

## Study of genetic divergence on vegetable cowpea [*Vigna unguiculata* (L.) Walp.]

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**Abstract:** The present investigation was carried out at Research Farm of the Department of Vegetable Science, CCS Haryana Agriculture University, Hisar during spring-summer season of the year 2011. Based on  $D^2$  values, forty six genotypes were grouped into eight clusters containing two to fifteen genotypes. These clusters consisted of genotypes with different geographical origins and indicated no correlation between genetic and geographical divergence. The genotypes of cluster VIII showed maximum genetic divergence with cluster V followed by Cluster II, hence, the genotypes belonging to cluster VIII and cluster V may be selected for generating genetic variability and hybridization. Cluster II having two genotypes was found to be the best performing for agronomic characters followed by cluster I with three genotypes and cluster V with three genotypes. Thus, to generate desirable genetic variability, the crossing between cluster II, I and V genotypes would be useful. It is suggested that hybridization among genotypes of above said clusters would produce segregants for more than one economic character which can serve as parents of hybrids. The number of seeds per pod contributed highest towards divergence followed by plant height at final harvest (cm).

**Keywords:** Cowpea,  $D^2$  statistics, cluster, genetic divergence

### Introduction

Cowpea is a multipurpose crop grown as green vegetable, grain, forage, green manure and cover crop under a wide range of climatic conditions. It is also a good companion crop with several food, fodder and fibre crops. Being a legume crop, it has the potential to fix atmospheric nitrogen to the tune of 240 kg/ha (Rachie 1985), and besides fulfilling its own nitrogen requirement, it leaves up to 60-70 kg/ha fixed nitrogen deposit in the soil for the succeeding crops. Being rich

source of protein (23-30%) and termed as vegetable meat, cowpea provides complementary proteins to the cereal based diets.

The average yield of cowpea is very low in India, and year to year variation in yield is also remarkably high, therefore, there is an urgent need to design breeding programme that can enhance productivity and stabilize the yield. It has also been well established that greater the genetic variability in the population greater will be the chance of obtaining desirable gene combination. Genetic divergence is of considerable practical interest in any crop improvement programme. The wide range in genetic diversity available in India has not been fully exploited to improve the yield of vegetable cowpea. Mahalanobis's  $D^2$  statistic as a tool for estimating genetic divergence in crop plants can be used to choose the parents without making crosses before the initiation of hybridization programme (Bhatt 1970). Therefore, the present investigation was undertaken to study the nature and magnitude of genetic divergence in forty six vegetable cowpea genotypes.

### Materials and Methods

The present investigation was carried out at Research Farm of the Department of Vegetable Science, Chaudhary Charan Singh Haryana Agriculture University, Hisar during spring-summer season of the year 2011. The 46 diverse cowpea genotypes procured from Indian Institute of Vegetable Research, Varanasi, Central State Farm, Hisar, Local market Hisar, Punjab Agricultural University, Ludhiana, Central Arid Zone Research Institute, Jodhpur and Chaudhary Charan Singh Haryana Agricultural University, Hisar and raised in a randomized block design (RBD) with three replications. There were two rows of three meter length of each genotype. Rows were spaced 60 cm apart and plants within a row at 15 cm. The data were recorded on five competitive plants selected randomly from each replication. The mean of five plants was used for

statistical analysis. For raising a healthy crop, the recommended package of practices was followed. The data were recorded on 13 parameters, *viz.* days to 50% flowering, days taken to horticultural maturity, days to first picking, days to last picking, total number of pickings, length of pod (cm), breadth of pod (cm), weight per pod (g), number of pods per plant, pod yield per plant (g), number of seeds per pod, plant height at final harvest (cm) and harvest index (%). The genetic divergence was worked out by using Mahalanobis  $D^2$  statistic as described by Rao (1952). Based on  $D^2$  values, these genotypes were grouped into different clusters by employing Euclidean cluster analysis.

### Results and Discussion

The analysis carried out for relative magnitude of  $D^2$  values for all the characters indicates that all the genotypes were grouped into eight clusters (Table 1). Among the clusters, the maximum number of genotypes (15) was included in cluster IV followed by cluster VII (11), cluster III (6), clusters I, V, VI and VIII (3 each) and cluster II (2). Generally, the geographical diversity has been considered as a measure of genetic diversity. However, this is an inferential criterion, and it may not be so effective in quantifying different populations. The present pattern of grouping of genotypes indicated that the genetic diversity was not fully associated with geographical diversity. These results are in close agreement with the findings of Venkatesan *et al.* (2004), Naher *et al.* (2005) and Anbumalarmathi and Nadarajan (2007).

There are forces other than geographical separation such as natural and artificial selection, exchange of breeding material, genetic drift, environmental variation, *etc.*, which are responsible for diversity in vegetable cowpea. Therefore, choice of the parents for hybridization should be decided on the basis of genetic diversity rather than geographic diversity.

The perusal of intra- and inter-cluster distances (Table 2) revealed that inter-cluster distance values were greater

than intra-cluster distance values. The maximum intra-cluster distance was observed for cluster-V (5.14) followed by cluster-I (4.25), cluster-VI (3.75), cluster-VII (3.35). The high intra-cluster distance in cluster-V indicated the presence of wide genetic diversity among the genotypes in this cluster, *viz.* Kashi Sudha, Arka Samrudhi and Kashi Unnati.

The nearest inter-cluster distance was found between cluster-III and IV (3.85) followed by cluster-IV and VII (4.26), cluster-III and VII (4.43). The widest inter-cluster distance was found between cluster-V and VIII (8.63) followed by cluster-II and VIII (8.49) and cluster-I and VIII (8.10). Cluster-VIII showed maximum genetic divergence with cluster-V and II. Based on these studies, the crosses may be attempted between the genotypes of cluster-V, *viz.* Kashi Sudha, Arka Samrudhi and Kashi Unnati followed by cluster- II, *viz.* Swarn Harita and Kashi Shyamal and cluster-VIII, *viz.* CST-5, CST-6 and CST-8 to obtain better recombinants in vegetable cowpea. For successful breeding programme, selection of genetically diverse parents is an important prerequisite so as to obtain better and desirable recombinants. Similar results were reported by Venkatesan *et al.* (2004), Naher *et al.* (2005), Anbumalarmathi and Nadarajan (2007) and Bertini *et al.* (2009).

The contribution of an individual character to the divergence has been worked out in terms of number of times it appeared first. This study helps in identifying the diversity in different proportion which ultimately helps in deciding the utilization of genetic material for the improvement of specific character. Among 13 characters studied, the highest contribution to the divergence was through number of seeds per pod followed by plant height at final harvest. Higher contribution of number of seeds per pod followed by plant height at final harvest to total divergence was also reported by Ushakumari *et al.* (2000) and Dalsaniya *et al.* (2009). The results imply that in order to select genetically diverse genotypes, the material should be screened for the important traits like number of seeds per pod and plant height at final harvest.

**Table 1:** Clustering pattern of 46 genotypes of cowpea based on  $D^2$  analysis

Clusters	Number of genotypes	Name of genotypes*
I	3	Pusa Komal, Kashi Kanchan and CST-10
II	2	Swarn Harita and Kashi Shyamal
III	6	Vanita, NDCP-13, Kashi Gauri, Kesari, Koninoor and Viscol
IV	15	CWP-11, CST-9, RCP-27, CST-1, CST-3, GC-3, BC-244002, NDCP-13-1, Lobia Banarsi, A.R. Garima, CST-11, Navkiran, Shalini, KBC-2 and RCV-319
V	3	Kashi Sudha, Arka Samrudhi and Kashi Unnati
VI	3	Pant Lobia-2, CST-7 and CST-2
VII	11	CST-4, A.P.-1, RCCP-1-1, DR-214, Chirodi, P-1-1-6, Ajeet-1, HC-46, FS-68, CST-12 and IRD-30
VIII	3	CST-5, CST-6 and CST-8

**Table 2:** Average intra- and inter-cluster D<sup>2</sup> values of cowpea genotypes in clusters

Clusters	I	II	III	IV	V	VI	VII	VIII
I	4.25	5.93	5.08	4.95	6.30	6.35	5.33	8.10
II		2.37	5.37	5.06	7.61	7.16	6.01	8.49
III			3.13	3.85	6.04	5.04	4.43	6.81
IV				3.26	6.87	4.72	4.26	6.12
V					5.14	7.67	7.78	8.63
VI						3.75	4.65	5.32
VII							3.35	6.18
VIII								2.90

**Table 4:** Cluster mean values for various characters in vegetable cowpea

Cluster	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	Total Score	Rank
I	53.11 (3)	22.55 (2)	78.77 (2)	97.22 (2)	3.00 (7)	16.08 (5)	0.91 (3)	4.91 (2)	23.66 (2)	99.45 (2)	7.80 (3)	52.59 (7)	19.41 (3)	43	II
II	54.66 (1)	23.16 (1)	80.00 (1)	100.33 (1)	4.00 (3)	34.98 (1)	1.01 (1)	2.72 (4)	13.16 (8)	40.61 (5)	6.80 (4)	107.99 (2)	17.22 (4)	36	I
III	54.22 (2)	17.50 (7)	74.61 (5)	95.00 (3)	3.61 (6)	19.15 (3)	0.82 (4)	3.86 (3)	17.94 (4)	74.85 (3)	4.99 (7)	126.19 (1)	20.54 (2)	50	IV
IV	53.04 (4)	19.64 (5)	75.15 (4)	94.60 (6)	3.95 (4)	17.58 (4)	0.91 (3)	2.44 (5)	17.22 (5)	39.49 (6)	5.44 (6)	87.73 (5)	13.61 (6)	63	V
V	51.77 (6)	19.44 (6)	73.44 (6)	94.66 (4)	4.00 (3)	20.53 (2)	1.00 (2)	10.19 (1)	24.77 (1)	153.25 (1)	4.84 (8)	73.62 (6)	34.36 (1)	46	III
VI	52.00 (5)	16.88 (8)	69.33 (7)	91.33 (7)	4.66 (2)	14.54 (6)	0.70 (6)	1.97 (8)	23.44 (3)	47.23 (4)	8.77 (1)	88.36 (4)	13.89 (5)	65	VI
VII	51.18 (7)	21.57 (3)	75.51 (3)	94.63 (5)	3.78 (5)	13.11 (8)	0.66 (6)	2.38 (6)	16.84 (6)	39.46 (7)	7.96 (2)	126.19 (1)	13.60 (7)	66	VII
VIII	37.66 (8)	20.88 (4)	61.88 (8)	86.66 (8)	4.88 (1)	13.49 (7)	0.82 (4)	2.30 (7)	16.44 (7)	33.44 (8)	6.35 (5)	94.36 (3)	13.55 (8)	78	VIII

In present investigation, it was observed that the genotype or genotypes grouped under cluster-II ranked first by having eight characters (1-3 scores) at desirable direction followed by genotypes under cluster-I with ten characters (1-3 scores) and cluster-V with seven characters (1-3 scores) (Table 4). The genotypes grouped under cluster-VIII (last rank) recorded eleven characters in negative direction (4-8 scores). Therefore, selection of genotypes followed in cluster-II, I and V would be useful to generate desirable genetic resource by crossing the genotypes under these clusters. It is suggested that hybridization among the genotypes of above said clusters would produce segregants for more than one economic character, which can serve as parents of hybrids.

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