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Characterization and evaluation of genetic divergence in Indian cowpea (*Vigna unguiculata* L. Walp.)

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Abstract
Genetic divergence studied in cowpea during *Kharif* 2016-17 at student farm of Chandra Shekhar Azad University of Agriculture& Technology, Kanpur (U.P.). The thirty two cowpea varieties were evaluated for eleven quantitative characters viz. days to flower initiation, days to maturity, plant height(cm),pod length(cm), number of pods per plant, number of branches per plant, leaf length (cm), leaf width (cm), leaf : stem ratio, st over of yield per plant (gm.) and seed yield per plant (gm.). Genetic divergence was determine using D^2 and all the thirty two genotype s were grouped into six cluster. Maximum inter cluster distance were observed between I and VI followed by cluster VI and IV and cluster VI and V. Cluster I hold first rank in days to initiation flowering, pod length, number of pods per plant, and Cluster II hold first rank in days to maturity, number of branches per plant and seed yield per plant and Cluster IV hold first rank in leaf width, leaf: stem ratio, st over yield per plant. It is suggested that the crosses between I, II and IV may be effective component characters in hybridization.

Keywords: Genetic divergence, genotype, cluster distance, hybridization

Introduction
Cowpea [*Vigna unguiculata* (L.) Walp.] Is a diploid species with (2n=2x=22) chromosome. It is an autogamous crop, with natural cross pollination of up to one percent. cowpea belongs to the class of Dicotyledonea, order Fabales, family Fabaceae, subfamily Faboideae, tribe Phaseoleae, sub tribe Phaseolinae, and genus *Vigna* (Pasquet *et al*. 2001) [12]. The Primary gene pool is composed of the domesticated cowpea (*V. unguiculata* sub sp. *Unguiculata var. unguiculata*) and its wild progenitor (*V. unguiculata sub sp. Unguiculata var. spontanea*). The secondary gene pool of cowpea includes nine perennial sub species.

All cultivated cowpeas are grouped under the species *Vigna unguiculata*, which is sub divided into four cultivar group such as unguiculata (common cowpea used as food and fooder), sesquipedalis (the yard long or aspergus been used as vegetables), biflora (catjang) and textilis (used for fibers). Cowpea exhibits different morphological forms; some are prostrate, erect or climbing. The leaves are trifoliate; inflorescences are axillary with few crowded flowers near the tip in alternate pairs. The anthers bear sticky and heavy pollen grains (Purseglove, 1984) [13]. Cowpea is produced for household purposes and as a cash crop. It is a multipurpose crop, since it is cultivated for leaf and seed yield**.** It is a multifunctional crop, providing food for man and livestock and serving as a valuable and dependable revenue-generating commodity for farmers and grain traders (Singh, 2002; Langyintuo *et al*., 2003) [15, 6]. Cowpea contributes 30-125 Kg N/ha in the soil due to its nitrogen fixing properties and also serves as a residue, which benefits the succeeding crops. It is also a shade tolerant crop and, therefore, compatible as an intercrop with a number of cereals and root crops, as well as with cotton, sugarcane and several plantation crops**.** In fresh form, the young leaves and immature pods are used as vegetables, while the grain is used in the preparation of several dishes. According to Bressani (1985) [5], the mature legume contains 23-25% protein and 50-67% carbohydrate, 1.9% fats, 6.35% fiber and small percentage of the B-vitamins such as folic acid, thiamine, riboflavin and niacin as well as some micronutrients such as iron and zinc. In India cowpea is a very important crop and cultivated for food, vegetables and fodder purpose. Crop due to its tremendous adoptability for various conditions cultivated from north Jammu& Kashmir to south Tamil Nadu. Cowpea is a very popular vegetable crops and being cultivated in all over country except hilly regions.

In India, it mainly grown in Rajasthan, Gujarat, Maharashtra, Karnataka, Tamil Nadu, Bihar and Uttar Pradesh. As a grain legume it has a great potential for sustainable agriculture in marginal land and semi-arid regions of country. It is estimated that about 6.5 lakh hectare is under different forms of Cowpea and the share of fodder cowpea is 3 lakh hectares.

In India a very systematic breeding programme is being carried in different research institution and universities. Cowpea varietal improvement programme in country has resulted in the development many improved and high yielding varieties for grain, vegetable and fodder purpose. Maximum varieties has been released for vegetable purpose followed by fodder cowpea more than 25 varieties so far has been released for the cultivation in different part of the country. Released varieties has been developed mostly by utilizing exotic lines as parent mainly introduced CG system Institute viz. IITA, Nigeria. In cowpea breeding programmes mostly emphasis is given to develop varieties for high yield, diverse maturity, suitable plant type, dual purpose use, resistant to biotic and abiotic stress and physiological and nutritional qualities of seed and fodder.

Material and method

The experimental materials of the study comprised of 32 cowpea varieties from Indian origin. These varieties were procured from germplasm lines available in cowpea Section, Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur. These thirty two genotypes are as under. A field experiment was conducted during *kharif* season 2016-17 at the student Research Farm, CSAUAT, Kanpur. All the genotypes were sown in Randomized Complete Block Design with three replications. Each genotype was sown in four lines in 3.0 m long and 1.50 m broad plots and space planted at 75 cm between row to row and plant to plant distance respective.

Result and discussion

The present investigation resulted in classification of thirty two national/ state released cowpea varieties into six clusters. Cluster IV comprises of eight genotypes followed by Cluster VI comprises of seven genotypes, followed by Cluster I and III comprises of six genotypes, Cluster V have four genotypes and Cluster II contain one genotype. The intra and inter-cluster distances did not very much in their magnitude which was in general low. Low value of intra and inter- cluster distance reflect that there is comparatively less expression of genetic differentiation between genotypes for the characters consider for the study Narayanankutty *et al.* (2005) [11] while classifying cowpea germplasm observed that number of pods per plant and pod length had the highest contribution to genetic divergence. In present study also these traits showed significant contributions.

The maximum cluster distance was observed between cluster VI and cluster I, followed by cluster VI to cluster IV, cluster VI and cluster V, cluster VI and cluster II, this indicates that strains include in these clusters had high genetic diversity so they can utilize in hybridization program for obtaining desirable recombinants in order to develop high yielding varieties. Lowest inter – cluster distance was observed between cluster II and cluster I, followed by cluster III and cluster IV and cluster IV and cluster V. This indicates that strains include in these clusters were closely related. So the clusters present in this genotypes present in these clusters may not yield better recombinants. To exploit genetic diversity through hybridization program inter- cluster distance must be taken into consideration. Genetic diversity is directly proportional to the inter- cluster distance. Higher the distance between cluster greater the diversity between them and vice versa.

Intra – cluster distance ranged from cluster I (447.919) to cluster VI (303.319). The cluster with lower intra – cluster distance indicates the compactness of the group (Table 1).

Cluster mean of the eleven characters under study marked considerable genetic differences among the group. Cluster I holds first rank in days to flower initiation, pod length, number of pod per plant. Cluster II holds first rank in days to maturity, number of branches per plant, seed yield per plant. Cluster IV hold first rank in leaf width, leaf: stem ratio, Stover yield per plant. Cluster V hold first rank in plant height and leaf length.

Maximum contribution to the divergence was made by number of pod per plant, followed by leaf: stem ratio, plant height, and days to maturity, leaf length, and pod length (Table 2 & 3).

Grouping of the varieties also observed a set trend. Vegetable type cowpea varieties (Kashi kanchan, Kashi nidhi, Kashi gauri, Kashi sudha, Kashi unnati) along with grain type varieties (Pant Lobia -1, and pant Lobia -2 accumulated in the cluster VI. The grouping genetic related varieties were also observed for cluster V where all the fodder varieties developed for GBPUA& T Pantnager and have genetic lineage pooled in one cluster. This showed the efficiency of clustering method to pool genetic similar varieties in one group (Table 3).

The above discussion clearly showed wide variation from one cluster to another in respect of cluster of cluster mean for eleven characters, which indicated that genotypes having distinctly different mean performance for various characters were separated into different clusters. The crossing between the genotypes belonging to cluster distance and possessing high cluster mean for one or other characters to be improved. It may be recommended for isolating desirable recombinants in segregating vary diverse genotypes, because the frequency of heterotic crosses and magnitude of heterosis for yield and it's components were found to be higher in crosses between parents with intermediate divergence than the extreme ones.

Based on the D^2 analysis it is reasonable to assume that the genetic material under study would form groups or clusters of genotypes in which measurement for various characters are normally distributed. The genotypes belonging to distant cluster with high cluster mean may be identified to be utilized further in the hybridization programme.

Table 1: Inter and intra cluster distances (D^2) among six clusters for thirty two genotype in cowpea.

Cluster number	I	II	III	IV	V	VI
I	447.919	845.575	1039.022	943.458	1827.994	4518.804
II		0.000	1292.443	1365.604	1255.993	2883.984
III			270.679	438.879	1197.095	2562.997
IV				315.188	905.685	3658.075
V					310.805	3231.180
VI						303.319

Table 2: Range of Cluster mean value for eleven characters in cowpea.

S No	Characters	Range	
		Min.	Max.
1	Days to flower initiation	36.762	57.056
2	Days to maturity	40.714	68.000
3	Pod length (cm)	16.667	20.444
4	Plant height (cm)	60.071	166.208
5	Number of pod per plant	13.833	48.000
6	Number of branches per plant	4.111	6.267
7	Leaf length (cm)	8.767	10.718
8	Leaf width (cm)	5.200	7.292
9	L:S ratio	0.376	0.769
10	Stover yield per plant (gm.)	89.081	227.417
11	Seed yield per plant (gm.)	51.429	121.667

Table 3: Cluster mean among six clusters for eleven characters of thirty two.

Cluster no	Days to flower initiation	Days to maturity	Pod Length (cm)	Plant Height (cm)	Number of Pod per plant (cm)	Number of Branches per plant	Leaf length (cm)	Leaf width (cm)	L:S ratio	Stover yield per plant (gm.)	Seed yield per plant (gm.)
I	57.056	64.000	20.444	140.944	48.000	5.211	9.272	6.592	0.749	206.156	64.444
II	55.667	68.000	16.667	122.667	29.000	6.267	8.767	5.200	0.643	177.500	121.667
III	38.333	44.333	17.000	139.089	39.778	4.111	10.288	7.379	0.684	190.739	67.944
IV	40.625	48.000	17.375	156.583	37.667	4.667	10.718	7.929	0.769	241.883	90.625
V	44.000	53.500	17.250	166.208	13.833	4.383	11.025	7.285	0.728	227.417	87.500
VI	36.762	40.714	17.381	60.071	19.429	5.648	10.650	5.778	0.376	89.081	51.429

Table 4: Grouping of thirty two genotypes of cowpea into six clusters on the basis of D^2 analysis.

S. No	Genotypes	No of genotype per cluster
1	CO-5,C-88,C-74,UPC-4200,COFC-8,UPC-287	6
2	Kokan Sadabahar	1
3	Aishwarya, BL-1, IL-1177, CL-367, EC-4216, UPC-618	6
4	Kohinoor, KFC, BL-2, UPC-621, UPC-625, UPC-628, UPC-8705, UPC-5287	8
5	UPC-5286, UPC-9202, UPC-622, UPC-607	4
6	Kashi Kanchan, Kashi Nidhi, Kashi Gauri, Kashi Sudha, Kashi Unnati, Pant Lobia -1, Pant Lobia-2	7

Genotypes in cowpea.

Summary & Conclusion

Mahalanobis D^2 statistics was used to the genetic divergence in the present group of material. All the thirty two genotypes were classified into six clusters. Cluster IV comprise the eight genotypes followed by cluster VI comprises of seven genotypes, followed by cluster I and III comprises of six genotypes, cluster V comprises four genotypes and cluster II having one genotypes.

Maximum inter-cluster distance was observed between cluster I and cluster VI, followed by cluster IV and cluster VI, cluster III and cluster VI, cluster IV and cluster VI, Cluster VI and cluster II and lowest inter-cluster distance was observed between cluster III and cluster IV followed by cluster I and cluster II, and cluster V and cluster IV. For high yield cluster I and cluster VI are found desirable because cluster I holds first rank in days to flower initiation, pod length, number of pods per plant, cluster IV holds first rank in leaf width, leaf : stem ratio Stover yield per plant. So the most desirable clusters is cluster I which is holding first rank in number of pods per plant followed by cluster IV stood first rank in Stover yield per plant, cluster II holds promise first rank in seed yield per plant. Number of pods per plant (31.45) had maximum contribution in the exixtance diversity of genotype followed by leaf: stem ratio (17.14), plant height (15.73), days to maturity (13.10), leaf length (8.87), pod length (4.64), while minimum contribution by leaf width (2.82) and Stover yield per plant (2.42).

Hence it is quite clear that these clusters are most desirable for breeding programme for creating the desired variability as well as for effective selections hitherto.

The maximum inter cluster distance had been observed between I and IV followed by cluster VI and IV, cluster VI and V, cluster VI and cluster II. Cluster IV holds first rank in leaf width, leaf: stem ratio, Stover yield per plant and cluster II holds first rank in days to maturity, number of branches per plant, seed yield per plant. For the development of superior hybrids we have to make the crosses between the inbred of cluster I & IV and II & IV. Number of pods per plant (31.45) had maximum contribution in the exixtance diversity of genotype followed by leaf: stem ratio (17.14), plant height (15.73), days to maturity (13.10), leaf length (8.87), pod length (4.64). Remaining traits had minimum or no contribution in divergence.

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