

Genetic Analysis for Yield and it's Attributing Traits in Pigeonpea [*Cajanus cajan* (L.) Mill sp.] under rainfed Condition

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ABSTRACT: Forty three germplasm accessions along with six checks, analyzed for morphological characterization, variability studies during *kharif* 2022-23, in alpha lattice design. Total twenty seven biometrical and nonbiometrical characters were evaluated on each accession at different growth stages. Germplasm was classified on the basis of fifteen morphological characters viz., anthocyanin coloration of hypocotyl, plant branching pattern, plant growth habit, stem: colour, leaf: shape, pubescence on lower surface of leaf, flower: colour of base of petal (standard), pattern of streaks on petal, pod: colour, pod: pubescence, pod: waxiness, pod: surface stickiness, seed: colour, seed: colour pattern and seed: shape. Variability analysis was carried out among twelve quantitative observations viz., days to 50% flowering, numbers of flowers at 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of pods per cluster, number of seeds per pod, 100 seed weight (g), days to 1st pod formation, days to 100% pod formation, seed yield per plant (g). Variability studies revealed the germplasm used in current study has ample amount of variability present and can be used as donor in pigeonpea improvement programme.

Keywords: *Cajanus cajan* (L.) Mill sp., DUS characterization, Variability.

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Mill sp.] is a multipurpose legume crop and is well adapted even in marginal lands (Joshi *et al.*, 2009). It has been recognized as a good source of vegetarian protein particularly in the developing countries like India where majority of the population depends on the low priced vegetarian foods. Pigeonpea plays a vital role in vegetarian diet as seeds constitutes protein (21–28%), vitamins, and mineral elements such as phosphorus (0.56 - 0.72 %), zinc (2.3- 2.5%), potassium and magnesium and it is also a good source of carbohydrate (57.3 - 58.7%), crude fibers (1.2 - 8.1%) and lipid (0.6 – 3.8%) (Phatak *et al.*, 1993). Pigeonpea seeds provide essential amino acids like lysine, tyrosine and arginine, whereas cystine and methionine contents are low (Saxena *et al.*, 2010).

Pigeonpea is an often cross pollinated (20-70%) crop with $2n = 2x = 22$ diploid chromosome number. India is considered as the native of pigeonpea because of its natural genetic variability available in the local germplasm and the presence of its wild relatives in the country. Pigeonpea is a hardy, widely adapted, and drought tolerant crop. It has a wide range of maturity which helps in its adaption in a wide range of environments and cropping systems. Information on the nature and magnitude of genetic diversity present in the genotypes is a pre-requisite for any breeding

programme. Morphological characterization is useful for the development of the core collection of germplasm (Reddy *et al.*, 2005). The concept of DUS was fundamental to the characterization of the variety as a unique creation (Sahu *et al.*, 2018).

According to FAO statistics (2019), worldwide pigeonpea is cultivated in about 4.5 million hectares area yielding approximately 3.68 million tons with an average yield of 832 kg/ha. Despite the substantial area under pigeonpea, productivity across the world is very low and stagnant as compared to other cereals. This low productivity can be attributed to the lack of effective selection indices for yield improvement while selecting parents for varietal development. Yield is a polygenic character and is the outcome of the direct or indirect association of several component characters. It is significantly impacted by the environment and has a low heritability in general (Luz *et al.*, 2011; Mukherjee *et al.*, 2016). Since direct selection for yield is less efficient, improvement in contributing traits is imperative. Understanding the nature and extent of genetic variation in pigeonpea genotypes is essential for any plant breeding program. The collection, conservation, and characterization of these genotypes form the foundation of crop improvement initiatives, which rely on the genetic diversity within the gene pool. This diversity offers plant breeders the chance to create new and enhanced cultivars with desirable traits. Since

the dawn of agriculture, natural genetic variability within crop species has been utilized to address subsistence food needs, and there is now an emphasis on increasing food production to meet the demands of a growing population.

Yield is a complex trait influenced by numerous cumulative, duplicate, and dominant genes, and it is directly or indirectly affected by environmental factors. Additionally, it tends to respond inadequately to direct selection. Considering this, various indigenous pigeonpea genotypes are being studied to identify suitable genotypes or donors that can help meet current and future demands for improving the pigeonpea crop.

Thus, there is a strong likelihood of discovering elite germplasms among locally adapted land races that possess desirable agro-morphological traits, which could lead to the development of high-yielding pigeonpea varieties. Genetic diversity plays a crucial role in successful plant breeding programs focused on enhancing productivity, quality traits, and stress tolerance (Walunjkar *et al.*, 2015).

The objective of the present studies were to evaluate a collection of promising and improved pigeonpea genotypes for their performance and generating knowledge on different genetic parameters to formulate the selection strategy (s) for yield improvement of this crop.

MATERIALS AND METHODS

The experimental materials include 43 germplasm lines along with six checks (C.G. Arhar-2, BDN-716, CORG-9701, UPAS-120, PT-0012 and KRG-33); for alpha lattice with 2 replications in kharif 2022-23, obtained from AICRP on pigeonpea, Department of Genetics & Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur. Germplasm was classified on the basis of fifteen morphological characters *viz.*, anthocyanin coloration of hypocotyl, plant branching pattern, plant growth habit, stem: colour, leaf: shape, pubescence on lower surface of leaf, flower: colour of base of petal (standard), pattern of streaks on petal, pod: colour, pod: pubescence, pod: waxiness, pod: surface stickiness, seed: colour, seed: colour pattern and seed: shape. Variability analysis was carried out among twelve quantitative observations *viz.*, days to 50% flowering, numbers of flowers at 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of pods per cluster, number of seeds per pod, 100 seed weight (g), days to 1st pod formation, days to 100% pod formation, seed yield per plant (g) according to Distinctness, Uniformity and Stability guidelines (Protection of Plant Varieties and Farmer's Rights Authority, 2007) and Morphological, Chemical and Electrophoretic Descriptors for Pigeonpea Varieties/ Hybrids (National Seed Project, 2004). The Pearson correlation coefficient was used to look for correlations and differences among analyzed genotypes.

RESULTS AND DISCUSSION

Morphological characterization of pigeonpea genotypes: The 43 pigeonpea germplasm accessions and six checks were classified for morphological

characters. The description for fifteen characters that was studied for 49 genotypes at different growth stages (Table 1) are described below:

Plant: Anthocyanin coloration of hypocotyls. The 49 genotypes studied were classified on different classes of anthocyanin coloration of hypocotyl on which 28.57% were grouped as purple (*i.e.*, anthocyanin present) and 71.42% as green (*i.e.*, anthocyanin absent).

Plant branching pattern. Out of 49 genotypes studied, 16.32% were classified as erect, 57.14% were classified as semi spreading and 26.53% were classified as spreading.

Plant: growth habit. The 49 genotypes studied were classified on different classes of plant growth habit and 100% genotypes were grouped as indeterminate.

Stem: colour. The 49 genotypes studied were classified on different classes of anthocyanin coloration of stem on which 16.32% were grouped as purple (*i.e.*, anthocyanin present) and 83.67% as green (*i.e.*, anthocyanin absent).

Leaf: shape. The 49 genotypes studied were classified on different classes of leaf shape out of which 71.42% were grouped under oblong, 4.08% were grouped under obovate and 24.48% under sesame.

Leaf: pubescence on lower surface of leaf. Out of 49 genotypes studied, on 95.91% of genotypes pubescence on lower leaf surface was absent and on 4.08% pubescence on lower leaf surface was present.

Flower: colour of base of petal. The 49 genotypes studied were classified on different classes of flower colour out of which 91.83% were grouped under yellow, 8.16% were grouped under orange yellow and none of the genotypes were found as light yellow, purple or red.

Flower: pattern of streaks on petal. The 49 genotypes studied were classified on different classes of pattern of streak out of which 6.12% were grouped under absent, 81.63% were grouped under sparse, 4.08% under medium and 8.16% under dense.

Pod: colour. Out of 49 genotypes studied, 4.08% were classified as green, 61.22% were classified as green with brown streak 32.65% were classified as green with purple streak, 2.04% were classified as purple and no genotypes were found in dark purple.

Pod: pubescence. The 49 genotypes studied were classified on different classes of pod pubescence and 100% genotypes had pod pubescence.

Pod: waxiness. The 49 genotypes studied were classified on different classes of pod waxiness and 100% genotypes had pod waxiness.

Pod: surface stickiness. The 49 genotypes studied were classified on different classes of pod stickiness and 100% genotypes had pod stickiness.

Seed: colour. Out of 49 genotypes studied, 14.28% were classified as cream, 73.46% were classified as brown, 8.16% were classified as dark brown, 2.04% were classified as grey and 8.16% were found in purple.

Seed: colour pattern. Out of 49 genotypes studied, on 75.51% of genotypes were uniform and 24.48% of genotypes were mottled.

Seed: shape. Out of 49 genotypes studied, 67.34% were classified as oval, 30.61% were classified as globular and 2.04% were classified as elongated.

Previous studies by Kimaro *et al.* (2021); Chauhan, 2021; Adegboyegun *et al.* (2020); Yuniastuti *et al.* (2020); Ramesh (2017); Sahu *et al.* (2018); Rupika and Kannan (2014); Upadhyaya *et al.* (2007); Upadhyaya *et al.* (2005); Majumder *et al.* (2008) have also demonstrated the existence of variation for various traits in pigeonpea germplasm accessions.



Fig. 1. Variations present in streak pattern of petal.

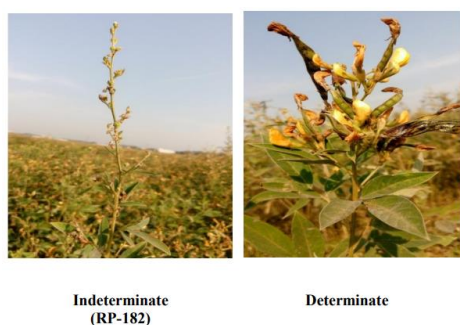


Fig. 2. Variations present in plant growth habit.

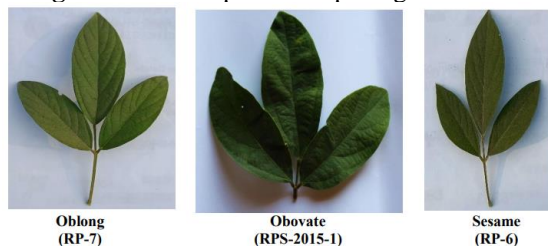


Fig. 3. Variations present in leaf shape.



Fig. 4. Variations present in seed colour.



Fig. 5. Variations present in stem colour.



Fig. 6. Variations present in seed colour pattern.

Table 1: Description of morphological characters.

Sr. No.	Characters	Categories or type	Symbols number frequency	Total no. of genotype	frequency%	Name of genotype				
1.	Plant: Anthocyanin coloration of hypocotyl	Absent	1	35	71.42	RPS 2015-4 RPS 2015-5 RPS 2015-14 RPS 2015-17 RPS 2015-21 RPS 2015-22 ICP-6994	RPS 2015-34 RPS 2015-35 RPS 2015-36 RPS 2015-38 RPS 2015-40 RPS 2015-41 RPS 2015-49	RPS 2015-50 RPS 2015-51 RPS 2014-6 RPS 2014-10 RPS 2014-23 RPS 2014-26 RPS 2015-23	BDN-716 ICP-7374 ICP-6996 RP-182 RP-204 RP-232 RPS 2015-27	RP-2 RP-3 RP-7 RP-89 RP-115 RP-130 CG ARHAR-2
		Present	9	14	28.57	KRG-33 PT-0012 UPAS-120	RPS 2015-1 RPS 2015-2 RPS 2015-13	RP-179 RP-187 RP-196	RP-206 RP-242 CORG-9701	RP-6 RP-93
2.	Plant branching pattern	Erect (<30°)	3	8	16.32	ICP-6994 RPS 2015-36	RPS 2015-35 KRG-33	RPS 2014-6 PT-0012	ICP-6996	RP-89
		Semi-spreading (30°-60°)	5	28	57.14	RPS 2015-5 PS 2015-13 RPS 2015-17 RPS	RPS 2015-34 RPS 2015-49 RPS 2015-50 RPS	ICP-7374 ICP-6996 BDN-716 UPAS-120 CORG-9701	RP-115 RP-179 RP-204 RP-206 RP-242	RP-2 RP-3 RP-7 RP-93

						2015-21 RPS 2015-22 RPS 2015-27	2014-10 RPS 2014-23 RPS 2014-26			
		Spreading (>60°)	7	13	26.53	RPS 2015-2 RPS 2015-4 RPS 2015-14	RPS 2015-38 RPS 2015-40 RPS 2015-49	CG ARHAR- 2 RP-130 RP-232	RP-187 RP-196	RP-6 RP-182
3	Plant: growth habit	Determinate	1	0	0					
		Indeterminate	3	49	100	RPS 2015-1 RPS 2015-2 RPS 2015-4 RPS 2015-5 RPS 2015-13 RPS 2015-14 RPS 2015-17 RPS 2015-21 RPS 2015-22 RPS 2015-23	RPS 2015-27 RPS 2015-34 RPS 2015-35 RPS 2015-36 RPS 2015-38 RPS 2015-40 RPS 2015-41 RPS 2015-49 RPS 2015-50 RPS 2015-51	RPS 2014-6 RPS 2014-10 RPS 2014-23 RPS 2014-26 KRG-33 UPAS- 120 BDN-716 CORG- 9701 CG ARHAR- 2 ICP-6994	ICP- 7374 ICP- 6996 RP-182 RP-187 RP-196 RP-204 RP-206 RP-232 RP-242 PT- 0012	RP-2 RP-3 RP-6 RP-7 RP-89 RP-93 RP-115 RP-130 RP-179
4.	Stem: colour	Green	1	41	83.67	RPS 2015-1 RPS 2015-2 RPS 2015-4 RPS 2015-5 RPS 2015-13 RPS 2015-14 RPS 2015-17 RPS 2015-21	RPS 2015-27 RPS 2015-34 RPS 2015-35 RPS 2015-36 RPS 2015-38 RPS 2015-40 RPS 2015-41 RPS 2015-49	RPS 2014-6 RPS 2014-10 RPS 2014-23 RPS 2014-26 KRG-33 BDN-716 CG ARHAR- 2	ICP- 7374 ICP- 6996 RP-196 RP-206 PT- 0012 ICP- 6994 RPS 2015-50 RPS 2015-51	RP-2 RP-3 RP-6 RP-7 RP-93 RP-130 RPS 2015-22 RPS 2015-23
		Purple	2	8	16.32	RP-182 RP-187	RP-115 RP-179	CORG- 9701 RP-204	UPAS- 120	RP-89
5	Leaf: shape	Oblong	1	35	71.42	RPS 2015-2 RPS 2015-4 RPS 2015-21 RPS 2015-22 RPS 2015-23 ICP-6994 RPS 2015-51	RPS 2015-27 RPS 2015-35 RPS 2015-36 RPS 2015-38 RPS 2015-40 RPS 2015-41 RPS 2015-49	RPS 2014-6 RPS 2014-10 RPS 2014-23 RPS 2014-26 CORG- 9701 CG ARHAR- 2 RPS 2015-50	ICP- 7374 ICP- 6996 RP-182 RP-187 RP-196 RP-204 RP-206	RP-2 RP-3 RP-7 RP-115 RP-232 RP-242 PT-0012
		Obovate	3	2	4.08	RPS 2015-1	RPS 2015-34			
		Sesame	5	12	24.48	RPS 2015-5 KRG-33 UPAS- 120	RPS 2015-13 RPS 2015-14 RPS 2015-17	RP-130 RP-179	RP-89 RP-93	RP-6 BDN-716
6.	Leaf: pubescence on lower surface of leaf	Absent	1	47	95.91	RPS 2015-1 RPS 2015-2 RPS 2015-4 RPS 2015-5 RPS 2015-13 RPS 2015-14 RPS	RPS 2015-27 RPS 2015-34 RPS 2015-35 RPS 2015-36 RPS 2015-38 RPS 2015-40 RPS	RPS 2014-6 RPS 2014-10 RPS 2014-23 RPS 2014-26 KRG-33 UPAS- 120 BDN-716 CORG-	ICP- 7374 ICP- 6996 RP-182 RP-187 RP-196 RP-204 PT- 0012 ICP- 6994	RP-2 RP-3 RP-6 RP-7 RP-89 RP-93 RP-115 RP-130 RP-179

						2015-17 RPS 2015-21 RPS 2015-22 RPS 2015-23	2015-41 RPS 2015-49 RPS 2015-50 RPS 2015-51	9701 CG ARHAR- 2		
7.	Flower: colour of base of petal (standard)	Present Yellow	9 3	2 45	4.08 91.83	RP-232 RPS 2015-1 RPS 2015-2 RPS 2015-4 RPS 2015-5 RPS 2015-17 RPS 2015-22 RPS 2015-23 RPS 2015-34 ICP-6994	RP-242 RPS 2015-35 RPS 2015-36 RPS 2015-38 RPS 2015-40 RPS 2015-41 RPS 2015-49 RPS 2015-50 RPS 2015-51 CG ARHAR- 2	RPS 2014-6 RPS 2014-10 RPS 2014-23 RPS 2014-26 KRG-33 UPAS- 120 BDN-716 CORG- 9701 PT-0012	ICP- 7374 ICP- 6996 RP-182 RP-187 RP-196 RP-204 RP-206 RP-232 RP-242	RP-2 RP-3 RP-6 RP-7 RP-89 RP-115 RP-130 RP-179
		Light yellow	1	0						
		Orange yellow	5	4	8.16	RP-93	RPS 2015-13	RPS 2015-21	RPS 2015-27	
		Purple	4	0						
		Red	5	0						
8.	Flower: pattern of streaks on petal (standard)	Absent	1	3	6.12	ICP-6996	RPS 2015-35	BDN-716		
		Sparse	3	40	81.63	RPS 2015-1 RPS 2015-2 RPS 2015-4 RPS 2015-5 RPS 2015-17 RPS 2015-22 CORG- 9701 CG ARHAR- 2	RPS 2015-27 RPS 2015-34 RPS 2015-36 RPS 2015-38 RPS 2015-40 RPS 2015-41 RPS 2015-49 RPS 2015-50	RPS 2014-6 RPS 2014-10 RPS 2014-23 RPS 2014-26 KRG-33 UPAS- 120 ICP-6994 RP-130	ICP- 7374 RP-182 RP-187 RP-196 RP-204 RP-206 RP-242 PT- 0012	RP-2 RP-3 RP-6 RP-7 RP-89 RP-93 RP-115
		Medium	5	2	4.08	RP-232	RP-179			
		Dense	7	4	8.16	RPS 2015-13	RPS 2015-23	RPS 2015-21	RPS 2015-51	
9.	Pod: colour	Green	1	2	4.08	BDN-716	RP-204			
		Green with brown streak	2	30	61.22	RPS 2015-4 RPS 2015-22 ICP-6994 RPS 2015-41 RPS 2015-50 CG ARHAR- 2	RPS 2015-34 RPS 2015-35 RPS 2015-36 RPS 2015-38 CORG- 9701 PT-0012	RPS 2014-6 RPS 2014-26 KRG-33 UPAS- 120 RP-179 RP-115	ICP- 7374 ICP- 6996 RP-182 RP-206 RP-232 RP-242	RP-3 RP-6 RP-7 RP-89 RP-93
		Green with purple streak	3	16	32.65	RPS 2015-1 RPS 2015-2 RPS 2015-5 RPS 2015-13	RPS 2015-21 RPS 2015-23 RPS 2015-27 RPS 2015-40	RP-2 RPS 2015-49 RPS 2015-51 RPS 2015-17	RP-187 RP-196 RPS 2014-23	RP-130
		Purple	4	1	2.04	RPS 2014-10				
10.	Pod: pubescence	Absent	1	0	0					
		Present	9	49	100	RPS 2015-1 RPS 2015-2 RPS 2015-4 RPS 2015-5 RPS	RPS 2015-27 RPS 2015-34 RPS 2015-35 RPS 2015-36 RPS	RPS 2014-6 RPS 2014-10 RPS 2014-23 RPS 2014-26 KRG-33	ICP- 7374 ICP- 6996 RP-182 RP-187 RP-196 RP-204 RP-206	RP-2 RP-3 RP-6 RP-7 RP-89 RP-93 RP-115 RP-130 RP-179

						2015-13 RPS 2015-17 RPS 2015-21 RPS 2015-22 RPS 2015-23 ICP-6994	2015-38 RPS 2015-40 RPS 2015-41 RPS 2015-49 RPS 2015-50 RPS 2015-51	UPAS- 120 BDN-716 CORG- 9701 CG ARHAR- 2 PT-0012	RP-232 RP-242	
11.	Pod: waxiness	Absent		0	0					
		Present		49	100	RPS 2015-1 RPS 2015-2 RPS 2015-4 RPS 2015-5 RPS 2015-13 RPS 2015-14 RPS 2015-17 RPS 2015-21 RPS 2015-22 RPS 2015-23	RPS 2015-27 RPS 2015-34 RPS 2015-35 RPS 2015-36 RPS 2015-38 RPS 2015-40 RPS 2015-41 RPS 2015-49 RPS 2015-50 RPS 2015-51	RPS 2014-6 RPS 2014-10 RPS 2014-23 RPS 2014-26 KRG-33 UPAS- 120 BDN-716 CORG- 9701 CG ARHAR- 2 ICP-6994	ICP- 7374 ICP- 6996 RP-182 RP-187 RP-196 RP-204 RP-206 RP-232 RP-242 PT- 0012	RP-2 RP-3 RP-6 RP-7 RP-89 RP-93 RP-115 RP-130 RP-179
12.	Pod: surface stickiness	Absent	1	0	0					
		Present	9	49	100	RPS 2015-1 RPS 2015-2 RPS 2015-4 RPS 2015-5 RPS 2015-13 RPS 2015-17 RPS 2015-21 RPS 2015-22 RPS 2015-23 ICP-6994	RPS 2015-27 RPS 2015-34 RPS 2015-35 RPS 2015-36 RPS 2015-38 RPS 2015-40 RPS 2015-41 RPS 2015-49 RPS 2015-50 RPS 2015-51	RPS 2014-6 RPS 2014-10 RPS 2014-23 RPS 2014-26 KRG-33 UPAS- 120 BDN-716 CORG- 9701 CG ARHAR- 2 PT-0012	ICP- 7374 ICP- 6996 RP-182 RP-187 RP-196 RP-204 RP-206 RP-232 RP-242	RP-2 RP-3 RP-6 RP-7 RP-89 RP-93 RP-115 RP-130 RP-179
13.	Seed: colour	Cream	1	7	14.28	RPS 2015-34 RPS 2015-50	RPS 2014-23 RPS 2015-14	RPS 2014-6	RP-182	RP-115
		Brown	2	36	73.46	RPS 2015-2 RPS 2015-4 RPS 2015-5 RPS 2015-21 RPS 2015-22 RPS 2015-23 ICP-6994	RPS 2015-27 RPS 2015-36 RPS 2015-38 RPS 2015-40 RPS 2015-41 RPS 2015-49 RPS 2015-51	RPS 2014-26 KRG-33 UPAS- 120 BDN-716 CORG- 9701 CG ARHAR- 2 RP-179	ICP- 7374 ICP- 6996 RP-187 RP-196 RP-206 RP-242	RP-2 RP-3 RP-6 RP-89 RP-93 RP-130
		Dark brown	3	4	8.16	RPS 2015-35	PT-0012	RP-204	RP-7	
		Grey	4	1	2.04	RPS 2015-1				
		Purple	5	4	8.16	RPS 2015-13 RPS 2015-17	RPS 2014-10	RP-232		
14.	Seed: colour pattern	Uniform	1	37	75.51	RPS 2015-1 RPS 2015-2 RPS 2015-5 RPS	RPS 2015-27 RPS 2015-34 RPS 2015-35 RPS	RPS 2014-6 RPS 2014-10 RPS 2014-23 RPS	ICP- 7374 ICP- 6996 RP-182 RP-187 RP-196	RP-2 RP-3 RP-7 RP-89 RP-93 RP-115

						2015-13 RPS 2015-14 RPS 2015-17 RPS 2015-21 ICP-6994	2015-36 RPS 2015-38 RPS 2015-49 RPS 2015-50 RP-242	2014-26 KRG-33 UPAS- 120 BDN-716 CORG- 9701	RP-204 RP-232	
		Mottled	2	12	24.48	RPS 2015-4 RPS 2015-22 RPS 2015-23	RPS 2015-40 RPS 2015-41 RPS 2015-51	CG ARHAR- 2 PT-0012 RP-206	RP-130 RP-179	RP-6
15.	Seed: shape	Oval	1	33	67.34	RPS 2015-1 RPS 2015-2 RPS 2015-5 RPS 2015-13 RPS 2015-17 RPS 2015-21 RPS 2015-22	RPS 2015-27 RPS 2015-34 RPS 2015-35 RPS 2015-36 RPS 2015-38 RPS 2015-40 RPS 2015-49	RPS 2014-23 RPS 2014-26 UPAS- 120 RPS 2015-23 ICP-6994 PT-0012	ICP- 7374 RP-187 RP-196 RP-204 RP-206 RP-242	RP-2 RP-3 RP-7 RP-93 RP-115 RP-179
		Globular	2	15	30.61	RPS 2015-4 RPS 2015-41 RPS 2015-50	RPS 2014-6 RPS 2014-10 RPS 2015-51	CG ARHAR- 2 BDN-716 CORG- 9701	RP-182 RP-232 KRG-33	RP-6 RP-89 RP-130
		Elongate	3	1	2.04	ICP-6996				

Table 2: Analysis of variance for different quantitative characters in pigeonpea germplasm.

Characters	Mean	Standard error	Standard deviation	CV	Range difference	Minimum	Maximum
Days to 50% flowering	120.347	0.817	5.662	3.298	21.500	108.500	130.000
Numbers of flowers at 50% flowering	198.480	1.612	11.169	4.012	48.000	164.000	212.000
Days to maturity	132.235	0.905	6.271	3.36	29.500	117.500	147.000
Plant height (cm)	194.551	3.141	21.763	10.551	70.500	150.000	220.500
Days to 50% flowering	304.044	13.143	91.055	29.925	395.000	130.000	525.000
Number of branches per plant	163.612	1.726	11.956	5.519	46.900	137.400	184.300
Number of pods per plant	6.382	0.186	1.286	20.008	5.900	4.600	10.500
Number of pods per cluster	83.027	3.282	22.741	27.16	108.600	44.900	153.500
Number of seeds per pod	3.904	0.047	0.328	6.166	1.800	3.000	4.800
100 seed weight (g)	4.155	0.046	0.318	5.452	1.400	3.500	4.900
Days to 1 st pod formation	8.867	0.184	1.275	12.991	5.200	6.685	11.885
Days to 100%pod formation	18.339	0.903	6.258	33.768	28.155	9.495	37.650
Seed yield per plant (g)	120.347	0.817	5.662	3.298	21.500	108.500	130.000

Determination of genetic variability of germplasm lines

Days to 50% flowering. Days to 50% flowering ranged from 130 to 108.50 with an average of 120.3 days, S.D observed for this trait was 5.66, S.E. recorded was 0.81 and coefficient of variation recorded for this trait was 3.2%. (Table 2)

Days to maturity. Range of days to maturity was observed between 212 to 164 with an average of 198.5 days, S.D observed for this trait was 11.16, S.E. recorded was 1.61 and coefficient of variation recorded for this trait was 4.01%.

Days to 1st pod formation. Days to 1st pod formation was measured with a range of 147 to 117.50 with an average of 132.2 days, S.D observed for this trait was

6.27, S.E. recorded was 0.90 and coefficient of variation recorded for this trait was 3.36%.

Days to 100%pod formation. It ranged from 220.5 to 150 with an average of 194.6 days, S.D observed for this trait was 21.76, S.E. recorded was 3.14 and coefficient of variation recorded for this trait was 10.55%.

Numbers of flowers at 50% flowering. Numbers of flowers at 50% flowering was measured with a range of 525 to 130 with an average of 304, S.D observed for this trait was 91.05, S.E. recorded was 13.14 and coefficient of variation recorded for this trait was 29.92%.

Plant height. Plant height was measured with a range of 184.3 to 137.4 with an average of 163.6 cm, S.D observed for this trait was 11.95, S.E. recorded was

1.72 and coefficient of variation recorded for this trait was 5.51%.

Number of branches per plant. Number of branches per plant ranged from 10.5 to 4.60 with an average of 6.4, S.D observed for this trait was 1.28, S.E. recorded was 0.18 and coefficient of variation recorded for this trait was 20%.

Number of pods per plant. Number of pods per plant was measured with a range of 153.5 to 44.9 with an average of 83, S.D observed for this trait was 22.74, S.E. recorded was 3.28 and coefficient of variation recorded for this trait was 27.16%.

Number of pods per cluster. Number of pods per cluster was observed between 4.8 to 3 with an average of 13.9, S.D. observed for this trait was 0.32, S.E. recorded was 0.047 and coefficient of variation recorded for this trait was 6.16%.

Number of seeds per pod. Number of seeds per pod was measured with a range of 4.9 to 3.5 with an average of 4.2, S.D observed for this trait was 0.31, S.E. recorded was 0.046 and coefficient of variation recorded for this trait was 5.45%.

100 seed weight (g). It ranged from 11.88 to 6.68 with an average of 8.9 g, S.D. observed for this trait was 1.27, S.E. recorded was 0.18 and coefficient of variation recorded for this trait was 12.99%.

Seed yield per plant (g). Seed yield per plant was measured with a range of 37.65 to 9.49 with an average of 18.3 g, S.D observed for this trait was 6.25, S.E. recorded was 0.90 and coefficient of variation recorded for this trait was 33.76%.

CONCLUSIONS

The germplasm used in current study has ample amount of variability present and can be used as donor in pigeonpea improvement programme. The genotypes having unique traits such as orange flower color (RP-93, RPS 2015-13, RPS 2015-21, RPS 2015-27), medium streak pattern on flower petal (RP-179, RP-232), obovate leaf shape (RPS 2015-34, RPS 2015-1), grey seed color (RPS 2015-1) and elongate seed shape (ICP-6996) can be used as morphological markers trait in pigeonpea breeding programmes.

Analysis of variance revealed that mean square due to genotypes were found significant at 1% and 5% level for all the traits, indicating variability present in the material studied. The high genotypic coefficient of variation and genotypic coefficient of variation was recorded for number of flowers at 50% flowering followed by number of branches per plant, seed yield per plant, number of pods per plant. Whereas lowest genotypic coefficient of variation and genotypic coefficient of variation was recorded for days to 50% flowering. The phenotypic coefficient of variation higher than genotypic coefficient of variation. This indicated that apparent variation is due to genotype but also due to influence of environment.

FUTURE SCOPE

Studying the genetic variability among different pigeonpea genotypes can enhance the effectiveness of crop improvement efforts. This study confirmed that characterizing and evaluating 49 pigeonpea accessions for agronomic traits is crucial for identifying genetic variability that can be utilized in plant breeding. As a result, phenotypic traits serve as a valuable indicator of genetic differences among pigeonpea genotypes, facilitating the identification of potential parent materials for future breeding programs, particularly for selecting donors of economically important traits.

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