

Genetic diversity studies for various quantitative traits in cowpea (*Vigna unguiculata* L.)

■ B.B. GORDE, D.V. KUSALKAR AND N.S. KUTE

SUMMARY

Fifty indigenous genotypes of cowpea were evaluated to assess genetic diversity for seed yield. The D^2 value ranged between 3.27 to 282.23 indicating that presence of substantial amount of genetic diversity. All 50 genotypes were grouped in to XIV clusters in which cluster I had maximum genotypes followed by cluster II and cluster III to XIV were monogenotypic in nature. The maximum inter cluster distance was observed between cluster-IV and cluster-XIV ($D = 16.80$) and maximum intra cluster distance was observed for cluster-II ($D=7.34$). The variance of cluster means revealed that plant height, 100 seed weight, protein per cent, days to 50 per cent flowering were the main characteristics contributing to the divergence. On the basis of inter-cluster distances, cluster means and *per se* performance the genotypes V-262, CAZC-04-1, JLCP-32, JLCP-37 were found to be superior which can be used in hybridization programme.

Key Words : Genetic diversity, Quantitative traits, Cowpea

How to cite this article : Gorde, B.B., Kusalkar, D.V. and Kute, N.S. (2013). Genetic diversity studies for various quantitative traits in cowpea (*Vigna unguiculata* L.). *Internat. J. Plant Sci.*, 8 (2) : 284-287.

Article chronicle : Received : 08.11.2012; **Revised :** 28.02.2013; **Accepted :** 26.04.2013

Cowpea (*Vigna unguiculata* L.) is multipurpose legume crop grown mainly for seed as a pulse, green pod as a vegetable and whole plant as a fodder in tropics and subtropics. It is rich in protein, calcium and phosphorus. It enriches soil fertility through biological nitrogen fixation and control soil erosion as cover crop. In view of low input requirement and short maturity, its cultivation is quite economic. As compared with other crops particularly the cereals, cowpea offers better chances of crop production under adverse conditions of moisture stress and low fertility. Genetic divergence, which is due to genetic factors is the basis for heritable improvement hence, the present investigation an attempt was made to study genetic diversity to identify suitable genotypes

for hybridization by using D^2 statistics.

MATERIAL AND METHODS

The experimental material consisted of fifty indigenous genotypes of cowpea obtained from Pulses Improvement Project, MPKV., Rahuri. The experiment was conducted in Randomized Block Design (RBD) with two replications during Kharif 2011.

The seeds were sown by dibbling with spacing of 45 x 15cm. Each entry was represented by single row of three meter length. Observations were recorded on five randomly selected plants for ten characters *viz.*, days to 50 per cent flowering, number of branches plant⁻¹, pod length, protein percent, plant height, days to maturity, number of pods plant⁻¹, number of seeds pod⁻¹, 100 seed weight and seed yield plant⁻¹. The analysis of divergence was carried out by D^2 statistics of Mahalanobis (1936) as described by Rao (1952). Analysis of variance for individual characters was worked out as per Panse and Sukhatme (1985).

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant

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differences among the genotypes for all the studied characters. All 50 genotypes evaluated for ten characters were grouped into 14 clusters (Table 1). The cluster-I was largest with 22 genotypes followed by cluster II with 16 genotypes. The remaining all other clusters viz., III, IV, V, VI, VII, VIII, IX, X, XI, XII, XIII and XIV were monogenotypic. This indicated that presence of diversity in the fifty genotypes studied. From the clustering pattern, it is observed that varieties from different sources were grouped into one cluster and similarly varieties having same source grouped into different clusters

which indicated that there is no relationship between geographical diversity and genetic divergence. Borah and Khan (2001) studied 60 cowpea cultivars which grouped into 10 clusters, Saini *et al.* (2004) studied 155 cowpea genotypes which grouped into 10 clusters, Bhandari and Verma (2007) studied 22 cowpea genotypes which grouped into seven clusters, Dalsaniya *et al.* (2009) studied 60 genotypes of cowpea which grouped in to 12 clusters.

The D^2 values of genotypes studied for seed yield was ranged from 3.27 to 282.23. Maximum intra cluster distance

Table 1: Distribution of 50 cowpea genotypes into different clusters

Cluster No.	No. of genotypes included	Name of genotypes
I	22	PCP-97296, GC-3-1, PCP-0404-6-01, PCP-97180, JLCP-26, PCP-9726-01, CPP-84, GC-3, VCM-8, HC-1-17, 4-2, Pusa komal, PCP-9741, VCM-8-1, Phule Pandhari, 4-55, KBC-WS-1, Gudagi cowpea, CPP-78, JLCP-15, T-944, DCP-5
II	16	DLCP-2, RC-101-1, PCP-97227, PCP-97137, HC-03-02, COCP-711, JLCP-37, JLCP-32, G-1, 4-40-1, GC-0102, PCP-97262, CAZC-04-1, PCP-97266, K13C-WS-1, DLCP-6
III	1	PCP-97215
IV	1	Nath-2
V	1	GC-0502
VI	1	Pusa Palghar
VII	1	VCM-8
VIII	1	DCP-12
IX	1	PCP-13
X	1	V-262
XI	1	PCP-9726
XII	1	EC-343057
XIII	1	RC-101
XIV	1	PCP-97261

Table 2: Average intra and inter cluster $D = \bar{D}^2$ values of 50 genotypes of cowpea

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	5.64	8.92	6.84	10.24	7.04	7.75	7.48	7.44	9.68	10.25	10.21	7.90	8.18	12.06
II		7.34	7.75	8.15	7.73	10.64	8.20	8.25	9.10	8.11	7.25	8.05	11.25	12.59
III			0.00	8.08	4.75	10.79	5.45	5.23	9.32	5.18	9.10	7.11	11.88	14.26
IV				0.00	9.19	13.38	6.90	9.80	10.04	6.99	4.58	10.11	13.81	16.80
V					0.00	9.97	4.28	6.07	9.85	6.58	10.22	5.79	11.63	14.07
VI						0.00	10.64	11.54	12.68	13.69	12.72	9.75	5.57	8.17
VII							0.00	7.52	9.85	6.57	8.96	6.35	11.99	16.05
VIII								0.00	8.56	6.94	10.40	6.47	12.00	13.93
IX									0.00	10.55	7.70	9.94	11.11	15.14
X										0.00	8.68	8.82	15.42	16.43
XI											0.00	11.19	12.48	15.00
XII												0.00	10.11	13.35
XIII													0.00	9.15
XIV														0.00

Digonal figures indicate the intra cluster distances

was observed for cluster II ($D = 7.34$) followed by cluster I ($D = 5.64$) (Table 2). The cluster-V and VII recorded the lowest inter cluster distance ($D = 4.28$) indicating genotypes in these clusters were genetically close to each other, whereas cluster IV and cluster XIV exhibited maximum inter-cluster distance ($D = 16.80$) indicating that genetic makeup of genotypes falling in those clusters may be entirely different from each other. However, the clusters III to XIV were monogenotypic. The monogenotypic nature of different clusters indicated maximum divergence from other clusters. Wide range of diversity was also reported by earlier workers. Similar findings were reported by Rewale *et al.* (1996), Borah and Khan (2001), Saini *et al.* (2004), Bhandari and Verma (2007), Dalsaniya *et al.* (2009) and Naglakshmi *et al.* (2010).

The highest cluster mean for grain yield per plant (26.40g) recorded by cluster-VII appeared to be due to contribution of component character *viz.*, plant height (122.50), days to

maturity (77.50), days to 50 per cent flowering (46.50), protein per cent (24.23), number of pods per plant (22.70), pod length (15.40), number of seeds per pod (14.00), number of branches per plant (5.00) and 100 seed weight (7.80 g) Table 3.

Relative contribution of all ten characters towards divergence revealed that (Table 4) the character plant height (33.47%) recorded the maximum contribution to divergence followed by 100 seed weight (21.55%), protein per cent (18.20%), days to 50 per cent flowering (11.51%) and number of seeds per pod (6.20%) indicating that these characters were considerably responsible for total divergence. These findings are similar to Thiyagarajan *et al.* (1988) for 100 seed weight, days to 50 per cent flowering and plant height, Thiyagrajan and Natarajan (1989) for number of seeds per pod, Sharma and Mishra (1997) for plant height, days to 50 per cent flowering, Vishwanathan *et al.* (1998) for 100 seed weight. Borah and Khan (2001) for plant height, Bhandari and Verma

Table 3 : Cluster mean performance for 10 characters in cowpea

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/Plant	Pod length (cm)	No. of pods/Plant	No. of seeds/ pod	100 seed wt. (g)	Protein %	Seed yield/ plant (g)
Cluster I	45.82	78.77	77.98	4.20	13.42	19.24	13.49	8.52	14.60	24.76
Cluster II	49.69	81.19	131.44	4.63	14.68	21.34	14.68	10.46	20.38	23.75
Cluster III	51.00	86.50	107.00	3.60	14.10	24.30	15.10	8.65	23.09	26.05
Cluster IV	44.50	77.50	163.00	4.70	14.10	24.10	14.90	9.05	20.40	24.85
Cluster V	52.50	79.00	112.50	4.20	15.70	18.40	14.80	8.85	21.41	26.15
Cluster VI	41.00	77.00	62.50	4.80	15.20	20.70	13.10	11.85	17.04	24.27
Cluster VII	46.50	77.50	122.50	5.00	15.40	22.70	14.00	7.80	24.23	26.40
Cluster VIII	54.00	86.50	105.00	5.20	14.00	23.70	15.00	7.96	13.95	25.20
Cluster IX	46.50	80.00	99.00	5.20	15.50	28.40	14.90	7.04	20.64	20.21
Cluster X	54.00	86.50	148.00	5.10	15.30	28.80	16.90	9.51	29.82	26.30
Cluster XI	44.50	75.50	144.00	4.60	13.80	25.30	15.30	9.75	22.94	21.96
Cluster XII	50.00	86.50	119.00	5.20	14.85	17.90	12.10	8.27	17.22	25.62
Cluster XIII	39.00	78.00	56.30	3.90	13.40	14.50	11.00	9.35	18.02	22.11
Cluster XIV	49.00	84.00	68.20	4.00	13.00	13.25	13.80	9.00	11.50	22.16

Table 4 : Contribution of various characters to divergence

Sr. No.	Characters	Per cent contribution
1.	Days to 50% flowering	11.51%
2.	Days to maturity	1.88%
3.	Plant height (cm)	33.47%
4.	No. of branches/plant	1.22%
5.	Pod length (cm)	2.45%
6.	No. of pods/plant	1.22%
7.	No. of seeds/pod	6.20%
8.	100 seed weight (g)	21.55%
9.	Seed yield/plant (g)	2.29%
10.	Protein%	18.20%

(2007) for protein content, Dalsania *et al.* (2009) for plant height and protein content, Nagalakshami *et al.* (2010) for days to 50 per cent flowering and 100 seed weight. The results obtained by earlier workers and in present study varied substantially which may be due to environment and dissimilarity of material under study.

On the basis of inter-cluster distances, cluster means and *per se* performance the genotypes *viz.*, V-262, CAZC-04-1, JLCP-32, JLCP-37 were found to be superior which should be used in hybridization programme so as to obtain desirable transgressive segregants.

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