

Genetic divergence in fodder cowpea (*Vigna unguiculata* (L.) walp.)

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Abstract: Sixty diverse genotypes of fodder cowpea (*Vigna unguiculata* (L.) walp.) evaluated for the genetic diversity were grouped into 10 clusters indicating high genetic divergence among them. The clustering pattern showed that geographic diversity is not an index of genetic diversity. Based on the intercluster distance and cluster mean for various characters, it could be seen that the clusters I, II, IX and X were the most divergent from the other clusters. The genotypes from these clusters may possibly be utilized for hybridization programme. Dry matter yield, green fodder yield and plant height contributed highly towards the genetic divergence among the types studied. (*Key words:* Genetic divergence, Geographic diversity, Fodder cowpea).

Selection is generally effective in a population developed by crossing two distantly related plants, as it possesses a broad spectrum of variability. Hence, knowledge of the genetic divergence among the various types in any germplasm collection is of paramount importance in any plant-breeding programme. Genetic divergence as measured by Mahalanobis (1936) generalized distance (D^2) has been one of the important statistical tools to provide a rational basis for selection of parents in breeding programmes. Application of D^2 statistic in fodder crops is very limited.

In the present investigation, the D^2 analysis was utilized to study the nature and magnitude of genetic divergence for green fodder yield and other related characters in a set of 60 cowpea (*Vigna unguiculata* (L.) walp.) genotypes, which is an important fodder legume grown in many parts of India in the summer and rainy seasons.

Materials and Methods

A set of 60 genotypes of fodder cowpea, representing types adapted to different geographical regions were obtained from the Department of Forage crops, TamilNadu Agricultural University, Coimbatore and were grown during *Kharif*, 1995 in randomized block design with three replications. Each genotype was raised in two rows of 4m length spaced at 30cm between rows and 20cm between plants. Observations were made at the time of 50 per cent flowering from five randomly selected plants from each replication in each genotype for green fodder yield and twelve of its component characters. Representative plant samples from each replication were collected after the harvest for estimating dry matter content and crude protein content. The mean values were transformed into uncorrelated linear functions for Mahalanobis' group distance (D^2) analysis (Rao, 1952). The genotypes were grouped into clusters by Tocher's method (Rao, 1952) and thereafter

the intra and inter-cluster distances were worked out.

Results and Discussion

The analysis of variance revealed that highly significant differences occur among the 60 genotypes for all the 13 characters studied. By the application of clustering technique, 60 types were grouped into ten different clusters (Table 1). Among the ten clusters, Cluster I was the largest having 22 genotypes. Cluster III consisted of 11 genotypes followed by cluster V having seven types. The clusters II and IV had five genotypes each, while the cluster VI had four types. Clusters VII and VIII had two genotypes each. The rest of the clusters had one type each. Thus, the large number of clusters indicated considerable genotypic diversity in cowpea for fodder characters. The clustering pattern revealed that the genotypes originating from different geographical regions got themselves grouped together into different clusters. This may perhaps be due to the free exchange of breeding materials from one place to other (Verma and Mehta, 1976) and/or due to the fact that the nature of selection forces operating under respective domestic conditions might have been similar across the geographic barriers. It was also observed that the exotic strains collected from NBPGR, New Delhi fell into different clusters indicating divergence among them. Strains collected from different states of India were also distributed among different clusters. This indicates the presence of wide genetic variability among the genotypes from various states of India. Thus, it is evident that geographic adaptation, though important, may not be the only factor in determining genetic divergence. In the present study the clustering pattern failed to indicate any relationship between genetic divergence and geographical distribution. This is in agreement with the findings of earlier workers *viz.* Thiyagarajan and Natarajan (1989).

Table 1. Composition of D² clusters

Cluster No.	No. of genotypes	Genotypes	Origin/source
I	22	IC 44696, EC 24024, EC 240215, EC 241044, EC 241053, EC 244024, EC 244021, EC 240884, EC 240764/1. UPC 9103, UPC 9202, U-13-15, UPC 941, UPC 942. IFC 8401, N-274, IFC 9304, Bundel lobia. CS-98, HCS-94. CL-348, Co-5	NBPGR, New Dell Pantnagar, U.P. Jhansi, U. P. Hissar, Haryana Ludhiana, Punjab Coimbatore, TN
II	5	IFC 9201, IFC 24094, N-311 RFC 8903 EC 24041	Jhansi, U.P. Rahuri, Maharastra NBPGR, New Delhi
III	11	UP 9001, UPC 951, UPC 952, UPC 953, UPC 5286, UPC 93-1, UPC 93-4. CL 321-1, CL 321-2 IFC 9503, IFC 9402	Pantnagar, U. P. Ludhiana, Punjab Jhansi, U. P.
IV	5	EC 24768, EC 240865, EC 240744 UPC 240806 CS-90	NBPGR, NewDelhi Pantnagar, U. P. Hissar, Haryana
V	7	EC 240687, EC 241024, EC 241027, EC 4216 UP 219 HCS-82 CL-341	NBPGR, New Delhi Pantnagar, U.P. Hissar, Haryana Ludhiana, Punjab
VI	4	IFC 9501, N-4300 CL-350 CS-91	Jhansi, U. P. Ludhiana, Punjab Hissar, Haryana
VII	2	EC 240166, EC 240768	NBPGR, New Delhi
VIII	2	UPC 287 CL-334	Pantnagar, U. P. Ludhiana, Punjab
IX	1	IFC 9502	Jhansi, U. P.
X	1	EC 240764/2	NBPGR, New Delhi

Sonawane and Patil (1991) and Beri and Soho (1991).

The intra and inter-cluster D² and D values among the ten clusters are presented in Table 2. The intra-cluster D values ranged from 13.59 to 16.01. The minimum intra-cluster distance was recorded by cluster VII and the maximum by cluster III. The highest inter-cluster distance was found between clusters I and X (41.60). It was least between cluster V and VI (17.52). The clusters I, II, IX and X were either moderately or highly

divergent from all the other clusters. Cluster III was closely related to clusters IV and VIII. Similarly cluster V was closely related to cluster VI and cluster VII to cluster VIII. The clusters IX and X were the most divergent clusters from the rest of the clusters. Intercrossing types from the most divergent clusters is expected to result in a wide spectrum of variability for important characters and selection for these characters would result in increased green fodder yield and dry matter production.

Table 2. Intra (Diagonal) and inter-cluster average of D^2 and D values (Within parentheses)

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	229.62 (15.15)	571.42 (23.90)	439.62 (20.97)	594.63 (24.39)	994.62 (31.54)	324.61 (36.40)	1059.28 (32.55)	674.61 (25.97)	1509.20 (33.85)	1730.69 (41.60)
II		240.45 (22.01)	694.64 (15.51)	808.49 (26.36)	1302.61 (28.43)	1238.621 (36.09)	046.41 (35.19)	1008.45 (32.35)	1429.70 (31.76)	484.62 (37.81)
III			256.19 (16.01)	315.46 (17.76)	864.31 (29.40)	624.63 (24.99)	1602.17 (40.03)	394.19 (19.85)	1004.58 (31.70)	1594.28 (39.93)
IV				248.65 (15.77)	850.63 (29.17)	714.66 (26.73)	828.49 (28.78)	961.68 (31.01)	914.63 (30.24)	1504.68 (38.79)
V					194.63 (13.95)	306.92 (17.52)	873.61 (29.56)	739.62 (27.20)	1246.18 (35.30)	1499.56 (38.72)
VI						229.37 (15.14)	394.29 (19.86)	1419.53 (37.68)	1038.61 (32.23)	1198.62 (34.62)
VII							184.63 (13.59)	1310.26 (36.20)	714.62 (26.73)	1313.67 (36.24)
VIII								201.68 (14.20)	968.64 (31.12)	1426.29 (37.70)
IX									0.00	1421.63 (37.70)
X										0.00

The cluster means of the various characters are presented in Table 3. High ranges of mean values among the clusters were recorded for the characters *viz.* dry matter yield, green fodder yield, plant height, number of leaves, number of branches and dry weight of stem.

The cluster IX had the highest mean values for number of leaves, leaflet width, dry matter yield, green fodder yield, dry weight of stem and crude protein content. For leaflet length, stem thickness, days to 50 per cent flowering and dry weight of leaves, cluster VII had maximum values. Cluster X recorded highest mean values for plant height and number of branches while cluster VIII had the maximum value for leaf: stem ratio. Cluster II had the minimum value for days to 50 per cent flowering. Thus, involving the genotypes of outstanding mean performance from these clusters in the intervarietal and interspecific crosses will be useful for creation of variability and the development of high fodder yielding cowpea varieties with superior quality. Their segregating progenies are also likely to yield good recombinants for economic traits.

The ranking technique was adopted to rank the characters in the order of contribution to total genetic divergence (Murthy *et al.* 1965). Dry matter yield had the highest contribution towards the genetic divergence followed by green fodder yield and plant height with rank totals of 7975, 8117 and 8832 respectively. The lowest rank total indicates the maximum contribution. Radha Manoharan (1978) reported that contribution of green fodder was maximum towards genetic divergence in fodder cowpea. The major contribution of dry matter yield, green fodder yield and plant

Table 3. Cluster means for 13 characters in fodder cowpea

Characters	I	II	III	IV	V	VI	VII	VIII	IX	X
Plant height(cm)	56.31	58.36	42.65	71.10	44.83	57.72	70.75	33.54	70.47	93.83
Number of Branches	4.41	4.86	3.17	4.77	3.37	4.08	4.45	1.67	3.07	5.83
Number of leaves	12.43	11.41	11.99	14.91	17.53	14.06	14.55	9.75	23.70	14.67
Leaflet length(cm)	11.11	10.94	10.75	10.82	11.09	10.84	14.22	8.99	11.00	13.30
Leaflet width(cm)	7.73	7.27	7.54	7.61	8.23	8.58	8.82	5.97	9.30	7.57
Stem thickness (mm)	7.53	8.39	7.58	8.02	7.85	7.28	8.47	7.70	7.22	7.79
Days to 50% flowering	55.27	52.53	53.94	57.87	58.33	57.75	62.67	52.84	58.33	55.00
Dry matter Yield(g)	13.11	9.38	12.52	12.03	18.44	19.52	19.51	14.27	20.76	8.66
Green fodder yield(g)	80.57	45.33	70.75	75.30	103.36	111.72	116.84	70.15	136.87	68.67
Dry weight of leaves(g)	3.93	2.74	3.12	3.55	5.42	5.57	6.20	4.59	5.65	2.22
Dry weight of stem(g)	9.18	6.64	9.11	8.48	13.03	13.95	132.31	9.70	15.11	6.44
Leaf/stem Ratio	0.44	0.42	0.39	0.43	0.42	0.41	0.47	0.50	0.37	0.35
Crude protein Content	20.34	19.63	19.31	19.25	19.52	19.03	18.79	20.64	21.68	21.07

height to genetic divergence in the present investigation was confirmed by their cluster mean (Table 3) where the ranges for these characters were very wide. This indicated that these attributes should form the criteria for selection of parents for future hybridization programmes.

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