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Short Communication

GENETIC DIVERGENCE IN FORAGE COWPEA

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Cowpea (*Vigna unguiculata* L. Walp) is a legume grown for vegetable, fodder or pulse in the tropics and sub-tropics. Further, the clustering of forage cowpea accessions on the basis of genetic divergence may provide the basis for selection of suitable parents to be used in hybridization programme. Therefore, the present study was undertaken on these aspects using multivariate statistical technique, for some fodder attributes in cowpea.

A total of 280 diverse genotypes (49 genotypes, *viz.*, IL 3939 to IL 3988 from Delhi, 81 genotypes, *viz.*, IL 93 to IL 174 from Punjab and 150 genotypes, *viz.*, IL 1520 to IL 1670 from Gujrat) of fodder cowpea along with 3 check varieties were studied in an augmented block design. Each plot consisted of one row of 4m length; spacing between and within rows were 60 and 15 cm, respectively. The crop was raised by adopting standard cultural practices. Observations were recorded on 5 competitive plants for 10 quantitative traits, *viz.*, days to 50 per cent flowering, plant height (cm), number of branches/plant, branch length (cm), leaf number/plant, fresh leaf weight (g), fresh stem weight (g), dry leaf weight (g), dry stem weight (g) and leaf/stem ratio. All the metric traits were analysed in augmented block design (Petersen, 1985). This analysis gave adjusted mean value, on which principal component analysis as given by Hotelling (1933) and Mardia (1971) was applied, to transform the interdependent variables into a set of independent variables. Further, these principal component scores were used for non-hierarchial euclidean cluster analysis (Beale, 1969; Spark, 1973). For assigning appropriate number of cluster F-test was applied. The analysis was carried out using SPAR1 package.

Correlation matrix of adjusted mean values was used to transform all the quantitative traits into a single index of similarity in the form of principal components, which yielded into 10 eigen vectors and eigen roots. Further, the maximum eigen root value 3.43 was obtained by eigen vector 1 and followed by 2.08, 1.11, 0.91, 0.67, 0.52, 0.51, 0.35, 0.27, and 0.16 respectively, for rest of the vectors. The first four principal components accounted for 34.29 per cent, 20.76 per cent, 11.125 per cent and 9.12 per cent of the variation. Thus, cumulative percentage of total variation reflected that more than 75 per cent variation was explained by first four principal components and rest by others.

The cluster analysis was initiated with 8 principal component scores, grouped 280 accessions into a convenient grouping of 10 non-overlapping clusters with like genotypes within clusters for different attributes. Further, F-test showed that 10 clusters (F ratio significant at 5% probability) were most suited. The maximum number of genotypes fell in cluster number 5 (61 genotypes), while cluster number 10 was solitary. The average inter- and intra-cluster distances are presented in Table 1. The intra-cluster distances ranged from 0.00 to 3.01. Maximum cluster distance (8.13) was found between cluster 8 and 9 followed by 5 and 8 (7.53). The minimum distance was observed between cluster 1 and 9 (1.97). The observed distances showed the genetic diversity among and within the clusters and clustering is useful to identify the diverse genotypes.

Table 1. Average inter and intra-cluster distances in forage cowpea

Cluster No.	1	2	3	4	5	6	7	8	9	10
1	**(1.6480)**									
2	2.670	**(2.131)**								
3	2.984	3.615	**(1.7500)**							
4	4.808	3.647	3.235	**(2.640)**						
5	2.156	3.664	3.635	5.592	**(1.681)**					
6	3.057	2.410	4.432	4.511	2.932	**(1.926)**				
7	2.531	2.768	2.598	3.824	2.944	2.959	**(2.064)**			
8	7.264	5.105	7.349	5.434	7.534	5.043	5.859	**(3.014)**		
9	1.967	4.048	2.548	5.231	2.264	4.242	2.559	8.128	**(1.595)**	
10	6.179	5.458	4.404	5.130	6.367	5.130	6.004	4.755	6.860	**(0.000)**

Values in parentheses shows intra-cluster distances

The relative superiority of different attributes is presented in the Table 2. The potential genetic donor for fresh leaf weight, fresh stem weight, dry leaf weight and dry stem weight fell into cluster number 8 (IL 102, IL 114, IL 1540, IL 1610, IL 1614, IL 3983 and IL 3987); for tallest plant height cluster number 2 (IL 107, IL 119, IL 140, IL 171, IL 1580, IL 1588, IL 1636, IL 1665, IL 1669, IL 1669, IL 3966, IL 3984 and IL 3986); for leaf/stem ratio cluster number 4 (IL 143, IL 174, IL 1589, IL 3939, IL 3952 and IL 3980).

Table 2. Cluster mean for various traits in forage cowpea

Character	1	2	3	4	5	6	7	8	9	10
1	55.12	142.92	6.93	223.85	59.93	88.92	181.60	17.07	38.70	0.44
2	71.00	183.33	8.78	230.97	107.00	152.89	287.39	26.03	62.92	0.45
3	48.49	163.35	8.38	160.12	62.95	161.83	166.59	23.61	22.88	1.08
4	49.17	163.75	9.63	190.23	98.62	264.63	261.35	44.84	77.36	1.24
5	87.52	106.25	7.40	188.04	66.95	66.06	135.76	15.00	32.76	0.49
6	87.65	101.48	8.89	244.46	121.14	132.04	260.60	28.19	68.63	0.43
7	51.46	124.52	10.20	157.71	107.82	133.61	208.55	21.59	43.40	0.53
8	82.00	136.23	12.26	203.20	265.80	246.11	486.86	46.95	101.85	0.47
9	49.21	126.63	6.81	147.59	54.73	76.08	125.60	12.35	23.03	0.60
10	88.00	83.30	8.00	293.00	115.30	183.30	431.60	37.50	100.22	0.34

1 = Days to 50 % flowering, 2 = Plant height (cm), 3 = Number of branches/plant, 4 = Branch length (cm), 5 = Leaf number/plant, 6 = Fresh stem weight (g), 8 = Dry leaf weight (g), 9 = Dry stem weight (g), 10 = Leaf/stem ratio

Therefore, the studies help in grouping of genotypes into clusters and selection of desired genotypes from a particular cluster for further utilization in hybridization programme.

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