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# Genetic diversity studies in F$_{2:3}$ segregating generation of cowpea (*Vigna unguiculata* L. Walp.)

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**Abstract**
Divergence studies through Mahalanobis D$^2$ statistics indicated the presence of considerable diversity by forming large number of clusters with wide range of inter cluster distances. The present investigation was carried out during *summer* 2021 to study F$_3$ segregating generation of two cowpea crosses *viz.,* VBN-1 × RC-19 and KBC-9 × PGCP-6 using augmented random block design at College of Agriculture, Kalaburagi. Data were recorded on 10 different quantitative traits. The Mahalanobis analysis revealed that 100 family rows of F$_{2:3}$ populations of VBN-1 × RC-19 cowpea were grouped into 7 clusters, while 70 family rows of F$_{2:3}$ populations of KBC-9 × PGCP-6 grouped into 7 clusters. In F$_{2:3}$ populations of VBN-1 × RC-19, cluster I was largest comprising of 65 genotypes, while in F$_{2:3}$ populations of KBC-9 × PGCP-6, cluster I was largest comprising of 55 genotypes. The inter-cluster distance was larger than intra-cluster distance which indicated that greater diversity is present among the genotypes of distant group. The maximum intra-cluster D$^2$ distances was recorded by cluster V in F$_{2:3}$ populations of VBN-1 × RC-19; cluster V in F$_{2:3}$ populations of KBC-9 × PGCP-6. The maximum inter cluster distance was observed between cluster VI and VII in F$_{2:3}$ populations of VBN-1 × RC-19; cluster V and VI in F$_{2:3}$ populations of KBC-9 × PGCP-6. Hence, segregants from these clusters may be utilized as parents for hybridization which would result in high heterotic combination for yield components. Seed yield/plant contributed maximum towards the divergence in both the segregating population, followed by dry matter content/plant and test weight.

**Keywords:** Cowpea, divergence, Mahalanobis D$^2$ statistics, F$_3$ segregating generation and clusters

## Introduction

Cowpea (*Vigna unguiculata* L. Walp.) is an annual self-pollinated diploid (2n = 2x = 22) warm-season grain legume with 620 Mb genome size [1]. It belongs to the family Fabaceae, tribe Phaseoleae, genus *Vigna* and section Catiang [2]. It is photo insensitive in nature and can be cultivated throughout the year. Cowpea is grown in different cropping system as it has relatively drought tolerant nature [3]. Cowpea can be grown in arid, semiarid and subtropical areas. It is resilient to high temperature and limited water stresses, and grows well on poor soil with a wide range of soil pH thus making it a good choice for resource-poor small-scale farmers for their sustenance [4]. It is cultivated in Africa, South and Central America, East/Southeast Asia, US and Southern Europe [5]. It plays an important role in the developing countries of the tropics and subtropics especially in sub Saharan Africa, Asia, Central and South America. In India, cowpea is grown in the states of Gujarat, West Bengal, Tamil Nadu, Andhra Pradesh, Kerala and Orissa [6].

Understanding the level of genetic diversity in germplasm is needful to plant breeders as it supports this decision on selection of superior parental segregating population and it is important in broadening the genetic base of cowpea breeding [7]. Morphological characters are routinely used for quantifying genetic diversity. Characterization and evaluation of available F$_3$ segregating populations of cowpea, quantification of magnitude of diversity and classification into homogeneous groups to facilitate identification of genetic variability enable breeders to select traits of interest for an improvement program [8]. The analysis of genetic diversity in germplasm collections can facilitate the classification and identification of groups of accessions with superior traits to be used for breeding purposes [9].

## Materials and Methods

The experimental material for the present study was generated by selfing the F$_2$ population of the cross I (VBN-1 × RC-19) and cross II (KBC-9 × PGCP-6). The experimental material was

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generated in the Department of Genetics and Plant Breeding, College of Agriculture, Kalaburagi, University of Agricultural Sciences, Raichur. The $F_3$ families of crosses (100 family rows of cross I and 70 family rows of cross II) were grown during summer 2021. The experiment material was evaluated using Augmented Block Design with five replications of checks (C-152, KBC-2, KBC-9, PGCP-6 and IT-803695-1) and parents. Each $F_3$ progeny family was sown in rows of 4 meter length with a spacing of 45 cm × 30 cm. The observation were recorded on ten traits *viz.*, days to initiation of flowering, days to physiological maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, pod length, test weight, dry matter per plant, seed yield per plant. The mean data of five randomly selected plants from each family row for all traits were recorded and utilized for statistical analysis *i.e.*, genetic divergence.

## Results and Discussion
Genetic diversity is considered as crucial criteria for selecting genetically diverse parents for a successful and efficient hybridization programme, which leads to the production of high yielding lines. The chance of evolving promising and desired types is higher when there is greater genetic diversity in crop species.

## Mahalanobis $D^2$ values
Genetic divergence using $D^2$ analysis was carried out in 170 $F_3$ family rows of two crosses of cowpea. Grouping of segregants into different clusters was done using Tocher's method [10].

## Group Constellations
Based on the divergence studies, 100 family rows of $F_{2:3}$ population of VBN-1 × RC-19 were grouped into seven clusters and is presented in Table 1 (Fig. 1) and 70 family rows of $F_{2:3}$ population of KBC-9 × PGCP-6 of cowpea grouped into seven clusters and presented in Table 2 (Fig. 2). In $F_{2:3}$ population of VBN-1 × RC-19, cluster I was largest comprising of sixty five segregants followed by cluster III and cluster VII containing 12 segregants in each cluster, cluster IV with ten segregants, cluster VI with six segregants, cluster III and cluster VII were solitary comprised of single segregant in each cluster indicating the presence of wide diversity from the rest and also from each other. In $F_{2:3}$ population of KBC-9 × PGCP-6, cluster I was largest comprising of fifty five segregants followed by cluster IV and cluster V with nine segregants in each cluster. Cluster II, cluster III, cluster VI and cluster VII were solitary comprised of single segregant in each cluster indicating presence of wide diversity from the rest and also from each other.
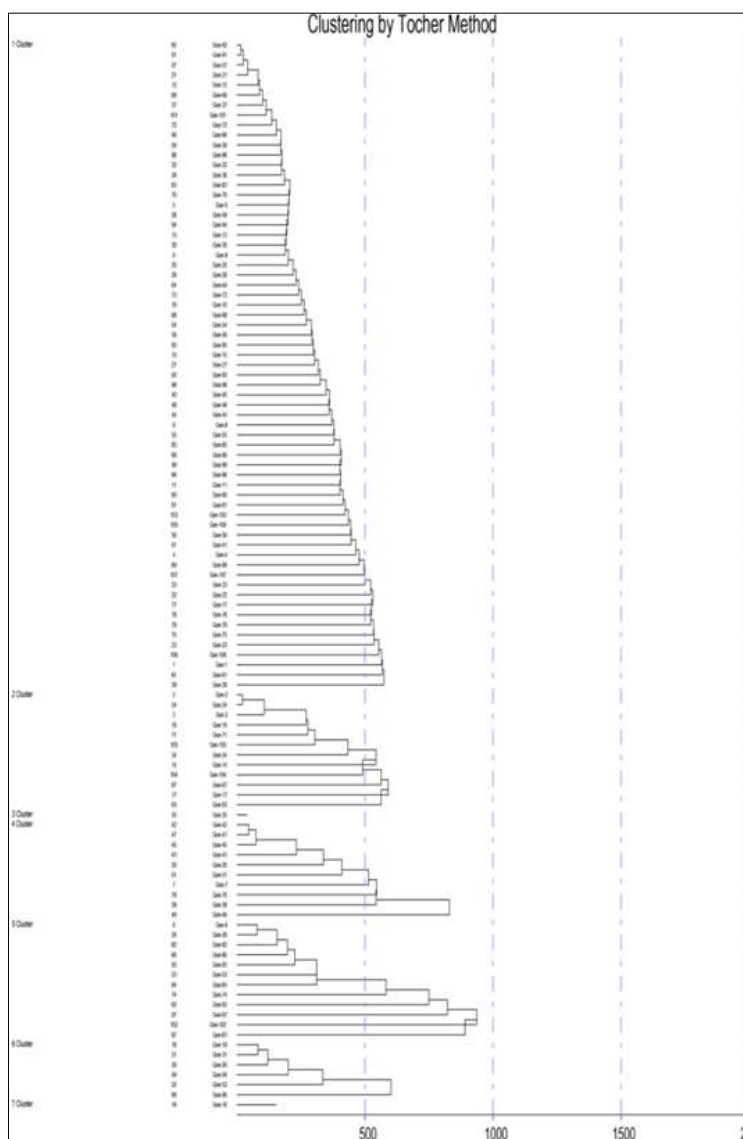
The formation of largest cluster I comprising of highest segregants might be due to free flow or exchange of breeding material from one place to another and the unidirectional selection practiced by breeders of different locations. Similar findings by Tigga and Tandekar [11] observed four clusters among thirty two genotypes. Vavilapalli *et al.* [12] grouped twenty-two genotypes into six clusters. Patil *et al.* [13] grouped the twenty genotypes could be into six clusters. Srinivas *et al.* [14] reported six clusters among thirty genotypes. Patel *et al.* [15] reported thirty two genotypes into eight clusters. Viswanatha and Yogeesh [16] grouped 169 genotypes into eight clusters, Tikka [17] grouped 28 populations into eight clusters, Rupesh *et al.* [18] grouped 21 genotypes into five clusters, Lovely *et al.* [19] grouped 50 genotypes into four clusters, Praveena *et al.* [20] grouped 30 genotypes into eleven clusters, Walle *et al.* [21] groups 324 genotypes into six clusters and Purohit *et al.* [22] divided forty-two cowpea genotypes into eight clusters.

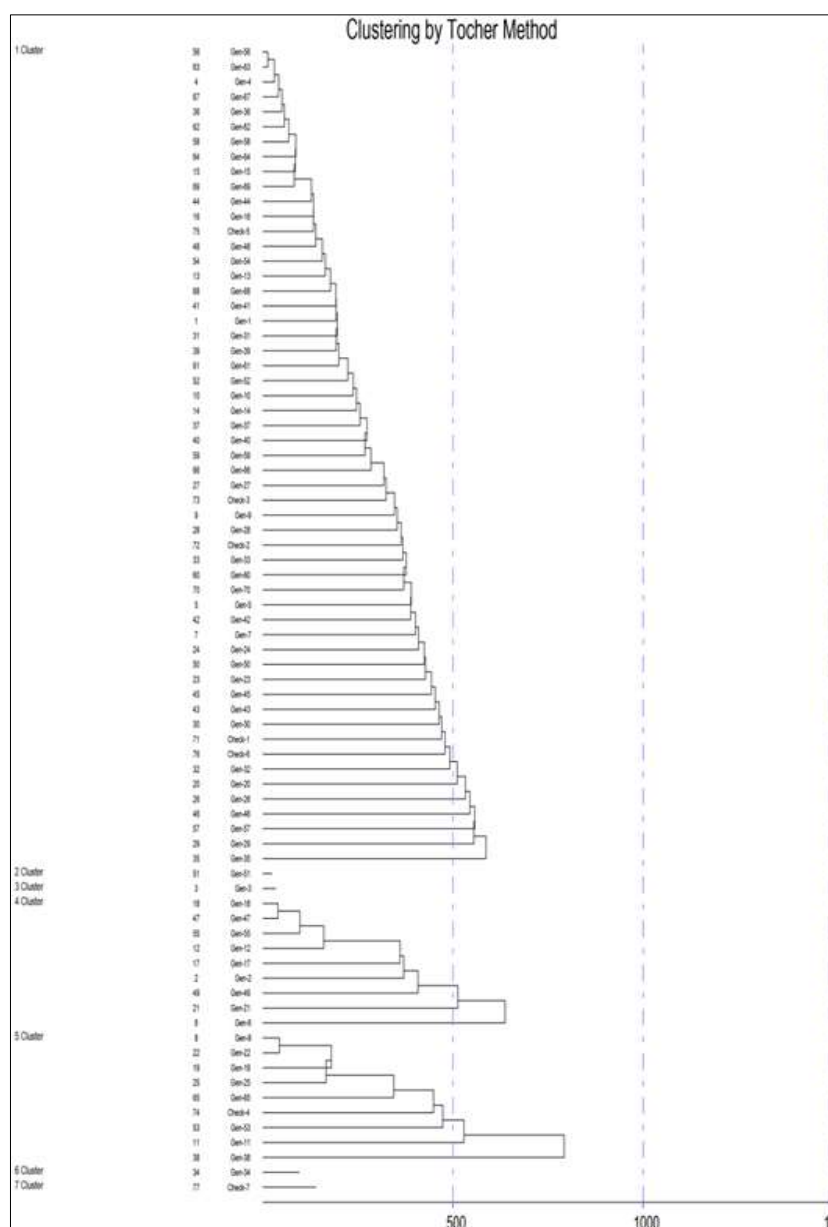**Table 1:** Clustering pattern in $F_3$ segregating population of VBN-1 × RC-19

| Cluster | No. of $F_3$ progeny families | $F_3$ progeny family |
|---|---|---|
| I. | 65 | $F_3$ progeny family-65, $F_3$ progeny family-91, $F_3$ progeny family-57, $F_3$ progeny family-21,$F_3$ progeny family-12, $F_3$ progeny family-69, $F_3$ progeny family-37, $F_3$ progeny family-72, $F_3$ progeny family-90, $F_3$ progeny family-59, $F_3$ progeny family-88, $F_3$ progeny family-32, $F_3$ progeny family-36, $F_3$ progeny family-83, $F_3$ progeny family-70, $F_3$ progeny family-5, $F_3$ progeny family -58, $F_3$ progeny family-94, $F_3$ progeny family-13, $F_3$ progeny family-30, $F_3$ progeny family-9, $F_3$ progeny family-25, $F_3$ progeny family-28, $F_3$ progeny family-64,$F_3$ progeny family-73, $F_3$ progeny family-10, $F_3$ progeny family-68, $F_3$ progeny family-54,$F_3$ progeny family-56, $F_3$ progeny family-95, $F_3$ progeny family-15, $F_3$ progeny family-27, $F_3$ progeny family-92, $F_3$ progeny family-98, $F_3$ progeny family-40, $F_3$ progeny family-48,$F_3$ progeny family-44, $F_3$ progeny family-8, $F_3$ progeny family-55, $F_3$ progeny family-85, $F_3$ progeny family-66, $F_3$ progeny family-99, $F_3$ progeny family-86, $F_3$ progeny family-11, $F_3$ progeny family-60, $F_3$ progeny family-61, $F_3$ progeny family-100, $F_3$ progeny family-50, $F_3$ progeny family-41, $F_3$ progeny family-4, $F_3$ progeny family-89, $F_3$ progeny family-33,$F_3$ progeny family-22, $F_3$ progeny family-77, $F_3$ progeny family-78, $F_3$ progeny family-79,$F_3$ progeny family-75, $F_3$ progeny family-23, $F_3$ progeny family-1, $F_3$ progeny family-81, $F_3$ progeny family-39, C-152, KBC-9, VBN-1, RC-19. |
| II. | 12 | $F_3$ progeny family-2, $F_3$ progeny family-24, $F_3$ progeny family-3, $F_3$ progeny family-19, $F_3$ progeny family-71, $F_3$ progeny family-34, $F_3$ progeny family-14, $F_3$ progeny family-67, $F_3$ progeny family-17, $F_3$ progeny family-63, PGCP-6, IT-803695-1. |
| III. | 1 | $F_3$ progeny family-35. |
| IV. | 10 | $F_3$ progeny family-42, $F_3$ progeny family-47, $F_3$ progeny family-45, $F_3$ progeny family-43, $F_3$ progeny family-20, $F_3$ progeny family-51, $F_3$ progeny family-7, $F_3$ progeny family-76, $F_3$ progeny family-38, $F_3$ progeny family-46. |
| V. | 12 | $F_3$ progeny family-6, $F_3$ progeny family-29, $F_3$ progeny family-82, $F_3$ progeny family-80, $F_3$ progeny family-93, $F_3$ progeny family-53, $F_3$ progeny family-84, $F_3$ progeny family-74, $F_3$ progeny family- 62, $F_3$ progeny family -97, $F_3$ progeny family -87, KBC-2. |
| VI. | 6 | $F_3$ progeny family-18, $F_3$ progeny family-31, $F_3$ progeny family-26, $F_3$ progeny family-49, $F_3$ progeny family-52, $F_3$ progeny family-96. |
| VII. | 1 | $F_3$ progeny family-16. |

**Table 2:** Clustering pattern in F$_3$ segregating population of KBC-9 × PGCP-6

| Cluster | No. of F$_3$ progeny Families | F$_3$ progeny family |
|---|---|---|
| I. | 55 | F$_3$ progeny family-56, F$_3$ progeny family-63, F$_3$ progeny family-4, F$_3$ progeny family-67, F$_3$ progeny family-36, F$_3$ progeny family-62, F$_3$ progeny family-58, F$_3$ progeny family-64, F$_3$ progeny family-15, F$_3$ progeny family-69, F$_3$ progeny family-44, F$_3$ progeny family-16, F$_3$ progeny family-48, F$_3$ progeny family-54, F$_3$ progeny family-13, F$_3$ progeny family-68, F$_3$ progeny family-41, F$_3$ progeny family-1, F$_3$ progeny family-31, F$_3$ progeny family-39, F$_3$ progeny family-61, F$_3$ progeny family-52, F$_3$ progeny family-10, F$_3$ progeny family-14, F$_3$ progeny family-37, F$_3$ progeny family-40, F$_3$ progeny family-59, F$_3$ progeny family-66, F$_3$ progeny family-27, F$_3$ progeny family-9, F$_3$ progeny family-28, F$_3$ progeny family-33, F$_3$ progeny family-60, F$_3$ progeny family-70, F$_3$ progeny family-5, F$_3$ progeny family-42, F$_3$ progeny family-7, F$_3$ progeny family-24, F$_3$ progeny family-50, F$_3$ progeny family-23, F$_3$ progeny family-45, F$_3$ progeny family-43, F$_3$ progeny family-30, F$_3$ progeny family-32, F$_3$ progeny family-20, F$_3$ progeny family-26, F$_3$ progeny family-46, F$_3$ progeny family-57, F$_3$ progeny family-29, F$_3$ progeny family-35, C-152, KBC-2, KBC-9, PGCP-6, VBN-1. |
| II. | 1 | F$_3$ progeny family - 51. |
| III. | 1 | F$_3$ progeny family - 3. |
| IV. | 9 | F$_3$ progeny family-18, F$_3$ progeny family-47, F$_3$ progeny family-55, F$_3$ progeny family-12, F$_3$ progeny family-17, F$_3$ progeny family-22, F$_3$ progeny family-49, F$_3$ progeny family-21, F$_3$ progeny family-6. |
| V. | 9 | F$_3$ progeny family-8, F$_3$ progeny family-22, F$_3$ progeny family-19, F$_3$ progeny family-25, F$_3$ progeny family-65, F$_3$ progeny family-53, F$_3$ progeny family-11, F$_3$ progeny family-38, IT-803695-1. |
| VI. | 1 | F$_3$ progeny family-34. |
| VII. | 1 | RC-19. |



**Fig 1:** Dendrogram of cowpea germplasm based on phenotypic data for F$_3$ segregating generation of VBN-1 × RC-19

**Fig 2:** Dendrogram of cowpea germplasm based on phenotypic data for F$_3$ segregating generation of KBC-9 × PGCP-6

**Intra and inter-cluster average distances**
F 2:3 population of VBN-1 × RC-19: The intra and inter-cluster D2 values among seven clusters for F2:3 population of VBN-1 × RC-19 are presented in Table 3 (Fig. 3). The inter cluster D2 values were greater than the intra cluster D2 values, further indicating the considerable amount of diversity present among the segregants. The intra cluster D2 values ranged from 00.00 to 713.99 units; the maximum intra-cluster D2 (713.99 units) distances was recorded by cluster V, followed by cluster IV (588.76 units), cluster II (535.15 units), cluster VI (435.50 units) and cluster I (412.81 units) indicating maximum diversity among these segregants. Minimum distance (0.00 units) was observed in cluster III and cluster VII as they consisted only one segregant. Whereas, closely related segregants which were grouped into each cluster indicates that less divergence is present among them.
Inter-cluster average D2 values in for F2:3 population of VBN-1 × RC-19 ranged from 306.07 to 2524.33 units. The maximum inter cluster distance was observed between cluster VI and VII (2524.33 units) followed by cluster III and VII (2261.75 units), cluster II and IV (2230.20 units) and cluster

IV and VI (1996.30 units) indicating maximum diversity among these segregants. While minimum inter cluster distance was observed between cluster III and VI (306.07 units) followed by cluster I and III (603.14 units), cluster I and VI (901.36 units) and cluster I and VI (916.94 units), indicating minimum diversity among these segregants i.e., most of the traits studied had similar values in these clusters.
F2:3 population of KBC 9 × PGCP 6: The intra and inter-cluster D2 values among seven clusters in F2:3 population of KBC-9 x PGCP-6 are presented in Table 4 (Fig. 4). The inter cluster D2 values were greater than the intra cluster D2 values, further indicating the considerable amount of diversity among the segregants. The intra cluster D2 values ranged from 00.00 to 564.91 units; the maximum intra-cluster D2 (564.91 units) distances was recorded by cluster V, followed by cluster IV (491.29 units) and cluster I (391.72 units) indicating maximum diversity among these segregants. While, minimum distance (0.00 units) was observed in cluster II, cluster III, cluster VI and cluster VII as they consisted only one genotype. Whereas, closely related segregants which were grouped into each cluster indicates the presence of less

divergence among them. Similar monogenotypic clusters were reported by Brahmaiah et al. [23] in cowpea.

Inter-cluster average D2 values in for F2:3 population of KBC-9 x PGCP-6 ranged from 174.89 to 1983.80 units. The maximum inter cluster distance was observed between cluster V and VI (1983.80 units) followed by cluster IV and VII (1686.42 units), cluster IV and V (1366.23 units) and cluster VI and VII (1298.42units) indicating maximum diversity among these segregants. The minimum inter-cluster distance was recorded between cluster II and VII (174.89 units), cluster III and IV (302.79 units), cluster I and VI (631.49 units) and cluster I and III (642.71 units) indicating minimum diversity among these segregants i.e., most of the characters studied had similar values in these clusters.

The intra-cluster distance was much lower than inter-clusters distance. Several researchers such as Ahamed et al. [24], Viswanatha and Yogeesh [16] and Walle et al. [21] reported similar findings. Segregants in these clusters were not genetically diverse. As a result, usage of segregants in these

clusters as parents might not give higher heterotic value and will not produce greater variability in subsequent generations. Similar findings by Nagalakshmi et al. [25], Vavilapalli et al. [12], Brahmaiah et al. [23] supported the present findings.

Cluster means for different characters

Cluster means for all the ten characters in seven clusters are presented in Table 5 for F2:3 population of VBN-1 × RC-19 and in Table 6 for F2:3 population of KBC-9 × PGCP-6. The findings clearly indicate appreciable difference among cluster means for most of the characters.

F2:3 population of VBN-1 × RC-19: Cluster mean values for days to initiation of flowering ranged from 51 days in cluster III to 70 days in cluster V. The cluster mean value for days to physiological maturity ranged between 88 and 110 days. The segregants under cluster III were early maturing (88 days). Whereas, the segregants under cluster VII were late maturing (110 days).For plant height, cluster mean values are maximum in cluster VI (69.85 cm) and minimum in cluster IV (30.82 cm).

**Table 3:** Average intra (bold) and inter cluster distance (D²) values in F2:3 population of VBN-1 × RC-19

|  | Cluster I | Cluster II | Cluster III | Cluster 1V | Cluster V | Cluster VI | Cluster VII |
|---|---|---|---|---|---|---|---|
| Cluster I | **412.81** | 773.97 | 603.14 | 1075.84 | 916.94 | 901.36 | 1017.35 |
| Cluster II |  | **535.15** | 1058.86 | 2230.20 | 1268.28 | 1057.21 | 1326.28 |
| Cluster III |  |  | **0.00** | 1415.36 | 1354.40 | 306.07 | 2261.75 |
| Cluster IV |  |  |  | **588.76** | 1858.99 | 1996.30 | 1247.43 |
| Cluster V |  |  |  |  | **713.99** | 1885.48 | 1462.93 |
| Cluster VI |  |  |  |  |  | **435.50** | 2524.33 |
| Cluster VII |  |  |  |  |  |  | **0.00** |

**Table 4:** Average intra (bold) and inter cluster distance (D²) values in F2:3 population of KBC-9 × PGCP-6

|  | Cluster I | Cluster II | Cluster III | Cluster 1V | Cluster V | Cluster VI | Cluster VII |
|---|---|---|---|---|---|---|---|
| Cluster I | **391.72** | 666.52 | 642.71 | 945.11 | 897.51 | 631.49 | 758.26 |
| Cluster II |  | **0.00** | 648.52 | 1291.36 | 1435.78 | 889.22 | 174.89 |
| Cluster III |  |  | **0.00** | 302.79 | 1217.39 | 883.49 | 1050.71 |
| Cluster IV |  |  |  | **491.29** | 1366.23 | 1244.44 | 1686.42 |
| Cluster V |  |  |  |  | **564.91** | 1983.80 | 1167.96 |
| Cluster VI |  |  |  |  |  | **0.00** | 1298.42 |
| Cluster VII |  |  |  |  |  |  | **0.00** |
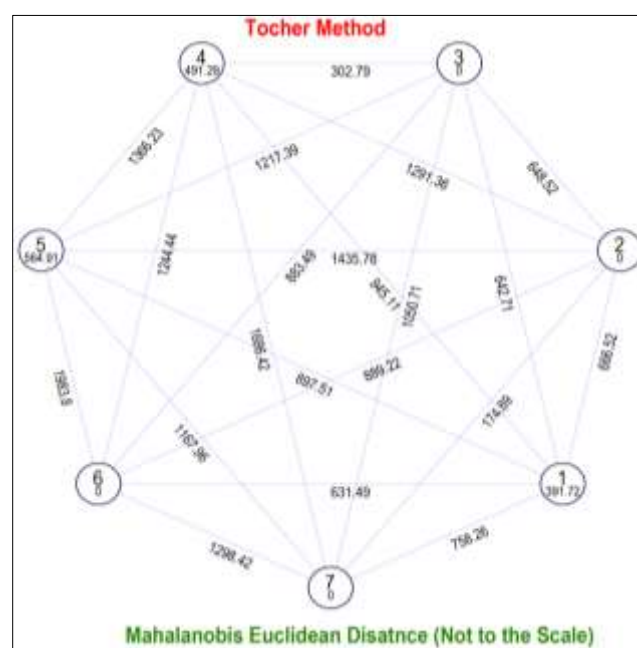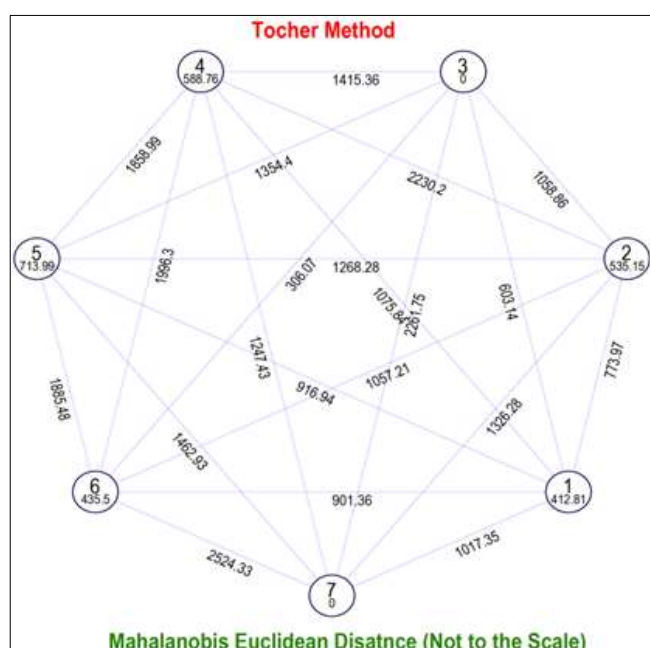


**Fig 3:** Diagrammatic presentation of intra and inter cluster distances in F3 segregating generation of VBN-1 × RC-19



**Fig 4:** Diagrammatic presentation of intra and inter cluster distances in F3 segregating generation of KBC-9 × PGCP-6

Cluster mean values for primary branches /plant recorded highest in cluster VII (5.00) and less in cluster V (3.29). The cluster mean value for number of pods /plant ranged between 8.00 and 16.29. The cluster V exhibited maximum pods /plant (16.29) and cluster VII showed minimum pods /plant (8.00). When considered pod length lowest value was found in cluster II (13.39 cm) and highest value in cluster III (16.84 cm). For the number of seeds/pod mean, highest value was found in cluster III (15.00) and lowest value in cluster II (11.52). The cluster means for 100 seed weight was recorded maximum value in cluster VI (11.50 g) and minimum in cluster VII (8.50 g). When considered total dry matter highest value was observed in cluster V (44.12 g) and lowest value recorded in cluster VII (19.05 g). Cluster mean values for seed yield /plant recorded maximum in cluster V (25.96 g) and minimum in cluster VII (11.21 g).

The mean value for days to initiation of flowering, number of pods /plant, total dry matter content /plant and seed yield /plant were highest in cluster V, cluster mean value for days to physiological maturity and number of branches /plant were highest in cluster VII, the cluster mean value for pod length and number of seeds/pod were highest in cluster III, the cluster mean value for plant height and test weight was maximum in cluster VI. The cluster III with overall score of 23 across 10 characters secured first rank followed by cluster V with overall score of 32 secured second rank. Cluster IV, VI, I, II and VII had score of 36, 36 41, 56 and 56 respectively, indicating that superior segregants are present in these clusters which could be used in future cowpea breeding programme.

**F$_{2:3}$ population of KBC 9 × PGCP 6:** Cluster mean values for days to initiation of flowering ranged from 55 days in cluster II to 74 days in cluster VI. The cluster mean value for days to physiological maturity ranged between 82 and 109 days. The segregants under cluster VII were early maturing (82 days). Whereas, the segregants under cluster IV were late maturing (109 days). For plant height, cluster mean values were maximum in cluster V (68.11 cm) and minimum in cluster VI (27.67 cm). Cluster mean values for number of primary branches /plant recorded highest in cluster III (5.00) and less primary branches segregants found in cluster II (2.00). The cluster mean value for number of pods /plant ranged between 9.00 and 17.00. The cluster III exhibited maximum number of pods /plant (17.00) and cluster VI showed minimum number of pods /plant (9.00). While, considered pod length mean of lowest value was found in cluster II (11.34 cm) and highest value was recorded in cluster VI (14.47 cm). For the number of seeds/pod mean, highest

value was found in cluster VI (12.44 g) and lowest value was recorded in cluster VI (8.00 g). The cluster means for 100 seed weight was recorded maximum value in cluster IV (12.38 g) and minimum in cluster VII (9.47 g). Whereas, highest value for total dry matter content/plant was recorded in cluster IV (42.26 g) and lowest value was recorded in cluster VI (23.90 g). Cluster mean values for seed yield/plant recorded maximum value in cluster IV (25.57 g) and minimum in cluster VI (12.47 g).

The mean value for days to physiological maturity, pod length, number of seeds/pod, test weight, total dry matter content/plant and seed yield/plant were highest in cluster IV, cluster mean value for number of pods/plant and number of branches/plant were highest in cluster I, the cluster mean value for plant height were highest in cluster V, the cluster mean value for days to initiation of flowering was maximum in cluster VI. The cluster III and IV with overall score of 26 across 10 characters secured first rank followed by cluster VII, II, V, I and VI had score of 38, 39, 42, 45 and 56 respectively indicating that superior segregants are present in these clusters which could be used in further cowpea breeding programme.

Similar findings by Brahmaiah et al. [23] supported the present findings for 100 seed weight, number of seeds/pod, seed yield and number of primary branches/plant. Srinivas et al. [14] reported highest cluster mean for days to 50 per cent flowering.

**F$_{2:3}$ population of VBN 1 × RC 19:** The analysis for estimating the contribution of various characters towards the expression of genetic divergence indicated that the character seed yield/plant (40.16%) contributed maximum to the genetic divergence by taking first rank 1223 times out of 3093 total number of combinations, followed by dry matter/plant (26.09%), test weight (16.43%), number of seeds/pod (8.10%), pod length (6.50%), plant height (1.80%), number of primary branches/plant (0.70%), days to physiological maturity (0.12%), days to initiation of flowering (0.08%), number of

seeds/pod (8.10%), pod length (6.50%), plant height (1.80%), number of primary branches/plant (0.70%), days to physiological maturity (0.12%), days to initiation of flowering (0.08%), number of pods/plant (0.08%), and contributed minimum towards the genetic divergence by taking 2 times ranked first in the present material (Table 7 and Fig. 5). The information on contribution of characters towards genetic divergence and cluster mean values would help in selection of better segregants for future cowpea breeding programmes.

**Table 5:** Cluster means for ten quantitative traits in F$_{2:3}$ population of VBN-1 × RC-19

|  | X$_1$ | X$_2$ | X$_3$ | X$_4$ | X$_5$ | X$_6$ | X$_7$ | X$_8$ | X$_9$ | X$_{10}$ | Score | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Cluster I | 61.46 (4) | 97.33 (4) | 51.85 (4) | 3.45 (6) | 13.70 (3) | 13.88 (5) | 12.35 (5) | 9.59 (3) | 33.23 (3) | 19.19 (4) | 41 | 4 |
| Cluster II | 68.10 (5) | 104.66 (5) | 65.28 (6) | 3.58 (5) | 12.31 (5) | 13.39 (7) | 11.52 (7) | 9.40 (4) | 27.27 (6) | 16.19(6) | 56 | 5 |
| Cluster III | 51.00 (1) | 88.00 (1) | 63.00 (5) | 4.00 (3) | 16.00 (2) | 16.84 (1) | 15.00 (1) | 9.00 (5) | 39.09 (2) | 24.00 (2) | 23 | 1 |
| Cluster IV | 53.10 (3) | 88.10 (2) | 30.82 (1) | 4.10 (2) | 12.10 (6) | 15.00 (3) | 13.40 (3) | 8.64(6) | 32.23 (5) | 17.51 (5) | 36 | 3 |
| Cluster V | 70.75 (7) | 108.03 (6) | 48.81 (3) | 3.29 (7) | 16.29 (1) | 15.54 (2) | 13.83 (2) | 10.38 (2) | 44.12 (1) | 25.96 (1) | 32 | 2 |
| Cluster VI | 51.50 (2) | 88.17 (3) | 69.85 (7) | 3.83 (4) | 12.67 (4) | 14.23(4) | 12.67 (4) | 11.50 (1) | 32.75 (4) | 21.25 (3) | 36 | 3 |
| Cluster VII | 69.00 (6) | 110.00 (7) | 34.66 (2) | 5.00 (1) | 8.00 (7) | 13.50 (6) | 12.00 (6) | 8.50 (7) | 19.05 (7) | 11.21 (7) | 56 | 5 |

**Table 6:** Cluster means for ten quantitative traits in F$_{2:3}$ population of KBC-9 × PGCP-6

| | X$_1$ | X$_2$ | X$_3$ | X$_4$ | X$_5$ | X$_6$ | X$_7$ | X$_8$ | X$_9$ | X$_{10}$ | Score | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Cluster I | 67.12 (4) | 102.93 (4) | 46.96 (4) | 3.19 (5) | 9.69 (5) | 12.31 (4) | 10.18 (5) | 11.15 (4) | 25.73 (6) | 13.72 (5) | 45 | 5 |
| Cluster II | 55.00 (1) | 89.00 (2) | 39.00 (2) | 2.00 (7) | 14.00 (3) | 11.34 (7) | 9.00 (6) | 10.50 (5) | 31.47 (3) | 17.5 (3) | 39 | 3 |
| Cluster III | 68.00 (5) | 105.00 (5) | 44.67 (3) | 5.00 (1) | 17.00 (1) | 14.00 (3) | 12.00 (2) | 10.50 (5) | 41.76 (2) | 24.67 (2) | 29 | 1 |
| Cluster IV | 73.44 (6) | 109.67 (7) | 48.86 (6) | 3.33 (3) | 14.22 (2) | 14.47 (1) | 12.44 (1) | 12.38 (1) | 42.26 (1) | 25.57 (1) | 29 | 1 |
| Cluster V | 66.78 (3) | 100.82 (3) | 68.11 (7) | 3.75 (2) | 9.55 (6) | 12.22 (5) | 10.34 (4) | 11.00 (4) | 27.02 (4) | 13.83 (4) | 42 | 4 |
| Cluster VI | 74.00 (7) | 106.00 (6) | 27.67 (1) | 3.00 (6) | 9.00 (7) | 11.84 (6) | 8.00 (7) | 11.50 (2) | 23.90 (7) | 12.47 (7) | 56 | 6 |
| Cluster VII | 56.48 (2) | 82.15 (1) | 47.15 (5) | 3.22 (4) | 13.48 (4) | 14.08 (2) | 10.89 (3) | 9.47 (6) | 25.97 (5) | 13.60 (6) | 38 | 2 |

**Table 7:** Relative contribution of different characters to genetic divergence in F$_{2:3}$ population of VBN-1 × RC-19

| Source | Contribution % | Times ranked 1st | Cumulative frequency |
|---|---|---|---|
| Seed yield per plant (g) | 40.16 | 1223 | 40.16 |
| Total dry matter content per plant (g) | 26.09 | 636 | 66.09 |
| Test weight (g) | 16.43 | 654 | 82.68 |
| Pod length (cm) | 6.50 | 167 | 89.18 |
| Number of seeds per pod | 8.10 | 345 | 97.28 |
| Plant height (cm) | 1.80 | 44 | 99.08 |
| Days to physiological maturity | 0.12 | 3 | 99.20 |
| Number of branches per plant | 0.70 | 17 | 99.90 |
| Number of pods per plant | 0.08 | 2 | 99.98 |
| Days to initiation of flowering | 0.08 | 2 | 100.06 |
| Total | 100.06 | 3093 | |

**Table 8:** Relative contribution of different characters to genetic divergence in F$_{2:3}$ population of KBC-9 × PGCP-6

| Source | Contribution % | Times ranked 1st | Cumulative frequency |
|---|---|---|---|
| Seed yield per plant (g) | 41.80 | 1223 | 41.80 |
| Test weight (g) | 22.35 | 654 | 64.15 |
| Total dry matter content per plant (g) | 21.74 | 636 | 85.89 |
| Number of seeds per pod | 6.75 | 345 | 92.64 |
| Pod length (cm) | 5.00 | 167 | 97.64 |
| Plant height (cm) | 1.50 | 44 | 99.14 |
| Number of branches per plant | 0.58 | 17 | 99.72 |
| Days to physiological maturity | 0.10 | 3 | 99.82 |
| Number of pods per plant | 0.07 | 2 | 99.89 |
| Days to initiation of flowering | 0.07 | 2 | 99.96 |
| Total | 99.96 | 3093 | |
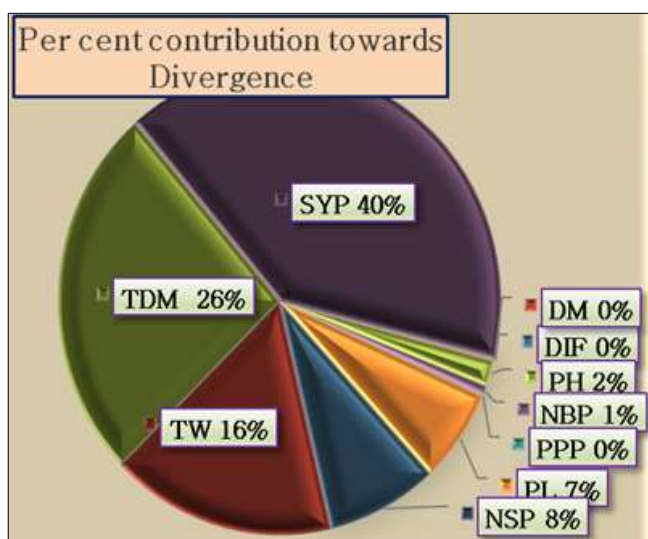


**Fig 5:** Relative contribution of quantitative traits towards genetic divergence in F$_3$ segregating generation of VBN-1 × RC-1
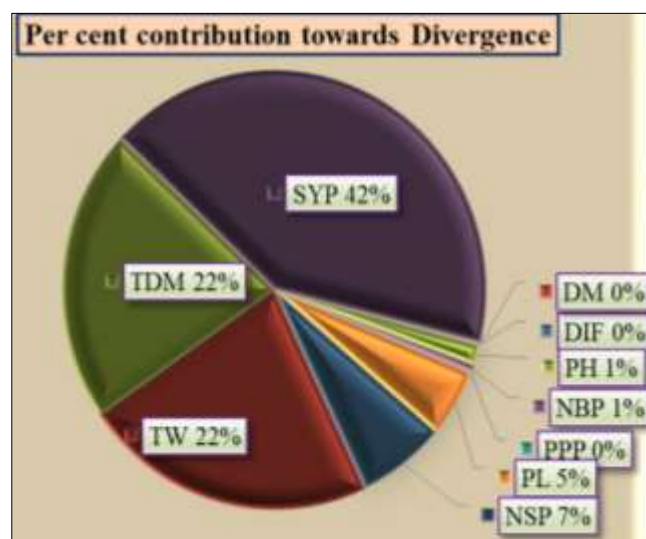


**Fig 6:** Relative contribution of quantitative traits towards genetic divergence in F$_3$ segregating generation of KBC-9 × PGCP-6

**F$_{2:3}$ population of KBC 9 × PGCP 6:** The analysis for estimating the contribution of various characters towards the expression of genetic divergence indicated that the characters *viz.*, seed yield/plant (41.80%) contributed maximum to the genetic divergence by taking first rank 1223 times out of 3093 total number of combinations, followed by test weight (22.35%), dry matter/plant (21.74%), number of seeds/pod (6.75%), pod length (5.00%) plant height (1.50%), number of primary branches/plant (0.58%), days to physiological maturity (0.10%), number of pods/plant (0.07%), days to initiation of flowering (0.07%) and contributed minimum towards the genetic divergence by taking 2 times ranked first in the present material (Table 8 and Fig. 6). The information on contribution of characters towards genetic divergence and cluster mean values would help in selection of better segregants.

Contribution of various characters towards divergence was earlier reported by Nagalakshmi *et al*. [25] for grain yield/plant contributed maximum followed by 100 seed weight; Vishwanatha and Yogeesh [16]. for seed yield and test weight; Srinivas *et al*. [14] for number of seeds/pod contributed maximum followed by pod length, plant height, 100 seed weight and number of primary branches/plant; Purohit *et al*. [22] for maximum contribution of 100 grain weight followed by number of seeds/pod while least contribution shown by pod length towards total divergence in cowpea.

## Conclusion
Genetic diversity study using Mahalanobies D$^2$ statistics grouped 100 F$_3$ progeny family of VBN-1 × RC-19 into 7 clusters, in which cluster I was largest comprising 65 segregants and cluster III secured first rank followed by cluster V. Similarly, 70 F$_3$ family progeny rows of KBC-9 × PGCP-6 grouped into 7 clusters, in which cluster I was largest comprising 55 segregants in it and cluster III and IV secured first rank followed by cluster VII. Seed-yield/plant contributed maximum towards the divergence in both the segregating population, followed by dry matter content/plant and test weight. Based on the information available and results obtained in present investigation following future line of work can be suggested that "the evaluated experimental materials possess potential variation for different traits and hence could be extensively evaluated for the exploitation in breeding programme".

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