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ASSESSMENT OF GENETIC DIVERSITY IN COWPEA [*VIGNA UNGUICULATA* (L.) WALP.] GERMPLASM

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ABSTRACT

In the present study, seventy two genotypes of cowpea were evaluated for assessing genetic diversity for ten different quantitative characters for exploitation in a breeding programme aimed at improving yield potential of cowpea by using Mahalanobis D^2 statistics. The intra cluster D^2 value ranged from 0.00 to 43.96 while Inter cluster D^2 value ranged from 30.9 to 375.97 indicated that the selected genotypes were highly divergent. The maximum intra cluster distance was recorded for cluster IV (43.96) while cluster III and IX (0.00) showed no intra-cluster distance values revealed homogenous nature of the genotype within the cluster. The genetically more divergent genotypes present in cluster V and VIII as indicated by inter cluster distance value (375.97). Inter cluster D^2 value and mean cluster values for characters indicated that hybridization of clusters VIII with clusters V genotypes would result in marked heterosis and produce better segregants with improved yield. Among the characters studied, seed yield per plant (38.81%) contributed highest towards genetic divergence followed by 100-seed weight (29.07%). Selecting parents of these clusters probably provide promising recombinants and better segregants for future breeding strategy.

INTRODUCTION

Cowpea is grown for dry seed as pulse in the northern drier tracts while some forms of cowpea are also grown as fodder crops in the semi-arid western regions and in the humid tropic regions and large grown for vegetable purpose. It is a great important crop in arid and semi-arid regions of India because of its short duration, high yield potential and quick growing habits along with high protein content. Cowpea young leaves, pods and beans contain vitamins and minerals which have fuelled its usage for human consumption and animal feeding (Nielson *et al.*, 1997).

To develop a new variety there is need of the magnitude of genetic variability in the base material and the vast of variability for desired characters. A good knowledge on genetic diversity or genetic similarity could be helpful in long term selection gain in plants (Kumar *et al.*, 2012). Hence, genetic variability and diversity is of prime interest to the plant breeder as it plays a key role in framing and successful breeding programme. The genetically diverse parents are always able to produce high heterotic effects and great frequency of desirable segregants in further generation as already reported by earlier workers (Kumar *et al.*, 1994). The genetic distance between pair of genotypes offers the basis for understanding the structure of the diversity of any intra-species population. It constructs an all-to-all matrix to describe the distance between each sequence pair of genotypes, thereby guiding plant breeder in their selection procedure (Adewale *et al.*, 2011). The multivariate analysis is a useful tool for choosing the parents for hybridization and has been well demonstrated by previous workers (Hazra *et al.*, 1992; Nath *et al.*, 2009). Therefore, an attempt was made to identify important selection indices influencing pod yield of vegetable cowpea and to choose promising parents that can profitably be utilized in a hybridization programme for the improvement of seed yield and other characters. D^2 statistic is a useful tool to measure genetic divergence among genotypes in any crop developed by Mahalanobis (1936). However, the main objective of present study to identify genetic divergent parents, so as to select the potential parents for breeding programme to attain the anticipated improvement in seed yield of cowpea.

MATERIALS AND METHODS

The experimental materials consisted of 72 genotypes of cowpea received from AICRP on Arid Legume, Jodhpur and Department of Plant Breeding and Genetics, S.K.N. College of Agriculture, Jobner, Jaipur were evaluated in a Randomized Completely Block Design with three replications during *Kharif* season 2013. Each genotype was sown in a three row plot of 5 m. length. The row to row distance and plant to plant distance was kept at 30cm and 10cm, respectively. All the recommended agronomic practices were followed to raise healthy crop. Observations on days to flowering and days to maturity were recorded on whole plot basis. Ten plants were selected randomly from each plot at maturity for measuring Plant height (cm), Primary branches per plant, Pods per plant, Pod length (cm), Seeds per pod, 100-Seed weight (g), Pod wall proportion (%) and Seed yield per plant (g). Replication wise data for each character were subjected for analysis of variance (Singh and Choudhary, 1995). Multivariate analysis was done utilizing Mahalanobis (1936) D^2 statistics and genotypes were grouped into different clusters following Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed that the significant differences were present for all the characters studied and the experimental materials were genetically divergent from each other (table 1). This indicates that there is ample scope for selection of promising genotypes to enhancing genetic yield potential of cowpea. Similar finding were also reported by Zargar *et al.* (2005). All the seventy two genotypes were grouped into nine clusters following by Tocher's methods (table 2). Cluster I was the largest and consists of 33 genotypes followed by cluster II with 11 genotypes, cluster VI with 9 genotypes, cluster VII with 8 genotypes, cluster V with 4 genotypes, cluster IV with 3 genotypes, cluster VIII with 2 genotypes and cluster III and IX had only 1 genotype in each. Clusters III and IX were unique, since each had only one genotype. The pattern of group constellation proved the existence of significant amount of variability.

The intra cluster D^2 value ranged from zero to 43.96 while inter cluster D^2 value ranged from 30.9 to 375.97 indicated that the selected genotypes were highly divergent (table 3 and figure 1). The maximum intra cluster distance was recorded for cluster IV (43.96) followed by cluster VII (41.60) while cluster III and IX (0.00) showed no intra-cluster distance values as they were solitary cluster indicating comparatively homogenous nature of the genotype within the cluster. This high intra-cluster distance indicated the wider genetic diversity among the genotypes which could be used in yield improvement of cowpea. The maximum inter cluster distance (D^2) was found between cluster V and VIII (375.97) followed by cluster IX and VIII (282.24), while the closest proximity was observed between cluster I and III (30.91) followed by the cluster II and III (40.45) suggesting that the genotypes belonging to these clusters may be used as parents for hybridization programme to develop desirable type because crosses between genetically divergent genotypes will generate heterotic segregants. Cluster means of each trait toward divergence are presented in table 4. It is evident that different cluster exhibit distinct mean values for almost all the ten characters. A wide range of variation was observed among different clusters for all the cluster means. Cluster IV had the highest mean value for primary branches per plant and seed yield per plant. Cluster VIII had the maximum mean value for plant height, pods per plant and pod wall proportion and Cluster IX had the maximum mean value for days to 50% flowering, days to maturity, pod length, seeds per pod and 100-seed weight. The maximum contribution to genetic divergence was made by seed yield per plant (38.81%) followed by 100-seed weight (29.07%), plant height (19.33%), and pod wall proportion (6.42%) had the greater contribution to genetic diversity therefore necessary attention is required to be focused on these characters (table-4 and figure 2). Similer finding were also observed by Kumawat and Raje (2005), Anbumalamarthi and Nadarajan (2007), Nagalakshmi *et al.,* (2010), Garje *et al.*, (2013) and Saxesena *et al.*, (2013). The clustering pattern could be utilized in crossing the parents and deciding the cross combinations which may generate maximum possible variability for various traits. The genotypes with high values of any cluster can be used either for direct adoption or for hybridization for further selection and improvement. On the basis of yield performance, maximum inter cluster distance and some specialized characters, genotypes KBC-4, DC-15 and KBC-5 from cluster IV, CPD-78 and CPD-118 from cluster VIII, Mutant-3, Mutant-11, Mutant-10 and Mutant-12 from cluster V and Goa Local from cluster IX may be selected as being the most diverse and high yielding genotypes. In this study, cluster IV had the highest mean value for primary branches per plant and seed yield per plant was suitable for seed yield and cluster III had the minimum mean value for days to 50% flowering and days to maturity was suitable for early maturity therefore, genotypes from this cluster may directly be evaluated on multi locations for yield

Table 1: Analysis of variance for different quantitative characters in cowpea

Characters	Mean sum of squares		
	Replication	Genotypes	Error
Degree of freedom	2	71	142
Days to 50% flowering	3.34	21.15**	4.66
Days to maturity	2.35	25.41**	8.78
Plant height	23.10	1095.81**	19.76
Primary branches/plant	0.59	1.10**	0.20
Pods/plant	0.58	1.65**	0.33
Pod length	1.73	10.21**	0.61
Seeds/pod	0.86	6.49**	0.58
100-Seed weight	0.13	19.30**	0.27
Pod wall proportion	0.38	117.86**	2.97
Seed yield/plant	0.06	1.21**	0.14

** Highly Significant at 0.01 level of significance

Table 2: Distribution of 72 cowpea genotypes in nine different clusters

Clusters	No. of genotypes	Genotypes
I	33	GC-723, GC-810, GC-3, CPD-127, CPD-134, JOB-11, CPD-129, MUTANT-7, CPD-108, MUTANT-5, CPD-119, CPD-115, CPD-105, CPD-132, GC-3,GC-703, JOB-80BR, CP-107 , JOB-80BR, CPD-121, CPD-119, JOB-129, GC-3, CPD-108, GC-501, MUTANT-9, GC-817,PHULE-CP-5030, CPD-77, CPD-142, PHULE-CP-5040, JOB-129, RC-101
II	11	RC-19, MUTANT-6, SUBHARA, MUTANT-8, MUTANT-4, MUTANT-1, RC-101, RC-19, GC-521, CPD-115, PGCP-6
III	1	JOB-129
IV	3	KBC-4, DC-15, KBC-5,
V	4	MUTANT-3,MUTANT-10, MUTANT-12, MUTANT-11
VI	9	CPD-118, CPD-103, GC-3,CPD-136 , CPD-121, PTB-1, MUTANT-1, DCS-47-1, HC-38
VII	8	GC-525, NBC-1, GC-815, NBC-2, PGCP-12, NBC-2, CPD-83, CPD-83
VIII	2	CPD-78, CPD-118
IX	1	GOA LOCAL

Table 3: Inter and intra cluster distance values for different quantitative characters in cowpea

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	4.57 (20.88)	7.33 (53.73)	5.56 (30.91)	9.93 (98.60)	7.11 (50.55)	7.69 (59.14)	8.54 (72.93)	14.52 (210.83)	13.95 (194.60)
II		4.81 (23.14)	6.36 (40.45)	6.59 (43.43)	11.88 (141.13)	8.91 (79.39)	11.24 (126.34)	10.47 (109.62)	15.93 (253.76)
III			0.00 (0.00)	8.08 (65.29)	9.93 (98.60)	8.78 (77.09)	6.95 (48.30)	12.7 (161.29)	13.13 (172.40)
IV				3.12 (9.73)	14.68 (215.50)	9.77 (95.45)	11.54 (133.17)	8.35 (69.72)	13.67 (186.87)
V					4.52 (20.43)	9.84 (96.83)	10.62 (112.78)	19.39 (375.97)	15.41 (237.47)
VI						6.63 (43.96)	9.99 (99.80)	12.63 (159.52)	12.27 (150.55)
VII							6.45 (41.60)	15.54 (241.49)	9.95 (99.00)
VIII								5.09 (25.91)	16.8 (282.24)
IX									0.00 (0.00)

Table 4: Cluster means for ten characters under study and their contribution to total divergence

Characters / Clusters	I	II	III	IV	V	VI	VII	VIII	IX	% Contribution
Days to 50% flowering	39.77	39.45	37.67	46.44	38.67	40.81	41.54	38.33	50.33	0.31
Days to maturity	67.10	67.45	65.33	73.33	68.67	68.07	67.96	65.83	75.67	0.16
Plant height (cm)	41.01	43.18	30.53	53.18	40.47	78.67	46.12	90.9	88.63	19.33
Primary branches/plant	4.18	4.04	3.50	5.18	4.49	4.53	4.40	4.25	4.40	0.70
Pods/plant	4.40	5.00	4.23	4.12	4.56	4.49	4.00	5.05	3.50	0.59
Pod length (cm)	11.25	11.60	11.57	15.79	11.03	12.61	12.77	12.38	20.47	4.26
Seeds/pod	10.10	10.88	10.80	14.16	10.47	11.2	11.43	11.55	15.63	0.35
100-seed weight (g)	9.24	7.97	11.93	9.54	8.42	9.16	14.93	10.07	17.34	29.07
Pod wall proportion (%)	29.09	37.11	31.09	39.1	20.12	28.07	26.8	47.70	25.02	6.42
Seed yield/plant (g)	3.42	3.96	4.17	4.49	3.38	4.28	3.97	4.22	4.27	38.81

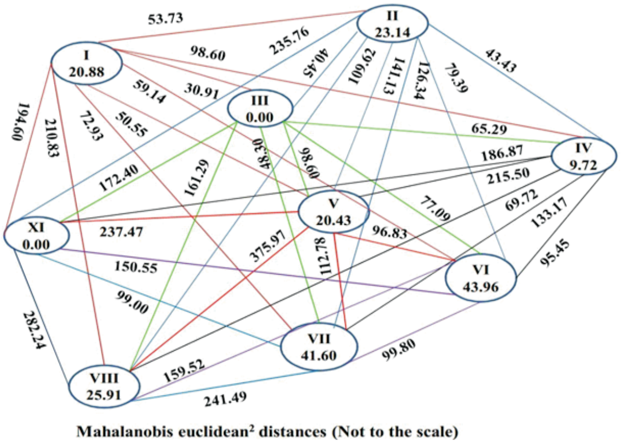

Figure 1: Diagram showing intra and inter cluster distances among IX cluster

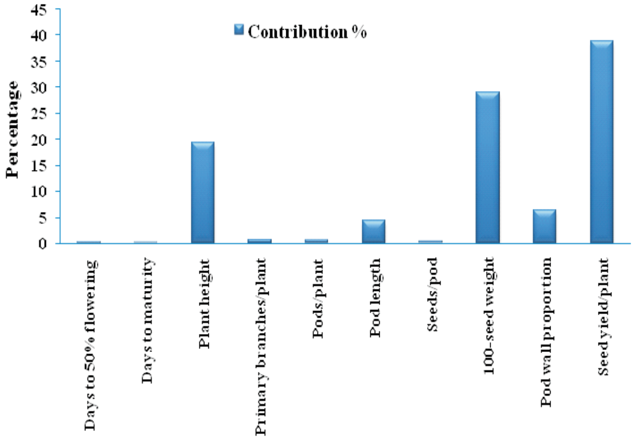

Figure 2: Contribution of different characters to total genetic divergence

or can be used as a donor parents in yield improvement programme.

On the basis of present investigation it can be concluded that vast amount of genetic variability was present in the genetic material. The genotypes fall into same cluster having lowest degree of divergence from each other and crosses among these genotypes of the same cluster unable to produce any transgressive segregants. While, the genotypes belonging to different clusters having maximum divergence and can be successfully utilize in hybridization programmes to get desirable transgressive segregants.

REFERENCES

Adewale, B. D., Adeigbe, O. O. and Aremu, C. O. 2011. Genetic distance and diversity among some cowpea (*Vigna unguiculata* L.

Walp) genotypes. *International Res. Plant Science*. **1(2):** 9-14.

Anbumalarmathi, J. and Nadarajan, N. 2007. Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]. *J. Ecobiology*. **19(2):**129-132.

Garje, U. A., Bhailume, M. S. And Nagawade, D. R. 2013. Genetic diversity analysis of green gram (*Vigna radiata* (L.) Wilczek.). *Bio Scan*. **8(4):** 1477-1480.

Hazra, P., Som, M. G. and Das, P. K. 1992. Selection of parents for vegetable cowpea breeding by multivariate analysis. *Veg. Science*. **19:** 166-173.

Kumar, D., Malik, B. P. S. and Singh, V. P. 1994. Assessing genetic divergence and identification of promising parents for hybridization in field pea (*Pisum sativum* L.). *Legume Research*. **17(3-4):** 225-228.

Kumar, H., Srivastava, A., Vishwakarma, M. K. and Lal, J. P. 2012. Genetic enhancement of variability through induced mutagenesis in two genotypes of *Brassica napus* L. *Madras Agric. J.* **99(4-6):** 228-231.

Kumawat, K. C. and Raje, R. S. 2005. Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]. *J. Arid. Legumes*. **2(1):** 25-27.

Mahalanobis, P. C. 1936. The generalized distance in statistics. *Proceeding of the National Ins. of Sci. of India*. **12:** 49-55.

Nagalakshmi, R. M., Usha, K. R. and Boranayak, M. B. 2010. Assessment of genetic diversity in cowpea [*Vigna unguiculata* (L.) Walp.]. *Electronic J. Plant Breedlng.* **1(4):** 453-461.

Nath, Vishwa., Lal, H., Rai, M., Rai, N. and Ram, D. 2009. Hierarchical Clustering and Character Association Studies in Cowpea [*Vigna unguiculata* (L.) Walp.]. *Indian J. Plant Genet. Resources.* **22:** 22-25.

Nielsen, S., Ohler, T. and Mitchell 1997. Cowpea leaves for human consumption, production, utilization and nutrient composition. In: *Advances in Cowpea Research*. Singh, B., Raj., Mohan., D. Dashiell, K. and Jackai, L. (Eds) International Institute of Tropical Agriculture (IITA) and Japan International Research Centre for Agricultural Sciences (JIRCAS), Ibadan, Nigeria. pp. 326-332.

Rao, C. R. 1952. Advanced statistical methods of Biometrical Research, *J. Willley and Sons, New York*. pp. 226-272.

Saxesena, R. R., Lal, G. M., Yadav, P. S. and Vishwakarma, M. K. 2013. Diversity analysis and identification of promising lines for hybridization in field pea (*Pisum sativum*). *The Bioscan.* **8(4):** 1437-1440.

Singh, R. K. and Choudhary, B. D. 1995. Biometrical Methods in Quantitative Genetic Analysis. *Kalyani Publisher*, New Delhi. pp. 215-238.

Zargar, S. A. and Tahirali, M. A. 2005. Genetic variability, heritability and genetic advance for seed yield and component traits in cowpea [*Vigna unguiculata* (L.) Walp.]. *J. Plant improvement.* **7(2):** 85-88.