Original Research Article

Characterization of pigeonpea (*Cajanus cajan* (L.) MillSp.) genotypes based on DUS traits

ABSTRACT

Aims: The ~~study involves the~~research entails morphological characterization of pigeonpea genotypes based on qualitative traits which aids in varietal description ~~thereby~~ and ~~ensuring~~ ensure genetic purity.

Study design: Randomized complete block design.

Place and Duration of Study: The study was conducted at the Department of Pulses, Tamil Nadu Agricultural University during *kharif*, 2019 and *rabi*, 2019-2020.

Methodology: The 68 short duration pigeonpea genotypes were characterized and grouped based on 17 qualitative traits.

Result: The morphological characterization revealed that, more variation was ~~observed~~ identified for traits *viz.,* pattern of streaks on standard petal, plant height, seed colour, seed shape and seed size. Sixty - eight genotypes were subjected to cluster analysis and were grouped into four major clusters with an average similarity of 80%~~at 80 per cent similarity~~. The similarity coefficient ranged from 0.65 to 1.00. The cluster I consisted of 60 genotypes. Two sub-groups were formed from Cluster I ~~The cluster I was divided into two sub-groups~~. The sub-group I had 59 genotypes at 84 per cent similarity, whereas the sub-group II consisted of the genotype ICPL19050. Cluster II was made up of six genotypes~~The cluster II consisted of six genotypes~~. The cluster II was divided into two sub-groups at 84 per cent similarity. Clusters III and IV were solitary clusters, each with a single genotype~~The cluster III and IV were solitary clusters with one genotype each~~.

Conclusion: The characterization of genotypes with specific traits could be used to identify the genotypes, maintenance of genetic purity and to utilize in future breeding programmes.

Key words: Clustering, DUS, morphological characterization, short duration, pigeonpea, qualitative traits.

1. INTRODUCTION

Pigeonpea *(Cajanus cajan* (L.) MillSp.) is a~~n important~~ popular legume crop, which is found in 82 countries around the world [10]. However, pigeonpea is grown only in 18 countries [11]. The average production of pigeonpea is 3.32 million tonnes in India with an area of 4.54 m. ha under pigeonpea cultivation [4]. Despite the numerous crop improvement programme ~~indulged in~~devoted to the development of varieties and hybrids in pigeonpea, the productivity of the crop has remained stagnant throughout time ~~over years~~. Any crop improvement programme begins with identification of plant genetic resources. Development of core and composite collections from the available germplasm facilitates ~~aids in~~ their utilization in crop improvement programmes. Core collections developed from the thousands of pigeonpea accessions around the world based on the qualitative traits have aided their utilization in the breeding programme [11-16]. The qualitative traits are ~~highly~~ quite stable and they can be ~~utilized~~ used as molecular markers in characterization and evaluation of genotypes. The characterization of cultivated species or genotypes aids in varietal description which can be used to maintain genetic purity. The genotypes of short-duration pigeonpeas were tested and characterized for numerous morphological features in this study.~~In the present study, the short duration pigeonpea genotypes were evaluated and characterised for various morphological traits.~~

2. MATERIAL AND METHODS

The experimental material consisted of 68 pigeonpea genotypes including a check variety, CO(Rg)7. The list of short duration (days to maturity 120-130 days) pigeonpea genotypes under study is given in Table 1. The experimental plot is located at a latitude of 11.0232°N and longitude of 76.9293°E. The altitude of the experimental location is 426.72 m above MSL(?). The soil type is red soil. The experiment was conducted during *kharif*, 2019 and *rabi*, 2019-2020. A total of 68 pigeonpea genotypes were raised in a randomized complete block design with two replications. The plants were raised in a 4 m row with a spacing of 90 × 30 cm. The pigeonpea genotypes were subjected to DUS (Distinctness, Uniformity and Stability) characterization based on 17 qualitative traits [2] *viz.,* anthocyanin colour on hypocotyl, plant branching pattern, time of flowering, plant growth habit, stem colour, leaf shape, colour of base of petal, pattern of streaks on standard petal, pod colour, pod constriction, pod length, number of seeds per pod, plant height, seed colour, seed colour pattern, seed shape and seed size (Table 2). The genotypes were scored for each trait based on the note values of the DUS characters given by PPV&FR (Protection of Plant Varieties and Farmers Right~~)~~, 2007). The morphological data was subjected to cluster analysis using NTSYSpc v 2.02i? software [12]. The similarity index was calculated using SimQual programme and the dendrogram was constructed using SAHN clustering(Reference).

Table 1. List of pigeonpea genotypes used in the study

S.No.	Genotypes	S.No.	Genotypes	S.No.	Genotypes
1	ICPL19001*	24	ICPL19026*	47	ICPL151*
2	ICPL19002*	25	ICPL19027*	48	ICPL89*
3	ICPL19003*	26	ICPL19028*	49	ICPL85010*
4	ICPL19004*	27	ICPL19029*	50	ICPL88039*
5	ICPL19007*	28	ICPL19030*	51	ICPL88034*
6	ICPL19008*	29	ICPL19031*	52	ICPL149*
7	ICPL19009*	30	ICPL19032*	53	ICPL86022*
8	ICPL19010*	31	ICPL19033*	54	ICPL161*
9	ICPL19011*	32	ICPL19034*	55	ICPL81-3*
10	ICPL19012*	33	ICPL19035*	56	ICPB2039*
11	ICPL19013*	34	ICPL19036*	57	ICPB2156*
12	ICPL19014*	35	ICPL19037*	58	CO2R**
13	ICPL19015*	36	ICPL19038*	59	CO3R**
14	ICPL19016*	37	ICPL19039*	60	CO4R**
15	ICPL19017*	38	ICPL19040*	61	CO5R**
16	ICPL19018*	39	ICPL19042*	62	CO6R**
17	ICPL19019*	40	ICPL19043*	63	CO7R**
18	ICPL19020*	41	ICPL19044*	64	CO8R**
19	ICPL19021*	42	ICPL19046*	65	CO9R**
20	ICPL19022*	43	ICPL19047*	66	CO10R**
21	ICPL19023*	44	ICPL19049*	67	CO11R**
22	ICPL19024*	45	ICPL19050*	68	CO(Rg)7**
23	ICPL19025*	46	ICPL87*		

'' -developed at ICRISAT; '**' – developed at the Department of Pulses, CPBG, TNAU.*

ICRISAT ? CPBG?`

3. RESULTS AND DISCUSSION

The diversity of any population can be estimated based on various ~~methodologies~~ approaches *viz.,* pedigree analysis, qualitative traits, quantitative or agronomical traits and molecular markers [14]. The classification of genotypes based on qualitative traits is the reliable and also the simplest method [6]. The expression of morphological traits is ~~not affected~~ unaffected by dynamic environmental factors and can be used as morphological markers in varietal identification and purification [9].

DUS characterization

The absolute and relative frequency for the qualitative traits of 68 pigeonpea genotypes are given in Table 2. The genotypes were assessed for 17 qualitative traits during two seasons *kharif,*

2019 and *rabi*, 2019-2020. The study ~~showed~~ found that~~,~~ all ~~the~~ genotypes had recorded unique characters and that there was no seasonal change in the expression of traits ~~showed no variation for the expression of traits in both the seasons~~. Thus, proving fact that, the qualitative characters are unaffected by the environment. The anthocyanin colour on the hypocotyl was observed during seedling stage and all the 68 genotypes possessed anthocyanin pigmentation. A total of 61 genotypes ~~had~~ exhibited a semi-spreading type of branching pattern, whereas seven genotypes had erect type of branching pattern and the spreading type was not observed among the genotypes ~~evaluated~~ studied (Fig.1). All the genotypes attained 50 % flowering within 61-90 days and fall in the early duration group. Out of 68 pigeonpea genotypes evaluated, 61 genotypes were indeterminate and seven with determinate plant type (Fig.2). The stem colour was green in all the genotypes. Oblong leaf shape was observed in 62 genotypes and obovate leaf shape was observed in six genotypes (Fig.3). The colour of the base petal was yellow for the 68 genotypes. The pattern of streaks on the standard petal showed a wide range of variation, where 18 genotypes had no streaks, 47 genotypes had sparse pattern of streaks, two genotypes had medium pattern of streaks and one genotype had dense streaks on the standard petal (Fig.4). Green pods with purple stripes were found in all 68 genotypes. Only one genotype, ICPL89, did not have the pod constriction. ~~The pod colour of all the 68 genotypes were green with purple streaks. The pod constriction was present in 67 genotypes and it was absent in only one genotype ICPL89~~ (Fig.5). Six genotypes had a pod length of 4-5 cm and 62 genotypes had above 5 cm. All the genotypes had four seeds per pod. The height of eight genotypes were less than 100 cm, 38 genotypes were of medium height (100-150 cm) and 22 genotypes were tall (>150 cm). The seed colour of four genotypes was cream, 15 genotypes was brown and 49 genotypes was with dark brown seeds (Fig.6). Only one genotype had a mottled seed color pattern, while 67 genotypes had uniform seed color patterns.~~Uniform seed colour pattern was observed for 67 genotypes and only one genotypes had mottled seed colour pattern~~ (Fig.7). A total of 32 genotypes had oval seed shape, whereas 36 genotypes had globular seed shape. The seed size was small in case of one genotype, medium in case of 24 genotypes, large for 33 genotypes and vary large in case of ten genotypes.

Characterization of genotypes using qualitative traits is vital for varietal identification and purification [13]. In the present study, variation was observed for qualitative traits *viz.,* pattern of streaks on standard petal, plant height, seed colour, seed shape and seed size. The limited variation was observed for traits *viz.,* plant branching pattern, plant growth habit, leaf shape, pod constriction, pod length and seed colour pattern, whereas no variation was observed for traits *viz.,* anthocyanin colour on hypocotyl, time of flowering, stem colour, base colour of standard petal, pod colour and number of seeds per pod. Seed characteristics, which are critical for genotype categorization, showed the most diversity. ~~The more variation was noted in case of seed characters, which is important for classification of genotypes~~ [7]. However, this study revealed a fact that the variation for qualitative traits among the pigeonpea genotypes studied was very less, which may be due to the narrow genetic base of the parents involved in the development of the study material. Manyasa et al. [8] evaluated 123 Tanzanian pigeonpea landraces based on eight qualitative traits and reported low variation among the accessions for various traits *viz.,* stem colour, growth habit, base flower colour, pod colour,

pod hairiness, seed eye colour and seed eye width. Sahu et al. [15] studied 60 pigeonpea genotypes using 21 quantitative characters and reported that, the variation was observed for traits *viz.,* branching pattern, growth habit, flower colour, pod colour and seed characters. Adegboyegun et al. [1] assessed 22 pigeonpea genotypes using six seed characteristics and found that more variation was observed for the traits seed colour pattern and primary seed colour. Chaudhary *et al.* [3] studied 243 pigeonpea genotypes based on 20 qualitative characters and reported more variations for traits *viz.,* time of flowering, pattern of streaks on standard petal, pod size and seed size.

Table 2. Classification of the short duration pigeonpea genotypes based on qualitative characters.

S.No.	Qualitative characters	Descriptors	Note	Absolute frequency	Relative frequency
1	Anthocyanin colour on hypocotyl	Absent	1	0	0.00
		Present	9	68	100.00
2	Plant branching pattern	Erect (<30°)	3	7	10.29
		Semi-spreading (30°-60°)	5	61	89.71
		Spreading (>60°)	7	0	0.00
3	Time of flowering (50% of the plants with at least one open flower)	Very early (<60 days)	1	0	0.00
		Early (61-90 days)	3	68	100.00
		Medium (90-130 days)	5	0	0.00
		Late(131-160days)	7	0	0.00
		Very late (>160 days)	9	0	0.00
4	Plant growth habit	Determinate	1	7	10.29
		Indeterminate	3	61	89.71
5	Stem colour	Green	1	68	100.00
		Purple	2	0	0.00
6	Leaf shape	Oblong	1	62	91.18
		Obovate	3	6	8.82
		Narrowly oblong	5	0	0.00
7	Flower colour of base of petal (standard)	Light yellow	1	0	0.00
		Yellow	2	68	100.00
		Orange yellow	3	0	0.00
		Purple	4	0	0.00
		Red	5	0	0.00
8	Flower pattern of streaks on petal (standard)	Absent	1	18	26.47
		Sparse	3	47	69.12
		Medium	5	2	2.94
		Dense	7	1	1.47
		Mosaic	9	0	0.00
9	Pod colour	Green	1	0	0.00
		Green with brown streak	2	0	0.00

		Green with purple streak	3	68	100.00
		Purple	4	0	0.00
		Dark purple	5	0	0.00
10	Pod constriction	Slight	3	1	1.47
		Prominent	7	67	98.53
11	Pod length	<4 cm	3	0	0.00
		4-5 cm	5	6	8.82
		>5 cm	7	62	91.18
12	Number of seeds per pod	2	3	0	0.00
		3	5	0	0.00
		4	7	68	100.00
13	Plant height	Short (<100cm)	3	8	11.76
		Medium (100-150)	5	38	55.88
		Tall(>150cm)	7	22	32.35
14	Seed colour	Cream	1	4	5.88
		Brown	2	15	22.06
		Dark brown	3	49	72.06
		Gray	4	0	0.00
		Purple	5	0	0.00
15	Seed colour pattern	Uniform	1	67	98.53
		mottled	2	1	1.47
16	Seed shape	Oval	1	32	47.06
		Globular	2	36	52.94
		Elongate	3	0	0.00
17	Seed size (100 seed weight)	Small(<7g)	3	1	1.47
		Medium(7-9g)	5	24	35.29
		Large(9-11g)	7	33	48.53
		Very large(>11)	9	10	14.71

Erect and compact

Semi – spreading

Fig.1. Plant branching pattern of the pigeonpea genotypes

Determinate plant Indeterminate plant

Fig.2. Plant growth habit of the pigeonpea genotypes

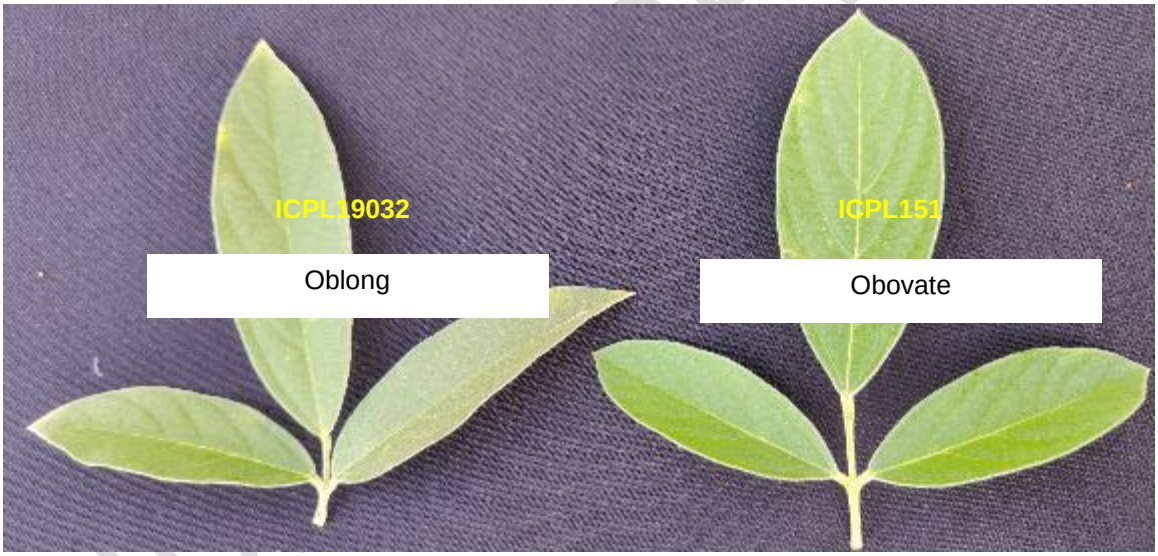

Fig.3. Leaf shape of the pigeonpea genotypes

Fig. ?.... Petal color

Fig.4. Pattern of streaks on the standard petal of the pigeonpea genotypes

Prominent

Slight

Fig.6. Seed colour of the pigeonpea genotypes

Uniform and Oval Mottled and Globular

Fig.7. Seed colour pattern and seed shape of the pigeonpea genotypes

Cluster~~ing~~ analysis

Sixty - eight genotypes were subjected to cluster analysis and were grouped into four major clusters with 80 per cent similarity (Fig.8). The coefficient of similarity ~~similarity coefficient~~ ranged from 0.65 to 1.00. The cluster I consisted of the 60 genotypes. The cluster I was divided into two sub-groups. The sub-group I had 59 genotypes at 84 per cent similarity, whereas the sub-group II consisted of the genotype ICPL19050. The cluster II consisted of six genotypes. The cluster was divided into two sub-groups at 84 per cent similarity. The sub-group one of cluster II consisted of the genotypes ICPL87 and ICPB2039, whereas the sub-group two of cluster II consisted of the genotypes *viz.,* ICPl85010, CO2R, CO3R and CO8R. Clusters III and IV were solitary clusters, each with a single genotype. ~~The cluster III and IV were solitary clusters with one genotype each.~~ The cluster III consisted of the genotype ICPL151 and cluster IV had ICPL89. A total of seven determinate plant types *viz.,* ICPL87, IPCB2039, ICPL85010, CO2R, CO3R, CO8R and ICPL151 were observed and were grouped together under the clusters II and III. The genotype ICPL89 was the only one genotype with compact and erect branching pattern in the indeterminate group having dense pattern of streaks on the standard petal and ~~slight~~ modest pod constriction. Hence, it was grouped separately in cluster IV. Thus, clustering of the pigeonpea genotypes revealed that, the genotypes with unique characteristics were grouped accordingly. The genotypes with 100 per cent similarity was observed in cluster I and cluster II (Fig.8:A – N). The genotypes with 100 per cent similarity with the other genotypes ~~believed~~ are thought to ~~decent~~ descend from closely related parental lines and reported

as ~~highly~~ storngly related. Adegboyegun *et al.* [1] reported three major clusters among 22 pigeonpea genotypes using qualitative traits. Geofroy *et al*. [5] studied 50 pigeonpea genotypes using 12 qualitative traits and reported eight different morphological clusters. Sahu *et al.* [15] reported two main clusters based on DUS characters in 60 pigeonpea genotypes.

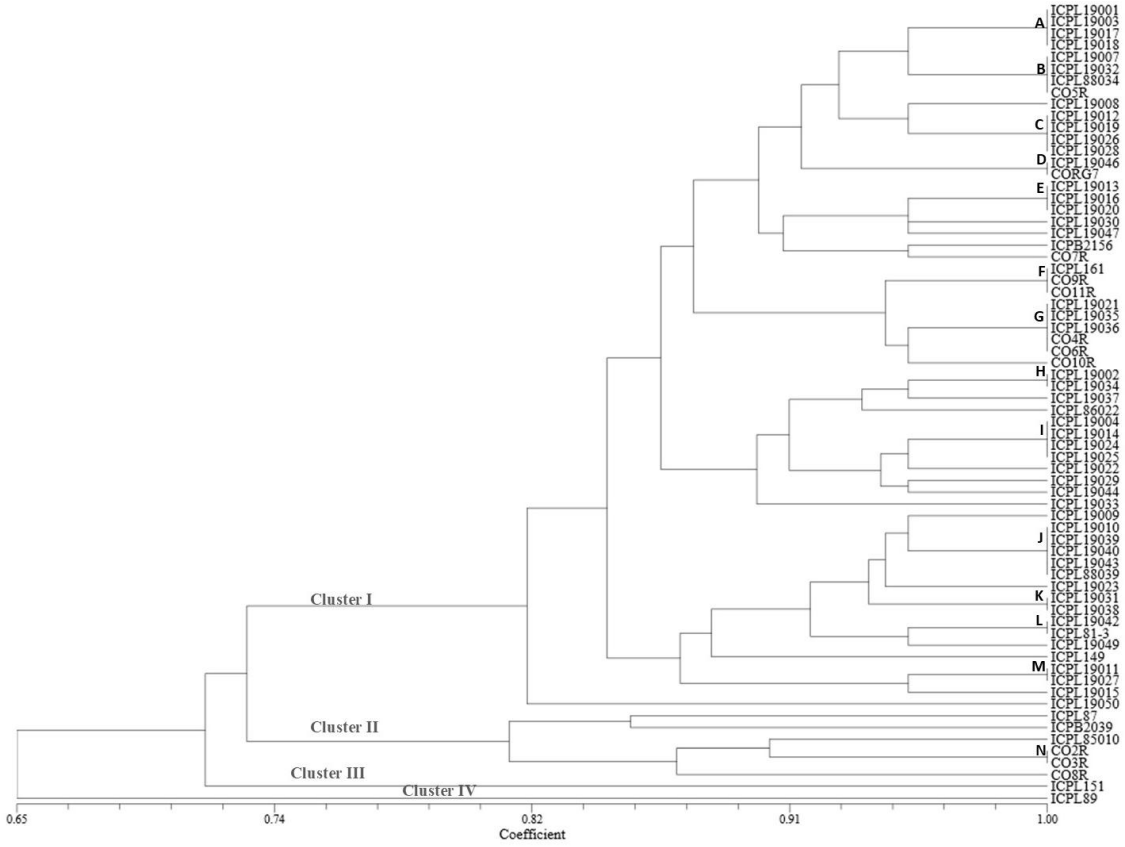

Fig.8. Clustering of the 68 genotypes based on the qualitative characters of pea genotypes

4. CONCLUSION

The DUS characterization and cluster analysis revealed that traits *viz*., plant branching pattern, plant growth habit, seed colour and flower based qualitative traits played a major role in the classification of genotypes. Hence, these traits can be used in identification and grouping of genotypes for utilization in future breeding programmes. This research may also provide insight into how to maintain the genetic purity of the materials under study and how to group them for use in future crop development programs. ~~This study may also serve as an insight to maintain the genetic purity of the studied materials and aids in their grouping for indulging in further crop improvement programmes.~~

REFERENCES

1. Adegboyegun K, Okpanachi FE, Akpanikot KE. Morphological Characterization of 22 Accessions of Pigeon Pea [*Cajanus cajan* (L) Millsp.]. Asian Journal of Biochemistry, Genetics and Molecular Biology. (2020); 20-28.
2. Anonymous. SG/07/2006,20/2/2007, Guidelines for the conduct of test for distinctness, uniformity and stability on pigeon pea (*Cajanus cajan* (L.)), Protection of Plant Varieties and Farmers' Rights Authority (PPV & FRA), GOI. 2007.
3. Chaudhary L, Sharma R, Kumar M, Kumar S. Morphological characterization and assessment of genetic diversity in pigeonpea [*Cajanus cajan* (L.) Millsp.] germplasm. Electronic Journal of Plant Breeding. 2021;12(3):707-711.
4. FAOSTAT.www.fao.org. 2019.
5. Géofroy K, Gustave D, Laura EYL, Relique IA, Saxena RK, Varshney RK, et al. (2020). Agro-morphological characterization of pigeonpea (*Cajanus cajan* L. Millspaugh) landraces grown in Benin: Implications for breeding and conservation. Journal of Plant Breeding and Crop Science.2020;*12*(1):34-49.
6. Kimaro D, Melis R, Sibiya J, Shimelis H. Agro-morphological characterization of pigeonpea (*Cajanus cajan* (L.) Millsp.).—Basis to—breeding. Agriculture and Natural Resources.2021;55(1):23-32.
7. Matthews S. Copeland LO, McDonald MB. Principles of seed science and technology. 4th edn.2002.
8. Manyasa EO, Silim SN, Githiri SM, Christiansen JL. Diversity in Tanzanian pigeonpea [*Cajanus cajan* (L.) Millsp.] landraces and their response to environments. Genetic Resources and Crop Evolution. 2008;*55*(3):379-387.
9. Muniswamy S, Lokesha R, Dharmaraj PS.Morphological characterization and assessment of genetic diversity in minicore collection of pigeonpea [*Cajanus Cajan* (L.) Millsp.]. Electronic Journal of Plant Breeding. 2014;*5*(2):179-186.
10. Nene YL, Sheila VK. Pigeonpea: geography and importance-.CAB International.1990;1-14.
11. Reddy LJ, Upadhyaya HD, Gowda CLL, Singh S. Development of core collection in pigeonpea [Cajanus cajan (L.) Millspaugh] using geographic and qualitative morphological descriptors. Genetic Resources and Crop Evolution. 2005;*52*(8):1049-1056.
12. Rohlf FJ.NTSYSpc numerical taxonomy and multivariate analysis system version 2.0 user guide.1998.
13. Rupika K, Bapu JK. Assessment of genetic diversity in pigeonpea germplasm collection using morphological characters. Electronic Journal of Plant Breeding. 2014;*5*(4):781-785.
14. Salem KFM, El-Zanaty AM, Esmail RM. Assessing wheat (*Triticum aestivum* L.) genetic diversity using morphological characters and microsatellite markers. World Journal of Agricultural Sciences. 2008;*4*(5):538-544.
15. Sahu JK, Sinha RE, Ekka RE, Tiwari JK. Morphological characterization of germplasm of pigeonpea (*Cajanus cajan* (L.) Millsp.). Multilogic in science; 2018; 8:181-183.

16. Upadhyaya HD, Pundir RPS, Gowda CLL, Reddy KN, Singh S. Geographical patterns of diversity for qualitative and quantitative traits in the pigeonpea germplasm collection. *Plant Genetic Resources*. 2005; *3*(3):331-352.