

**STUDIES ON GENETIC DIVERSITY IN INDIAN COWPEA (*VIGNA UNGUICULATA* (L.) WALP) GERMPLASM**V.Sandeep^{1*}, V. Hemalatha², D. Shashi Bushan³ and V. Swarnalatha³

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ABSTARCT: Genetic divergence using D^2 analysis was carried out in 50 diverse genotypes of cowpea. All the 50 genotypes were grouped into twelve clusters. Cluster I was largest comprising of twenty seven genotypes followed by Cluster II with twelve genotypes, cluster IV with three genotypes, and cluster III, V, VI, VII and VIII, IX, X, XI, XII were represented each by single genotype. Intra-cluster D^2 values ranged from 0 to 38.06. The inter-cluster D^2 values ranged from 44.08 to 276.55. The maximum inter cluster distance was observed between VII and XII clusters followed by clusters IV and XII and cluster X and VII. The maximum contribution towards genetic divergence is by days to 50% flowering (25.22%) followed by plant height (12.24%) and biological yield per plant.

Key words: Genetic diversity, cowpea and D^2 analysis.

Abbreviations: g- grams, %- per cent and cm- centimetres.

INTRODUCTION

Cowpea is an important multipurpose grain legume extensively cultivated in arid and semi arid regions of Africa, South Asia and Latin America. However, the productivity is low. To develop elite genotypes, knowledge on genetic diversity is essential. Assessment of genetic diversity in cowpea genotypes would facilitate development of elite cultivars. Better knowledge of the genetic differences of breeding materials could help to maintain genetic diversity and helps in development of breeding strategy. The utility of D^2 analysis have not been sufficiently tested so far in the genetic improvement of cowpea. Therefore an attempt was made to identify diverse genotypes and their utilisation in breeding programme.

MATERIAL AND METHODS

The experimental material used for the present investigation comprised of 50 genotypes of cowpea collected from different states of India. Each genotype was sown in 2 rows of 5 meter length with a spacing of 45 cm between rows and 15 cm between plants in Randomized Block Design (RBD) with two replications at Regional Agricultural Research Station, Palem, Mahaboobnagar, during *kharif*-2013. The observations were recorded on five randomly selected plants from each treatment in each replication for twelve morphological characters *viz.*, Plant height, number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, 100-seed weight, biological yield, harvest index and seed yield per plant except days to 50% flowering. Data on days to 50% flowering as noted on plot basis. Diversity analysis was carried out using Mahalanobis (1936) D^2 statistics [2]. Grouping of populations into different clusters was done using Tocher's method as described by Rao (1952) [3].

RESULTS AND DISCUSSION

Analysis of variance revealed that the genotypes under study differed significantly for all the twelve characters. Based on the divergence studies fifty genotypes were grouped into twelve clusters have been given in Table 1. Out of twelve clusters, cluster I was largest comprising of twenty seven genotypes followed by Cluster II with twelve genotypes, cluster IV with three genotypes, and cluster III, V, VI, VII, VIII, IX, X, XI, XII were represented by single genotype each. Intra and inter cluster distances were presented in the Table 2. Intra-cluster D^2 values ranged from 0 to 38.06.

Maximum intra cluster distance was observed in cluster IV (38.06), followed by cluster II (37.08) and cluster I (32.49). Lowest intra cluster was observed in clusters III, V, VI, VII, VIII, IX, X, XI and XII (0). The inter-cluster D^2 values ranged from 44.08 to 276.55. The maximum inter cluster distance (276.55) was observed between VII and XII clusters followed by clusters IV and XII (248.37) and cluster X and VII (201.64), while the minimum inter cluster distance of 44.08 was recorded between cluster IV and III.

Table-1. Distribution of cowpea genotypes into different clusters

S. No	Clusters	Number of genotypes	Genotypes
1	I	30	ACM-37,ACM-48,CO-2,CPD-132,ACM-10, CPD-150, GC-909, ACM-34, GC-3, NBC-1, PHULE-CP, NBC-2, ACM-31, VCP-09-19, ACM-38, ACM-35, Surabhi, GC-815, ACM-30, Ever green, ACM-36, ACM-32,GC-901, CPD-115, GC-911, ACM-39, ACM-43, ACM-44, KBC-4, Lalima
2	II	8	Bhagyalaxmi, KBC-5, DC-47-1, PGP-306, IT-38915, RC-101, COCP-7, KBC-2
3	III	1	PGCP-15
4	IV	3	GC-3 (1), Kanakamuni, IT-38956
5	V	1	PGCP-16
6	VI	1	DC-150
7	VII	1	Lola
8	VIII	1	Aneshwara
9	IX	1	HC-98-64
10	X	1	Shwetha
11	XI	1	VCP-09
12	XII	1	ACM-27

The clusters means for each of twelve characters are presented in Table.3. From the data it can be seen that considerable differences existed for all the characters under study. Cluster VI had high mean value for 100 seed weight (21.84), cluster VIII had high mean value for seed yield (49.64) and biological yield (206.24), cluster X had high mean value for pod length (28.70), number of seeds per pod (24.80) and low mean value for days to 50 % flowering(40.5) and the cluster XII had high mean value for number of primary branches (5.30), number of secondary branches (15.70), number of clusters per plant (14.20), number of pods per plant (27.90), harvest index (43.67).

Table-2. Mean intra (bold) and inter cluster distances among twelve clusters formed by Tocher's method in cowpea

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	5.87 (32.49)	8.65 (74.82)	7.85 (61.62)	7.75 (60.06)	7.04 (49.56)	7.79 (60.68)	9.06 (82.08)	9.18 (84.27)	8.29 (68.72)	10.65 (113.42)	9.21 (84.82)	11.91 (141.84)
II		6.09 (37.08)	11.21 (125.66)	12.46 (155.25)	8.12 (65.93)	9.94 (98.80)	13.44 (180.63)	7.87 (61.93)	7.88 (62.09)	13.56 (183.87)	12.27 (150.55)	8.12 (65.93)
III			0.00 (0.00)	6.64 (44.08)	9.16 (83.90)	9.86 (97.21)	9.31 (86.67)	9.66 (93.31)	11.04 (121.88)	8.24 (67.89)	10.89 (118.59)	12.31 (151.53)
IV				6.17 (38.06)	8.78 (77.08)	11.06 (122.32)	8.94 (79.92)	12.30 (151.29)	11.10 (123.21)	10.75 (115.56)	11.42 (130.41)	15.76 (248.37)
V					0.00 (0.00)	9.71 (94.28)	11.74 (137.82)	10.57 (111.72)	8.40 (70.56)	11.98 (143.52)	11.62 (135.02)	11.36 (129.04)
VI						0.00 (0.00)	8.79 (77.26)	8.36 (69.88)	10.90 (118.81)	11.42 (130.41)	6.73 (45.29)	12.00 (144.00)
VII							0.00 (0.00)	10.21 (104.24)	12.13 (157.00)	14.20 (201.64)	10.00 (100.00)	16.63 (276.55)
VII								0.00 (0.00)	9.86 (97.21)	13.67 (186.86)	10.79 (116.42)	9.53 (90.82)
IX									0.00 (0.00)	13.18 (173.71)	12.06 (145.44)	11.29 (127.46)
X										0.00 (0.00)	9.41 (88.54)	12.93 (167.18)
XI											0.00 (0.00)	13.76 (189.33)
XII												0.00 (0.00)

Cluster VIII had high mean value for seed yield (49.64), followed by cluster VI and cluster XI. The per cent contribution towards genetic divergence by all the twelve contributing characters is presented in Table 4. The maximum contribution towards genetic divergence is by days to 50% flowering (25.22%), plant height (12.24%) and biological yield per plant (10.78%). Followed by the other characters viz., number of primary branches per plant (9.14%), 100 seed weight (7.92%) seed yield (7.67%), pod length (6.37%), number of clusters per plant (6.20), number of secondary branches (5.31%), seeds per pod (4.49%), number of pods per plant (2.29%) and harvest index (2.37%). These results are in accordance with the reports of Rewale *et al.* (1996) [4] and Kumawat and Raje (2005) [1].

Table-3. Cluster means for twelve characters in cowpea using ward's minimum variance method

Clusters	Days to 50% flowering	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of Clusters Per plant	Number of pods per plant	Pod length (cm)	Number of seed per pod	100 seed weight (g)	Biological yield per plant (g)	Seed yield per plant (g)	Harvest index (%)
I	47.82	50.19	3.16	10.54	9.45	17.94	16.58	15.60	13.31	36.12	144.68	25.42
II	50.06	54.79	4.76	13.46	12.24	23.78	14.26	15.11	12.87	40.62	157.03	26.66
III	42.50	31.82	3.00	12.10	9.30	16.00	15.19	16.70	15.39	44.51	114.40	39.17
IV	42.83	40.77	2.50	8.53	8.50	13.40	15.39	12.53	12.75	33.98	135.84	25.40
V	48.00	56.66	2.80	11.10	13.50	16.60	15.10	11.20	17.99	34.40	142.00	24.30
VI	51.50	54.00	2.90	11.40	8.10	17.90	18.65	21.50	21.84	49.11	149.69	33.13
VII	50.50	29.51	2.90	7.90	7.40	14.80	14.58	15.10	16.48	35.84	182.34	19.77
VIII	50.50	34.86	5.20	13.10	12.10	26.40	12.60	18.10	15.57	49.64	206.24	24.17
IX	47.50	57.18	4.80	13.00	8.70	19.70	15.12	12.20	10.80	33.35	201.33	16.57
X	40.50	52.12	3.00	10.00	10.10	18.40	28.70	24.80	13.54	44.19	111.15	40.25
XI	50.50	57.78	3.00	9.60	10.10	17.70	30.92	22.50	13.82	46.67	181.40	25.75
XII	50.00	49.96	5.30	15.70	14.20	27.90	20.21	19.40	15.37	45.44	104.03	43.67

Table-4. Relative contribution (%) of each character to the genetic diversity in cowpea

S.No	Character	Times Ranked 1st	Contribution (%)
1	Days to 50% flowering	309	25.22
2	Plant height (cm)	150	12.24
3	No. of primary branches	112	9.14
4	No. of secondary branches	65	5.31
5	No. of clusters per plant	76	6.20
6	No. of pods per plant	28	2.29
7	Pod length (cm)	78	6.37
8	No. of Seed per pod	55	4.49
9	100 seed weight(g)	97	7.92
10	Seed yield per plant(g)	94	7.67
11	Biological yield per plant(g)	132	10.78
12	Harvest index %	29	2.37

Hybridization between genotypes falling in the most distant clusters will result in maximum hybrid vigour and eventually desirable segregants or combinations leading to the development of useful varieties. Sharma and Mishra (1997) [5] reported diversity in cowpea and suggested selection of parents for hybridization and improvement of character.

CONCLUSION

Hence it can be concluded that the diverse parent belonging to different cluster should be involved in the hybridization programme based on their merits of characters. Beside this more number of germ plasm should be incorporated in hybridization programme.

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