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## Assessment of genetic variability and diversity in cowpea (*Vigna unguiculata* (L.) Walp)

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#### Abstract

Genetic divergence using  $D^2$  analysis was carried out to assess the 60 diverse genotypes of cowpea. All the 60 genotypes were grouped into nine clusters. The analysis of variances has shown that there was a significant variation among the genotypes in all traits. Out of the nine clusters, Cluster II was a largest cluster had maximum 21 genotypes, followed by cluster I (14 genotypes), cluster III (11 genotypes), cluster IV (7 genotypes), cluster VII (3 genotypes) and all other clusters viz., V, VI, VIII, IX had only single genotype. The calculated  $D^2$  values ranged from 1.18 to 173.78. The highest genetic distance was observed between cluster VI-IX (10.65), while lowest genetic distance between cluster V-VI (3.77). The maximum value between PCP-13-12 and GTC-22 were observed whereas, lowest value between the pairs of genotypes VWB-5 and VWB-3-1. Under this investigation, the maximum contribution towards genetic divergence is by plant height (39.89%) contributed more to genetic diversity, it was followed by harvest index (23.33%), 100 seed weight (17.80%) and seed yield per plant (7.91%).

**Keywords:** Genetic diversity, cowpea and  $D^2$  values

#### Introduction

Pulses production in India is characterized by diversity of crops and their regional specificity based on adaption to prevailing agro climatic conditions. This group of crops can utilize limited soil moisture and nutrients more efficiently than cereals. Pulses have a significant role in farming systems as a substitute for fallow in cereal rotations, where it contributes to the sustainability of production. Cowpea (*Vigna unguiculata* (L.) walp.) is one of the most important leguminous crop native to central Africa. Cowpea commonly known as Lobia is also known by different vernacular names viz., Rawan (Hindi), Chavali (Marathi), Barbati (Bengali) and Lobia (Orissa). The cultivars grown for their immature pods (vegetable purpose) are known as asparagus bean, snake bean, yard long bean and when grown for dry seeds, it is known as black eye pea, kaffir pea and southern pea. Vavilov (1951) [20] recognized India and Africa as the centres of origin, while china is considered as secondary centre of origin of cowpea.

Cowpea is a self-pollinated crop which belongs to family Leguminosae, sub family Papilionaceae or fabaceae with chromosome number  $2n = 2x = 22$ . According to Vedcourt (1970) [21] there are five sub-species of *V. unguiculata*. Two subspecies are wild viz., *dekinditiana* and *mensensis*. However, remaining three subspecies viz., *unguiculata* syn. *V. sinensis* (common cowpea); *sesquipedalis* (L.) vedcourt, syn. *V. sesquipedalis* and *V. sinensis* var. *sesquipedalis* (asparagus bean or yard long bean) are cultivated and wide spread in India and far east (Steele, 1976) [18].

Cowpea is mainly grown in tropical and subtropical regions in the world for vegetable and seed purpose as a warm seasonal annual herbaceous legume and to a lesser extent as a fodder crop. It is a most versatile pulse crop because of its smothering nature, drought tolerant characters, soil restoring properties and multipurpose uses. It's growth habit ranges from erect, determinate, non-branching types. It has strong tap root system. Stem may be green or pigmented, leaves are alternate trifoliate, with one symmetrical leaflet and two asymmetrical leaflets. Inflorescence is an unbranched axillary raceme bearing several flowers at the end and peduncles. Pods are pendent or vertically attached to the raceme axis, mostly linear. Cowpea is multipurpose legume which can be grown in rainfed conditions where as little as 300 mm rains are received and also in irrigated condition.

Cowpea can be grown as pure crop or inter crop with cereal fodders like maize or sorghum or pearl millet. Its young leaves, pod and peas contain vitamins and minerals which have fuelled its usage for animal and human consumption.

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Cowpea fodder is much relished by cattle and being dicot improves the animal performance.

Cowpea is the cheapest source of proteins and minerals. It is indispensable source of protein predominantly for vegetarian population in India. In fresh forms the young leaves, immature pods and peas are used as vegetable. The nutritive value of cowpea (per 100 g of edible portion), is moisture (84.6 g), protein (4.3 g), fat (0.2 g), minerals (0.9 g), carbohydrates (8.0 g), calcium (0.08 mg), phosphorus (0.74 mg) and iron (0.25 mg) are indicative of its importance in the diet. It is also rich in vitamin B2 (0.09 mg), B12 (0.07 mg) and C (13.0 mg). (Aykroyd, 1963) [1]. Mature cowpea seed contain 24.8% protein, 1.9% fat, 6.3% fibre, 63.6% carbohydrate, 0.00074% thiamine, 0.00042% riboflavin and 0.0028% niacin (Davis *et al.*, 2000) [4].

In view of low input requirement and short maturity, its cultivation is quite economic. As compared with crops particularly the cereals, cowpea offers better chances of crop production under adverse conditions of moisture stress and low fertility. Though India is leading producer of cowpea, its grain productivity is very low. Therefore, there is a great scope for its improvement and to increase the production by developing high yielding, disease and pest resistant, moisture stress resistant varieties (Ehlers and hall, 1997) [5] and improved nutritional value by increasing protein content specially.

The variability studies enable the breeder to have a group of genotypes to be used as parents, but unless they produce desirable progenies in combination with each other it has limited scope. Hence their combining ability needs to be studied. A study of combining ability analysis gives useful information regarding selection of parents based on performance of their hybrids. Further, it serves as a powerful tool to elucidate the nature and magnitude of various types of gene action involved in the expression of quantitative traits.

In a self-pollinating crop like cowpea, variability is often created through hybridization between carefully chosen parents. The scope of exploitation of hybrid vigour will depend on the direction and magnitude of heterosis, biological feasibilities and the type of gene action involved. The information of such estimates is essential to plan efficient breeding programme for the improvement of the crop. Although the hybrid vigour cannot be exploited commercially in highly self-pollinated crop like cowpea, the heterotic  $F_1$ s can be used to isolate a higher frequency of productive derivatives in their later generations. Also, Cowpea being a self-pollinated crop, the diversification of genotypes is expected to be limited compared to cross-pollinated crops. The divergence studies of parents involved and their  $F_1$ s may provide a tool for selection for ensuring occurrence of more number of desirable attributes in progenies and also for planning future crossing programme. Choice of parents is considered an important aspect in any breeding programme aimed at improving yield and its related attributes because the high yielding parent may not necessarily transfer its superiority to the progenies in the crosses.

The present investigation entitled "Genetic Studies in Cowpea (*Vigna unguiculata* (L) walp.)" was therefore undertaken with following objectives.

### Material and Methods

The experimental material used for the present investigation comprised of sixty genotypes of cowpea, collected from

Agriculture Research Station, Pandharpur and Pulses Improvement Project M.P.K.V Rahuri. The experiment was carried out in Randomized Block Design (RBD) with three replications at Pulses Improvement Project M.P.K.V Rahuri, during *kharif*-2013. Each genotype was sown in single row of 3 meter length with a spacing of 45 cm between rows and 10 cm between plants. The observations were recorded on five randomly selected plants from each treatment in each replication for eleven morphological characters *viz.*, Days to maturity, Days to 50% flowering, Plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, 100-seed weight, harvest index and seed yield per plant (g).

Analysis of variance was performed the standard procedures described by Panse and Sukhatme (1995) [13]. The multivariate analysis such as Grouping of populations into different clusters was done using Tocher's method as described by Rao (1952) [15]. Genetic distance between clusters was calculated using the carried out by using  $D^2$  statistics Mahalanobis (1936) [10].

### Results and Discussion

Analysis of variance revealed that the genotypes under study differed significantly for all the eleven characters. This indicates that existence of considerable genetic variability for selection and breeding. Mean and range traits of the genotypes are presented in Table 1. The estimate of genetic variability exhibited the highest GCV for No. of clusters per plant (32.09), followed by seed yield per plant (28.84), No. of pods per plant (27.62), No. of primary branches (25.03), plant height (16.42), 100 seed weight (15.78) and Harvest Index % (15.00). The differences between GCV and PCV were very low for all the characters, was mostly due to genetic factors.

The presence of high genetic variability is an indication of good for their improvement through hybridization followed by selection. High heritability (b.s.) estimates for all characters and it ranged between 66.00 and 95.60 percent. In the present study, high heritability with high genetic advance as a percent of mean indicating additive gene action was observed for traits *viz.*, plant height at maturity, harvest index, seed yield per plant and 100 seed weight.

High heritability coupled with high genetic advance as percent of mean was recorded for plant height, seed yield per plant, No. of clusters per plant, No. of pods per plant and harvest index are revealed the influence of additive gene action for these traits. Hence the improvement of these traits can made through direct phenotypic selection. Thus, selection for these traits in cowpea may be effective for increasing seed yield as stated by Johnson *et al.* (1955a) [7], These results are in conformity with the results of Kalaiyarasai and Palanisamy (2000) [8] for plant height and seed yield per plant Narayana kutty *et al.* (2003) [11] for yield per plant; Nigude *et al.* (2004) [12] for plant height, seed yield, test weight.

The genetic distance during the crossing programme to create the genetic diversity between genotypes in the terms of gene frequencies which may result of heterotic group and transgressive segregants. In this divergence studies sixty genotypes evaluated for eleven characters were grouped into nine clusters. Cluster II had maximum (21) genotypes, followed by cluster I (14 genotypes), cluster III (11 genotypes), cluster IV (7 genotypes), cluster VII (3 genotypes) and other 4 clusters *viz.*, V, VI, VIII, IX were

solitary in regard to multivariate composition. This indicates the presence of diversity in the sixty genotypes studied. These findings confirmed the earlier reports of Puneet *et al.* (2006) [14], Bhandari and Verma (2007) [2], Suganthi and Murugan (2007) [19] and Francisco *et al.* (2009) [6].

Genetic distance among the most clusters was significant. Intra and inter cluster distances were presented in the Table 3. Intra-cluster D<sup>2</sup> values ranged from 0 to 6.02. Maximum intra cluster distance was observed in cluster VII (6.02), followed by cluster IV (5.81) and cluster III (5.66). Lowest intra cluster

was observed in clusters V, VI, VIII and IX (0). The inter-cluster D<sup>2</sup> values ranged from 3.77 to 10.65. The maximum inter cluster distance (10.65) was observed between VI and IX clusters followed by clusters V and IX (10.05) and cluster I and VII (9.85), while the minimum inter cluster distance of 3.77 was recorded between cluster V and VI. Dalsaniya *et al.* (2009) [3], suggesting that the genetic divergence value is the best criteria for choosing diverse parent for hybridization programme.

**Table 1:** Range and estimate of genetic parameters of different characters in Cowpea

Sr. No.	Characters	Mean Range	$\sigma^2g$	$\sigma^2p$	$\sigma^2e$	GCV (%)	PCV (%)	ECV (%)	h <sup>2</sup> (BS%)	GA	GA as % mean
1	Days to 50% flowering	36 – 44	3.40	5.16	1.75	4.64	5.71	3.33	66.00	3.08	7.72
2	Day to maturity	62.33 – 71	7.02	9.08	2.05	4.01	4.56	2.17	74.40	4.80	7.27
3	Plant height (cm)	27.20 - 55.00	46.18	48.95	2.14	16.42	16.79	3.51	95.60	13.78	33.08
4	No. of primary branches	1.96 – 5.23	0.65	0.82	0.17	25.03	28.22	13.03	78.70	1.47	45.73
5	No. of clusters per plant	2.20 – 7.03	1.97	2.22	0.25	32.09	34.10	11.53	88.60	2.71	62.21
6	No. of pods per plant	3.76 – 13.93	5.52	6.15	0.89	27.62	29.86	11.35	85.50	4.37	52.62
7	Pod length (cm)	6.70 – 10.53	0.91	1.35	0.43	11.24	13.64	7.73	67.90	1.62	19.09
8	No. of seeds per pod	7.80 - 13.36	1.46	2.16	0.70	11.03	13.45	7.69	67.30	2.04	18.64
9	100 seed weight (g)	2.76 – 5.63	0.42	0.57	0.15	15.78	18.43	9.52	73.30	1.14	27.85
10	Seed yield per plant (g)	2.06 – 5.83	1.14	1.20	0.06	28.84	29.60	6.66	94.90	2.15	57.88
11	Harvest Index (%)	15.93 - 30.76	12.93	15.67	2.74	15.00	16.51	6.91	82.50	6.72	28.06

**Table 2:** Distribution of sixty cowpea genotypes in different clusters.

Sr. No	Clusters No.	Total No. of genotypes in cluster	Genotype included in clusters
1	I	14	VWB-5, VWB-3-1, PCP-23-2, VWB-3, DLCP-6-1, KBC-1-M, GTC-22, EC-34302, HC-03-2, PCPP-3201-1, PCP-97180, TC-2010-82, V-240, TPTC-1.
2	II	21	COVU-702, RC-101, HC-1-17, PCP-4-55, PHULE CP-05040, PHULE CP-109, PHULE CP-104, CAZC-13-1, PGCP-5, GC-525, CAZC-13, PCP-12-11, KBC-WS-1, VCM-8, TC-701, VWB-4, PCP-9741, IC-201081, GC-3, HC-03-3, CPD-71.
3	III	11	DLCP-6, PCP-97226-1, G-1, DCS-6, PUSA KOMAL, PCP-97198, PCP-2011-5, DCP-17, GCS-7, T-944-1, JLCP-38.
4	IV	7	T-944, JLCP-5, PCP-M-10, PCP-04-04-6-01, PHULE CP-629, PCP-13-11, PHULE PANDHARI.
5	V	1	GC-0121.
6	VI	1	PCP-4-2.
7	VII	3	PUSA PALGHAR, PGCP-4, PCP-97262-01.
8	VIII	1	HC-08-02.
9	IX	1	GUDAGI COWPEA.

The clusters mean for each of eleven characters are presented in Table 4. From the data it can be seen that considerable differences existed for all the characters under study. The cluster means observed for days to 50% flowering varied from 51 (cluster IX) to 59.67 days (cluster VI). The genotypes of clusters IX (51 days) appeared to be early in flowering followed by cluster II (51.46), V (52), I (53.9). The cluster means for days to maturity varied from 76.00 (cluster IX) to 88.67 days (cluster VI). The clusters VI (88.67 days), VIII (86.67 days) and III (84.09 days) showed relatively more days to maturity. The range of cluster means for plant height varied from 39.73 (cluster VII) to 63.33 cm (cluster I). The cluster I (63.33 cm) followed by cluster IX (60.2 cm), VIII (58.93 cm) and III (57.36 cm) showed relatively more plant height. The cluster IX (2.8) recorded the highest cluster mean for number of primary branches per plant and it was followed by cluster I (2.62), II (2.59) and IV (2.55). The lowest cluster mean was recorded for cluster V (1.6) followed by cluster VI (2.4) and VIII (2.47).

The cluster IX (2.6) recorded the highest cluster mean number of cluster per plant and it was followed by cluster I (2.52), VII

(2.49) and III (2.47). The lowest cluster mean was recorded for cluster V (1.47) followed by cluster VIII (1.53) and VI (2.4). The highest number of pods per plant was observed in the genotypes of cluster IX (7.47) and it was followed by cluster II (5.9) and cluster IV (5.43). The cluster VIII (4.4) recorded the lowest cluster mean followed by cluster III (4.99) and VII (5.07). The cluster means for pod length varied from 11.33 to 14.53 cm. The cluster VIII (14.53 cm) recorded highest means pod length followed by cluster III (14.40 cm). The cluster IX (11.33 cm) showed lowest cluster mean followed by cluster V (11.67 cm) and VI (11.87 cm). The cluster IX (12.93) recorded highest seeds per pod followed by cluster I (12.73) and III (12.53). The genotypes in cluster V (9.07) recorded the lowest number of seeds per plant followed by cluster VII (10.24) and VI (11.13). The cluster means for 100 seed weight ranged from 7.18 to 13.67 g. The cluster V (13.67 g) recorded highest cluster mean followed by cluster III (13.47 g) and VI (12.66 g). The cluster IX (7.18 g) recorded the lowest cluster mean followed by cluster VIII (7.41 g) and cluster IV (10.11 g) for this trait. The cluster VI (7.61 g) recorded highest seed yield per plant (g) followed by

cluster II (6.34 g). The cluster IV (4.4 g) recorded lowest cluster mean followed by cluster IX (5.07 g) and cluster I (5.15 g). The cluster VII (27.86%) recorded highest mean harvest index followed by cluster V (26.1%), VI (25.56%), IX

(25.35%), III (23.86%) and II (23.07%). The cluster IV (14.97%) recorded lowest cluster mean followed by cluster (17.92%).

**Table 3:** Average intra and inter cluster square distance ( $D^2$ ) among sixty genotypes for nine cluster based on morphological traits in cowpea.

Cluster No	C-I	C-II	C-III	C-IV	C-V	C-VI	C-VII	C-VIII	C-IX
C-I	4.44	7.43	6.25	7.39	9.05	9.79	9.85	5.88	6.99
C-II		5.12	7.04	6.99	5.89	6.55	6.3	7.12	7.27
C-III			5.66	8.69	6.92	7.6	8.18	7.15	8.59
C-IV				5.81	8.73	9.5	8.61	7.25	8.15
C-V					0.00	3.77	5.19	8.56	10.05
C-VI						0.00	5.69	8.74	10.65
C-VII							6.02	8.92	9.63
C-VIII								0.00	5.82
C-IX									0.00

Where, Underline figures indicate intra cluster  $D^2$  values, C-Cluster

**Table 4:** Clusters mean values for eleven characters of sixty cowpea genotypes.

Clusters No.	Days to 50% Flowering	Days to maturity	Plant height (cm)	No. of primary branches	No. of cluster per plant	No. of pod per plant	Pod length (cm)	No. of seed per pod	100 seed weight (gm)	Seed yield /plant (gm)	Harvest Index (%)
C-I	53.9	82.98	63.33	2.62	2.52	5.18	14.35	12.73	11.4	5.15	17.92
C-II	51.46	78.19	48.08	2.59	2.41	5.9	13.31	11.29	11.18	6.34	23.07
C-III	55.58	84.09	57.36	2.5	2.47	4.99	14.4	12.53	13.47	5.58	23.86
C-IV	54.52	78.05	49.1	2.55	2.32	5.43	13.73	11.69	10.11	4.4	14.97
C-V	52	84	42.73	1.6	1.47	6.13	11.67	9.07	13.67	6.05	26.1
C-VI	59.67	88.67	40.93	2.4	2.4	5.47	11.87	11.13	12.66	7.61	25.56
C-VII	54.44	79.33	39.73	2.8	2.49	5.07	13.42	10.24	12.29	5.45	27.86
C-VIII	58	86.67	58.93	2.47	1.53	4.4	14.53	12.93	7.41	5.38	21.59
C-IX	51	76	60.2	2.8	2.6	7.47	11.33	11.4	7.18	5.07	25.35

Where, C-Cluster

**Table 5:** Percent contributions of traits into total divergence.

Sr. No	Characters	Times Ranked	Percent contribution
1	Days to 50% Flowering	74	4.16
2	Days to maturity	99	5.57
3	Plant height (cm)	706	39.71
4	No. of primary branches	2	0.11
5	No. of cluster per plant	14	0.79
6	No. of pod per plant	7	0.39
7	Pod length (cm)	5	0.28
8	No. of seed per pod	3	0.17
9	100 seed weight (gm)	315	17.72
10	Seed yield per plant (gm)	140	7.87
11	Harvest Index (%)	413	23.23
	Total	1778	100.00

The percent contribution towards genetic divergence by all the eleven contributing characters is presented in Table 5. The maximum contribution towards genetic divergence is by plant height (39.89%) contributed more to genetic diversity. It was followed by harvest index (23.33%), 100 seed weight (17.80%), seed yield per plant (7.91%), days to maturity (5.59%), days to 50% flowering (4.18%), number of cluster per plant (0.79%), number of pods per plant (0.40%), pod length (0.36%), number of seed per pod (0.28%) and number of primary branches per plant (0.11%).

These results are in accordance with the reports of Rewale *et al.* (1996)<sup>[16]</sup> and Kumawat and Rajee (2005)<sup>[9]</sup>. Hybridization between genotypes falling in the most distant clusters will result in maximum hybrid vigour and eventually desirable

segregants or combinations leading to the development of useful varieties. Sharma and Mishra (1997)<sup>[17]</sup> reported diversity in cowpea and suggested selection of parents for hybridization and improvement of character.

Hence it can be concluded that the diverse parent belonging to different cluster should be involved in the hybridization programme based on their merits of characters. This study indicates that there is possibility of beside this more number of germplasm should be incorporated with seed yield per plant of genotypes through further hybridization programme such as inter crossing between genotypes *viz.*, VCM-8, PCP-12-11, PCP-97262-01, JLCP-38, G-1, Pusa palghar, Phule CP-629, Gudagi cowpea, DLCP-6, CPD-71, PCP-4-2 and CAZC-13-1 were selected as per se performance of genotypes and divergent cluster combination observed in the present study. The present investigation also revealed that diverse geographic origins of the genotypes could not necessarily be an index of variation and the factors other than geographic diversity such as selection, genetic drift and environment may be responsible for inconsistency of genotype.

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