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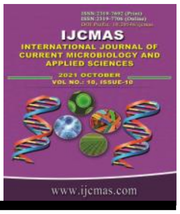

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Genetic Diversity Studies in Seed Cowpea (*Vigna unguiculata* L. Walp) Genotypes

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ABSTRACT

Thirty three seed cow genotypes (*Vigna unguiculata* L. WALP) collected from different geographical region were assessed for their genetic divergence based on ten characters during kharif-2020 at Post Graduate Farm, MPKV, Rahuri. The genotypes were grouped into six clusters which indicating high genetic diversity among them. It indicated that genetic diversity and geographic diversity are not related. The present study revealed that days to 50% flowering contributed maximum (34.09%) for divergence followed by plant height (32.58%), number of pods per plant (10.98%) and test weight (8.71%). Based on inter-cluster distance, intra-cluster distance and *per se* performance the genotypes viz., CP-04, CP-10, CP-10R, PCP-1411, CP-37, CP-10R,CP-39 and Phule Sonali are suggested to utilize for future breeding programme.

Introduction

Cowpea is a tropical grain legume which plays nutritional role of the tropics and sub tropics, especially in Sub-Saharan Africa, Asia, Central and South America (Singh *et al.*, 1997). Cowpea is grown worldwide on 12.61 million ha with an annual grain production about 5.59 million tons and the productivity of 20-25 kg/ha. In India the Cowpea is grown in an area of about 1.3 million ha with a production of 2.1 million tones having a productivity of 607 kg/ha (www.cazri.res.in). Cowpea is one of oldest legume used as protein source for humans and livestock. Dry seeds of cowpea are used to prepare several meal and snacks dishes. It contains high amount of quality protein (23.4 %), carbohydrate (60.3 %), fat (1.8 %) and sufficient amount of calcium (76 mg/100gm), iron (57 mg/100gm) and vitamins such as thiamine (0.92 mg/100g.), riboflavin (0.18 mg/100g.) and nicotinic acid (1.9mg/100g) (Chatterjee and Bhattaacharya, 1986).

The nature and magnitude of genetic divergence in a population is essential for selection of diverse parents, which upon hybridization leads to a wide spectrum of gene recombination for quantitatively inherited traits. Multivariate analysis is a powerful tool in quantifying the degree of divergence in germplasm collection of crop plants. In present study, genetic divergence among thirty three genotypes of seed cowpea collected from different geographical region were quantitatively assessed by adopting Mahalanobis D^2 statistics based on seed yield and yield attributes.

Materials and Methods

Experiment was conducted at Post Graduate Farm, MPKV, Rahuri comprised of thirty three during *kharif*, 2020-21 in RBD design with two replication. Observation were recorded on five randomly selected plants for ten *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), number of main branches, number of pods per plant, pod length cm), number of seeds per pod, test weight (g), seed yield per plant (g), and crude protein content (%). Analysis of variance was estimated as per procedure proposed by Panse and Sukhatme (1995). Significant differences between genotypes based on the pooled effects of all the traits were tested by Wilk's 'λ' (Statistics) criterion (1932). Genetic divergence estimated by multivariate analysis using Mahalanobis D^2 statistics (1936). The genotypes were grouped into different clusters as per Tocher's method as described by Rao (1952).

Results and Discussion

The analysis of variance showed highly significant difference among the genotypes for all the characters studied.

Thirty three genotypes were grouped into 6 clusters (Table 1) as per Tocher's method as described by Rao (1952). Cluster I was the largest with 24 genotypes, followed by cluster III with 4 genotypes, followed by cluster IV with 2 genotypes. Cluster II, V and VI were monogenotypic. These genotypes grouped in monogenetic clusters maintained separate identity and exhibited high genetic diversity with most of the other clusters. Earlier workers Lal *et al.*, (2017) who also grouped 89 genotypes genotypes into 11 clusters; Patel *et al.*, (2017) grouped 32 genotypes into 8 clusters and Purohit *et al.*, (2020) grouped 42 genotypes into 8 clusters.

Distribution of genotypes in different clusters was random but it has clearly shown relationship with the characters for which they were bred. It indicated that genetic diversity and geographic diversity are not related. Similar findings were also reported by Nagalakshmi *et al.*, (2010) and Tigga and Tandekar (2013) in seed cowpea.

The averages inter and intra cluster D values are presented in (Table No.2). The maximum intra cluster distance observed by cluster III (11.88) followed by cluster I (10.30), IV (8.32), and rest of cluster had zero intra cluster distance as they have only one genotype (monogenic).

The maximum inter cluster distance showed by cluster I and cluster VI (31.31) followed by cluster III and VI (29.49), cluster II and VI (27.39), cluster I and IV (27.26), cluster III and IV (21.10) and cluster IV and V (20.94). These results suggest maximum divergence between genotypes grouped in these clusters indicating the fact that the genotypes included in one cluster differ entirely from those present in other clusters.

A comparison of the mean value of ten characters of different clusters is presented in the (Table 3). Considerable differences in cluster mean values were evident for all the characters. Cluster V was identified for the earliness for flowering, high crude protein content and seed yield par plant. The highest mean value for pod length and test weight was for II while, highest cluster mean for number of branches and pods per plant were recorded by cluster IV.

Table.1 Distribution of 33 cowpea genotypes into different clusters

Clusters	No. of genotypes included	Name of genotype
I	24	PCP-1124, PCP-1409, PMCP-1018, CP-07, PCP-1403, PCP-1408, CP- 16CP- 38, CP-01R, CP-02R, PCP-1110, PCP-1402, PMCP-1016, PCP-1106, CP-05, CP-06, CP-12, CP 03R, CP- 36, CP-41, CP-09R CP-10R, Phule Pandhari and Phule Vittai
II	1	CP-10
III	4	PCP-1411, CP-17, CP-04, PCP-1404
IV	2	CP-13R, CP-39
V	1	Phule Sonali
VI	1	CP-37

Table.2 Average intra (bold) and inter cluster distance (D) and D^2(in bracket) values for six clusters in thirty three cowpea genotypes

Cluster	I	II	III	IV	V	VI
I	**10.30 (106.09)**	13.69 (187.41)	14.35 (205.92)	27.26 (773.10)	14.00 (196)	31.31 (980.31)
II		**0.00**	8.22 (67.56)	18.11 (327.97)	14.83 (219.92)	27.39 (750.21)
III			**11.88 (141.13)**	21.10 (445.21)	16.75 (280.56)	29.49 (869.66)
IV				**8.32 (69.22)**	20.94 (438.48)	18.00 (324)
V					**0.00**	19.78 (391.24)
VI						**0.00**

Table.3 Mean values of the six clusters for ten characters in thirty three cowpea genotypes

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of main branches	No. of Pods Per Plant	Pod Length (cm)	No. of seed per pod	Test Weight (g)	Crude protein content (%)	Seed yield per plant (g)
CL-I	52.94	78.81	38.41	9.21	13.56	12.49	10.48	11.54	19.85	16.06
CL-II	67.00	87.50	52.45	8.20	14.90	**14.99**	9.60	**13.85**	19.99	19.80
CL-III	66.38	89.00	50.24	9.55	12.73	14.31	11.20	12.70	19.66	17.71
CL-IV	68.00	91.25	92.85	**13.20**	**18.38**	14.08	9.58	12.05	19.72	20.90
CL-V	**47.00**	74.50	58.00	6.90	17.05	11.88	11.25	10.90	**20.47**	**20.91**
CL-VI	48.50	**73.50**	**93.40**	11.40	17.80	14.51	**12.10**	9.45	17.20	20.36

Table.4 Percent contribution of 10 characters for divergence

Sr. No.	Source	Times ranked first	Contribution %
1	Days to 50% flowering	180	34.09
2	Days to maturity	19	3.60
3	Plant height (cm)	172	32.58
4	Number of main branches	10	1.89
5	Number of Pods Per Plant	58	10.98
6	Pod Length (cm)	17	3.22
7	Number of seed per pod	7	1.33
8	Test Weight (g)	46	8.71
9	Crude protein content (%)	9	1.70
10	Seed yield per plant (g)	10	1.89
		Total	**100**

The cluster VI found superior for early maturity, tall plant height and more number of seeds per pod. The present study revealed that days to 50% flowering contributed maximum (34.09%) for divergence (Table 4) followed by plant height (32.58%), number of pods per plant (10.98%), test weight (8.71%). This result was in accordance with Thiyagarajan *et al.*, (1988), Kumawat and Raje (2005), Sulnathi *et al.*, (2007) and Nagalakshmi *et al.*, (2010) who also reported maximum contribution towards genetic divergence of characters days to 50 per cent flowering, 100-seed weight and plant height and pods per plant.

Based on inter-cluster distance, intra-cluster distance and *per se* performance the genotypes *viz.*, CP-04, CP-10, CP-10R, PCP-1411, CP-37, CP-10R, CP-39 and Phule Sonali are suggested to utilize for future breeding programme.

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