cluster analysis dendrogram showing relationship among 20 pigeon pea (*Cajanus cajan*) genotypes collected from IITA and Landraces respectively.

DISCUSSION

Character used for characterisation reveal some important component of variability in the germplasm. One or more characters were able to discriminate accessions depending on their discriminating power. All accessions collected from local farmer in Oyo state were closely clustered in group III, IV and V, these might be due to closed similarity in their ecological and environmental factor. Therefore, all characters were found to have a distinct influence in selection of the accessions. Also, there is a great variation among accessions collected from local farmer with the accession PG/OY/2018/004 being a single and distinct genotypes despite their closed similarity in their ecological zone were the accessions were grown. Accessions TCC-8156 and TCC-8111 are cluster has the same genotype, this imply that accessions are the same but might have been move or migrate to different geographical area. This result was in line with the observation of Thombre *et al.* (2000) who observed 15 clusters in 64 genotypes of pigeon pea in India. Phillip (2002) also observed 4 clusters in 28 accessions of Zambian pigeon pea germplasm using



morphological characters. Katiyar *et al.* (2004), observed 14 clusters in 221 genotypes in India, and Romi *et al.* (2015), observed 7 clusters in 40 accessions in genetic diversity study of pigeon pea genotypes using SSR markers. Hence, the characters used were very important and effective criteria in distinguishing among the accession of pigeon pea. The use of seed coat colour as a selection criterion has been previously established in Bambara groundnut (Sinefu, 2011). Zondi (2013) also reported the significant contribution of seed coat colour and seed characteristics to the total variation in Bambara groundnut.

CONCLUSION

Seed characters like, seed colour, seed colour pattern, Seed Eye Colour, Seed Eye Width and seed shape can also be used to characterize genotypes, which helps in varietal or genotype identification and serves as morphological indicators in breeding at field level. Hence, they may serve as morphological markers in varietal identification, helps in purification of a variety or genotype. Also, accession may be similar morphologically and yet they are genetically distinct to each other. Therefore, morphological characterisation should be further subjected to molecular tools such as Random Amplified Polymorphic DNA (RAPD) or Simple Sequence Repeat (SSR) to detect their variation at molecular level.

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