

18(4): 1-5, 2019; Article no.AIR.47670 ISSN: 2348-0394, NLM ID: 101666096



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## Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

#### Article Information

DOI: 10.9734/AIR/2019/v18i430096 <u>Editor(s):</u> (1) Dr. Martin Kröger, Professor, Computational Polymer Physics, Swiss Federal Institute of Technology (ETH Zürich), Switzerland. <u>Reviewers:</u> (1) Schirley Costalonga, Universidade Federal do Espírito Santo, Brazil. (2) Toungos, Adamawa State University Mubi, Nigeria. Complete Peer review History: <u>http://www.sdiarticle3.com/review-history/47670</u>

Original Research Article

Received 08 November 2018 Accepted 28 February 2019 Published 12 March 2019

# ABSTRACT

Advances in Research

A field experiment was conducted with 25 hybrids and their 14 parents of cowpea to study the diversity among the genotypes which were grouped in to 7 clusters revealing the presence of considerable diversity in the material. The clustering pattern of the varieties usually did not confirm to geographical distribution. Cluster-II got desirable rating in respect of maximum harvest index, seed yield per plant and minimum days to maturity where cluster V got maximum number of pods per plant, green pod yield per plant and dry pod yield per plant where all yield related components that could be directly tested in multilocation trials for their suitability or could be used as a donor parent in breeding programme. The characters like plant height, green pod yield per plant and dry pod yield per plant were found to contribute much to the total genetic divergence in cowpea.

Keywords: Cowpea; divergence; cluster;  $F_2$  generation; interspecific hybrids.

# **1. INTRODUCTION**

Cowpea (*Vigna unguiculata* (L). Walp) 2n=22 is one of the most widely adapted; drought-tolerant, versatile, and nutritious grain legumes or pulse crop. It is used as dry seed or green pod as vegetable or as forage crop. 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

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breeding programmes that can enhance productivity and stabilize the yield. According to Jain [1], this is possible only when diverse parents are available for breeding programme. The basic rationale in crop improvement programme is the selection of parents. It is well known that there is a likelihood of getting better segregants, when the parents used in crossing are genetically diversed [2]. This segregants will be useful in identification of better inbreds in the future and development of improved varieties. Therefore, present study was attempted to determine the divergence among the cowpea genotypes.

## 2. MATERIALS AND METHODS

The experimental material comprised of twenty five crosses and their fourteen parents of cowpea, which were obtained from germplasm maintained at Department of Agricultural Botany, College of Agriculture, Dapoli. The experiment was carried out in a randomized block design (RBD) with three replications at education and research Farm, College of Agriculture, Dapoli during rabi 2016-17. Each genotype was represented by double row plot with a spacing of 45 x 30 cm. Observations were recorded on five competitive plants from each genotype which were randomly selected. The data were subjected to statistical analysis usina Mahalanobis D<sup>2</sup>statistics [3] and Tocher's method as described by Rao [4] by using INDOSTAT software [5].

## 3. RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters studied (Table 1). Based on D<sup>2</sup> statistics, (Table 2) the thirty nine genotypes grouped in to 7 clusters (Table 3) with variable numbers of genotypes revealing the presence of considerable amount genetic diversity in the materials. The clustering pattern of genotypes showed that genotypes of different origins were clubbed in one cluster whereas the genotypes belonging to same origin were grouped in different clusters indicating that there is no formal relationship between geographical and genetic diversity. Cluster I, II, III, and VII contained as many as seven genotypes which complete 28 genotypes out of the total. On the other hand cluster V possessed only two genotypes which was minimum which was followed by cluster VI with three genotypes. In general, (Table 2) inter cluster distances were higher than the intracluster distances. Higher intra and inter cluster

D<sup>2</sup> values revealed very interesting trend of aenetic diversity. Thus, the aenotypes included within a cluster tended to diverse less from each other. The lowest intra-cluster (Table 2) distance was in cluster-III (D = 15.89). Whereas, the highest intra-cluster distance was in cluster-V (D 29.82). This high intra-cluster distance = indicated the wider genetic diversity among the genotypes which could be used in yield improvement of cowpea. The maximum inter cluster distance (D) was noticed between cluster V and III (D = 49.63) followed by that between cluster VII and V (D =41.43), while the closest proximity was observed between cluster-VI and IV (D = 24.67) followed by the cluster-IV and I (D = 25.32). Pawar [6], Sharma and Mishra [7], Valarmathi and Surendran [8], Usha kumari et al. [9] Nagalakshmi et al. [10] and Dalsania et al. [11], also reported diversity in cowpea. Cluster means of each trait toward divergence are presented in Table 3. The cluster-II got desirable rating in respect of maximum harvest index, seed yield per plant and minimum days to maturity where cluster V got maximum number of pods per plant, green pod yield per plant and dry pod yield per plant, which are all yield related components. Therefore, genotypes from these clusters may directly be evaluated on multilocations for yield or can be used as a donor parents in vield improvement programme. The cluster-VII had higher mean value for pod length.

A wide range of variation for several characters among single as well as multi-genotypic clusters was observed. However, the differences were clear for plant height, pod length, number of clusters per plant, number of pods per plant, green pod yield per plant, dry seed yield and seed yield per plant which have contributed maximum to the divergence. Dalsania et al. [10], also reported the same in case of plant height and green pod yield per plant.

The clustering pattern could be utilized in crossing the parents and deciding the cross combinations which may generate maximum possible variability for various traits. The genotypes with high values of any cluster can be used either for direct adoption or for hybridization for further selection and improvement as per Brahmiah [12], In the present study, the cluster VII had maximum plant height where the minimum plant height observed in cluster III, in which the selection for vegetable and grain purpose cowpea can be done. Cluster number V got desirable mean value for number of pods per plant, green pod yield per plant and dry pod yield per plant. Seed yield per plant observed

Source of variation	df	<b>X</b> <sub>1</sub>	<b>X</b> <sub>2</sub>	X <sub>3</sub>	<b>X</b> 4	<b>X</b> 5	<b>X</b> <sub>6</sub>	<b>X</b> <sub>7</sub>	<b>X</b> <sub>8</sub>	X <sub>9</sub>	<b>X</b> <sub>10</sub>	<b>X</b> <sub>11</sub>	<b>X</b> <sub>12</sub>	<b>X</b> <sub>13</sub>	<b>X</b> <sub>14</sub>
Replication	2	19.44	0.1132	1.564	65.444	0.730	0.157	0.014	0.462	2.198	7.365	5.755	0.119	0.809	1.151
Genotypes	38	10473.2*	4.27*	76.63*	500.83*	123.60*	7.38*	0.52*	63.84*	543.87*	6249.44*	1829.51*	10.95*	420.87*	140.61*
Error	76	194.90	0.288	3.853	25.084	1.186	0.705	0.028	0.827	6.728	33.239	14.154	0.459	3.836	1.388
*indicate 5 % level of significance															

#### Table 1. Analysis of variance for fourteen quantitative characters

\*indicate 5 % level of significance

 $X_1$  = plant height,  $X_2$  = No. of primary branches per plant,  $X_3$  = days to first flowering,  $X_4$  = days to maturity,  $X_5$  = pod length,  $X_6$  = No. of seeds per pod,  $X_7$  = No. of pods per cluster, X<sub>8</sub>= No. of clusters per plant, X<sub>9</sub>= No. of pods per plant, X<sub>10</sub>= green pod yield per plant, X<sub>11</sub>= dry pod yield per plant, X<sub>12</sub>= hundred seed weight, X<sub>13</sub>= harvest index,  $X_{14}$ = seed yield per plant

# Table 2. Average intra and inter-cluster ( $D=\sqrt{D^2}$ ) values for 39 genotypes of cowpea

Cluster		II	III	IV	V	VI	VII	
	20.84	25.59	27.39	25.32	37.69	28.22	31.52	
II		21.95	28.33	27.00	40.83	30.48	38.94	
111			15.89	28.74	49.63	27.04	30.45	
IV				16.82	30.76	24.67	27.42	
V					29.82	35.88	41.43	
VI						16.46	26.35	
VII							22.80	

#### Table 3. Clustering pattern of 39 genotypes of cowpea on the basis of genetic divergence

Cluster no.	No. of genotypes/ cluster	Name of the genotype							
I	7	K.safed×A. gerima, K.sadabahar, K.safed×K.wali, Pusa dophasali×DPL-YB-5,ACP-109×A.gerima,ACP-109×DPL-YB- 5,Pusa dophasali							
II	7	PCP-97102 × UBA-1, ACP-1264 × Konkan wali, Konkan safed, PCP- 97100, Pusa phalguni × DPL-YB-5 ,Pusa phalguni, PCP- 9723							
III	7	Konkan sadabahar × UBA-1, PCP-97100 × Arka garima, PCP- 9723× Arka garima, ACP- 1264, ACP- 109, V-585, PCP- 7102							
IV	6	K. safed × DPL-YB-5,Pusa dophasali × K. wali,ACP-109 × Konkan wali PCP- 9723× UBA-1, V-585 × Konkan wali, V-585 × UBA-1							
V	2	Pusa phalguni × Konkan wali, ACP-1264 × UBA-1							
VI	3	Pusa dophasali × UBA-1, ACP-1264 × DPL-YB-5, PCP- 9723 × Konkan wali							
VII	7	PCP-97100 × Konkan wali, Konkan waliPusa dophasali × Arka garima, PCP-97100 × UBA-1, UBA-1, Arka garima, DPL- YB-5							

Table 4. Cluster means for 14 characters in 39 genotypes of cowpea

Clusters	<b>X</b> <sub>1</sub>	<b>X</b> <sub>2</sub>	<b>X</b> <sub>3</sub>	$X_4$	<b>X</b> 5	<b>X</b> <sub>6</sub>	<b>X</b> <sub>7</sub>	<b>X</b> 8	<b>X</b> 9	<b>X</b> <sub>10</sub>	<b>X</b> <sub>11</sub>	<b>X</b> <sub>12</sub>	<b>X</b> <sub>13</sub>	<b>X</b> <sub>14</sub>
	56.667	3.801	55.286	97.667	17.157	13.102	2.488	20.830	52.149	87.303	74.194	13.318	41.526	21.520
11	52.905	3.535	59.476	95.000	12.543	11.664	2.360	16.832	39.579	82.832	79.472	12.877	55.139	25.625
	50.714	3.748	59.381	96.095	13.048	12.836	1.930	12.674	24.388	73.275	55.574	12.179	32.432	14.878
IV	129.833	3.392	62.333	99.333	18.717	13.461	2.106	18.189	38.669	158.898	63.941	13.306	41.504	18.100
V	118.000	5.290	60.833	112.667	20.053	13.598	2.603	24.365	64.528	209.152	115.817	13.293	48.380	23.967
VI	62.889	4.528	60.333	106.778	17.996	14.756	1.958	14.987	29.499	124.438	116.233	12.013	32.369	19.922
VII	167.238	4.254	57.905	105.333	26.922	13.560	2.164	16.266	34.865	142.969	69.390	14.172	23.943	12.596
Mean	89.650	3.894	59.000	100.009	17.797	13.086	2.213	17.155	38.627	114.094	74.728	13.084	38.825	18.939

 $X_1$  = plant height,  $X_2$  = No. of primary branches per plant,  $X_3$  = days to first flowering,  $X_4$  = -days to maturity,  $X_5$  = pod length,  $X_6$  = No. of seeds per pod,  $X_7$  = No. of pods per cluster,  $X_8$  = No. of clusters per plant,  $X_9$  = No. of pods per plant,  $X_{10}$  = green pod yield per plant,  $X_{11}$  = dry pod yield per plant,  $X_{12}$  = hundred seed weight,  $X_{13}$  = harvest index,  $X_{14}$  = seed yield per plant

maximum mean in cluster II. The highest (Table 4) contribution in this regard was from green pod yield per plant (114.09) followed by days to maturity (100.00) and plant height (89.65). Hence plant height, green pod yield per plant and days to maturity were considered to be important traits contributing towards genetic divergence. Usha Kumari et al. [9], also reported the highest contribution of plant height (22.69%) towards divergence followed by number of seeds per pod, number of branches, number of pods per cluster and pod length. Shiva Kumar et al. [13] reported that pod yield per plant contributed maximum divergence (66.23%) which was followed by pod weight (20.78%) and plant height (8.23%).

## 4. CONCLUSION

In conclusion, the genetic diversity study conducted in 14 parents and 25  $F_2$  generations from their cross combination resulted in formation of seven clusters. This proves the existence of large amount of variation and diversity among the parents and cross combination. This diversity is useful in the selection of suitable parents for hybridization programme as the diverse parent will provide maximum heterosis and useful in development of efficient segregants and in future identification of better inbreds and development of elite cultivar or variety.

## **COMPETING INTERESTS**

Authors have declared that no competing interests exist.

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