

Morphological Characterization of 22 Accessions of Pigeon Pea [*Cajanus cajan* (L) Millsp.]

Kemi Adegboyegun^{1*}, Fidelis Etuh Okpanachi¹ and Kufre Ededet Akpanikot¹

¹*Department of Cell Biology and Genetics, University of Lagos, Lagos, Nigeria.*

Authors' contributions

This work was carried out in collaboration among all authors. Authors KA and FEO designed the study, performed the statistical analysis, wrote the protocol. Authors KA and KEA wrote the first draft of the manuscript and managed the analyses of the study. Author KEA managed the literature searches. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/AJBGMB/2020/v4i330107

Editor(s):

(1) Dr. Arulselvan Palanisamy, Muthayammal College of Arts and Science, India.

Reviewers:

- (1) Janilson Pinheiro de Assis, Federal Rural University of the Semi-Arid, Brazil.
(2) Muhammad Mubashar Zafar, Chinese Academy of Agricultural Sciences, China.
Complete Peer review History: <http://www.sdiarticle4.com/review-history/56175>

Original Research Article

Received 26 February 2020

Accepted 03 May 2020

Published 16 July 2020

ABSTRACT

Pigeon pea (*Cajanus cajan* [L] Millsp.) is a multipurpose legume crop that provides food fodder and wood for small scale farmers. However, it remains one of the underutilised crops with limited research done so far for the crop diversification and improvement. In this study, the phenotypic diversity of 22 accessions of pigeon pea was evaluated. The Seeds were collected from ICRISAT Niamey, Niger. The study was carried out at the biological garden and at the central research laboratory of the University of Lagos. Viability test was done on the collected seeds before planting in a polythene pot. The phenotypic traits measured include both the quantitative and qualitative traits. Analysis of variance revealed significant differences among accessions for all quantitative traits, except the seed length, seed breadth, seed thickness and the number of germinated seeds per pot. For qualitative traits, seed colour pattern and primary seed colour were diverse, other qualitative traits measured in this study showed moderate level of variation. The results for cluster analysis for both qualitative and quantitative traits grouped the accessions into two major clusters. In all the dendrograms, accessions ISC 147, ISC 24, ISC 157 and ISC 185 were varied and showed good performance for morphological traits analysed as well. The result of the phenotypic diversity observed in this study can help in parental selection for subsequent plant breeding.

*Corresponding author: E-mail: kemide37@gmail.com;

Keywords: Variability; morphological; genetics; food; *Cajanus cajan*.

1. INTRODUCTION

Pigeon pea, *Cajanus cajan* [L] Millsp. is one of the most important legumes grown in the tropics and sub tropics [1]. It is considered as a drought tolerant and a post-rainy season crop. It is often subjected to water stress at one or several stages of crop growth and development, and it has the ability to survive under different environmental conditions and cropping systems [2]. The crop plays an important role in food and nutritional security for rural communities in developing countries. The seed of pigeon is eaten as a green vegetable, and is an important source of protein, vitamin B, carotene and ascorbic acid [3;4]. It is a major source of protein to about 20% of the world population [5]. The plant seed is reported to contain 20 – 22% protein, 1 – 2% fat, 65% carbohydrate, and 6.8% ash. It is also rich in useful mineral elements such as calcium, phosphorous and magnesium [6].

Pigeon pea is a locally available, affordable and as a result of this, it has been reported as a crop that can supply reasonable amount of nutrition and protein in place of animal protein. Moreover, its high nutritional value has also made the plant a good source of fodder. There are reports of improved performance of poultry fed with the plant [7;8]. Due to its versatility, pigeon pea is an established and valued crop among small scale farmers. It is generally planted by small holder farmers in low input and rain-fed conditions [9].

The crop originated in India [10] and is grown in over 4 million hectares in tropical and sub-tropical areas of the world [11]. India is still the largest producer with over 3 million tons of pigeon peas produced per annum. The total number of hectares grown to pigeon pea is estimated at 5.4 million. India accounts for 72% of area grown to pigeon pea or 3.9 million hectares [12]. The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) maintains a large ex-situ collection of over 13,000 accessions of *Cajanus* species from around 75 countries (<http://singer.cgiar.org>).

Analyzing genetic relationships in species is important for revealing genetic diversity. It shows variability among cultivars and provides useful information for successful breeding programs [13]. The knowledge about morphological diversity in available germplasm though has

been shown to have limited genetic resolution still helps plant breeders in decision making during selection of cross combinations from large sets of parental genotypes and is always useful when widening the genetic basis of a breeding program.

Despite the potential benefits of pigeon pea, unfortunately it is considered as an orphan crop in many countries in sub sahara Africa [3;14]. Recently, the national agricultural program study defined the crop as one of the nineteen neglected and underutilised priority crop that merit attention and support [15;16]. The neglected status of pigeon pea affects its varietal diversity. In order to integrate its conservation and provides good parental line in the strategies of increasing agricultural production of this crop, it is necessary for more research work to be done on its diversity.

This study aims to assess the morphological diversity in a collection of pigeon pea accessions with the objective of evaluating the phenotypic variations in a collection of pigeon pea accessions using quantitative and qualitative morphological traits.

2. MATERIALS AND METHODS

2.1 Source of Materials and Planting

Twenty-two (22) accessions of pigeon pea seeds were sourced from ICRISAT in Niamey, Nigeria. Viability test was done by soaking method. These (viable seeds) were planted inside pots containing loamy soil. Each pot was labelled according to accession using a paper tape and permanent marker. Standard agronomic practices were followed to raise the crop. The crop was occasionally irrigated and weeding was done as the need arose. The pots were kept in the screen house provided at the Biological Garden, University of Lagos.

2.2 Morphological Evaluation

Different qualitative and quantitative characters were observed. These include seed length, seed breadth, thickness of seed, seed colour pattern, secondary seed colour, seed shape, plant height, leave length, leave width, number of branches, seed colour and number of plant that germinate per pot. They were recorded on selected plants from each accession following the morphological and taxonomical descriptors from ICRISAT.

2.3 Analysis of Data

Data generated were analysed using the IBM SPSS v25 (IBM SPSS Inc., USA). Treatment groups were compared using Analysis of variance (ANOVA) and mean differences were separated using the Duncan Multiple Range Test (DMRT). Differences were considered significant at 5% level of significance.

3. RESULTS

Twenty two pigeon pea accessions were characterized based on quantitative and qualitative characters. Among the morphological traits observed as shown in Table 1, the highest level of variation was shown in Leaf breadth (CV = 83.07). Another trait which exhibited a high variability among the accessions was the number of germinated seeds per pot (CV = 62.33). The least value of variation was observed in the seed thickness with CV = 7.96. Moderate levels of variation were observed in plant height and number of branches at 23.46 and 27.80 respectively. For seed length and seed breadth, the levels of variation were low at 10.10 and 14.37 respectively.

The various morphological traits recorded were shown in Tables 2 and 3. For quantitative traits, the accessions analyzed were significantly different for some of the traits measured. The study showed a significant level of variation in all the characters except seed length, seed breadth, seed thickness and number of plant per pot. Traits such as plant height, leaf length and leaf breadth showed significant differences ($P < 0.05$) among the accessions evaluated (Table 4).

Seed colour pattern showed a moderate level of variation. Out of 22 different accessions, 3 accessions showed plain seed colour pattern, 13 accession was speckled, 6 has mottled/speckled and one accession has speckled/ringed colour pattern. Seed shape was observed as oval in 12

accessions, 9 accessions has pea shape and one accession has elongated shape. There were no much differences in other qualitative traits measured in this study such as seed eye colour width, , primary seed colour and secondary seed colour (Table 3).

3.1 Cluster Analysis Based on Dendrogram

Cluster analysis using dendrogram for quantitative traits as shown in Fig. 1 grouped the accessions into three major clusters. Cluster A has two accessions, cluster B has 17 accessions and cluster C has two accessions. Of all the accessions analysed for quantitative trait, accession ISC 147 formed an outgroup with other accessions. Cluster B was further sub-group into two. Sub-group A consist of two accessions, sub-group B consist of 14 accessions. Accession ISC 24 was an outgroup in cluster A.

The accessions were grouped into three major clusters based on their quantitative traits (Fig. 2). Cluster A has 2 accessions, cluster B has 7 accessions and cluster C has 13 accessions. Cluster B was further divided into two group; Group BI has four accessions while Group BII has three accessions. In the same way, cluster C was further divided into two sub-group; sub-group CI has three accessions and sub-group CII has nine accessions. Accession ISC 157 was an outgroup in cluster C.

Combining both qualitative and quantitative traits together, two major clusters were observed from samples evaluated. Cluster A has two accessions and cluster B has nineteen accessions. Again accession 147 formed an outgroup with other accessions. Cluster B had two sub-clusters which includes Cluster BI consisting of two accessions, while cluster BII has seventeen accessions.

Table 1. Coefficient of variation among traits

Traits	Mean	Standard deviation	Minimum	Maximum	Coefficient of variation
Seed length (cm)	6.49	0.66	4.90	8.62	10.10
Seed breadth (cm)	5.71	0.82	0.32	8.00	14.37
Seed thickness (cm)	4.61	0.37	3.38	5.52	7.96
Leaf length (cm)	5.87	1.41	1.10	8.60	24.05
Leaf breadth (cm)	2.10	1.74	1.00	18.90	83.07
Plant height (cm)	32.84	7.70	6.00	44.70	23.46
Number of branches	5.61	1.56	1.00	8.00	27.80
Number of germinated seed	1.54	0.96	0.00	3.00	62.33

Table 2. Quantitative traits evaluated

Accessions	S.LTH	S.BRTH	S. TKS	LF. LNT	LF. BRTH	PT.H	N.O.B	N.O.GS
ISC 2	5.97±0.28	5.52±0.35	4.43±0.14	5.26±0.31a	1.72±0.23ab	26.20a	5.00b	1.00
ISC 4	6.64±0.28	5.66±0.32	4.58±0.36	5.88±0.57b	2.06±0.28bc	36.00b	7.00b	3.00
ISC 9	5.90±0.55	5.35±0.26	4.36±0.16	6.86±0.88c	2.60±1.57c	35.50b	6.00b	3.00
ISC 14	6.18±0.30	5.60±0.53	4.13±0.37	6.66±0.58bc	2.56±0.27c	33.40ab	6.00b	2.50
ISC 22	6.08±0.30	6.21±0.33	4.79±0.32	6.60±1.14b	2.08±0.36bc	35.40ab	7.00b	2.00
ISC 24	7.59±0.50	7.10±0.56	4.96±0.39	7.86±0.83c	2.54±0.44c	38.60b	6.00b	0.50
ISC 29	6.54±0.34	5.90±0.51	4.61±0.27	6.40±0.67b	2.04±0.27bc	34.50b	6.00b	2.00
ISC 32	6.35±0.32	5.11±0.45	4.42±0.40	5.96±0.66b	1.74±0.28ab	35.50b	7.00b	2.00
ISC 34	6.39±0.35	6.56±0.75	4.58±0.51	5.98±0.66b	1.72±0.31ab	30.70b	6.00b	1.00
ISC 38	6.99±0.27	5.64±0.35	4.81±0.22	5.54±0.53b	1.72±0.33ab	33.50b	5.00b	2.00
ISC 65	5.61±0.19	5.45±0.16	4.33±0.17	5.56±0.63b	1.82±0.40ab	32.30ab	6.00b	1.00
ISC 88	6.54±0.36	4.74±1.26	4.50±0.42	5.70±0.44b	1.82±0.31ab	35.50b	7.00b	1.50
ISC 157	6.73±0.49	5.79±0.41	4.89±0.19	7.58±1.06c	2.66±0.41c	44.70b	8.00b	0.50
ISC 12	5.65±0.35	5.20±0.42	4.33±0.34	5.86±0.84b	1.68±0.34ab	32.00ab	5.00b	1.00
ISC 90	6.58±0.38	5.78±0.29	4.74±0.35	6.20±0.61c	1.98±0.41abc	44.00b	7.00b	1.00
ISC 185	6.61±0.41	5.73±0.33	4.69±0.33	4.36±0.73a	1.28±0.24a	22.00a	2.00a	1.00
ISC 74	6.21±0.39	4.97±1.69	4.95±0.23	4.90±0.58a	1.58±0.27ab	31.80ab	5.00b	1.00
ISC 195	7.85±0.45	7.22±0.28	4.98±0.34	7.06±0.97c	2.08±0.40bc	30.40ab	5.00b	1.50
ISC 104	6.04±0.28	5.69±0.44	4.61±0.23	5.74±1.13b	1.58±0.38ab	34.70ab	6.00b	2.00
ISC 86	7.22±0.28	5.37±0.27	4.63±0.26	5.38±0.65ab	1.66±0.29ab	35.40b	5.00b	1.00
ISC 18	6.19±0.34	5.29±0.31	4.47±0.20	6.18±0.82b	1.74±0.43ab	34.40ab	6.00b	1.00
ISC 147	6.87±0.12	5.65±0.20	4.71±0.11	5.34±1.74a	1.56±0.38ab	18.90a	6.00b	1.00
F	1.13ns	0.97ns	1.17ns	5.08*	3.20*	15.67*	69.02*	10.42ns

ns: differences not significant at $p>0.05$. Column values with different alphabet are significantly different (DMRT, $P<0.05$). S.LTH - seed length; S.BRTH - seed breadth; S.TKS - seed thickness; LF. BRTH - leaf breadth; PL.HT - plant height; N.O.B - number of branches; N.O.GS - number of germinated seed per pot

Table 3. Qualitative traits evaluated

ACC	S. CLR. P	P. S. CLR	S. S. CLR	Eye. CLR	S. Shape	S. Eye. CLR. WT
ISC 2	Plain	R.Brown	L.Cream	L.Cream	Elongate	Wide
ISC 4	Speckled	L.Brwn	L.Cream	Cream	Pea	Medium
ISC 9	Plain	R.Brown	-	Cream	Oval	Narrow
ISC 14	Speckled	L.Brwn	L.Cream	L.Grey	Oval	Narrow
ISC 22	Speckled	L.Cream	L.Brwn	L.Grey	Pea	Wide
ISC 24	Speckled	L.Cream	L.Brwn	L.Grey	Pea	Medium
ISC 29	Speckled	L.Brwn	L.Cream	Cream	Oval	Wide
ISC 32	M/Specked	L.Brwn	R.Brwn	Cream	Pea	Narrow
ISC 34	Speckled	L.Cream	L.Brwn	Cream	Oval	Medium
ISC 38	M/Specked	L.Brwn	R.Brown	Cream	Pea	Wide
ISC 65	Speckled	L.Cream	Lb/Lg	Cream	Oval	Wide
ISC 88	Plain	L.Brwn	-	Cream	Pea	Narrow
ISC 157	Speckled	R.Brwn	L.Brwn	Cream	Pea	Narrow
ISC 12	Speckled	L.Brwn	R.Brwn	Cream	Oval	Narrow
ISC 90	S/Motled	L.Cream	R.Brwn	Cream	Oval	Wide
ISC 185	Speckled	L.Cream	L.Brwn	Cream	Oval	Medium
ISC 74	S/Motled	L.Brwn	R.Brwn	Cream	Oval	Medium
ISC 195	Speckled	L.Grey	L.Brwn	L.Grey	Oval	Wide
ISC 104	Speckled	L.Cream	L.Brwn	Cream	Oval	Narrow
ISC 86	Speckled	L.Brwn	R.Brown	Cream	Pea	Narrow
ISC 18	M/Speckd	L.Brwn	R.Brown	Cream	Pea	Medium
ISC 147	S/Ringed	L.Cream	L.Brwn	L.Grey	Oval	Medium

S.CLR.P - seed colour pattern; *P.S.CLR* - primary seed colour; *EYE. CLR* - eye colour; *S.SHAPE* - seed shape; *S.EYE.CLR.WT* - seed eye colour width; *R.BROWN* - reddish brown; *L.BROWN*- light brown; *L.GREY* - light grey

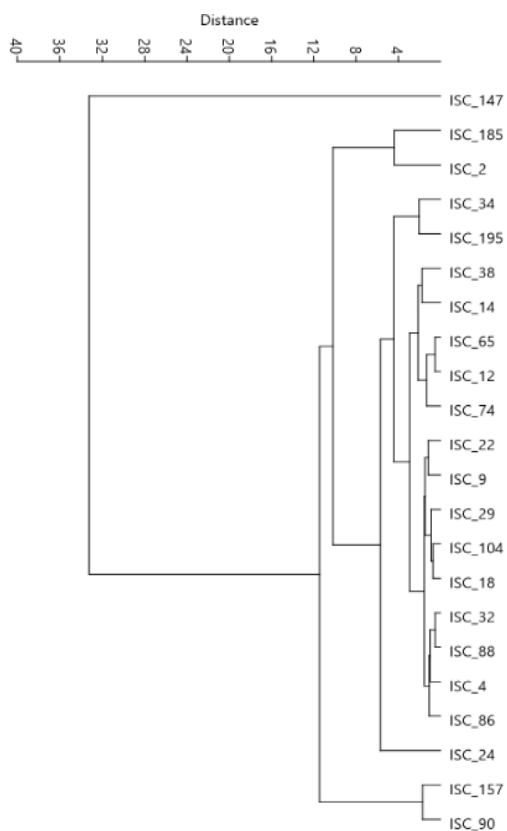


Fig. 1. Dendrogram for quantitative traits

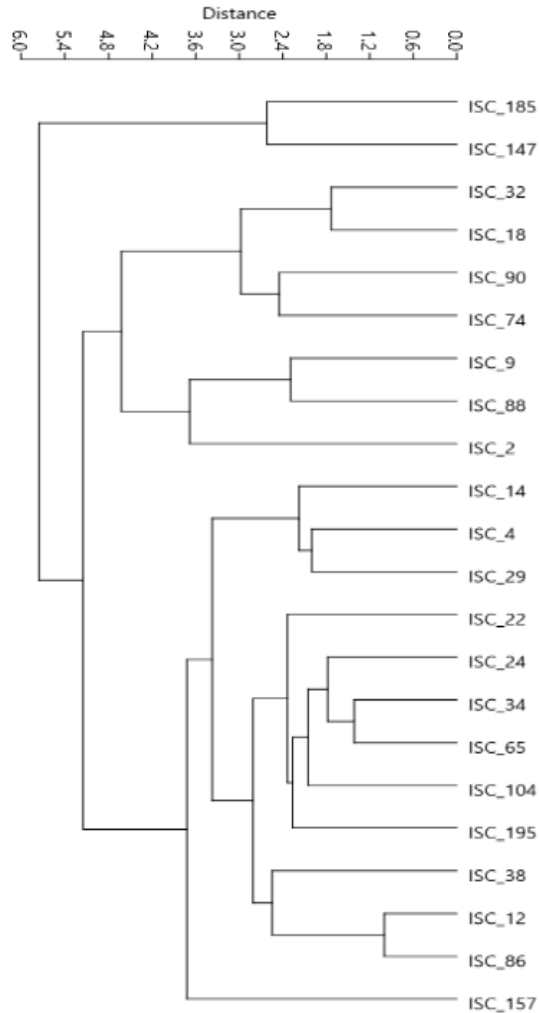


Fig. 2. Dendrogram for qualitative traits

4. DISCUSSION

Determination of the genetic diversity of any crop species is a suitable precursor for crop improvement. Several studies have been conducted previously for estimating genetic diversity in pigeon pea. Various techniques such as morphological variability [17;18], biochemical characterization [19] and molecular marker analysis [20;21;22] have been used in the pigeon pea diversity assessment. Although morphological characterization is susceptible to environmental effects, it is the first step in the description and classification of the germplasm [16].

The present study revealed a wide range of variation in qualitative traits as well as in

quantitative variables. Among the quantitative traits measured, leaf breadth was varied followed by the plant number of germinated seeds per pot. Moderate coefficient of variation (CV) was observed in a number of branches and plant height. However, this result was not in agreement with the report of [16] who observed a high value of variability in number of branches. He explained that his result could arise from large inter-row spacing adopted in his study. As reported by [23] that at low population density, pigeon pea was known to produce greater biomass (branches). It is then assumed that the moderate CV value observed in the number of branches in this present study could be attributed to increase in population density of plant per pot. Low level of variation was observed in plant height, and this might be due to influence of

exposure to short day condition resulting from lack of exposure to adequate sunlight. Also the study was conducted during the raining season. [24] reported that plant height could be substantially increased through prolong of the vegetative phase by exposure to the long day situations. The fact that germplasm collections were not made up of the same accessions may also explain the differences observed in trait diversity.

Among the qualitative traits measured in this study, seed colour pattern and primary seed colour has the highest level of variation. This

result is in congruence with the finding of [17] who also reported the highest variability in primary seed colour. However, [25] in their study reported the highest variation in flowering pattern and seed eye colour; but they observed nonetheless a moderate level of variation in seed colour. In general, the heterogeneity observed for qualitative traits in pigeon pea germplasm depends often on its natural out-crossing rate [17] which ranges from 3% to 26% and varies according to locations, genotype, and the intensity of the insect population and time of flowering [26;27].

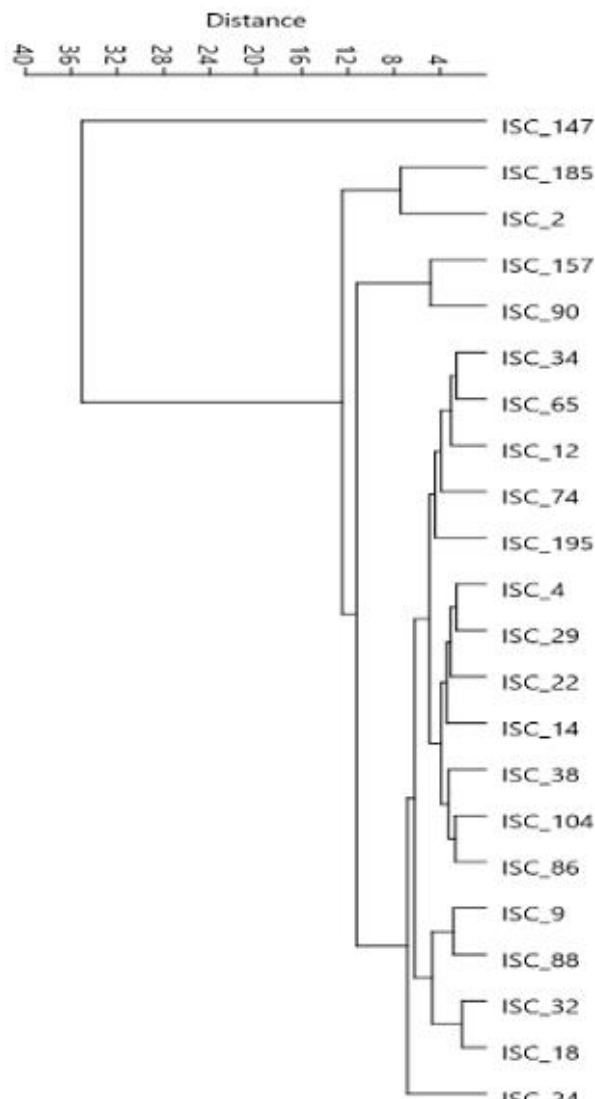


Fig. 3. Dendrogram for quantitative and qualitative traits

The results of cluster analysis for both qualitative and quantitative traits grouped the accessions into clusters. In all the dendrograms as shown in the Fig. 3, accession ISC 147 was the most varied, followed by accession ISC 24, ISC 157 and ISC 185. These accessions (ISC 147, ISC 24, ISC 157 and ISC 185) appeared to show similar character for most of the qualitative traits evaluated. They equally showed good performance for quantitative traits. This may suggest that they are genetically related. However, morphological characterization alone cannot be used to ascertain relatedness as they can be easily influenced by environmental factors.

5. CONCLUSION

The results obtained from this study showed a wide morphological variability in the collection of pigeon pea analysed. Based on qualitative traits, seed colour pattern and primary seed colour were the most varied trait. A great variability was observed in quantitative traits such as leaf breadth, plant height, number of branches and number of germinated seeds per pot. Of all the accessions of pigeon pea evaluated, accessions ISC 147, ISC 24, ISC 157 and ISC 185 were varied and showed good performance for both qualitative and quantitative traits evaluated. The result of the morphological characterization observed in this study can help in subsequent plant breeding program. However, molecular studies using specific *Cajanus cajan* primers may also be carried out to ascertain their genetic relatedness and variability.

DISCLAIMER

The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Varshney RK, Penmetsa RV, Dutta S, Kulwal PL, Saxena RK, Data S, Sharma TR, Rosen B, Carrasquilla-Garcia N, Farmer AD, Dubey A, Saxena KB, Gao J, Fakrudin B, Singh MN, Singh BP, Wanjari KB, Yuan M, Srivastava RK, Kilian A, Upadhyaya HD, Mallikarjuna N, Town CD, Bruening GE, He G, May GD, McCombie R, Jackson SA, Singh NK, Cook DR. Pigeon pea genomics initiative (PGI): an international effort to improve crop productivity of pigeonpea (*Cajanus cajan* L.). *Molecular Breeding*. 2010;26:393–408.
2. Choudhary DK, Sharma KP, Gaur RK. Biotechnological perspective of microbes in agro-ecosystems. *Biotechnol Lett*. 2011;33:1905-1910.
3. Odeny DA. The potential of pigeon pea (*Cajanus cajan* (L.) Millsp.) in Africa. *Natural Resources Forum*. 2007;31:297-305.
4. Choudhary AK, Kumar S, Patil BS, Bhat JS, Sharma M. Narrowing yield gaps through genetic improvement for Fusarium wilt resistance in three pulse crops of the semi-arid tropics. *Breeding Genetics*. 2013;45:341–370.
5. Odeny DA. Microsatellite development and application in Pigeon pea. MSc. diss., Rheinischen-Friedrich Willhelms University. Kisumu; 2006.
6. Morake TK, Munthali DC, Karikari SK, Amarteifio JO. The composition of pigeon pea grown in Botswana. *Plant Foods for Human Nutrition*. 2002;57:173-177.
7. Amaefule KU, Obioha FC. Performance of pullet chicks fed raw or processed pigeonpea seed meal diets. *Livestock Research for Rural Development*. 2005;17:29-32.
8. Abdelati KA, Mohammed HAR, Ahmed ME. Influence of feeding processed pigeonpea seeds on broiler chick performance. *Journal of Poultry Science*. 2009;8(10):971-975.
9. Saxena RK, Patel K, Kumar CV, Tyagi K, Saxena KB, Varshney RK. Molecular mapping and inheritance of restoration of fertility in A4 hybrid system in pigeon pea. *Theoretical and Applied Genetics*. 2018;131:1605-1614.
10. Ladizinsky G, Hamel A. Seed protein profiles of pigeon pea and some *Atylosia* species. *Euphytica*. 1980;29:313-317.
11. Matthew C, Saxena KB. Prospects for pigeon pea evaluation in drought-prone areas of South Africa, South Africa. *Pigeon Pea Newsletter*. 2001;8:52-53.

12. FAO. Food and Agriculture Organization of the United Nations, Rome, Italy "FAOSTAT"; 2018. Available:www.fao.org
13. Sneller CH, Nelson RL, Carter TE, Cui Z. Genetic diversity in crop improvement: The soybean experience. *Journal of Crop Improvement*. 2005;14:1-2
14. Varshney RK, Chen W, Li Y, Bharti AK, Saxena RK, Schlueter JA, Donoghue MT. Draft genome sequence of pigeon pea, an orphan legume crop of resource-poor farmers. *Nature Biotechnology*. 2012;30:83–89.
15. Dansi A, Vodouhè R, Azokpota P, Yedomonhan H, Assogba P, Adjatin A, Loko YL, Dossou-Aminon I, Akpagana K. Diversity of the neglected and underutilized crop species of importance in Benin. *Science World Journal*. 2012;19:932-947.
16. Zavinon F, Adoukonou-Sagbadja H, Ahoton L, Vodouhè R, Ahanhanzo C. Quantitative Analysis, Distribution and traditional management of pigeon pea landraces' diversity in Southern Benin. *European Scientific Journal*. 2018;14:184-211.
17. Upadhyaya HD, Reddy KN, Gowda CLL, Singh S. Phenotypic diversity in the pigeonpea core collection. *Genetic Resources and Crop Evolution*. 2007;54:1167–1184.
18. Manyasa EO, Silim SN, Githiri SM, Christiansen JL. Diversity in Tanzanian pigeonpea landraces and their response to environments. *Genetic Resources and Crop Evolution*. 2008;55: 379–387.
19. Joshi BK, Bimb HP, Gauchan D, Bajracharya J, Shrestha P, Upadhyay MP. Genetic Diversity and Population Structure of Pigeon Pea. *BSN E-Bulletin*. 2009;1:16-17.
20. Saxena RK, Prathima C, Saxena KB, Hoisington DA, Singh NK, Varshney RK. Novel SSR markers for polymorphism detection in pigeon pea. *Plant Breeding*. 2010;129:142–148.
21. Njung'e V, Deshpande S, Siambi M, Jones R, Silim S, Villiers S. SSR genetic diversity assessment of popular pigeon pea varieties in Malawi reveals unique fingerprints. *Electronic Journal of Biotechnology*. 2016;21:65–71.
22. Bohra A, Jha R, Pandey G, Patil PG, Saxena RK, Singh IP, Singh D, Mishra RK, Mishra A, Singh F, Varshney RK, Singh NP. New Hypervariable SSR Markers for Diversity Analysis, Hybrid Purity Testing and Trait Mapping in Pigeon pea. *Frontier of Plant Science*. 2017;8:370-377
23. Mula M, Saxena K, Rathore A, Kumar R. Response of A x B and A x R CMS-Lines of hybrid pigeon pea on spacing in late sown condition. *Green Farming*. 2011;2:379-381.
24. Reddy SS, Bhaduri SK, Sen SK. Infrared spectra of alkali treated juice stick. *Journal of Applied Polymer Science*. 1990;41:1-2.
25. Manyasa EO, Silim SN, Christiansen JL. Variability patterns in Ugandan pigeon pea landraces. *Journal of SAT Agricultural Research*. 2009;16:9-11.
26. Saxena KB, Sharma D. Pigeon pea: Genetics. In: Nene YL, Hall SD, Shiela VK (editions) *The pigeon pea*. C.A.B. International, Wallingford, UK. 1990;18:44–87.
27. Reddy LJ, Chandra S, Pooni H, Bramel PJ. Rate of outcrossing in pigeon pea under intercropped conditions. In: Bramel PJ (editions) *Assessing the risk of losses in biodiversity in traditional cropping systems: A case study of Pigeon pea in Andhra Pradesh*. International Crops Research Institute for the Semi-Arid Tropics. Patancheru. 2004;168:502-324.

© 2020 Adegboyegun et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:
<http://www.sdiarticle4.com/review-history/56175>