

GENETIC DIVERGENCE IN COWPEA

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The genetic divergence among seven parents and their twelve hybrids of cowpea was assessed using Mahalanobis D^2 statistic. Ten characters were studied and utilised for multi variate analysis. The genotypes were grouped into seven different clusters. The characters namely days to 50 per cent flowering, 100 grain weight and plant height contributed maximum towards genetic divergence. The seven parents fell into five clusters. The twelve hybrids also fell into five different clusters. The genotypes from diverge groups such as KC 199 and KC 195 could be utilized in the breeding programme for improvement of yield in cowpea.

Cowpea (*Vigna unguiculata* (L.) Walp.) is an important pulse crop of India and one of the main sources of protein. The importance of genetic diversity has been stressed by many workers in cross pollinated as well as self pollinated crops. In cowpea little information is available on genetic diversity of parents and their F₁s. Therefore, the present investigation was undertaken to estimate the nature and magnitude of genetic diversity in seven parents and their twelve F₁s in cowpea.

MATERIALS AND METHODS

Seven parents and their 12 F₁s of cowpea were grown in a randomised block design with three replications at the National Pulses Research Centre, Pudukkottai, Tamil Nadu during kharif 1984. Each plot consisted of two rows of 1.5 m long with inter and intra-row spacings of 45 cm and 15 cm respectively. Observations were recorded on five competitive randomly selected plants from each plot for ten characters namely, days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of clusters per

plant, number of pods per plant, pod length, number of seeds per pod, 100 grain weight and yield per plant. Plot means were used for the statistical analysis. The diversity in characters was studied using Mahalanobis D^2 statistic described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters. On the basis of relative magnitude of D^2 values, all the nineteen genotypes were grouped into seven clusters (Table 1). Mutual relationship among the clusters is shown in Fig. 1. Maximum inter-cluster divergence was observed between genotypes of cluster VI and VII and the minimum was found between genotypes of clusters II and III (Table 2). The intra-cluster divergence varied from 0.00 to 6.951, the maximum being in cluster V which comprised of two genotype.

The clustering pattern indicated that genotypes KC 199 and KC 195 were genetically distant among themselves and from the rest of the genotypes and formed most divergent single genotypic cluster viz. VI and VII. The

characteristic features of the selection KC 199 contributing towards diversity was late flowering, long duration, more number of branches per plant, clusters per plant, pods per plant and seeds per pod (KC 199). The selection KC 195 had dwarfness, less number of branches per plant, lower pod length, seeds per pod, 100 grain weight and yield per plant.

The cluster V which showed highest intra-cluster variation included two genotypes V 87 and V 87 x CoVu 4, both of which had highest plant height (146.96 cm), less number of clusters per plant (10.38) and pods per plant (18.71) (Table 3). Cluster I was the most compact with minimum intra-cluster distance. The seven parents fell into five clusters, the inter-cluster distance being appreciable in most

cases. The twelve F₁s also fell into five different clusters. The parents and their F₁s tended to cluster together in the clusters I, IV and V.

The results of the present study indicate that the population is genetically fairly diverse. Similar reports were made by Ramanujam (1975) in the study with 10 parents and their 25 F₁s in mungbean. Days to 50 per cent flowering, 100 grain weight and plant height were to contribute the maximum towards divergence.

The characters like maturity and plant height are known to substantial by contribute to genetic divergence in several crops (Murthy and Arunachalam, 1966). Bainiwal and Jatasra (1980) reported that plant height, pod length and days to flower contri-

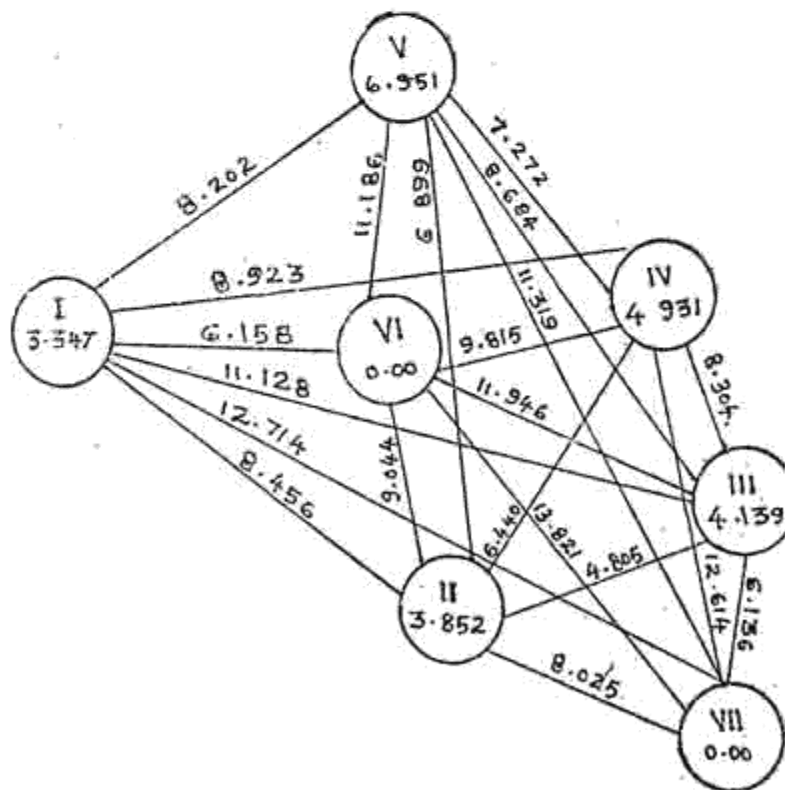


Table 1. Distribution of 7 parents and 12 hybrids in different clusters formed by D² analysis in cowpea

Clusters	No. of		Population included
	parents	hybride	
I	2	2	Co 3, C 152, Co 3 x C 152, KC 199 x C 152
II	—	4	Co 3 x KC 195, Co 3 x CoVu 4, Co 4 x KC 195 and KC 199 x CoVu 4
III	—	2	KC 199 x KC 195 & V 87 x KC 195
IV	2	3	CoVu 4, Co 4, Co 4 x C 152, Co 4 x CoVu and V 87 x C 152
V	1	1	V 87, V 87 x CoVu 4
VI	1	—	KC 199
VII	1	—	KC 195

Table 2. The intra and inter-cluster distances (\bar{VD}^2) among seven clusters in cowpea

Clusters	I	II	III	IV	V	VI	VII
I	3.347	8.456	11.128	8.923	8.202	6.158	12.714
II		3.852	4.805	6.440	6.899	9.044	8.025
III			4.139	8.304	8.684	11.946	6.136
IV				4.931	7.272	9.815	12.614
V					6.951	11.186	11.319
VI						0.000	13.821
VII							0.000

Table 3. Cluster means for ten characters in cowpea

Clusters	Days to 50 percent flowering	Days to maturity	Plant height (cm)	Branches per plant	Clusters per plant	Pods per plant	Pod length (cm)	Seeds per pod	100 grain weight (g)	Yield per plant (g)
I	45.89	65.72	125.58	6.25	14.37	22.30	16.67	15.70	11.26	32.75
II	42.97	62.80	120.99	5.64	12.56	19.88	17.04	14.97	13.02	28.69
III	40.95	59.80	98.59	5.36	13.29	20.13	16.76	14.90	13.15	29.46
IV	42.30	62.82	138.65	5.80	12.10	21.81	17.75	16.16	12.62	37.40
V	42.80	62.66	146.96	5.11	10.38	18.71	17.09	14.53	12.75	26.54
VI	48.66	68.66	134.50	6.33	16.13	25.53	17.63	16.60	12.93	35.93
VII	42.00	61.00	54.20	4.93	13.93	20.06	15.30	12.93	13.26	24.06

buted the maximum to genetic divergence in pigeonpea.

The genetically diverse genotypes of clusters VI (KC 199) and VII (KC 195) could be utilized for the improvement of yield in cowpea by crossing them. Further, KC 199 can be crossed with Co 3, Co 4 and V 87 for incorporating the characters of KC 199 namely, more number of branches per plant, clusters per plant, pods per plant and seeds per pod. The seed size of C 152 and CoVu 4 could be improved by crossing them with KC 195. Thus it could be possible to generate a gene pool possessing immense variability by appropriate inter crossing.

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