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Research Note

Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp] for yield components and seed quality parameters

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Abstract
Forty cowpea genotypes were evaluated for 18 quantitative characters to estimate the genetic diversity existing among them by using Mahalanobis D^2statistics. The genotypes were grouped into six clusters. The cluster strength varied from single genotype (Clusters III, IV and V) to 25 genotypes (Cluster I). Clusteres IV and VI had high inter cluster distance. Clusters II, III and I had maximum 100-seed weight, number of seeds per pod and seed yield respectively. Cluster IV had maximum seedling vigour index, germination per cent, peduncle length, number of clusters per plant and number of primary branches. The genotypes from clusters IV and IV may be inter crossed to obtain high variation.

Key words: Cowpea, diversity, variability

Cowpea [*Vigna unguiculata* (L.)Walp] is one of the most important pulse crops native to West Africa (Vavilov, 1951) but Steele (1976) suggested Ethiopia as the primary and Africa as the secondary centres of diversity. The estimated world wide area under cowpea is over 14 million hectares, with production of 4.5 million tonnes and productivity of 387 kg ha^{-1} (Anonymous, 2009). In India it occupies an area of 3.9 million hectares with production of 2.2 million tonnes and productivity of 564 kg ha^{-1} (Kurer *et al.,* 2010). In Andhra Pradesh cowpea was grown in an area of 0.21 lakh hectares with a production of 0.14 lakh tonnes and productivity of 632 kg ha^{-1} (INDIASTAT, 2011). It is relatively drought tolerant and an important food and fodder legume. The present study was taken up with an objective to estimate the genetic diversity for yield components and seed quality parameters in cowpea genotypes.

The experiment was laid out in Randomized Block Design with two replications.The present study comprised of 40 (36 accessions and four check varieties) genotypes of cowpea at National Bureau of Plant Genetic Resources (NBPGR), Regional station, Hyderabad, Andhra Pradesh during *Kharif* 2012. Each genotype was sown in one row of five meter length by adopting a spacing of 45 cm × 10 cm. Data was recorded on five randomly selected competitive plants per replication for 15 yield components and three seed quality parameters *viz.,* days to 50% flowering, leaf length (cm), leaf width (cm), days to maturity, plant height (cm), number of primary branches per plant, length of main branch (cm), number of clusters per plant, peduncle length (cm), pod length (cm), number of pods per plant, days to 80% flowering, number of seeds per pod, 100-seed weight (g), seed yield per plant (g), protein content (%), germination (%), seedling vigour index-I and seedling vigour index-II. The seedling vigour indices-I and II were calculated by using the following formulae as suggested by Abdul-Baki and Anderson (1973). Seedling vigour index (SVI-I) = Germination (%) x Seedling length (cm); Seedling vigour index (SVI-II) = Germination (%) x Seedling dry weight (mg). The method by using bovine serum albumin as described by Lowry *et al.* (1951) was used for estimation of seed protein. Multivariate analysis was done by using Mahalanobis D^2 statistic (Mahalanobis, 1936) and genotypes were grouped into different clusters following Tocher’s method (Rao, 1952).

The magnitude of D^2 values suggested that there was considerable variability in the material studied, which led to genetic diversity. Significant differences among the genotypes for individual characters were first determined and later the statistical significant differences between the genotypes based on the pooled effects of all the characters were carried out using the Wilk’s criterion‘Λ’. The Wilk’s criterion thus obtained was used in calculations of ‘v’ statistic. The statistic 2202.51 was highly significant indicating that genotypes differed significantly when all the characters were considered simultaneously.

Based on the D^2 values, the 40 genotypes were grouped into six clusters using the Tocher’s method. The distribution of genotypes into different clusters is shown in Table 1. Among the six clusters, cluster I was the largest with 25 genotypes followed by cluster II which comprised of 10 genotypes and cluster VI had two genotypes. Clusters III, IV and V were solitary comprised of single genotype *i.e.,* NSJ 161, NSJ 007 and NSJ 044 respectively, indicating wide diversity from the rest and also from each other.

Grouping of genotypes evolved from the same location into different clusters indicated that geographical and genetic diversity were not related. This suggests forces such as exchange of breeding material, natural and artificial selection, genetic drift, migration and gene flow may be responsible for this diversity. The choice of suitable diverse parents selected on the basis of genetic diversity analysis would be more rewarding than the choice made on the basis of geographic diversity. Results are in agreement with Deshpande *et al.* (2011), Girish *et al.* (2001), Nigude *et al.* (2004), Pandey (2007) and Venkatesan *et al.* (2004) in cowpea.

The average intra and inter cluster D values were given in Table 2. Intra-cluster D values ranged from zero (cluster III, IV, V) to 26.01(cluster VI). The maximum intra cluster distance was observed in cluster VI (26.01), followed by cluster I (20.42) and Cluster II (19.44) indicating the genotypes included in these cluster may have different genetic architecture. Selection of genotypes from cluster I and II based on high mean value for characters may yield desirable breeding material. The intra cluster distance was zero in clusters III, IV, V as they consisted only one genotype. The monogenotypic clusters were reported by Jindal and Gupta (1985) and Kumar *et al.* (1982) in cowpea.

The maximum inter cluster distance (72.77) was observed between IV and VI clusters suggesting that genetic makeup of genotypes included in these cluster may have entirely different from one another. The lowest inter cluster distance of 26.71 was recorded between cluster I and III, indicating similar genetic constitution of the genotypes included in these clusters. Cluster VI was the most diverse as many other clusters showed maximum inter cluster distances with it. The diversity among the genotypes measured by inter-cluster distance was adequate for improvement of cowpea by hybridization and selection. The genotypes included in these diverse clusters may be used as promising parents for hybridization to obtain better segregants.

Hybridization between genotypes falling in the most distant clusters should result in maximum hybrid vigour and eventually desirable segregates or combinations leading to the development of useful varieties. Sharma and Mishra (1997) reported diversity in cowpea and suggested selection of parents for hybridization and improvement of characters. Similar reports were given by Dahiya *et al.* (2007), Pandey (2007), Suganthi *et al.* (2007), Sulanthi *et al.* (2007) and Valarmathi *et al.* (2007) in cowpea.

The cluster mean values for all the 18 characters are presented in Table 3. Cluster IV had high mean value for SVI-II (4364.00), SVI-I (2534.50), germination per cent (95.00), peduncle length (29.40 cm), number of clusters per plant (27.50) and number of primary branches (4.70). Cluster VI had high mean value for length of main branch (197.08 cm), plant height (131.98 cm), days to 80 percent flowering (74.50), days to 50 per cent flowering (62.00) and leaf width (8.08 cm). Cluster I had high mean value for seed yield (67.79 g). Cluster II had high mean value for 100 -seed weight (12.39 g). Cluster III had high mean value for number of seeds per pod (19.50). Cluster V had high mean value for pod length (24.35 cm), protein content (30%) and leaf length (11.25 cm). Higher differences were observed in respect of SVI-II, SVI-I, length of main branch and plant height. Lower differences were observed in case of days to 80 per cent flowering, pod length, number of seeds per pod, 100-seed weight, number of primary branches, leaf width and leaf length.

The heterosis and better recombinants were obtained by crossing parents between clusters of high and low means (Kumari *et al.,* 2000 and Girish *et al.,* 2001). Cluster mean values showed a wide range among the characters studied which indicated presence of variation among the genotypes studied. (Sharma and Roy, 1994). Intercrossing these genotypes from clusters (I and IV) might result in wide array of variability for exercising effective selection for yield as well as seed quality parameters similar to the report of Venkatesan *et al. (*2004). Singh *et al.* (2007) earlier reported that since grain yield was the major objective in crop like cowpea, the genotypes falling in different clusters with high mean grain yield and high mean for component characters can be selected to recombine them in future hybridization programme. The per cent contribution towards genetic divergence by all the 18 characters is presented in Table 3. The maximum contribution towards genetic divergence was by number of clusters per plant (36.79%) followed by protein content (33.21%). Number of clusters per plant and protein content can be considered for selecting diverse parents. Contribution of various characters towards divergence in cowpea was earlier reported by Backiyarani *et al.* (2000), Jindal and Gupta (1985) for number of branches per plant, Jain *et al.*(2006) for number of pods and pod length and Saini *et al.* (2004) for days to flowering. Kumari *et al.* (2000) and Sharma and Mishra (1997) reported maximum contribution of green pod yield per plant, plant height, days to 50 per cent flowering and leaf area towards total divergence in cowpea.

In addition to the genetic divergence, considering the mean performance, two genotypes for seed yield *viz.,* NSJ 007 from cluster IV, two genotypes for earliness *viz., PSR 13279 and PSR 12994* from cluster VI may be intercrossed to obtain high variability.

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Table 1.Distribution of cowpea genotypes in different clusters based on analysis of morphological data

Cluster number	No. of genotypes	Name of the Genotype
1	**25**	NSJ 185, PSR 13201, NSJ 009, NSJ 008, SNJ 24, RJR 257, NSJ 51, RJR 256, NSJ 336, SNJ 93,PSR 13295, RJR 47, NSJ 180, NSJ 149, RJR 260,SNJ 7, PSR 12991, NSJ 159, CoVu 702, NSJ 133, NSJ 029, C 152, NSJ 197, RJR 180, PSR 13200
2	**10**	PSRJ 13020, RJR 229, NSJ 65, NSJ 66, RJR 316, Hridya, NSJ 79, PSR 13266, PSRJ 13022, GC 3.
3	**1**	NSJ 161
4	**1**	NSJ 007
5	**1**	NSJ 044
6	**2**	PSR 13279, PSR 12994

Table 2. Average intra (bold) and inter cluster D values for six clusters in 40 genotypes of cowpea

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	**20.42**	31.19	26.71	29.95	28.87	57.50
Cluster II		**19.44**	34.71	51.42	36.66	46.62
Cluster III			**0.00**	37.82	36.94	56.72
Cluster IV				**0.00**	33.17	72.77
Cluster V					**0.00**	51.20
Cluster VI						**26.01**

Table 2. Cluster mean values for quantitative characters in cowpea genotypes

Cluster	Days to 50% flowering	Leaf length (cm)	Leaf width (cm)	Plant height (cm)	No. of primary branches	Length of main branch (cm)	No. of clusters per plant	Peduncle length (cm)	Pod length (cm)	Pods per plant	Days to 80% flowering	No. of seeds per pod	Seed yield per plant (g)	100 seed weight (g)	Germination (%)	SVI I	SVI II	Protein (%)
I	45.26	9.76	7.27	70.09	4.45	78.10	16.79	25.73	14.48	21.75	62.36	15.83	67.79	9.42	82.36	2254	3479	23.93
II	43.70	9.51	6.78	62.91	3.54	59.98	7.43	20.98	13.37	11.14	61.25	12.59	23.41	12.39	80.50	2227	3632	21.48
III	47.50	8.35	7.30	59.05	3.90	67.90	16.50	26.10	16.85	13.85	66.50	19.50	61.14	8.75	66.00	1576	2173	14.78
IV	46.50	8..80	6.55	86.80	4.70	71.90	27.50	29.40	14.85	23.10	65.00	15.10	44.20	8.05	95.00	2534	4364	27.88
V	47.00	11.25	8.05	48.50	3.00	59.00	20.50	4.70	24.35	10.25	61.00	9.85	8.49	4.30	80.00	2193	3490	30.00
VI	62.00	9.90	8.08	131.98	3.65	197.08	7.63	21.25	16.70	8.65	74.50	14.55	20.01	9.05	72.50	1751	3112	14.00
Contribution towards divergence	8.72	0.26	0.26	1.15	0	0.13	36.79	0	6.79	0.13	0	6.03	0.77	0	0.51	0.64	4.62	33.21