Received: 31 May 2021 | Revised: 12 Jun 2021 | Accepted:28 Jun 2021

Electronic Journal of Plant Breeding

Research Article

Genetic analysis and diversity in early duration pigeonpea (*Cajanus cajan* (L.) MillSp.) genotypes

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Abstract

Genetic analysis and diversity study was done involving 68 early duration pigeonpea based on 12 quantitative traits. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was high for traits *viz.,* plant height (20.22, 20.77 %) pod bearing length (22.14, 23.44 %), the number of clusters per plant (23.03, 25.06 %), the number of pods per plant (21.21, 23.64 %) and the single plant yield (23.61, 34.89 %). The traits *viz.,* plant height (94.77, 40.54 %), the number of branches per plant (78.20, 31.04 %), pod bearing length (89.18, 43.07 %), the number of clusters per plant (84.49, 43.61 %), the number pods per plant (80.51, 39.20 %) and 100 seed weight (94.37, 29.56 %) existed high heritability combined with high genetic advance as a proof for additive gene action and aiding in selection of these traits. The 68 pigeonpea genotypes were grouped into seven clusters based on Mahalanobis D^2 statistic. The cluster II contains the maximum number of genotypes (44 genotypes) followed by cluster V with 10 genotypes. The maximum inter cluster distance (22.18) was observed for clusters VI and VII and the minimum distance (7.76) was between clusters III and IV. The cluster II recorded the maximum average cluster mean for traits *viz*., plant height (143.02 cm), pod bearing length (83.47 cm), the number of cluster per plant (91) and single plant yield (41.79 g). The lowest average cluster mean for single plant yield (27.42 g) and the yield attributing traits *viz.,* the number of clusters per plant (60), the number of pods per plant (112) was observed for cluster I. The highest per cent contribution to genetic diversity is rendered by days to fifty per cent flowering (21.12 %) and the lowest contribution is observed for pod bearing length (0.83%). The genotypes CO2R (61 days) of cluster VI and ICPL19024 (64 days) of cluster I had reduced days to fifty per cent flowering and can be utilized in the breeding of early maturing pigeonpea genotypes. The genotypes *viz.,* ICPL19002, ICPL19004, ICPL19007, ICPL19009, ICPL19010, ICPL19018 and ICPL19028 were found to be superior for yield and yeld attributing traits.Genotypes identified in the present study, could be used to develop varieties with early maturity and increased yield in pigeonpea.

Key words

Early duration pigeonpea, genetic advance as per cent of mean, genetic diversity, genetic variability, heritability.

INTRODUCTION

Pigeonpea (*Cajanus cajan* L. MillSp.) is an important pulse crop grown in the tropical and subtropical regions (Sarkar *et al.,*2020). It is a versatile food legume, helping in resource-free cultivation by poor farmers (Chandavenkata *et al.,* 2019). Pigeonpea is a protein rich (20-22%) and drought resistant crop. It can be grown as an intercrop with wide range of crops and improves soil fertility due to its nitrogen fixing capacity. The early duration pigeonpea are photo-insensitive types with compact plant stature suitable for intercropping. Globally pigeonpea is grown in an area of 5.6 m. ha. owing to a production and yield of 4.4 m. t. and 788 kg/ha, respectively. In India, the area under pigeonpea cultivation is about 4.54 m.ha. with a production of 3.3 m. t. (FAOSTAT, 2019). The lack of diversity and photosensitivity is causing stagnant productivity of pigeonpea leading to a gap between demand and supply over the years (Sameerkumar *et al.,* 2016). In order to break the yield plateau several remedies have been considered like utilizing the genetic diversity within the primary gene pool or creating variability by involving wild species from secondary and tertiary gene pool, exploiting the heterosis and development of photo-insensitive early maturing genotypes.The present study was formulated to study the genetic variability and diversity present in the early duration pigeonpea germplasm and to utilize for the development of early duration pigeonpea varieties or hybrids.

MATERIALS AND METHODS

The study was conducted at the Department of Pulses, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India during *rabi* 2019-2020 and *rabi* 2020-2021. The latitude and longitudinal coordinates of the experimental plot is 11.01°N and 76.93°E, respectively and the soil type is red loam. The experimental material includes 67 early duration pigeonpea genotypes and a local check variety Co(Rg)7. A total of 57 genotypes obtained from ICRISAT and 11 genotypes available in the Department of Pulses, Tamil Nadu Agricultural University were evaluated.The pigeonpea genotypes were raised in a 4 m row each with a spacing of 90 X 30cm.The experimental design employed was randomized complete block design (RCBD) with two replications. The field operations were carried out as per the standard recommendations. The genotypes were evaluated for genetic variability and genetic diversity based on twelve quantitative traits *viz.,* days to fifty per cent flowering, days to maturity, plant height (cm), the number of branches per plant, pod bearing length (cm), the number of clusters per plant, the number of pods per plant, pod length (cm), the number of seeds per pod, shelling percentage (%), 100 seed weight (g) and single plant yield (g). The biometrical traits were recorded from three randomly selected competitive plants from each genotype for the two replications. The two season data was pooled and the mean value calculated was subjected for statistical analysis.Genotypic coefficient of variation and phenotypic coefficient of variation was calculated according to the procedures given by Burton, (1952). Heritability and genetic advance was estimated utilizing the methodology by Lush, (1940) and Johnson *et al.*(1955), respectively. The genetic diversity was calculated based on Mahalanobis D^2 statistic (Mahalanobis, 1936). The analysis was done with help of GENRES vs 7.01 software.

RESULTS AND DISCUSSION

The principle of systematic plant breeding entails the exploitation of available natural variability and diversity for utilization in crop improvement programme (Bhandari *et al.,* 2017). The present study involves the assessment of genetic variability and genetic diversity present within the pigeonpea genotypes. The analysis of variance showed a significant variation for all the traits. The mean and the range of all the traits were mentioned in **Table1.** The range for each trait showcased a wider value indicating the possibility of presence of variability among the genotypes. The days to fifty per cent flowering of 68 pigeonpea genotypes ranged from 61 days to 79 days and their mean value was 70 days. A total of 34 pigeonpea genotypes was observed to have days to fifty per cent flowering lesser than the overall mean and these genotypes can be used for the development of early maturity pigeonpea genotypes. Days to maturity ranged from 112 to 128 days with a mean value of 119 days. The days to maturity of 33 pigeonpea genotypes were lesser than the overall mean for days to maturity (119 days) and these genotypes may be utilized to develop high yielding early duration pigeonpea genotypes for Tamil Nadu. The mean value of single plant yield was 38.93g and the range was 21.67 to 80.75g. The wide variation in single plant yield projects the possibility of improvement of the particular trait in pigeonpea. The mean value for yield contributing traits *viz.,* the number of pods per plant and 100 seed weight was 158 and 9.65g, respectively. The early maturing pigeonpea genotypes having elite plant stature, superiror yield and yield contributing traits can be selected based on the mean values for utilization in the future breeding programmes.

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) showcast supremacy in representing the variability present among the genotypes (**Table 2**). The phenotypic coefficient of variation is higher in magnitude than the genotypic coefficient of variation for all the traits. The GCV and PCV was higher for traits *viz.,* plant height (20.22, 20.77 %), pod bearing length (22.14, 23.44 %), the number of clusters per plant (23.03, 25.06 %), the number of pods per plant (21.21, 23.64 %) and the single plant yield (23.61, 34.89 %). The presence of high GCV and PCV indicates high variability for the traits and aids in the selection of genotypes based on these traits.The traits *viz.,* days to fifty per cent flowering (5.84,5.91 %), days to maturity (3.85, 3.96 %), pod length (7.71, 8.35 %), the number of seeds per pod (5.85, 6.99 %) and shelling percentage (6.70, 9.34 %) possessed low GCV and PCV. Reddy *et al.*(2019) had observed low GCV and PCV for most of the quantitative traits considered for the study in pigeonpea. The selection for such traits shows no significance.The relative difference in magnitude between GCV and PCV was very less for all the traits except for single plant yield indicating the lesser influence of environment on the expression of traits. Ranjani *et al.*(2018), Pushpavalli *et al.* (2018) and Hemavathy *et al.* (2019) recorded less difference between GCV and PCV for various traits in pigeonpea.

Table 1. Mean performance of pigeonpea genotypes for twelve quantitative traits

S.No.	Genotypes	Days to fifty per cent flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Pod bearing length (cm)	Number clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Shelling percentage (%)	100 seed weight (g)	Single plant yield (g)
1	ICPL19001	78	123	157.74	13	86.56	110	190	5.20	4	52.60	10.74	38.59
2	ICPL19002	71	120	135.13	11	79.86	127	215	5.51	4	70.05	8.48	45.10
3	ICPL19003	71	123	150.94	12	82.84	94	160	6.20	5	65.82	10.29	39.10
4	ICPL19004	66	120	143.16	11	93.43	105	182	6.15	4	62.84	10.98	52.00
5	ICPL19007	68	115	129.39	10	77.80	119	169	5.66	4	70.70	10.69	59.20
6	ICPL19008	67	118	141.09	9	90.54	81	133	5.63	4	68.33	11.24	48.50
7	ICPL19009	69	115	131.68	12	74.84	106	195	5.65	4	65.37	10.41	45.83
8	ICPL19010	71	123	149.32	11	94.04	134	239	5.99	4	65.63	10.34	66.92
9	ICPL19011	78	127	179.84	11	90.05	89	131	6.30	4	57.02	12.17	45.24
10	ICPL19012	73	118	153.00	8	87.70	86	130	6.24	4	63.64	11.80	33.60
11	ICPL19013	63	113	150.90	9	80.90	79	120	5.96	4	68.91	10.96	35.70
12	ICPL19014	63	113	143.91	9	90.75	103	179	5.70	4	64.67	10.05	38.14
13	ICPL19015	70	124	185.09	12	103.42	123	147	5.80	4	65.88	11.95	54.33
14	ICPL19016	67	120	165.59	8	92.25	83	143	5.54	4	68.93	10.23	38.75
15	ICPL19017	66	117	152.75	8	92.84	99	198	5.88	4	64.82	9.87	46.00
16	ICPL19018	75	124	162.50	10	81.75	88	169	5.67	4	60.34	10.57	42.50
17	ICPL19019	75	125	162.96	10	88.13	81	166	6.42	4	51.61	11.99	40.25
18	ICPL19020	72	120	158.55	9	92.19	80	177	5.97	4	64.33	9.71	56.54
19	ICPL19021	65	114	109.67	9	73.08	65	110	5.69	4	71.53	9.02	24.17
20	ICPL19022	65	117	108.67	9	73.17	67	128	5.43	4	67.24	9.67	30.59
21	ICPL19023	66	120	121.70	7	68.40	55	114	5.77	4	73.41	10.08	35.33
22	ICPL19024	64	117	119.25	8	80.59	63	116	5.91	4	66.68	10.44	29.00
23	ICPL19025	65	119	124.67	7	76.59	58	108	5.82	4	67.10	10.03	25.83
24	ICPL19026	71	124	161.50	13	92.84	96	190	6.22	4	61.56	11.61	53.35
25	ICPL19027	73	125	151.29	11	86.00	79	123	6.20	4	60.30	11.76	34.83
26	ICPL19028	76	126	161.00	10	95.80	87	181	6.48	4	64.88	12.00	51.00
27	ICPL19029	67	124	143.54	11	85.55	84	131	6.09	4	63.64	11.27	34.17
28	ICPL19030	72	126	182.50	10	109.13	112	227	5.79	4	56.66	9.28	40.84
29	ICPL19031	78	128	194.21	10	109.67	106	165	5.72	4	56.36	9.62	25.42
30	ICPL19032	71	125	142.88	10	76.50	73	150	6.05	4	64.61	9.75	34.13
31	ICPL19033	69	118	140.65	8	76.55	73	143	5.91	4	64.15	8.90	38.05
32	ICPL19034	73	121	149.75	11	91.17	96	202	5.37	4	62.57	8.95	46.12
33	ICPL19035	74	124	128.80	6	77.65	99	170	5.13	4	64.61	8.13	36.40
34	ICPL19036	73	122	144.05	8	91.25	93	170	5.76	4	73.76	9.05	41.50

35	ICPL19037	69	118	130.46	8	77.13	96	173	5.71	4	70.91	9.75	51.42
36	ICPL19038	70	120	150.80	10	95.09	111	215	5.26	4	64.45	9.23	65.40
37	ICPL19039	76	125	120.94	8	81.80	85	194	6.01	4	62.73	9.82	51.63
38	ICPL19040	70	123	120.25	7	70.50	94	187	5.89	4	60.81	9.20	32.50
39	ICPL19042	72	127	126.75	7	77.00	90	138	5.87	4	68.28	9.09	30.00
40	ICPL19043	69	123	140.38	12	71.13	106	185	6.07	4	59.96	10.26	38.50
41	ICPL19044	68	116	128.50	10	75.25	83	146	5.78	5	66.97	7.72	34.88
42	ICPL19046	71	117	159.90	7	97.21	97	180	6.01	4	63.43	9.51	47.60
43	ICPL19047	68	123	159.05	7	93.30	84	166	5.76	4	66.04	9.45	43.04
44	ICPL19049	71	118	96.00	7	57.84	76	142	5.22	4	71.14	8.36	29.33
45	ICPL19050	67	113	93.78	8	55.11	60	138	5.27	4	71.81	7.38	28.13
46	ICPL87	68	116	72.50	9	34.75	57	128	5.58	4	75.05	9.01	34.33
47	ICPL151	74	112	100.34	13	37.13	45	111	7.10	5	60.54	14.93	34.13
48	ICPL89	70	113	109.00	7	70.17	63	124	4.40	4	67.06	7.73	27.09
49	ICPL85010	64	113	72.25	9	38.03	54	115	5.69	4	53.33	9.16	27.34
50	ICPL88039	72	118	138.89	10	89.14	105	169	5.66	4	64.26	9.96	38.37
51	ICPL88034	72	115	144.59	11	82.67	118	241	6.04	4	60.84	9.76	53.50
52	ICPL149	72	115	102.13	9	61.63	75	146	5.03	4	69.42	6.95	22.67
53	ICPL86022	78	123	131.17	9	84.25	55	100	5.46	4	58.94	8.30	21.67
54	ICPL161	67	113	116.75	9	74.75	84	169	4.85	4	66.92	7.84	35.25
55	ICPL81-3	67	118	111.50	8	72.13	64	149	5.22	4	67.56	8.24	31.17
56	ICPB2039	73	120	90.60	10	41.72	68	154	5.48	4	65.99	8.81	33.70
57	ICPB2156	67	121	154.87	7	91.37	84	184	5.86	4	68.48	8.74	42.63
58	CO2R	61	112	75.33	9	35.25	54	109	5.19	4	67.79	10.29	27.92
59	CO3R	65	112	79.00	10	38.00	58	142	5.15	4	64.00	9.88	38.75
60	CO4R	64	116	137.07	11	68.57	108	167	5.15	4	59.77	8.17	23.38
61	CO5R	72	123	149.50	12	85.34	104	143	5.86	4	63.32	9.11	40.84
62	CO6R	67	112	135.59	8	71.17	92	147	5.43	4	68.84	8.68	38.92
63	CO7R	79	128	157.25	12	92.75	111	170	5.26	4	55.35	8.32	29.00
64	CO8R	69	112	73.59	9	31.89	48	98	5.04	4	64.70	8.27	24.41
65	CO9R	68	113	113.09	8	68.34	69	115	4.76	4	65.33	7.07	27.67
66	CO10R	69	113	129.90	10	72.10	89	149	5.20	4	68.56	7.52	32.57
67	CO11R	72	118	136.96	7	81.17	78	134	4.88	4	69.69	7.36	22.09
68	Co(Rg)7	73	123	156.83	11	96.25	115	258	5.68	4	67.65	10.10	80.75
	Mean	70	119	134.60	9	78.14	86	158	5.67	4	64.86	9.65	38.93
	Range	61.00-79.00	112.00-128.00	72.24-194.21	6.00-13.00	31.89-109.67	45.00-134.00	98.00-258.00	4.40-7.10	4.00-5.00	51.61-75.05	6.95-14.93	21.67-80.75
	SED	**0.604**	**1.082**	**6.395**	**0.843**	**6.025**	**8.521**	**16.499**	**0.182**	**0.153**	**4.234**	**0.348**	**10.001**
	CD at 5%	**1.205**	**2.160**	**12.765**	**1.682**	**12.026**	**17.009**	**32.933**	**0.362**	**0.305**	**8.451**	**0.695**	**19.963**

Table 2. Genetic variability, heritability and genetic advance as per cent mean for the quantitative traits in pigeonpea

Characters	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	Genetic advance as per cent of mean
Days to fifty per cent flowering	5.84	5.91	97.85	8.31	11.90
Days to maturity	3.85	3.96	94.74	9.21	7.72
Plant height	20.22	20.77	94.77	54.57	40.54
Number of branches per plant	17.04	19.27	78.20	2.91	31.04
Pod bearing length	22.14	23.44	89.18	33.66	43.07
Number of clusters per plant	23.03	25.06	84.49	37.66	43.61
Number of pods per plant	21.21	23.64	80.51	61.98	39.20
Pod length	7.71	8.35	85.29	0.83	14.68
Number of seeds per pod	5.85	6.99	70.03	0.40	10.09
Shelling percentage	6.70	9.34	51.44	6.44	9.90
100 seed weight	14.77	15.21	94.37	2.85	29.56
Single plant yield	23.61	34.89	45.80	12.82	32.92

Heritability was high for traits *viz.,* days to fifty per cent flowering (97.85 %), days to maturity (94.74 %), plant height (94.77 %), the number of branches per plant (78.20 %), pod bearing length (89.18 %), the number of clusters per plant (84.49 %), the number of pods per plant (80.51 %), the number of seeds per pod (70.03 %) and 100 seed weight (94.37 %). The highest genetic advance as per cent mean was recorded for the number of clusters per plant (43.61 %) followed by pod bearing length (43.07 %), plant height (40.54 %), the number of pods per plant (39.20 %), single plant yield (32.92 %) and the number of branches per plant (31.04 %). The traits *viz.,* plant height (94.77, 40.54 %), the number of branches per plant (78.20, 31.04 %), pod bearing length (89.18, 43.07 %), the number of clusters per plant (84.49, 43.61 %), the number pods per plant (80.51, 39.20 %) and 100 seed weight (94.37, 29.56 %) existed a high heritability combined with high genetic advance as per cent of mean. The high heritability with high genetic advance implies additive gene action and selection for these traits leads to crop improvement. The high heritability combined with high genetic advance as per cent mean was reported for traits *viz.,*plant height, the number of primary branches per plant, the number of pods per plant, 100 seed weight and seed yield per plant by Rekha *et al.*(2013). Ajay *et al.*(2014) observed a high heritability and genetic advance as per cent mean in pigeonpea for the traits *viz.,* plant height, primary branches per plant, the number of pods per plant, seed yield per plant and shelling per cent. Sharma *et al.*(2021) reported high heritability and genetic advance as per cent of mean for traits *viz.,*the number of primary branches per plant, the number of pods per plant, 100 seed weight and single plant yield in pigeonpea.

Table 3. Cluster distribution of 68 pigeonpea genotypes based on D^2 statistic

Cluster	Number of Genotypes	Genotypes
Cluster I	2	ICPL19024, ICPL19025
Cluster II	44	ICPL19001, ICPL19002, ICPL19003, ICPL19004, ICPL19007, ICPL19008, ICPL19009, ICPL19010, ICPL19011, ICPL19012, ICPL19013, ICPL19014, ICPL19015, ICPL19016, ICPL19017, ICPL19018, ICPL19019, ICPL19020, ICPL19021,ICPL19022,ICPL19023,ICPL19026,ICPL19027,ICPL19028,ICPL19029, ICPL19030, ICPL19031, ICPL19032, ICPL19033, ICPL19034, ICPL19035, ICPL19036, ICPL19037, ICPL19038, ICPL19039, ICPL19040, ICPL19042, ICPL19043, ICPL19044, ICPL19046, ICPL19047, ICPL19049, ICPL19050, ICPL87
Cluster III	2	ICPL161, CO9R
Cluster IV	2	CO6R, CO10R
Cluster V	10	ICPL151, ICPL89, ICPL85010, ICPL88039, ICPL88034, ICPL149, ICPL86022, ICPL81-3, ICPB2039, ICPB2156
Cluster VI	4	CO2R, CO3R, CO4R, CO5R
Cluster VII	4	CO7R, CO8R, CO11R, Co(Rg)7

https://doi.org/10.37992/2021.1202.076

The most appropriate method to estimate the diversity within any crop species is the D^2 statistics (Bhandari *et al.,* 2017; Priyanka *et al.,* 2021). The 68 pigeonpea genotypes were grouped into seven clusters. Reddy *et al.*(2015) reported ten clusters formed from 47 pigeonpea genotypes based on D^2statistic whereas, Sharma *et al.* (2018) observed nine clusters formed from 68 pigeonpea genotypes.The cluster II contained the maximum number of genotypes (44), followed by cluster V with 10 genotypes (**Table 3**). The clusters VI and VII were observed to have four genotypes each, whereas the clusters I, III and IV had two genotypes each . The highest inter cluster distance was observed between the clusters VI and VII (22.18) followed by clusters I and VII (21.08) (**Table 4**). The lowest inter cluster distance was noticed in case of cluster III and IV (7.76). The higher inter cluster distance indicates the genotypes of those clusters were distantly related, whereas the lowest inter cluster distance indicates the likeliness among the genotypes of the different clusters. The intra cluster distance was high for cluster VII (18.22) and cluster V (18.11). The lowest intra cluster distance was recorded in the case of cluster I (3.61). The highest intra cluster distance confirms that the genotypes grouped within a cluster are comparatively distantly related, whereas the lowest intra cluster distance implies the closeness of the genotypes confined to a cluster. Muniswamy *et al.* (2014) reported the highest inter cluster and intra cluster distance of 147.38 and 51.96, respectively for 18 clusters of 196 pigeonpea genotypes. The highest inter and intra cluster distance of 842.70 and 90.03, respectively was reported by Reddy *et al.*(2015) for ten clusters of 47 pigeonpea genotypes. Singh *et al.* (2015) also reported the highest inter cluster distance of 128.60 and intra cluster distance of 17.81 for six clusters formed from 21 pigeonpea genotypes.

The average cluster mean values for the seven clusters is represented in **Table 5**. The earliest days to fifty per cent flowering was recorded in cluster I and VI (64 and 65 days). The shortest days to maturity was observed in the case of cluster III and IV (113 days). The genotypes CO2R (61 days) of cluster VI and ICPL19024 (64 days) of cluster I had reduced days to fifty per cent flowering and can be utilized in the breeding of early maturing pigeonpea genotypes. The cluster II recorded maximum plant height (143.02 cm), pod bearing length (83.47 cm), the number of clusters per plant (91) and single plant yield (41.79 g). The highest average cluster mean value for the number of pods per plant (165) was recorded in case of cluster VII followed by cluster II (164). The highest pod length (5.86 cm) and 100 seed weight (10.24 g) was confined to cluster I followed by cluster II (5.80 cm and 10.01 g, respectively). Cluster IV had greater shelling percentage (68.70 %) followed by cluster I (66.89 %). Number of branches per plant (11) was observed to be the highest for the cluster VI followed by cluster VII (10). All the cluster showed similarity for number of seeds per pod and consisted the average mean value of four seeds per pod. The clusters with high average mean value for yield and yield contributing traits can be utilized in crop

Table 4. The inter and intra (diagonal) cluster distance for the seven clusters of pigeonpea genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	**3.61**	15.88	13.93	13.67	18.00	14.91	21.08
Cluster II		**15.11**	17.37	15.96	17.40	19.58	17.42
Cluster III			**5.88**	7.76	15.85	15.18	17.24
Cluster IV				**6.63**	15.78	14.41	17.22
Cluster V					**18.11**	19.66	17.73
Cluster VI						**17.85**	22.18
Cluster VII							**18.22**

Table 5. Cluster mean of the quantitative traits for seven clusters in pigeonpea

	Days to fifty per cent flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Pod bearing length (cm)	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Shelling percentage (%)	100 seed weight (g)	Single plant yield (g)
Cluster I	64	118	121.96	7	78.59	60	112	5.86	4	66.89	10.24	27.42
Cluster II	70	121	143.02	9	83.47	91	164	5.80	4	65.22	10.01	41.79
Cluster III	67	113	114.92	8	71.54	76	142	4.80	4	66.12	7.45	31.46
Cluster IV	68	113	132.74	9	71.63	91	148	5.31	4	68.70	8.10	35.74
Cluster V	71	117	115.53	9	66.82	73	149	5.59	4	63.64	9.26	33.22
Cluster VI	65	116	110.22	11	56.79	81	140	5.33	4	63.72	9.36	32.72
Cluster VII	73	120	131.16	10	75.51	88	165	5.21	4	64.34	8.51	39.06

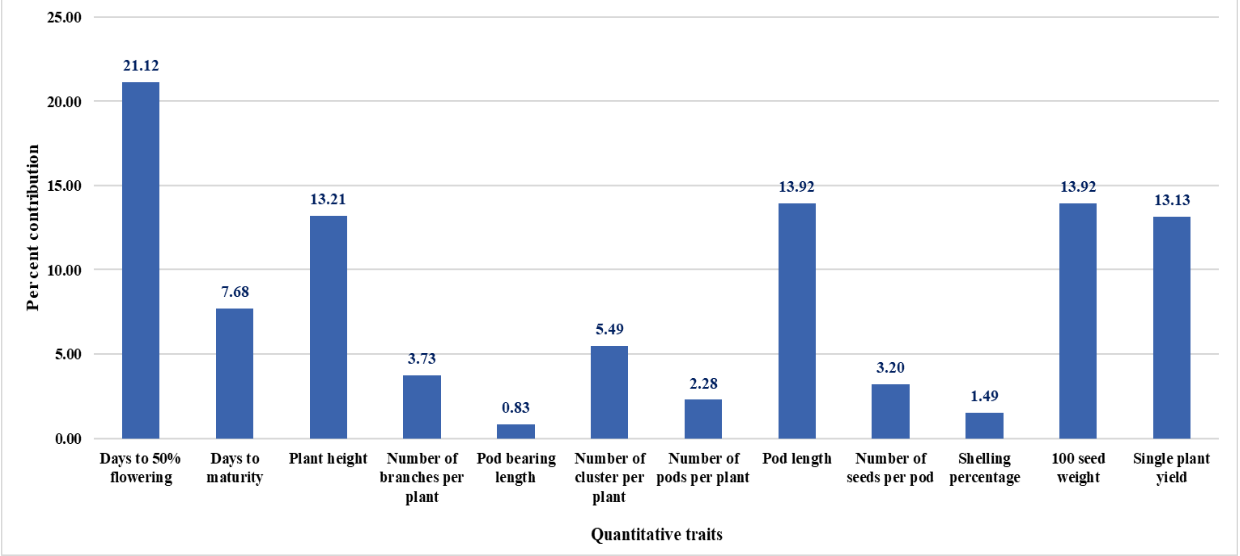

Fig. 1. Per cent contribution of the 12 quantitative traits towards genetic diversity of 68 pigeonpea genotypes

improvement to obtain high productivity. The genotypes *viz.,* ICPL19002, ICPL19004, ICPL19007, ICPL19009, ICPL19010, ICPL19018 and ICPL19028 of cluster II were found to be superior for yield and yield attributing traits *viz.,* the number of clusters per plant, the number of pods per plant and 100 seed weight. The above genotypes may be utilized for breaking the stagnant yield plateau in pigeonpea and improve production.

The lowest average mean values for the number of branches per plant (7), the number of pods per plant (112), the number of clusters per plant (60) and single plant yield (27.42 g) was observed for the cluster I. The cluster III contained the lowest mean values for pod length (4.80 cm) and 100 seed weight (7.45 g). Cluster VI exhibited a lowest plant height (110.22 cm) and pod bearing length (56.79 cm). Cluster V showed a low average cluster mean value for shelling percentage (63.64 %).The genotypes of different or same clusters with extreme average mean values can be selected according to the breeding objectives to create variability, to develop a hybrid or a mapping population.The above conclusions were also given by Singh *et al.* (2010), Shunyu *et al.* (2013) and Satapathy and Panigrahi, (2014).

The per cent contribution of each quantitative trait towards genetic diversity is given in **Fig.1**. Days to 50 per cent flowering (21.12 %) contributed more to genetic diversity followed by 100 seed weight (13.92 %) , pod length (13.92 %), plant height (13.21 %) and single plant yield (13.13 %). The minimum contribution for total genetic diversity was offered by pod bearing length (0.83 %) and shelling percentage (1.49 %). Satapathy and Panigrahi, (2014) reported that traits *viz.,* yield per plant, pod length, 100 seed weight and days to maturity contributed more to diversity, whereas least contribution was rendred by plant height and the number of branches per plant in pigeonpea.The biometrical traits *viz.,* the number of seeds per pod, plant height, 100 seed weight and days to maturity showed the highest contribution towards diversity and the lowest contribution was executed by days to fifty per cent flowering and the number of pods in pigeonpea (Reddy *et al.,*2015).

The significant variation present for each quantitative trait summarize the posssiblity for improvement of yield and other yield related traits. The high heritability and genetic advance as per cent mean for traits *viz.,* the number of clusters per plant, the number of pods per plant and 100 seed weight represents selection for these traits is feasible thereby improving the yield in pigeonpea. The classification of 68 pigeonpea genotypes into seven different clusters based on D^2 statistic helps in the selection of desirable parents for different breeding aspects based on the inter cluster distance and cluster mean. The genotypes identified in the present study *viz.*, ICPL19002, ICPL19004, ICPL19007, ICPL19009, ICPL19010, ICPL19018 and ICPL19028 for various traits could be used in the breeding program to develop early duration and photo insensitive varieties in pigeonpea.

ACKNOWLEDGEMENT

The authors would like to express our gratitude to Dr. Anupama. J. Hinagane, Pigeonpea Breeder, ICRISAT and NPBGR, New Delhi for sharing the pigeonpea genotypes for the present study.

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