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 D2 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 yield 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...
Genetic analysis and diversity in early duration pigeonpea

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 Table 1. 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, superior 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) showcase 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 (22.14, 23.44 %), seed weight (6.70, 9.34 %) and shelling percentage (6.70, 9.34 %). 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 %) possesses 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.

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 D² statistic (Mahalanobis, 1936). The analysis was done with help of GENRES vs 7.01 software.

RESULTS AND DISCUSSION

In order to generate productive genotypes for 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.

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| S.No. | Genotypes      | Days to flowering (days) | Days to maturity (days) | Plant height (cm) | Pod length (cm) | Number of clusters per plant | Pod bearing number of branches per plant | Shelling percentage (%) | Number of seeds per plant (g) | 100 seed weight (g) | Single plant weight (g) | Pod length (cm) | Days to flowering (days) | Number of clusters per plant | Pod bearing number of branches per plant | Shelling percentage (%) | Number of seeds per plant (g) | 100 seed weight (g) | Single plant weight (g) | Pod length (cm) |
|-------|----------------|--------------------------|-------------------------|-------------------|----------------|-----------------------------|------------------------------------------|------------------------|-------------------------------|-----------------|------------------------|----------------|--------------------------------|-----------------------------|------------------------------------------|------------------------|-------------------------------|-----------------|------------------------|----------------|
| 1     | ICPL 19001     | 123                      | 13                      | 157.74            | 13             | 86.56                       | 110                                       | 3.85                   | 50.00                         | 4              | 50.00                  | 10.74          | 120                                         | 12              | 190                                         | 190                       | 5.20                         | 4              | 5.20                   | 10.74 |
| No. | ID          | Mean   | Range  | SED  | CD at 5%  |
|-----|-------------|--------|--------|------|-----------|
| 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 | 9.62 | 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    | 159.95 | 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  | ICPL2039    | 73     | 120    | 90.60  | 10 | 41.72 | 68  | 154 | 5.48 | 4 | 65.99 | 8.81 | 33.70 |
| 57  | ICPL2156    | 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 | 56  | 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

Range

SED

CD at 5%
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 (80.51 %), the number of pods per plant (78.20 %), the number of clusters per plant (80.51, 39.20 %) and 100 seed weight (94.37, 29.56 %). The highest genetic advance as per cent of mean was reported for traits viz., plant height (94.77, 40.54 %), 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 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 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 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             |
|           |                     | 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 II| 44                  | ICPL161, CO9R                     |
|           |                     | ICPL151, ICPL89, ICPL85010, ICPL88039, ICPL8034, ICPL149, ICPL86022, ICPL81-3, ICPB2039, ICPB2156 |
| Cluster III| 2                   | ICPL19024, ICPL19025             |
|           |                     | 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 IV| 2                   | ICPL19024, ICPL19025             |
|           |                     | 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 V | 10                  | ICPL151, ICPL89, ICPL85010, ICPL88039, ICPL149, ICPL86022, ICPL81-3, ICPB2039, ICPB2156 |
| Cluster VI| 4                   | ICPL151, ICPL89, ICPL85010, ICPL88039, ICPL149, ICPL86022, ICPL81-3, ICPB2039, ICPB2156 |
| Cluster VII| 4                  | ICPL151, ICPL89, ICPL85010, ICPL88039, ICPL149, ICPL86022, ICPL81-3, ICPB2039, ICPB2156 |

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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 $D^2$ statistic 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 likeness 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 | 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       |
| Cluster II | 15.11      | 7.76        | 15.78      | 18.11     | 17.85      | 17.24       |
| Cluster III | 5.88       | 18.11       | 17.76      | 19.58     | 19.66      | 17.73       |
| Cluster IV | 6.63       | 4.80        | 17.85      | 15.18     | 14.41      | 17.22       |
| Cluster V | 17.85      | 19.66       | 16.67      | 17.73     | 17.24      | 18.22       |
| Cluster VII |            |             |            |           |            |             |

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

| Cluster | 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 pod | 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                   | 414                         | 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                   | 51                          | 184                   | 5.31             | 4                       | 63.64                  | 9.26                 | 32.22                  |
| Cluster V | 71                             | 117              | 115.53           | 9                             | 66.82                   | 53                          | 149                   | 5.59             | 4                       | 67.32                  | 9.36                 | 32.72                  |
| Cluster VI | 65                            | 116              | 110.22           | 11                            | 56.89                   | 51                          | 140                   | 5.33             | 4                       | 63.72                  | 8.51                 | 39.06                  |
| Cluster VII | 73                            | 120              | 131.16           | 10                            | 75.51                   | 88                          | 165                   | 5.21             | 4                       | 64.34                  | 8.51                 | 39.06                  |
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 (9.83 %) and shelling percentage (1.49 %).

The significant variation present for each quantitative trait summarize the possibility 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, 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 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.

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