Genetic Diversity in Cowpea [*Vigna unguiculata* (L.) Walp]

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One hundred cowpea genotypes were evaluated for eleven metric characters to quantify the genetic diversity existing among them by using Mahalanobis D^2 statistics. The genotypes fell into eleven clusters. Among the eleven quantitative characters studied, 100-seed weight contributed maximum (75.73%) towards divergence followed by plant height (8.28%) and seed yield (6.30%). Cluster VI had minimum days to first flower opening and days to maturity, and also had maximum number of pods per plant, pod length, number of seeds per pod and seed yield. Cluster IX exhibited lowest means for seed yield, 100 seed weight, number of seeds per pod, pod length, primary branches and plant height. The genotypes from Cluster VI and IX, which have high and low cluster means for the majority of the characters are suggested as parents for hybridization.

Key words: Cluster, Cowpea (*Vigna unguiculata*), D^2, Germplasm, Genetic Diversity

Genetic variability is the basic requirement for any crop improvement programme to be effective. When the existing variability is exploited by way of selection, for further improvement, the breeder has to resort to hybridization to succeed in evolving new recombinants with desirable traits of different genotypes. Accumulation of different desirable traits spread over the diverse genotypes into one genotype is important for the rapid advancement in yield improvement of any crop. To initiate hybridization, the genotypes are to be classified into clusters based on genetic divergence and the extent of genetic diversity between them need to be estimated so that the parents could be chosen from the clusters with wide genetic divergence. The characters for which the clusters excel and the objective of the breeding programme also need to be considered. In the present investigation, genetic diversity in a set of cowpea genotypes was assessed by Mahalanobis D^2 statistics for seed yield and related traits.

Material and Methods

In the present study, 100 cowpea genotypes were selected from those maintained at the All India Coordinated Research Programme (AICRP) on Arid legumes, University of Agricultural Sciences (UAS), Bangalore. These represented collections from different parts of India and Nigeria. The crop was sown in simple lattice design with two replications during summer season of 2000, with a spacing of 60x30 cm. Observations were recorded on ten randomly selected plants in each genotype, from each replication excluding the border plant, for eleven quantitative characters namely, plant height, primary branches, secondary branches, days to first flower opening, days to 50 per cent flowering, days to maturity, number of pods per plant, pod length, number of seeds per pod, seed yield per plant and hundred seed weight (test weight). The analysis of variance was carried out for all the characters individually and then the data were subjected to multivariate analysis of Mahalanobis (1936). The genotypes were grouped into different clusters following Teachers method (Rao, 1952).

Results and Discussion

The analysis of variance (ANOVA) exhibited significant differences among the varieties for all the eleven characters studied (Table 1). Based on D^2 values, 100 cowpea genotypes were grouped into 11 clusters (Table 2). The cluster strength varied from single/ solitary genotype (cluster X and XI) to 25 genotypes (cluster I). The pattern of distribution of these germplasm lines into 11 clusters confirmed the existence of diversity among the genotypes indicated by ANOVA.

Table 1. Analysis of variance for quantitative characters in 100 cowpea genotypes

Source of variation	D.F.	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
Genotypes	99	145.9**	2.09**	5.17**	7.59*	6.02*	10.57*	31.15*	5.68*	5.74*	33.6*	6.41**
Replication	1	-0.03	2.42	0.58	1.44	1.44	6.5	1.74	6.83	1.76	3.23	0.003
Error	99	3.89	0.14	0.48	0.52	0.439	1.91	1.79	0.56	0.68	1.05	0.01
S.E.		1.97	0.37	0.09	0.72	0.65	1.38	1.33	0.75	0.82	1.02	0.11
C.V.		5.11	9.69	9.28	1.32	1.13	1.76	9.27	5.79	7.44	11.05	1.10

X_1 = Plant height; X_2 = Primary branches; X_3 = Secondary branches; X_4 = Days to first flower opening; X_5 = Days to 50% flowering; X_6 = Days to maturity; X_7 = Number of pods/plant; X_8 = Pod length; X_9 = Number of seeds/pod; X_{10} = Seed yield per plant; X_{11} = 100 seed weight

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Table 2. Composition of genotypes in cluster

Cluster	No. of Genotypes	Included of Genotypes
I	25	KAB-13, CAS-15, CAP-8, CAS-11, KAP-7, CAP-2, KAB-9, TAP-1, TAP-3, TAS-21, TAP-2, CAS-5, TAP-8, APC-401, APC-966, TVX-944, C-152, APC-455, APC-988, TAS-13, ITTA-958, C-40, MS-2, C-27, C-66.
II	22	A-4-3-3, C-130, APC-217, P-695, EC-394822, ITTA-784, VCP-9, GC-89322, GC-8929, APC-68, C-30, TCM-101-4, Lolitha, Pattambi, A-4-4-1, KAB-12, CAB-6, CAP-6, KAB-32, CAP-4, KAB-36, TA-9, APC-331.
III	21	APC-97C11, CAZC-11, LD-SP, CAZC-3, BDC-547-46, KBC-1, TCM-121-9, APC-121-132-P, TCM-42-1, V-585, V-422, APC-105-TVX-2460, CS-88, CAB-3, CAB-7, CAB-7, KAP-2, TAP-12, CAS-6, TAP-7, TAP-4.
IV	12	GC-2, CA2C-10, TCM-75-3, APC-565-56, V-16, S-488, APC-578-57, APC-946, TAS-12, CAS-8, CAP-13, KAP-2.
V	9	TCM-77-4, CPT-10, ITTA-1010, V-585, V-130, APC-645, CAP-5, KAP-1, KAP-5.
VI	2	APC-855-Sel 46, KBC-2.
VII	3	APC-384, APC-949, TCM-14-1.
VIII	2	APC-748, KAB-3.
IX	2	APC-332, APC-379 (C0-1)
X	1	ITTA Cowpea Black.
XI	1	KAB-2

The average intra- and inter-cluster distances are given in Table 3 and Figure 1. The intra-cluster distance ranged from 0.00 (X and XI) to 363.90 (IX) and did not transgress the limits of any of the cluster distances. Maximum inter-cluster distance (4509.19) was recorded between Cluster II and Cluster IX, revealing that these two clusters were most diverse, followed by Cluster IX and XI (4160.82).

The average cluster mean for different characters (Table 4) showed that the genotypes included in Cluster VII had maximum plant height, Cluster XI had maximum primary and secondary branches. Cluster VI had minimum days to first flower opening and days to maturity in addition to maximum number of pods per plant, pod length, number of seeds per pod and seed yield. Cluster X had maximum 100-seed weight. The Cluster IX exhibited lowest means for plant height, primary branches, pod length, number of seeds per pod, seed yield and 100-seed weight. Based on the earlier reports, heterosis and better recombinants were obtained by crossing parents between clusters of high and low means (Shweta *et al.*, 1972, Usha Kumari *et al.*, 2000). Selection of parents is most critical to isolate desirable recombinants. It can be suggested that for creating variability and to get better heterosis, the genotypes from Cluster VI (KBC-2 and APC-855-sel46) and Cluster IX (APC-332 and APC-379) with high and low cluster means respectively for majority of the characters, may be selected for

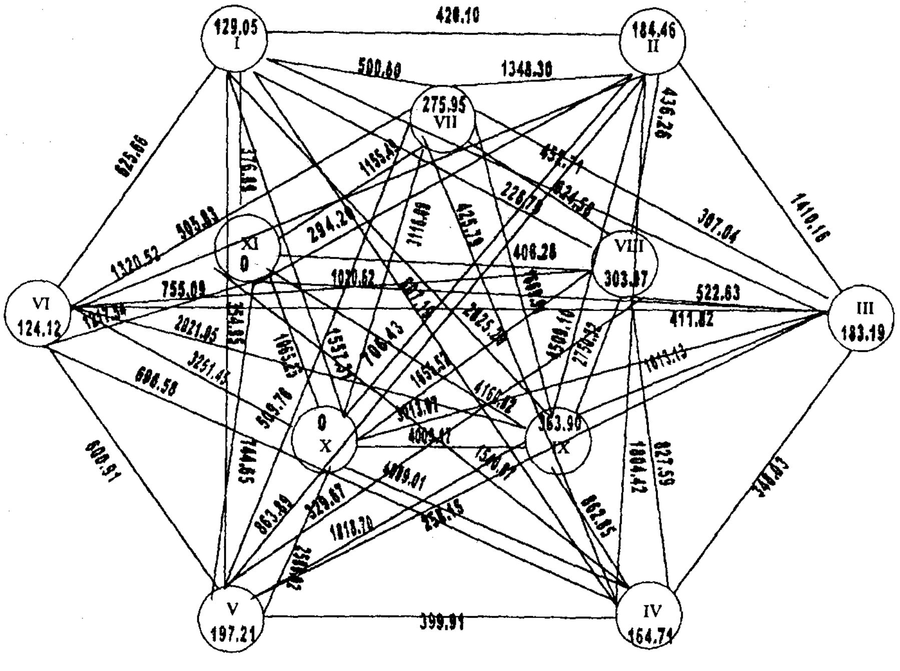

Fig. 1: Intra- and inter-cluster distance (D) in the cowpea germplasm

Table 3. Intra and Inter cluster distance (D^2) in the cowpea genotypes

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	129.05	420.10	452.71	807.19	354.95	625.66	500.60	226.79	2825.29	1557.31	376.89
II		184.46	1410.16	1804.42	863.89	1320.52	1348.30	463.26	4509.10	706.43	294.20
III			183.19	348.03	285.15	411.82	307.04	522.63	1613.13	3013.07	1020.62
IV				164.71	399.91	696.58	425.79	827.59	862.85	4089.01	1540.67
V					197.21	600.91	509.76	329.67	1818.70	2589.92	744.65
VI						124.12	505.83	755.09	2021.05	3251.45	1217.54
VII							275.95	624.58	1669.91	3116.09	1155.49
VIII								303.07	2750.32	1655.52	406.28
IX									363.90	4009.17	4160.82
X										0	1065.25
XI											0

Table 4. Cluster means for 11 characters of cowpea

Cluster	Plant height (cm)	Primary branches (No)	Secondary branches (No)	Days to first flower opening	Days to 50% flowering	Days to maturity	No of pods/plant	Pod Length (cm)	No of seeds/pod	Seed yield (g)	100 seed weight (g)
I	42.06	3.87	7.26	55.10	58.32	79.10	12.63	12.97	10.99	8.16	11.02
II	34.60	4.08	7.47	54.36	58.10	77.36	12.97	13.72	11.36	10.24	12.56
III	41.74	3.55	7.18	53.57	55.60	78.37	13.67	13.71	11.77	10.36	9.36
IV	33.90	3.57	7.27	55.50	58.75	79.16	13.23	11.56	9.98	7.95	8.33
V	33.39	4.14	7.49	54.38	58.05	78.05	13.71	13.39	11.40	6.64	9.78
VI	48.97	4.04	12.25	52.50	56.00	75.25	22.57	15.33	13.39	25.25	9.60
VII	55.90	3.71	9.48	54.50	57.16	79.16	17.85	12.76	11.36	8.11	9.33
VIII	38.27	4.22	7.37	55.00	59.00	79.00	20.50	11.20	9.73	8.84	11.05
IX	26.34	2.64	6.58	55.00	58.25	78.25	21.92	9.435	7.23	6.49	5.75
X	34.40	2.78	5.05	52.50	56.50	78.50	8.25	11.94	8.91	7.64	15.16
XI	39.83	8.25	13.20	56.50	59.50	80.50	12.94	12.75	10.88	8.95	12.06

hybridization, in achieving improvement in yield in cowpea.

In addition to classifying the genotypes into clusters based on genetic divergence, this study also provided information on the characters that contributed maximum to the total divergence among genotypes (Table 5). Test weight was the trait, which contributed for maximum genetic distance. Plant height, seed yield, days to first flower opening, primary branches and number of pods per plant were the next important traits responsible for the divergence recorded. Similar results were observed by Thiyagarajan *et al.*, (1988) in cowpea. Number of seeds per pod contributed minimum to the genetic divergence among the genotypes studied leading to the inference that in general, the variability for this character is less in cowpea genotypes used in this study.

Table 5. Contribution of each character to divergence

Character	Number of times D^2 values scored	% Contribution of each character
Plant height	402	8.28
Primary branches	111	2.28
Secondary branches	18	0.35
Days to first flower opening	123	2.53
Days to 50 % Flower opening	34	0.70
Days to maturity	10	0.2
Number of pods per plant	107	2.20
Pod length	58	1.19
Number of seeds per pod	9	1.18
Seed yield	306	6.30
100 seed weight	3674	75.73
Total	4851	100.00

References

Mahalanobis PC (1936) On the generalized distance in statistics. *Proc. Natl. Acad. Sci.* India, 2: 49-55.

Rao CR (1952) *Advanced Statistical Methods in Biometrical Research*, John Wiley and Sons. Inc. New York.

Shweta UH, BR Murthy, HB Singh and UMB Rao (1972) Genetic divergence in recent elite strains of soybean and groundnut in India. *Indian J. Genet.* **32**: 285.

Thiyagarajan KR, Rathinaswamy and S Rajashekaran (1988) Genetic divergence in cowpea. *Madras Agric. J.* **75**: 125-128.

Usha Kumari, RS Backiyarani and CV Dhanakodi (2000) Character contribution to diversity in cowpea. *Legume Res.* **23**: 122-125.