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Research Note

Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.] for yield components parameters

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Abstract
Thirty two cowpea [*Vigna unguiculata* (L.) Walp.] genotypes were evaluated for 12 quantitative characters to estimate the genetic diversity existing among them by using Mahalanobis D^2 statistics. The genotypes were grouped into eight clusters. The cluster strength varied from single genotype (Clusters IV, V, VI, VII and VIII) to 12 genotypes (Cluster II). The maximum inter-cluster distance ($D^2 = 35.43$) was observed between cluster-VI and VIII. Clusters II, III and I had maximum 100-seed weight, number of seeds per pod and seed yield respectively. Cluster VIII had the highest mean value for the characters *viz.,* number of pod per plant, number of green pods per plant and green pod yield per hectare (kg/ha), while the cluster III had a lowest mean value for days to 50 per cent flowering. On the basis of inter cluster distances, cluster VIII was found to be more divergent. Therefore, it was concluded that the genotypes belonging to these cluster should be inter-crossed in order to generate more variability.

Key words
Cowpea, diversity, variability

Vegetables are considered potential crops for improving nutrition, food security and also to generate employments in the country. Among all the legume vegetable crops, cowpea (*Vigna unguiculata* (L.) Walp.) is grown as one of the most important vegetable crop in almost all parts of our country during rainy and summer season and has got potential to solve the protein problem.India and Ethiopia are recognized as primary and China as a secondary centre of origin (Vavilov, 1951). Cowpea adjusts well in a variety of cropping system and also grown as catch crop and green manure crop as it fix atmospheric nitrogen in the soil by symbiotic bacteria to a range of 64 to 131 kg/ha (Ayanaba and Dart, 1977). In India, cowpea is grown in almost all states. The largest cultivating states are Gujarat, West Bengal, Tamil Nadu, Andhra Pradesh, Kerala and Orissa. In Gujarat, vegetable cowpea occupies an area of 0.26 lakh hectares with an annual production of 2.83 lakh metric tons green tender pods (Annon., 2014).The present study was taken up with an objective to determine the genetic divergence among the genotypes by D^2 statistics and to provide a basis for selection of parents for crop improvement in cowpea.

The experiment was laid out in Randomized Block Design with three replications. The present study comprised of 32genotypes of cowpea at Regional Horticultural Research Station (RHRS), Navsari during *kharif* 2015. Each genotype consists of two row of spaced at 45cm between the lines. Plant to plant distance was 30cm. Data was recorded on five randomly selected competitive plants per replication for 12 parameters *viz.,* days to 50 per cent flowering, number of branches per plant, number of clusters per plant, pod length (cm), number of seeds per pod, number of pods per plant, plant height at final harvest (cm), sugar content (%), shelling (%), crop duration, green pod yield per plant (g), green pod yield per hectare (kg/ha). The sugar content was estimated according to the method described by Ranganna (1986). Multivariate analysis was done by using Mahalanobis D^2statistic (Mahalanobis, 1936) and genotypes were grouped into different clusters following Tocher's method (Rao, 1952).

The magnitude of D^2 values suggested that there was considerable variability in the material studied, which led to genetic diversity. After testing the difference in regard to individual character through "Anova" a simultaneous test of significant difference with regard to the pooled effect of nine characters was carried out using Wilk's criterion (Wilk's, 1932 and Rao, 1952).

Based on the D^2 values, 32 genotypes of cowpea were grouped into eight clusters by Tocher's method. The composition of clusters is given in Table 1. The results indicate that a maximum number of diverse genotypes (12 genotypes) appeared in cluster II followed by cluster I (11 genotypes), cluster III (4 genotypes). All other five clusters were composed by single genotype.

The clustering pattern showed that varieties from different sources were clubbed into one group and also varieties of same source forming different cluster indicated no relationship between geographical diversity and genetic divergence. There was no parallelism between genetic diversity and geographical distribution. Genetic drift and selection in different environment could cause greater diversity than geographical distance. Further, there was a free exchange of seed material among different regions consequently character constellations that might be associated with particular region in nature, lose their individuality under human interference. Backiyarani *et al.* (2000) had suggested that geographical diversity may not be necessarily being related to genetic diversity. Cluster - II contained as many as 12 genotypes. Out of 8 clusters, five had only one genotype. The maximum inter-cluster distance was observed between cluster VI and VIII (D^2=35.43) followed by cluster III and VII (D^2=34.02). Hence, crosses between the genotypes involving these clusters might give more variability in the segregating generations.

The intra and inter cluster distances (D^2) between all possible pairs of nine clusters were computed and presented in Table 2. The inter-cluster distance (D^2) ranged from 10.49 to 35.43. The maximum inter-cluster distance (D^2 = 35.43) was observed between cluster-VI and VIII followed by those between cluster III and VII (D^2 = 34.02). The minimum inter-cluster distance (D^2 = 10.49) was observed between cluster IV and VIII followed by the cluster II and IV (D^2= 13.05). Intra-cluster distance (D^2) ranged from 8.15 to 10.74. At intra-cluster level cluster-II had the highest value (D^2 = 10.74) which was followed by the cluster-III (D^2 = 9.95). The minimum intra-cluster distance (D^2= 8.15) was observed in cluster-I which included eleven genotypes.

Cluster VIII had the highest mean values for number of pods per plant, number of green pods per plant and green pod yield per hectare (kg/ha). The cluster VI had highest mean value for the characters number of branches per plant, number of cluster per plant and pod length, the cluster III had highest mean values for days to 50 per cent flowering, plant height at final harvest and sugar content, cluster V had maximum mean for number of seeds per pod and cluster IV had maximum mean value for shelling % and crop duration. Therefore, inter crossing of such genotypes involved in these cluster will be useful for variability in the respective traits.

The analysis for estimating the contribution of various characters towards the expression of genetic divergence indicated that the characters *viz.*, plant height at final harvest (51.81%), number of pods per plant (44.15%), green pod yield per plant (1.21%), number of branches per plant (0.81%), shelling % (0.81%), number of clusters per plant (0.40%), days to 50 per cent flowering (0.20%), pod length (0.20%), number of seeds per pod (0.20%) and sugar content (0.20%) contributed very much towards genetic divergence in the present material (Table 3). Those accounted nearly 100 per cent of total divergence in the material.

Cluster mean for all the twelve characters are presented in Table 4. The results clearly indicate appreciable difference among cluster means for most of the characters. As far as cluster means are concerned, cluster VIII had the highest mean value for the characters *viz.*, number of pod per plant (30.56), number of green pods per plant (130.15 g) and green pod yield per hectare (kg/ha) (9641 kg), while the cluster III had a lowest mean value for days to 50 per cent flowering. The cluster VI had highest mean value for the characters *viz.*, number of branches per plant (11.69), number of cluster per plant (5.52) and pod length (27.85 cm), while it had lowest mean value for number of pods per plant (10.23), shelling % (28.21%) and crop duration (83.67). The cluster VII had highest mean values for days to 50 per cent flowering (42.60), plant height at final harvest (271.64) and sugar content (12.38) but it had also lowest mean value for number of branches per plant. The cluster V had maximum mean for number of seeds per pod (13.42) but cluster II had lowest mean, while cluster III had lowest mean value for plant height (73.64). The cluster IV had maximum mean value for shelling % (51.65) and crop duration (91.82), while it had also minimum mean value for number of cluster per plant (4.15), pod length (14.96 cm), green pod yield per plant (79.45 g) and green pod yield per hectare (5585 kg).

The clustering pattern could be utilized in crossing the parents and deciding the cross combinations which may generate highest variability for various traits. The superior genotypes for breeding programme can also be selected on the basis of cluster means and to increase yield by inter crossing the genotypes of cluster VII had the highest mean values for the characters number of pod per plant, number of green pods per plant and green pod yield per hectare, cluster VII for days to 50 per cent flowering, plant height at final harvest and sugar content while cluster II for number of seed per pod. Whereas, for inducing earliness genotypes of cluster VII will be desirable.

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Table 1. Distribution of 32 genotypes of cowpea into eight different clusters on the basis of Mahalanobis D^2 statistics

Clusters	No. of genotypes	Genotypes
I	11	Phule CP-5040, W-3-1, W-203-1, Subra, W-502-2, W-5, GC-4, Pusa Phalguni, Arka Nidhi, GAC-19, W-3-2
II	12	DVCP-2, Swarna Harita, AVCP-1, W-502, PKB-6, Arka Samrudhi, AV-5, Kashi Gauri, Arka Garima, W-203-3, CPD-107, Arka Suman
III	4	Kashi Unnati, W-203, PKB-4, Kashi Kanchan
IV	1	CDP-11
V	1	W-601
VI	1	Kashi Shyamal
VII	1	Pusa Komal
VIII	1	GC-3

Table 2. Average intra and inter cluster (D^2) values for 32 genotypes of cowpea

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**8.15**	20.82	18.41	13.11	32.87	29.18	33.98	19.34
II		**10.74**	18.77	13.05	16.51	20.19	19.38	19.33
III			**9.95**	20.27	13.77	15.36	34.02	28.91
IV				0.00	25.25	26.90	22.19	10.49
V					0.00	15.53	19.64	30.81
VI						0.00	32.03	35.43
VII							0.00	21.33
VIII								0.00

Table 3. Contribution of twelve characters under study to total divergence

S. No.	Characters	% contribution towards divergence
1	Days to 50 per cent flowering	0.20
2	Number of branches per plant	0.81
3	Number of clusters per plant	0.40
4	Pod length (cm)	0.20
5	Number of seeds per pod	0.20
6	Number of pods per plant	44.15
7	Plant height at final harvest (cm)	51.81
8	Sugar content (%)	0.20
9	Shelling (%)	0.81
10	Crop duration	0.00
11	Green pod yield per plant (g)	1.21
12	Green pod yield per hectare (kg/ha)	0.00

Table 4. Cluster means for twelve characters in thirty two genotypes of cowpea

Clusters	Days to 50 per cent flowering	Number of branches per plant	Number of clusters per plant	Pod length (cm)	Number of seeds per pod	Number of pods per plant	Plant height at final harvest (cm)	Sugar content (%)	Shelling (%)	Crop duration	Green pod yield per plant (g)	Green pod yield per hectare (kg/ha)
I	41.18	7.60	4.95	15.64	10.99	22.96	98.82	8.24	47.11	88.05	84.36	6249
II	40.61	8.38	5.16	17.86	10.14	16.79	158.42	8.10	48.54	87.75	101.24	7499
III	36.69	7.35	4.45	24.49	12.33	16.31	73.64	8.29	47.46	84.79	123.87	9175
IV	40.94	9.02	4.15	14.96	10.42	22.45	162.92	10.18	51.65	91.82	79.45	5885
V	40.94	7.69	4.30	25.51	13.42	12.80	178.44	8.09	38.36	84.67	101.66	7530
VI	39.28	11.69	5.52	27.85	10.42	10.23	78.47	11.28	28.21	83.67	98.36	7286
VII	42.60	5.02	4.43	15.63	11.75	18.57	271.64	12.38	49.36	86.46	126.07	9339
VIII	36.27	5.35	4.24	15.66	11.08	30.56	248.98	9.30	35.71	87.82	130.15	9641