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Study of Genetic Divergence for Yield and Quality Traits in Cowpea [*Vigna unguiculata* (L.) Walp.]

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ABSTRACT

Background: The genetic divergence analysis was done using Mahalanobis D^2 statistics. The mean intra-cluster and inter-cluster D^2 values are compared for drawing conclusions on superiority of cowpea genotypes for various plant yield and quality attributes.

Method: In the field of Vegetable Research Farm of Department of Horticulture, RPCAU, Pusa, Indiaduring 2018-19 (Rainy season) thirty-three cowpea genotypes were taken for genetic divergence analysis. The genotypes exhibited marked divergence and thus grouped into clusters following Tocher's method of clustering. The mean intra-cluster and inter-cluster D^2 values among the clusters were compared for their superiority of yield and quality attributes.

Result: All the selected genotypes displayed marked divergence. Among the five clusters, Cluster I consisted eight, Cluster II had three, Cluster III had eleven, Cluster IV had nine and Cluster V had two genotypes.The clustering pattern had no parallelism between genetic diversity and geographical distribution, suggesting that the selection of parental genotypes for hybridization will be more appropriate based on genetic diversity. The intra-cluster D^2 values ranged from 0.00in cluster II, cluster III, cluster IV and cluster V to 16.12 in cluster I. The inter-cluster D^2 values revealed that highest inter-cluster generalized distance (44.50) was between cluster V and cluster III, while it was the lowest (20.12) between cluster II and cluster I. From this study it can be concluded that for selection and heterotic recombinants emphasis may be given to attributes such as seed germination percentage, peduncle length and average pod weight to enhance the yield of cowpea. Similarly, with respect to the clusters for obtaining the heterotic recombinants, genotypes placed in cluster V, cluster II and cluster III may be used in the crossing program.

Key words: Clusters, Cowpea, Divergence, Genotype, Mahalanobis D^2.

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INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp.] is an annual, autogamous leguminous crop belonging to family Leguminaceae (Mackie and Smith, 1935) with a diploid chromosome number of 2n=2x=22 (Darlington and Wylie, 1955). It is native to India (Vavilov, 1949) but tropical and central Africa is also considered as a secondary center of origin (Ng and Marechal, 1985). Cowpea is considered as one of the most important food legumes of the world, especially in countries of the tropics and sub-tropics, such as Africa, Asia, Central and South America (Singh *et al*., 1997; Anonymous, 2017). Due to high protein content, cowpea is called 'Vegetable meat' and has high grain and biological value on a dry weight basis. It is commercially grown throughout India and is used for multiple purposes such as long green pods, seeds as pulses, foliage as fodder for the milch animal, green manuring and cover crop (Meena *et al.,* 2017). Cowpea cultivars grown for immature green pods are commonly referred to as southern pea, black eye pea, crowder pea, lobia, niebe, caupi or frijole (Dahiya *et al.,* 2007; Mishra, 2007; Diouf, 2014). Globally India ranks second in vegetable production as it contributes 15.7% to the global vegetable area and 14.5% to global production *i.e.*187.47 million tonnes (Anonymous, 2020b).

As per the nutritional profile is concerned, cowpea grain contains 23.4% protein, 1.8% fat and 60.3% carbohydrates and it is a good source of vitamins and phosphorus (Venkatesan *et al*., 2003). In India and South East Asia, cowpea is well known for immature tender pods and dry seeds are considered as an economical source of protein (20.25%) (Salimath *et al*., 2007; Anonymous, 2020a). Cowpea is also valued for the fact that it is low in fat and high in fibers and the protein in pod legumes has been shown to reduce low-density lipoproteins that are implicated in heart diseases when harvested at appropriate maturity stage (Prasad *et al.,* 2018b). Some recent uses of cowpea include vegetable mixture, baking powder of biscuits, vegetable milk and legume starch (Hall *et al.,* 2003; Manggoel *et al*., 2012; Dovi, 2013). Cowpea is also well known for its postharvest value and responds very well to postharvest treatments such as edible coatings, packaging, *etc.* (Prasad *et al.,* 2018a). It is a most versatile pulse crop because of its smothering nature, drought-tolerant character, soil-restoring properties and multi-purpose uses (Hall *et al.,* 2003).

As a pulse crop, cowpea fits well into most of the cropping system (Singh *et al.,* 2018) varieties of cowpea with a "persistent-green" grain have been developed by the breeding program in the USA that is a versatile product for frozen vegetable applications. (Nwosu *et al*., 2013; Anonymous, 2020b). The variability of qualitative and quantitative characters of the breeding material will help to a breeder in its genetic improvement. Since the improvement in cowpea is concerned with the selection of superior genotypes for which the most suitable individuals from their phenotypic expression, estimates of genotypic and phenotypic variance for various quantitative characters and their heritability are necessary (Jogdhande *et al.,* 2017).

The D^2 statistics developed by Mahalanobis (1936) is a potential tool for obtaining quantitative estimates of divergence among biological populations and has extensively been utilized to assess diversity. Moreover, the relative contribution of different yield components to total divergence using Mahalanobis's D^2 analysis helps in the identification of selected parameters to be used as criteria for improvement in yield (Dalsaniya *et al*., 2009).

MATERIALS AND METHODS

The experiment was conducted during 2018-19 (Rainy season) at Vegetable Research Farm of Department of Horticulture, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar. Pusa of state Bihar is located at a longitude of 85.67^0 E and latitude of 25.98^0 N. This place is situated at an altitude of 52.0 meters above mean sea level. The soil of Pusa (Samastipur) is mainly young alluvium and calcareous. Soil is deep, light to heavy in texture having $CaCO_3$ more than 10 percent and up to 30 percent. This region has a subtropical climate with an extreme of summer and winter. The experimental materials consisted of thirty-three lines of cowpea genotypes including one check variety *viz.* Kashi Unnati. The genotypes were collected from IIVR-Varanasi, GBPUA andT Pantnagar, CAZRI Jodhpur and from local. The experiment was conducted in a randomized block design with three replications at RPCAU, vegetable research farm, Pusa Samastipur. The seeds were sown on the 21st of August, during monsoon-season 2018 in plot size 378 m^2. After the final preparation of the land, the field was divided into 99 plots of size 378m^2. The seeds of cowpea were dibbled in 60×45 cm apart. The observations were recorded from five randomly selected plants in each replication for all characters following *viz*., seed germination percentage, plant height (cm), number of branches per plant, days to first flowering, first flowering node, number of nodes on the main stem, peduncle length (cm), number of pods per cluster, day to first picking, pod length(cm), pod diameter (cm), average pod weight (g), number of pods per plant, number of seeds per pod,100 seed weight (g), pod yield per plant (g).

Table 1: Analysis of variance for sixteen characters in cowpea.

Source of variation / Characters	Mean sum of squares		
	Replication	Treatments	Error
	(d.f=2)	(d.f=32)	(d.f=64)
Seed germination percentage	9.114	23.427*	6.485
Plant height (cm)	73.098	2268.543*	30.642
Number of branches per plant	9.114	23.427*	6.485
Days to first flowering	0.545	14.015*	1.375
First flowering node	0.025	0.398*	0.034
Number of nodes on main stem	0.001	0.397*.	0.042
Peduncle length (cm)	5.336	24.075*	2.191
Number of pods per cluster	0.075	0.153*	0.051
Days to first picking	1.828	13.017*	2.161
Pod length (cm)	5.180	72.077*	3.679
Pod diameter (cm)	0.008	0.035*	0.005
Average pod weight (g)	29.360	1311.66*	9.715
Number of pods per plant	18.468	105.138*	7.101
Number of seed per pod	1.887	7.863*	1.361
100 seed weight (g)	0.220	6.034*	0.106
Pod yield per plant (g)	232.180	13655.57*	231.209

**Significant at p = 0.01 * Significant at p = 0.05.

Statistical analysis

The collected data were subjected to Analysis of Variance (ANOVA) using MS-Excel, OP-STAT software available from HAU, Hisar and presented in Table 1 and genetic divergence (D^2) was worked out according to Mahalanobis (1936) using SPAR-1 software. A dendrogram was generated using the

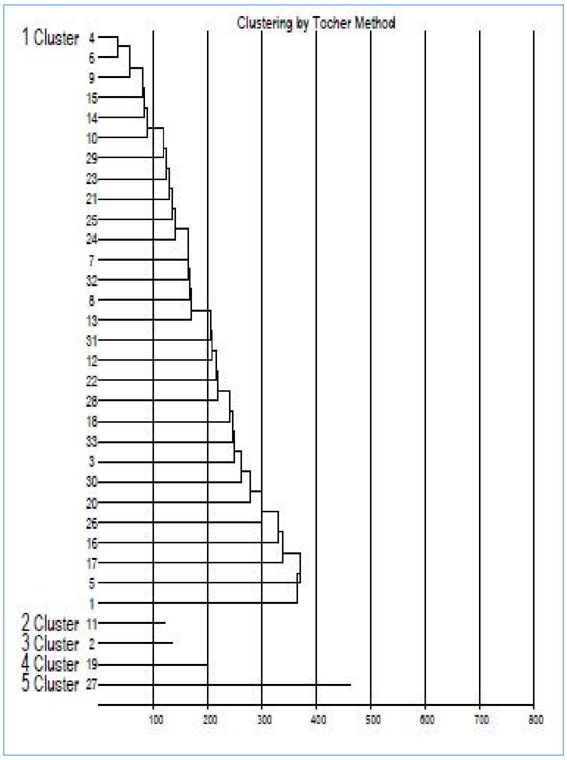

Fig 1: Clustering pattern of thirty-three genotypes of cowpea based on D^2 statistics by Tocher's method.

Table 2: Clustering pattern of thirty-three genotypes of cowpea.

Cluster	Number of genotypes	Name of genotypes
Cluster I	8	EC-724729, PL-2, EC-724678, EC-724651, EC-725167, PL-1, PL-4, EC-19736.
Cluster II	3	Kashi Unnati, Kashi Kanchan, Kashi Gouri.
Cluster III	11	EC-390252, EC-724767, PL-5, GP-56, EC-725189, EC-724765, EC-725167, EC-724761, EC-725141, Triguna, Chirag.
Cluster IV	9	Bihar Germplasm-1, Bihar Germplasm-2, Bihar Germplasm-3, Bihar Germplasm-4, Bihar Germplasm-5, Anupama, Nikita, Bodichilmarakodihar and PL-3.
Cluster V	2	EC-390237, EC-725197

Wards method and Euclidean distance as a measure of similarity with the help of SPSS software version 16 and is presented in Fig 1.

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the characters studied, indicating the existence of wide genetic divergence among them. Information on genetic diversity was also used to identify promising diverse genotypes, which may further be used in breeding programs.

In context to the performance of various traits, the thirty-three genotypes were grouped into five clusters based on the genetic divergence D^2 values (Table 2). Cluster III had the largest number of eleven genotypes followed by nine genotypes in cluster IV, eight genotypes in cluster I, three genotypes in cluster II while only two genotypes in cluster V. Similar results were also reported by Venkatesan *et al*. (2004), Madheshia and Pandey (2005) and Brahmaiah *et al*. (2014).

The cluster means of different traits shown the wider difference between the cluster means (Table 5). The highest cluster mean values for the first flowering node were maximum in cluster I, cluster II had maximum cluster mean value for seed germination percentage, 100 seed weight and pod yield per plant. Cluster III had a maximum cluster mean value for plant height and pod diameter. Cluster IV had a maximum cluster mean value for the number of branches per plant, pod length and average pod weight.

Cluster V had maximum cluster mean value for days to first flowering, number of nodes on the main stem, peduncle length, number of pods per cluster, days to first picking, number of pods per plant, number of seeds per pod, number of pods per cluster, number of nodes on main stem and number of seeds per pod. Genotypes namely EC-390237 and EC-725197 can be used further for enhancing the pod yield per plant. Whereas, the genotypes Kashi Unnati, Kashi Gouri and Kashi Kanchan may be used as one of the diverse parents to develop a more number of recombinants for yield improvement. Similar approaches as mentioned in the above discussion suggestion were given by Venkatesan *et al*. (2004), Dalsaniya *et al*. (2009), Kumari *et al.* (2010), Brahmaiah *et al*. (2014), Kumar and Kumar (2015).

Table 3: Intra and Inter-cluster distance (D^2) among five clusters in cowpea.

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	**16.12**	20.12	20.62	23.83	32.29
Cluster II		**0.00**	21,17	30.81	38.32
Cluster III			**0.00**	27.50	44.50
Cluster IV				**0.00**	27.65
Cluster V					**0.00**

Table 4: Contribution percentage of sixteen characters towards genetic divergence in cowpea.

Source	Times ranked 1st	Contribution percentage
Seed germination percentage (%)	0	0.00%
Plant height (cm)	125	23.67%
Number of branches per plant	0	0.00%
Days to first flowering	12	2.27%
First flowering node	17	3.22%
Number of the node on the main stem	20	3.79%
Peduncle length (cm)	3	0.57%
Number of pods per cluster	0	0.00%
Days to first picking	3	0.57%
Pod length (cm)	9	1.70%
Pod diameter(cm)	1	0.19%
Average pod weight (g)	95	17.99%
Number of pods per plant	4	0.76%
Number of seed per pod	0	0.00%
100 seed weight (g)	158	29.52%
Pod yield per plant (g)	81	15.34%

The maximum inter-cluster distance was recorded between cluster V and cluster III followed by cluster V and cluster II (Table 3). The maximum mean value for the characters was recorded in cluster V *viz*, first flowering node, number of nodes on the main stem, peduncle length, number of pods per cluster, days to first picking, number of pods per plant and number of seeds per pod and followed by cluster II for the traits namely seed germination percentage, days to first flowering, 100 seed weight and pod yield per plant, suggesting that to have the heterotic recombinants for the improvement of above mentioned eleven traits. Genotypes from cluster V and cluster II may be used in crossing program as it is evident that high cluster means value recorded for seed germination percentage and peduncle length having the positive and high direct effect

Table 5: Cluster mean value for sixteen characters in cow pea.

Clusters	SGP	PH	BPP	DFF	FFN	NMS	PDL	PPC	DFP	PL	PD	APW	PPP	SPP	SW	PYP
Cluster I	92.52	73.57	4.81	43.45	3.51	3.13	35.84	3.54	54.09	28.51	0.66	62.12	34.59	16.27	13.45	127.05
Cluster II	96.75	60.14	3.29	39.52	3.18	3.39	34.68	3.81	49.41	28.17	0.60	66.56	23.69	14.60	13.72	275.75
Cluster III	91.89	113.38	4.62	44.04	3.17	3.39	37.41	3.79	54.48	27.65	0.71	57.51	31.34	16.87	12.27	171.21
Cluster IV	96.47	82.20	4.85	43.98	3.33	3.49	35.38	3.59	55.02	33.96	0.62	79.94	38.18	16.12	11.19	236.16
Cluster V	93.89	70.54	3.41	44.49	3.08	3.61	38.38	3.92	55.74	20.59	0.53	36.83	44.55	18.19	13.54	139.79

SGP=seed germination percentage, PH=plant height(cm), BPP=number of branch per plant, DFF=days to first flowering, FFN=first flowering node, NMS=number of nodes on main stem, PDL=peduncle length(cm), PPC=number of pods per cluster, DFP=days to first picking, PL=pod length(cm), PD=pod diameter(cm), APW=average 10 pod weight(g), PPP=number of pods per plant, SPP=number of seeds per pod, SW= 100 seed weight (g), PYP=pod yield per plant

on pod yield per plant. Similar results were also obtained by Dalsaniya *et al.* (2009), Kumar and Kumar *et al.* (2015), Jogdhande *et al*. (2016) and Singh and Srivastava (2017).

The contribution of different plant characters towards divergence is important for further selection and choice of the parents for hybridization (Table 4). The maximum character contribution towards divergence was recorded for 100 seed weight followed by plant height, average pod weight, pod yield per plant and very meager contributions were found for the rest of the traits. Similar results were obtained by Bakiyarani (2000), Borah and Khan (2002), Kumar and Kumar (2015) and Kwaga (2014) in legume crops.

CONCLUSION

Based on all these results we can conclude that during selection emphasis may be given to seed germination percentage, peduncle length and average pod weight to enhance the yield of cowpea. For obtaining the heterotic recombinant genotypes placed in cluster V, cluster II and cluster III may be used in the crossing program. Further heterotic recombinants may be obtained for enhancing peduncle length, average pod weight and seed germination percentage.

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