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Genetic diversity studies for seed yield in cowpea [Vigna unguiculata (L.) Walp.]

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SUMMARY

The present investigation on genetic diversity studies for seed yield in cowpea [*Vigna unguiculata* (L.) Walp.] was conducted by using 44 genotypes of cowpea. There was substantial genetic diversity among the genotypes studied. 44 genotypes were grouped into 6 clusters to study the genetic divergence for seed yield per plant. There was no parallelism between genetic diversity and geographical distribution. For seed yield, the pair of genotypes *viz.*,Phule CP 05001 and UPC-5286 were most divergent from one another ($D^2 = 1225.35$). On the basis of inter-cluster distance, cluster means and *per se* performance observed in the present studies, following genotypes are suggested for hybridization to improve seed yield in cowpea. 1.UPC-5286, 2.Phule Pandhari, 3.NBPGR-05-66, 4. Pusa-do-fasali, 5.Shweta, 6.NBPGR-05-67, 7.CP-23-GPM, 8.NBPGR 05-71.

Key Words : Cowpea, Genetic, Diversity, D², Seed yield

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owpea is multipurpose legume grown for seed as a pulse, green pod as a vegetable and whole plant as a fodder in tropics and subtropics. Because of its high protein content (20-25 %) cowpea has been referred as "poor man's meat". Genetic diversity is a variability available among the different genotypes of a species. A method suggested by Mahalnobis (1936) known as "Mahalanobis D² statistic" is widely used to know genetic diversity in the available germplasm. This technique measures the forces of differentiation at intracluster and intercluster levels and thus helps in the selection of genetically divergent parents for their exploitation in hybridization programme. The D² statistics also measures the degree of diversificiation and determines the

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relative proportion of each component character to the total divergence. The present investigation was, therefore, undertaken to study extent of genetic diversity for seed yield and its components in cowpea.

MATERIAL AND METHODS

In the present study forty four genotypes of cowpea were used and grown in RBD with two replications. The experiment was conducted at Pulses Improvement Project Farm, Mahatma Phule Krishi Vidyapeeth, Rahuri. Each genotype was sown in single row of 4 meter length. The spacing of 30×10 cm was maintained. Five competitive plants per genotype were selected at random from each replication for recording observations for eight characters *i.e.* days to maturity (no), plant height at maturity (cm), number of pods per plant, number of seeds per plant, seed yield per plant (g).Tocher's method as described by Rao (1952) was followed for cluster formation.The forces of differentiation at intracluster and intercluster levels measures the Mahalanobis D² statistic method.

RESULTS AND DISCUSSION

The experimental findings obtained from the present

study have been discussed in following heads:

Diversity based on a set of fourteen characters:

Analysis of variance revealed highly significant differences among the genotypes for all the characters under study.

Cluster formation intra and inter-clusters distance and mean performance:

In present study for seed trial, 44 genotypes evaluated for six characters were grouped into six clusters. The cluster-I was largest with 31 genotypes followed by cluster II with 7 genotypes and cluster III with 3 genotypes. The remaining all other clusters *viz.*, IV, V and VI were monogenotypic. This indicated that presence of diversity in the 44 genotypes studied. These findings confirmed earlier reports of Kumar *et al.* (1982), Patil and Bhapkar (1987), Rewale *et al.* (1996), Sharma and Mishra (1997). The clustering pattern showed that varieties from different sources were clubbed into one group and also varieties of same source forming different clusters indicated no relationship between geographical diversity and genetic divergence. Murthy and Arunachalam (1966) stated that 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, loose their individuality under human interference. Similar results were reported by Marangappanavar (1986), Patil and Bhapkar (1987), Rewale et al. (1996). Similarly in case of seed trial maximum intra cluster distance was observed for cluster II (D = 11.63) followed by cluster III (D = 11.22) and cluster-I (D = 8.90). The cluster-I and IV recorded the lowest inter cluster distance (D = 12.50) indicating genotypes in these

Table 1 : Average intra and inter cluster D=õD ² values of 44 genotypes of cowpea evaluated for seed yield its components						
Clusters	I	II	III	IV	V	VI
Ι	8.90	13.41	23.38	12.50	12.90	15.26
II		11.63	18.17	19.92	13.79	14.76
III			11.22	31.39	18.04	18.64
IV				0.00	20.57	21.49
V					0.00	17.72
VI						0.00

Sr. No.	Chamatan	Clusters						Cluster average
	Characters	Ι	П	Ш	IV	V	VI	
1.	Days to maturity	73.29	76.29	92.83	67.00	87.50	74.00	75.30
2.	Plant height at maturity(cm)	68.01	85.87	118.20	59.10	68.50	88.10	74.54
3.	No. of pods per plant	7.83	8.86	12.20	7.50	7.80	16.30	8.47
4.	No. of seeds per pod	12.10	13.97	14.63	7.90	13.60	15.70	12.59
5.	100 seed weight(g)	8.62	12.44	10.52	8.19	9.04	7.31	9.33
6.	Seed yield per plant(g)	8.23	15.05	18.48	4.82	9.70	18.02	10.19

Table 3 : Relative contribution of different characters towards genetic diversity in cowpea genotypes evaluated for seed yield

Sr. No.	Characters	Times ranked 1 st	Contribution to divergence (%)
1.	Days to maturity	240	25.37
2.	Plant height at maturity(cm)	173	18.29
3.	No. of pods per plant	73	7.72
4.	No. of seeds per pod	296	31.29
5.	100 seed weight(g)	124	13.11
6.	Seed yield per plant(g)	40	4.23

Table 4 : Putative parents suggested for hybridization for seed yield improvement					
Characters	Source cluster	No. of genotypes	Name of genotypes		
Seed yield per plant	III, VI, II	5	UPC-5286, Bundel lobia-1, PhulePandhari, NBPGR-05-66, Pusa-do-Fasali		
No. of pods per plant	VI, III, II	5	PhulePandhari, UPC-5286, Shweta, NBPGR-05-66, NBPGR-05-67		
100 seed weight	II, III, V	5	Pusa-do-fasali, CP-23-GPM, Bundel-lobia-1, NBPGR 05-71, UPC-5286		
No. of seeds per pod	VI, III, II	5	PhulePandhari, UPC-5286, Bundel lobia-1, CP-4-74, NBPGR 05-66.		

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clusters were genetically close to each other, whereas cluster III and cluster IV exhibited maximum inter-cluster distance (D = 31.39) indicating that genetic makeup of genotypes falling in those clusters may be entirely different from one another (Table 1). The highest cluster mean for grain yield per plant (18.48 g) recorded by cluster-III appeared to be due to contribution of component character *viz.*, plant height (118.20 cm), days to maturity (92.83 days), number of pods per plant (12.20), number of seeds per pod (14.63) and 100 seed weight (10.52 g) (Table 2).

Relative contribution of characters towards divergence:

In seed trial plot, the character number of seeds per pod (31.29 %) made the maximum contribution to divergence followed by days to maturity (25.37 %), plant height at maturity (18.29%) and 100 seed weight (13.11%) indicating that these characters were considerably responsible for total divergence in the material under study (Table 3). These results are similar to the findings of Kumar et al. (1982) and Thiyagarajan et al. (1988) for 100 seed weight, Kumar et al. (1982) for days to maturity, Thiyagrajan and Natarajan (1989) for number of seeds per pod, Sharma and Mishra (1997) for plant height, Vishwanathan et al. (1998) for 100 seed weight and days to maturity. Taking into account the cluster mean, cluster distance and per se performance for important seed yield components, the various clusters which can provide the desired parents for hybridization for improvement in characters are listed in Table 4. On the basis of inter-cluster distances, cluster means, path analysis and per se performance observed in the present study, for seed purpose the genotypes UPC-5286, PhulePandhari, NBPGR-05-66, Pusa-do-fasali, Shweta, NBPGR-05-067, CP-23-GPM, NBPGR-05-071 were found to be overall superior genotypes for hybridization programme.

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