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Genetic Diversity Study in Cowpea (*Vigna unguiculata* (L.) Walp.)

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Abstract Forty nine cowpea germplasm lines were collected from different places of Karnataka and they were evaluated for twelve different traits in *kharif* 2013 to asses diversity. Genetic diversity was calculated by using Mahalanobis D^2 statistics and also it helped to know the relative distances between these germplasm lines. Based on D^2 values 49 cowpea genotypes were grouped into thirteen clusters. The cluster I was the largest cluster with 31 genotypes, 7 genotypes in cluster IV and remaining clusters are solitary. The solitary clusters may be due to total isolation preventing the formation of gene flow or natural or human selection for diverse adaptive complexes. The maximum D^2 value of 5.10 was observed between the cluster VII and XIII, while the lowest D^2 value of 1.95 between cluster V and VII. Among studied twelve characters day to 50% flowering contribute more to genetic diversity that is 28.43% followed by grain yield per plant (24.04%), number of primary branches, test weight, days to maturity, number of secondary branches per plant, plant height, number of pods per plant, pod length and number of clusters per plant.

Keywords Cowpea, Genetic diversity, Germplasm, Solitary cluster.

Introduction

Cowpea (*Vigna unguiculata* (L.) (Walp.) is one of the most important drought tolerant pulse crop [1], native of West Africa. It is used as a pulse, vegetable and fodder. Cowpea is called as poor man's meat or vegetable mean due to its high amount of protein in grain with better biological value on dry weight basis. Cowpea grain contains 23.4% protein, 1.8% fat and 60.3% carbohydrates and also it is a good source of vitamins and phosphorus [2]. Among the different pulses grown in the world, cowpea is grown in 12.76 million ha with production of 7.56 million tones and the productivity of 750 kg per ha [3]. In India, the cowpea is grown in an area of about 3.9 million ha with a production of 2.21 million tonnes having a productivity of 625 kg per ha compare to world India productivity is low, so still there is scope to improve

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Table 1. Percent contribution of 12 characters towards diversity in cowpea.

Sl. No.	Characters	Contribution in percentage
1	Days to 50% flower	28.43
2	Grain yield per plant	24.03
3	Number of primary branches	4.34
4	100 grain weight	4.08
5	Days to maturity	3.48
6	Number of secondary branches	2.75
7	Plant height	2.51
8	Number of pods per plant	2.43
9	Number of clusters per plant	1.63
10	Grains per pod	1.27
11	Pod length	0.90
12	Number of pods per cluster	0.86

Table 2. Clustering pattern of 49 germplasm lines of cowpea on D^2 analysis.

Sl. No.	Clusters	No. of genotypes	Name of genotype genotypes
1	I	31	MFC-09-01, MFC-09-03, MFC-09-04, MFC-09-05, MFC-09-06, MFC-09-07, MFC-09-08, MFC-09-09, MFC-09-10, MFC-09-11, MFC-09-12, MFC-09-13, MFC-09-15, MFC-09-16, MFC-09-17, MFC-09-18, MFC-09-19, MFC-09-20, MFC-09-21, MFC-09-22, MFC-09-23, MFC-09-24, C-325, IC-402182, V-578, EC-458489, MBC-25, NBC-36, IC-202867 (99) and CB-10
2	II	1	EC-394839
3	III	1	NBC-21
4	IV	7	EC-458480, IC-201 (C), NBC-41, IC-402161, 198355 (45), IT-9715499-38 and IC-1071
5	V	1	IC-402180
6	VI	1	KBC-2
7	VII	1	MFC-08-14
8	VIII	1	EC-170574-6
9	IX	1	V-585
10	X	1	IC-202290
11	XI	1	C-720
12	XII	1	NBC-29
13	XIII	1	IC-402048

the productivity of the cowpea.

Genetic diversity is the fundamental requirement for any successful breeding program. Collection and evaluation of genotypes of any crop is a pre-requisite for any crop improvement program, which provides a greater scope for exploiting genetic diversity [4]. A quantitative assessment of the genetic divergence among the collected germplasm lines and their relative contribution of different traits towards the genetic divergence provides very important and useful information to breeders for selecting parents in hybridization program and further genetic improvement of yield. The necessity for identifying genetically distant among the germplasm is because, hybridization between genetically diverse parents produce high heterotic effect and wide spectrum of variability could be expected in the segregating generation. With this back ground information we studied

Table 3. Average intra and inter cluster D^2 values of clusters in cowpea.

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	2.11	2.95	2.63	3.13	2.61	4.09	2.89	2.92	3.16	3.19	2.96	3.03	3.72
II		0.00	3.70	3.23	2.92	4.24	3.38	4.15	3.41	2.39	2.31	3.06	3.56
III			0.00	3.23	2.87	4.28	3.89	2.60	1.96	4.39	2.85	3.04	2.76
IV				2.52	3.20	4.31	3.25	2.98	3.32	3.16	3.33	3.53	4.03
V					0.00	4.63	1.95	3.41	3.48	3.22	3.29	3.40	4.39
VI						0.00	4.75	4.59	4.34	4.35	4.44	4.25	4.71
VII							0.00	3.39	4.67	2.60	4.28	4.02	5.10
VIII								0.00	3.64	4.04	3.60	3.68	3.95
IX									0.00	4.38	2.32	3.06	2.75
X										0.00	3.73	3.02	4.28
XI											0.00	2.48	2.76
XII												0.00	2.33
XIII													0.00

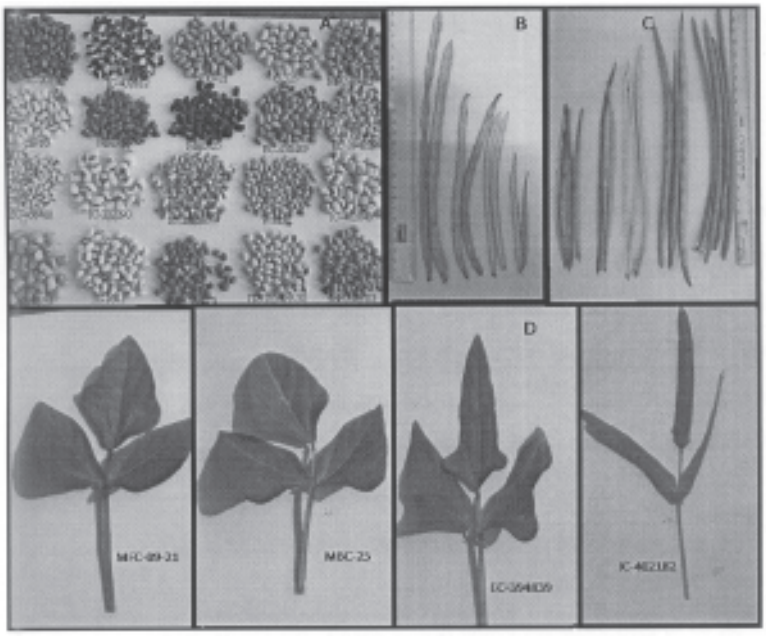

Fig. 1. The A, B, C and D are variations observed in grain, dry pods, green pods and leaves respectively.

genetic diversity in the collected germplasm lines.

Materials and Methods

The investigation on genetic diversity of cowpea was studied at College of Agriculture, University of Agriculture and Horticultural Sciences, Shimoga. The experiment comprised of 49 genotypes, collected from different parts of Karnataka. The experiment was laid out in simple lattice design with two replications during August 2013. The observations were recorded on five randomly selected plants in each lines and replication for twelve traits viz. days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, number of pods per cluster, pod length, number of grains per pod, test weight and grain yield per plant.

The statistical analysis of the data on the individual characters was carried out on the mean values of five random plants and analyzed genetic diversity with INDOSTAT software, verified through formulas given by Mahalanobis' [5] D^2 statistics for assessing the genetic divergence between populations. Germplasm lines were clustered using Tocher's method as described by Rao [6]. The intra and inter cluster distances were calculated as for the Singh and Chowdhary [7].

Results and Discussion

Genetic relationship among germplasm lines can be measured by similarity or dissimilarity of any number of quantitative characters assuming that the differences between characters of genotypes reflect the divergence of genotypes. In heterosis breeding program, the diversity of parents is always emphasized. More diverse among the parent within a reasonable range, better the chances of improving economic character under consideration, in the resulting off spring.

Collected germplasm lines showed lot of observable variations for grains, leafs and pods (Fig. 1). The genetic diversity among 49 genotypes was measured by employing D^2bstatistics and results are given in

Table 4. Cluster mean analysis. Where, X_1=Days to 50% flowering, X_2=Days to maturity, X_3=Plant height, X_4=Number of primary branches, X_5=Number of secondary branches, X_6=Number of clusters per plant, X_7=Number of pods per plant, X_9=Pod length, X_{10}=Number of grains per pod, X_{11}=Test weight, X_8=Number of pods per cluster, X_{12}=Grain yield per plant.

Sl. No.	Clus-ters	No. of geno-types	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	Cluster score	Cluster rank
1	I	31	48.24 (3)	79.80 (6)	112.44 (5)	4.42 (8)	4.83 (6)	11.48 (9)	20.23 (9)	1.78 (7)	15.59 (8)	13.41 (4)	10.00 (11)	20.34 (10)	85	VIII
2	II	1	44.50 (10)	79.50 (7)	66.40 (11)	4.80 (6)	2.80 (13)	12.40 (7)	18.60 (12)	1.50 (10)	15.60 (7)	12.10 (8)	12.05 (6)	14.80 (12)	104	XIII
3	III	1	46.00 (8)	74.00 (10)	84.20 (10)	4.40 (10)	5.20 (3)	10.60 (13)	19.70 (11)	1.86 (5)	15.35 (10)	12.80 (7)	12.08 (5)	23.80 (6)	98	XII
4	IV	7	47.36 (6)	80.40 (3)	96.61 (6)	5.55 (1)	4.86 (5)	13.91 (4)	26.88 (2)	1.97 (3)	14.44 (11)	13.90 (2)	9.94 (12)	24.49 (4)	68	IV
5	V	1	44.00 (11)	73.00 (11)	85.10 (9)	4.70 (7)	4.90 (4)	12.80 (6)	24.40 (6)	1.93 (4)	16.20 (6)	11.40 (10)	10.35 (8)	20.40 (9)	91	XI
6	VI	1	48.50 (2)	79.00 (8)	96.10 (7)	4.30 (3)	4.86 (11)	11.20 (11)	22.40 (8)	2.04 (2)	13.96 (12)	16.30 (1)	10.10 (10)	21.40 (8)	83	VI
7	VII	1	45.50 (9)	79.00 (8)	118.10 (4)	5.10 (4)	4.80 (7)	11.30 (10)	21.70 (9)	1.93 (4)	17.10 (3)	12.90 (6)	9.45 (13)	19.30 (11)	87	IX
8	VIII	1	49.00 (1)	84.00 (1)	120.00 (2)	5.40 (2)	6.00 (1)	14.50 (3)	25.70 (3)	1.78 (7)	15.50 (9)	12.10 (8)	10.33 (9)	32.10 (1)	47	II
9	IX	1	47.00 (7)	80.00 (4)	66.40 (11)	4.30 (10)	4.60 (8)	12.10 (8)	25.10 (4)	2.08 (1)	13.10 (13)	11.50 (9)	11.40 (7)	21.80 (7)	90	X
10	X	1	47.00 (7)	83.00 (5)	127.00 (1)	4.90 (5)	4.30 (9)	13.80 (5)	24.80 (5)	1.82 (6)	16.45 (5)	13.10 (5)	12.60 (4)	21.40 (8)	61	III
11	XI	1	47.00 (5)	74.00 (4)	57.40 (13)	4.40 (9)	3.30 (12)	14.70 (2)	24.30 (7)	1.64 (8)	16.75 (4)	12.50 (8)	12.89 (3)	23.90 (5)	84	VII
12	XII	1	48.00 (4)	83.00 (9)	119.95 (3)	4.00 (12)	5.40 (2)	15.80 (1)	26.90 (1)	1.64 (8)	18.35 (2)	13.80 (3)	16.60 (2)	31.10 (2)	40	I
13	XIII	1	47.50 (5)	83.50 (2)	85.20 (8)	4.20 (11)	4.10 (10)	10.70 (12)	16.70 (13)	1.61 (9)	18.65 (1)	12.90 (6)	18.90 (1)	25.60 (3)	76	V

Table 1. Out of 12 character studied, days to 50% flowering contributed maximum to the diversity (28.43%) followed by grain yield per plant (24.03%), number of primary branches, test weight, days to maturity, number of secondary branches per plant, plant height, number of pods per plant, pod length and number of clusters per plant. Similarly Sharma and Mishra [8] reported that days to 50% flowering is a major contributing characters to total diversity. Nagalakshmi and associates [4] reported that grain yield per plant contributed maximum to the total divergence followed by 100 grain weight and days to 50% flowering.

Based on D^2 values the genotypes were grouped into thirteen clusters (Table 2) using Tocher's method given by Rao [6]. Cluster I was found largest with 31 genotypes followed by cluster IV comprising 7 genotypes and remaining clusters were solitary. The solitary clusters may be due to total isolation preventing the formation of gene flow or natural or human selection for diverse adaptive complexes. The maximum D^2 value of 5.10 was observed between VII and XIII clusters, while the lower between clusters V and VII with D^2 value of 1.95 (Table 3). The intra clusters distance varies from 4.52 in cluster IV and 2.11 in cluster I. This indicates the presence of divergent genotypes within these clusters. However, in solitary clusters intra cluster distance was nil because they are composed with single genotype. Cluster IV was must diverse, showed maximum intra cluster distance within it. It is desirable to select genotypes from clusters showing high inter cluster distance (cluster VII and XIII) for parents for hybridization program to exploit hybrid vigor and also to get desirable segregants for crop improvement.

Table 5. Genotypes recorded significant higher grain yield than local check in cowpea.

Genotypes	Days to 50% flowering	Days to maturity	Plant height	Number of clusters/ plant	Number of pods/ plant	Pod length	Grains/ pod	100 grain weight	Grain yield/ plant	Yield over local check check
MFC-09-02	50.50	79.50	119.60	12.00	22.20	15.70	14.10	9.42	25.00	5.04
MFC-09-12	48.00	82.00	167.40	12.80	22.50	15.20	15.55	9.71	25.40	6.72
MFC-09-15	49.00	82.00	119.10	14.70	28.70	16.05	7.40	12.83	29.30	23.11
MFC-09-23	50.00	83.00	121.50	20.60	29.30	15.40	15.40	10.95	29.10	22.27
NBC-29	48.50	83.00	118.70	12.50	16.50	22.35	14.70	22.92	27.90	17.23
C-720	46.50	74.00	61.30	18.30	32.20	13.85	10.60	12.28	28.10	18.07
EC-170574-6	49.00	84.00	116.00	14.80	27.50	15.30	12.00	11.87	29.70	24.79
IC-402161	48.50	80.00	125.30	15.10	25.20	15.90	13.80	8.92	31.00	30.25
IT-9715499-38	47.00	84.00	120.55	18.80	38.30	14.50	13.40	10.22	34.20	43.70
NBC-41	48.50	80.00	103.90	18.30	34.55	15.65	15.20	9.55	35.30	48.32
KBC-2	49.50	79.00	123.70	13.10	24.30	15.45	13.80	10.27	23.80	Check

Thirteen clusters were ranked based on overall score obtained from the all 12 characters (Table 4). The highest cluster mean was given the first rank and next cluster possessing next best means were given 2nd, 3rd and so on up to 13th rank for all the traits. Finally the clusters are ranked based on the overall score obtained across 12 characters. The lowest scoring cluster was given first rank and next cluster possessing the score above the previous ones were given 2nd, 3rd and so on up to 13th rank. Accordingly, cluster XII with overall score of 40 across the 12 characters elected first rank followed by cluster VIII, X, IV, XIII, VI, XI, I, VII, IX, V and III indicating presence of most promising genotypes in them and further breeding program to generate new material. Cluster II with overall score of 104 recorded last rank (13th) reflecting lower mean values across 12 characters.

These forty nine genotypes exhibited observable variability for twelve yield and yield related traits. Among the 49 genotypes, ten were recorded grain yield more than local check (KBC-2) significantly. The genotypes along with their performance presented in Table 5. The genotype NBC-41 recorded highest grain yield of 35 g per plant, while it recorded higher number of pods (34.55), followed by IT-9715499-38 (34.20 g), IC-402161 (31.00 g), EC-170574-6 (29.70 g), MFC-09-15 (29.30 g), MFG-09-23 (29.10 g), C-720 (28.10 g) and NBC-29 (27.90 g). These genotypes can be used for further evaluation for yield and also used for parental material for existing variety improvement.

Diversity studies indicates low diversity among genotypes as 31 in cluster I and individual genotypes in solitary clusters are more diverse and can be involved in hybridization program to create new variable. The 50% flowering, grain weight, number of primary branches and test weight are the major contributors to total diversity. High yielded germplasm lines can be used for yield improvement program.

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