

STUDIES ON GENETIC DIVERGENCE IN COWPEA (*VIGNA UNGUICULATA*) BY USING D² STATISTICS UNDER SEMI-ARID CONDITIONS

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SUMMARY

The field experiment was carried out by using the 30 genotypes of cowpea during *Kharif* season, 2017 at Directorate of Farms, CCS Haryana Agricultural University, Hisar, Haryana, India. Based on D² analysis, these genotypes were grouped into six clusters. Cluster pattern revealed that cluster I and II were the largest groups, each has the eight genotypes, followed by cluster III (6 genotypes), cluster V (4 genotypes), cluster IV (3 genotypes) and cluster VI (1 genotype). The maximum intra-cluster D² value was shown by cluster V (19.85) followed by cluster III (19.35), cluster IV (18.49) and cluster I (15.63). The intra-cluster D² values ranged from 15.63 (cluster I) to 19.85 (cluster V). Highest inter-cluster D² values among genotypes existed between clusters III and VI (52.08), followed by clusters III and V (45.99), clusters IV and V (43.62) and clusters II and III (41.21). There were high variations among six clusters for all characters, cluster V revealed the highest mean value for almost desirable seed yield characters *i.e.* seed yield per plant, number of clusters per plant, number of pods per plant, harvest index, seed protein content and early in maturity). Cluster III had exhibited superior characters of biological yield and plant height. On the contrary, cluster VI had smallest mean values for almost important characters. It can be concluded that, the crossing between the genotypes of most divergent clusters *i.e.* cluster III (KBC-8, GC 901, VCP 09-019, KBC-6, PTB-1, UCP 12-007) and cluster VI (TC 150) could able to produce highest seed yielding transgressive segregants.

Keywords : Genetic divergence, cowpea, *Vigna unguiculata*, D² statistics, transgressive segregants

Cowpea [*Vigna unguiculata* L.Walp] (2n=22) is an important annual legume crop which is tolerant to drought as well as rain water stagnation conditions. Like other legumes, it also has unique ability to fix atmospheric nitrogen into nitrate, thus allows it to grow on and improve fertility status of soils (Kumar *et al.*, 2015).

Cowpea provides nutritious grain and an inexpensive source of protein for both rural poor and urban consumers that it is also called as vegetable meat (Ram, 2014). Cowpea grain contains about 23-28% protein and 64% carbohydrate and therefore, has an enormous potential to contribute to the alleviation of malnutrition among resource-poor farmers (Lal and Vashisht, 2008). Besides being used as pulse in form of dry seed, cowpea's immature pod and green leaf and growing twig can be utilized as vegetable. However, it is more important as the source of green as well as dry fodder. Among fodder legumes, cowpea is grown for both grain and fodder in all tropical and sub-tropical regions.

The evaluation of cowpea germplasm, quantification of the magnitude of variability existing for different characters and classification into different groups help in identifying potential distinct genotypes

which are having contrasting characters, can be used to operate effective selection of genetically diverse genotypes for the improvement of yield. Keeping these aspects in view, the proposed study was undertaken with the objectives to assess the extent of genetic diversity in cowpea.

MATERIALS AND METHODS

The experimental material was comprised of 30 genotypes of cowpea (Table 1), collected from various parts of India. These genotypes were selected from available germplasm maintained in Forage section, Department of Genetics & Plant breeding, CCS, Haryana Agricultural University, Hisar. The field experiment was carried out during *Kharif* season 2017 at Directorate of Farms, CCS Haryana Agricultural University, Hisar, Haryana, India. Geographically, Hisar is situated in the semi-arid sub-tropics at 29°10' latitude and 75°46' E longitude with an altitude of 215.2 meters above the mean sea level.

The experiment was carried out in RBD with three replications. Each genotype was sown in paired

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TABLE 1
List of genotypes evaluated during experiment

S. No.	Genotype	Sources	S. No.	Genotype	Sources
1.	PL-3	Pant Nagar	16.	KBC-8	UAS, Bangalore
2.	GC 1203	Gujarat	17.	Goa Cowpea-3	Goa
3.	PGCP 28	Pant Nagar	18.	Pant Lobia-3	Pant Nagar
4.	TC 161	-	19.	DCS 47-1	Dharwad
5.	RC 101	Rajasthan	20.	KBC-6	UAS, Bangalore
6.	CPD 240	NAU, Navsari	21.	GC 1207	Gujarat
7.	KBC 10	UAS, Bangalore	22.	TPTC-29	Andha Pradesh
8.	CPD 29	NAU, Navsari	23.	PCP-07-272	-
9.	UCP 12-007	Uttar Pradesh	24.	TC 150	-
10.	GC 1304	Gujarat	25.	KBC 9	UAS, Bangalore
11.	VCP 09-019	-	26.	PGCP-54	Pant Nagar
12.	DC 7-15	Dharwad	27.	GC 901	Gujarat
13.	Chirodi	-	28.	PGCP-23	Pant Nagar
14.	CS 88	HAU, Hisar	29.	GC1110	Gujarat
15.	PTB-1	Pattampi	30.	GC-3	Gujarat

row of 4 m length with a row-to-row distance 0.45 m and plant to plant spacing of 15 cm. The recommended cultural and agronomic practices were followed to raise crop. During experimentation weather parameters were also recorded. The mean minimum and maximum temperature exhibited a wide range (17.3 to 40.8°C) and relative humidity (28.0-90.0%). The high rain fall also was found this season, maximum up to 283.8 mm per month in June.

For recording of observations five competitive plants of each genotype were randomly selected in each replication. Observations were recorded on the characters, namely, plant height (cm), days to 50% flowering, days to maturity, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), pod breadth (mm), pod weight (g), pod yield per plant (g), number of seeds per pod, 100 seeds weight (g), seed yield per plant (g), biological yield per plant (g), harvest index and seed protein content (%). The D^2 analysis was done by using the method as suggested by Mahalanobis (1936) and elaborated by Rao (1952); Murty and Arunachalam (1966). The character contribution towards genetic divergence was computed using the method given by Singh and Chaudhary (1977), Nadarajan and Gunasekaran (2012).

RESULTS AND DISCUSSION

Grouping of genotypes

The 30 cowpea genotypes were grouped into six clusters (Table 2) using Tocher's method (Rao 1952) employed on the Mahalanobis's (D^2) values. The grouping of genotypes into different clusters revealed that cluster I and II was the largest groups (8 genotypes) followed by cluster III (6 genotypes), cluster V (4 genotypes), cluster IV (3 genotypes) and cluster VI (1 genotype). The genotypes included in cluster I were Goa Cowpea-3, TPTC-29, PCP-07-272, Pant Lobia-3, GC1110, GC-3, Chirodi and GC 1304, whereas in cluster II were KBC 10, CPD 29, PGCP 28, PL-3,

GC 1207, DCS 47-1, PGCP-54 and PGCP-23. The cluster III had six genotypes (KBC-8, GC 901, VCP 09-019, KBC-6, PTB-1, UCP 12-007). Cluster V was comprised of 4 genotypes (GC 1203, TC 161, RC 101, CPD 240). While, cluster IV consisted of three genotypes viz., DC 7-15, CS 88, KBC 9 and remaining one genotype (TC 150) was placed in VI cluster.

The cluster analysis using Tocher's method grouped 30 cowpea genotypes into six non-overlapping clusters for the discrimination of germplasm lines into discrete clusters indicated presence of substantial amount of diversity in the material evaluated. Previous workers have also reported existence of high degree of genetic diversity in cowpea materials (Jain *et al.*, 2006; Costa *et al.*, 2013; Nancee *et al.*, 2013; Nath and Tajane, 2014; Sandeep *et al.*, 2014; Vavilapalli *et al.*, 2014; Animasaun *et al.*, 2015; Khan and Viswanatha, 2016; Srinivas *et al.*, 2016; Asoontha and Meena, 2017; Lal *et al.*, 2017; Lovely *et al.*, 2017). Presence of substantial genetic divergence among the genotypes screened in present investigation suggested that this material might serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable combination for seed yield as well as other characters.

Intra- and inter-cluster D^2 value

The intra- and inter-cluster D^2 values among six clusters are presented in Table 3 and Fig.1 The inter-cluster D^2 values were greater than the intra-cluster D^2 values, further indicating the considerable amount of diversity among the genotypes studied. The intra-cluster D^2 values ranged from 15.63 (cluster I) to 19.85 (cluster V). Moreover, the cluster VI was monogenic, as a result, its value was zero. The maximum inter-cluster D^2 values among genotypes existed between clusters III and VI (52.08), followed by clusters III and V (45.99), clusters IV and V (43.62)

TABLE 2
Grouping of genotypes into different clusters

Clusters	No. of genotypes	Name of genotypes
I	8	Goa Cowpea-3, TPTC-29, PCP-07-272, Pant Lobia-3, GC1110, GC-3, Chirodi, GC 1304
II	8	KBC 10, CPD 29, PGCP 28, PL-3, GC 1207, DCS 47-1, PGCP-54, PGCP-23
III	6	KBC-8, GC 901, VCP 09-019, KBC-6, PTB-1, UCP 12-007
IV	3	DC 7-15, CS 88, KBC 9
V	4	GC 1203, TC 161, RC 101, CPD 240
VI	1	TC 150

TABLE 3
Intra and inter cluster D₂ values

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	15.63	29.05	37.97	33.33	29.14	35.91
Cluster II		17.56	41.21	33.67	28.18	24.59
Cluster III			19.35	27.90	45.99	52.08
Cluster IV				18.49	43.62	41.73
Cluster V					19.85	32.96
Cluster VI						0.00

and clusters II and III (41.21). Therefore, the crossing between the genotypes of most divergence clusters *i.e.* III (KBC-8, GC 901, VCP 09-019, KBC-6, PTB-1, UCP 12-007) and VI (TC 150) could able to produce high seed yielding transgressive segregants. Similar findings were also reported by Jain *et al.* (2006); Bhandari and Verma (2007) and Patel (2017).

Cluster mean and contribution of individual characters towards genetic divergence

The cluster means for the 17 quantitative characters studied in 30 cowpea genotypes revealed that considerable difference among all the clusters exists (Table 4). From the data, it was evident that cluster I had the highest mean value for number of clusters per plant (2.71) and lowest in pod breadth (6.72 mm). Cluster II was highest in pod breadth (7.98 mm), pod weight (1.63g) and harvest index (0.24). Cluster III had the highest mean values for plant height (481.54 cm), pod length (15.16 cm), number of seeds per pod (11.34) and biological yield per plant (375.57g), but lowest in harvest index (0.07). Cluster IV had showed the highest mean values for days to 50% flowering (92.78), days to maturity (118.67) and seed protein content (24.45%) but lowest in 100 seed weight (7.91g) and harvest index (0.07). Cluster V had exhibited the highest mean values for number of branches per plant (6.70), number of clusters per plant (34.33), number of pods per plant (56.55), pod yield per plant (68.11g), seed yield per plant (37.74g) and harvest index (0.24) but lowest in days to 50% flowering (51.33), days to maturity (79.00) and pod

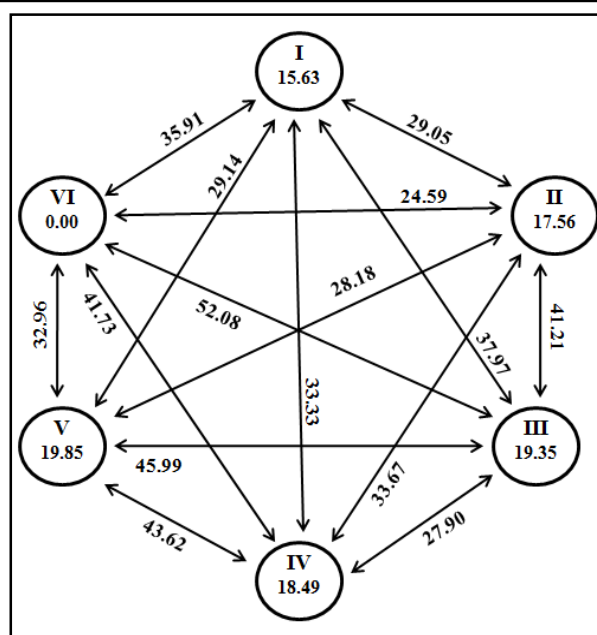


Fig. 1. Diagram showing the intra- and inter-cluster D² values.

length (11.13 cm). Cluster VI was having the highest mean values for 100-seed weight (11.97g). However, it has low mean value for other characters.

The results had showed that, there were high variations of mean values among six clusters for all characters. Therefore, depend on the purpose of breeding for particular *e.g.* seed yield per plant, fodder, seed size, nutrition value, earliness, resistance etc. The genotypes with high mean values according to that purpose to be selected.

The above comparison indicated that cluster V had the highest mean value for desirable yield

characters (number of branches per plant, number of clusters per plant, number of pods per plant, pod yield per plant, seed yield per plant, harvest index, seed protein content and early in days to 50% flowering, days to maturity). Cluster III had exhibited superior characters of biological yield, plant height. However, cluster VI had smallest mean values for almost important characters.

Contribution of individual characters (Table 4) towards total genetic divergence had been presented in which the maximum per cent contribution observed for plant height (34.71%) followed by biological yield per plant (26.44%), number of cluster per plant (17.24%) and days to 50% flowering (9.89%). Characters as number of pods per cluster, number of pod per plant, pod yield per plant and harvest index have given negligible contribution to genetic divergence. The above finding are broadly in agreement with previous workers (Bhandari and Verma, 2007; Costa *et al.*, 2013; Nancee *et al.*, 2013; Ahamed *et al.*, 2014; Nath and Tajane, 2014; Sandeep *et al.*, 2014; Vavilapalli *et al.*, 2014; Animasaun *et al.*, 2015; Khan and Viswanatha, 2016; Srinivas *et al.*, 2016; Asoontha and Meena, 2017; Lal *et al.*, 2017; Lovely *et al.*, 2017 and Patel *et al.*, 2017).

The genotypes of different clusters having high seed yield and high in contributing characters are presented in Table 5. The present research exhibited a high level of genetic diversity among 30 cowpea genotypes, which they were grouped into six distinct clusters based on D² statistic. The estimates of intra- and inter-cluster D² values for six clusters revealed that the genotypes of the same cluster have little genetic divergence from each other with respect

to aggregate effects of 17 characters under study while much more genetic diversity was observed between the genotypes of different clusters. Since high or optimum genetic divergence is required between the parents of hybridization plan for obtaining high frequency of desirable recombinants, the chances of obtaining good segregants in the segregating generations. It would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster D² values. This clearly showed presence of wide variation from one cluster to another in respect of cluster mean for six clusters, which indicate that genotypes having distinctly different mean performance for various characters were separated into different clusters.

Saini *et al.* (2004) proposed that the crossing between the genotypes which showing high mean values coupled with relatively large inter-cluster D² values results in high heterotic expression. In present study, genotypes from cluster III and from cluster V indicated highest mean values for seed yield per plant and some desirable characters *viz.*, number of clusters per plant, number of pods per plant, seed yield per plant, pod length, number of seeds per pod, pod yield per plant and early in maturing, and relatively high inter-cluster D² value, therefore, this two genotypes can be selected for hybridization to develop high seed yielding variety in cowpea.

The results of study could be also helpful in improving the knowledge of the divergences among the evaluated cowpea genotypes and would be basic to select appropriate methods in cowpea improvement programmes and other utilizations.

TABLE 4
Mean value of different clusters for different characters along with per cent contribution

Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Per cent contribution
Plant height (cm)	379.09	195.04	481.54	406.76	129.08	61.47	34.71
Days to 50% flowering	65.67	55.54	72.22	92.78	51.33	58.00	9.89
Days to maturity	89.58	82.38	99.06	118.67	79.00	86.00	0.23
Number of branches per plant	5.64	5.64	6.13	5.80	6.70	4.13	1.15
Number of clusters per plant	28.31	17.30	17.91	12.24	34.33	10.00	17.24
Number of pods per cluster	2.71	2.23	2.35	2.52	2.70	2.10	-
Number of pods per plant	45.00	28.86	35.87	29.04	56.55	18.00	-
Pod length (cm)	11.57	14.45	15.16	13.47	11.13	12.27	0.23
Pod breadth (cm)	6.72	7.98	7.27	6.84	7.03	7.77	0.23
Pod weight (g)	1.01	1.63	1.59	1.36	1.28	0.89	1.84
Pod yield per plant (g)	40.32	42.64	45.74	36.09	68.11	12.78	-
Number of seeds per pod	9.03	10.89	11.34	10.61	8.16	7.00	2.30
100 seeds weight (g)	8.32	11.50	9.59	7.91	10.72	11.97	0.69
Seed yield per plant (g)	24.24	27.22	26.85	21.48	37.74	8.67	2.99
Biological yield per plant (g)	134.14	108.26	375.57	290.35	159.22	55.56	26.44
Harvest index	0.18	0.24	0.07	0.07	0.24	0.16	-
Seed protein content (%)	24.19	23.99	24.43	24.45	23.52	23.19	2.07

TABLE 5
Diverse and superior genotypes selected from different clusters

Cluster	Genotypes	Superior characters
I	PCP-07-272	Seed yield, number of pods per cluster, number of pod per plant, seed protein content
II	PL-3	Seed yield, pod breadth, pod weight, and harvest index
III	GC 901	Seed yield per plant, plant height, pod length, number of seeds per pod and biological yield per plant
IV	KBC 9	Seed yield per plant, plant height, medium in maturity
V	CPD 240	Seed yield per plant, pod yield per plant, number of clusters per plant, number of pod per plant
VI	TC 150	Dwarf plant height and high in 100 seeds weight

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