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Research Note

Genetic variability for quantitative and quality traits in cowpea [*Vigna unguiculata* (L.) Walp]

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Abstract

The field experiment comprised of 30 cowpea genotypes were evaluated for genetic variability for important quantitative and quality traits during the Summer 2019 season. Analysis of variance showed that there was significant differences among the genotypes evaluated for all the characters studied. A high value of phenotypic coefficient of variation than genotypic coefficient of variation was observed for all the characters which revealed the influence of environment for phenotypic expression of the traits. High heritability and the high genetic advance were observed for days to 50% flowering, leaf width, the number of nodes on main stem, the number of main branches, the number of pods per plant, length of pod, the number of seeds per pod, test weight, seed yield per plant, fat content, lignin content and host preference mechanism of pulse beetle on the grain of cowpea indicating that the characters are governed by additive gene action and the characters which can be improved by simple selection. On Mahalanobis D^2 statistics, the genotypes were grouped into four clusters. A maximum number of genotypes was observed in cluster I with 16 genotypes followed by clusters II and III with 8 genotypes each and cluster IV with solitary genotype. On the basis of divergence classes studied the genotypes *viz.,* PMCP-1021, CP-20, CP-25, CP-26, CP-7, CP-2-1, CP-15, CP-9-1, CP-17, CP-2-1, PCP-1809, PCP-1124, PCP-1123, Phule Rukmini and Phule Pandhari can be used for the further breeding programme.

Keywords: Cowpea, Genetic diversity, Heritability, Genetic advance

Cowpea [*Vigna unguiculata* (L.) Walp] is identified as one of the important leguminous crops in India. India and Africa are the centers of origin of cowpea which is recognized by Vavilov (1951). Cowpea is grown for a vegetable purpose known as yard long bean, snake bean, asparagus bean and catjang bean, while it is grown for dry seeds is known as kaffir pea, southern pea, black eye pea and china pea. Cowpea has characteristics to neutralize fatty acids during the digestion of food. Cowpea is a self pollinated crop belongs to the family Leguminosae and subfamily *Fabaeace* or *Papilionaceae* with chromosome number 2n=2x=22. Verdcourt (1970) reported five sub-species in which *Vigna unguiculata, Vigna dekinditiana* and *Vigna mensensis* are wild sub-species and cultivable subspecies are *V. unguiculata* syn *V. sinensis* (common) and *V. sesquipedalis* ((yard long or asparagus bean) which are popular in India (Steele,1976). Erect, determinant, indeterminant and non-branching are the range of growing

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habits of cowpea. It is an annual herbaceous and warm seasonal legume crop with well built tap root system. It has been called as "poor man's meat" due to its well protein content (20-25%). Cowpea plays a vital role in the tropics and subtropics region of developing countries like Asia, sub-Saharan Africa, Central and South America.

Cowpea stands well in dry environments, it is noticeable characteristics of cowpea. It helps to improve soil fertility as it has ability to fix nitrogen from the atmosphere. It has maximum forage as it has maximum vegetative growth covers maximum ground area results in less soil erosion. Cowpea cultivation requires pH about 6-7 with a loamy type of soil with 250-300 mm rainfall and 27^0C temperature for the pod formation and seed yield. It is cultivated in dry zone of the world, where other leguminous crops cannot withstand hence it is known as "The Crop of Choice". Cultivated area and yield increased by the development of new genotypes with early maturity, resistance to pests and diseases and good grain quality (Ehlers and Hall, 1997).

For the breeding programme genetic variability is necessary. The collection and evaluation of genotypes is a pre-requirement of the breeding programme resulted in scope for the genetic diversity. In hybridization for genetical yield improvement the quantitative assessment of diversity within the collection of cultivars and diversity traits provides effective and important guidance to a breeder. To create a more heterotic effect in hybridization if genetically diverse parents are involved with distantly related parents and a vast spectrum of variability could be predicted in the segregation generation of crosses are the two reasons for the genetic diversity among the types.

The experimental material consists of 33 cowpea genotypes obtained from Pulses and Oilseed Crops Research and Training Centre, Pandharpur was raised in a randomized block design with three replications at Post Graduate Research Farm, RCSM, College of Agriculture, Kolhapur during the Summer 2019 season **(Table1)**.

The genotypes were sown in a spacing of 45 cm between rows and 10 cm among the plants in four rows of 5 meter length. Observations were recorded on days to 50% flowering, days to maturity, length of leaf, width of leaf, the number of nodes on main stem, the number of main branches, the number of pods per plant, length of pod, seeds per pod, 100 seed weight, yield of seed per plant, protein, tannin, carbohydrate, fat, lignin, starch content and host preference mechanism of pulses beetle. The statistical analysis was carried out as per the procedure outlined by Panse and Sukhatme (1958) by using the WINDOSTAT programme.

The analysis of divergence was carried out by D^2 statistics of Mahalnobis (1936) as described by Rao (1952). The analysis of covariance for character pairs, based on plot averages was carried out (Cochran and Cox, 1957).

Analysis of variance showed significant differences within genotypes for all the characters taken for the study (**Table 2**). The characters lignin content, the number of pods per plant, host preference mechanism of pulse beetle, seed yield per plant, the number of nodes on main stem, test weight, pod length and the number of main branches showed higher estimates of GCV and PCV. This showed presence of large variation in the genotypes for these characters. Therefore, simple selection can be applied for the improvement of these characters. Also, these characters provide a good source of variation and hence they are useful in crop improvement programme in cowpea. High PCV and GCV were observed in the traits namely the number of nodes on main stem (24.45, 26.07), the number of pods per plant (34.42, 35.39), test weight (20.01, 20.25), seed yield per plant (31.82,

Table 1. List of 33 genotypes of Cowpea used in the present study

S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes
1	CP-5(RARI,Durgapura)	12	CP-25(GBPAU,Pantnagar)	23	PCP-1805(ARS,Pandharpur)
2	CP-6(RARI,Durgapura)	13	CP-26(UAS,Dharwad)	24	PCP-1809(ARS,Pandharpur)
3	CP-7(UAS,Banglore)	14	CP-2-1(RARI,Durgapura)	25	PCP-1810(ARS,Pandharpur)
4	CP-8(UAS,Banglore)	15	CP-9-1(RARI,Durgapura)	26	PCP-1814(ARS,Pandharpur)
5	CP-13(PRC,Vamban)	16	CP-17-1(RARI,Durgapura)	27	PMCP-1002(ARS,Pandharpur)
6	CP-15(PRC,Vamban)	17	PCP-1110(ARS,Pandharpur)	28	PMCP-1005(ARS,Pandharpur)
7	CP-16(SKRU,Bikaner)	18	PCP-1115(ARS,Pandharpur)	29	PMCP-1008(ARS,Pandharpur)
8	CP-17(RARS,Pittambi)	19	PCP-1116(ARS,Pandharpur)	30	PMCP-1021(ARS,Pandharpur)
9	CP-18(SDAU,Srinagar)	20	PCP-1123(ARS,Pandharpur)	31	Phule Pandhari(C)(ARS,Pandharpur)
10	CP-19(ARS,Tirupati)	21	PCP-1124(ARS,Pandharpur)	32	Phule Rukmini(C)(ARS,Pandharpur)
11	CP-20(UAS,Dharwad)	22	PCP-1126(ARS,Pandharpur)	33	Phule Vithai(C)(ARS,Pandharpur)

Table 2. Parameters of genetic variability of 18 characters in 33 genotypes of cowpea.

S. No.	Characters	Mean sum of square of treatments	Range		Mean	Coefficient of variation (%)		Heritability in broad sense (h^2_{bs})	Genetic advance (GA)	Genetic advance as per cent of mean (GAM)
			Minimum	Maximum		Genotypic (GCV)	Phenotypic (PCV)			
1	Days to 50% flowering	180.39**	45.33	69.00	56.40	13.24	14.69	81.24	13.87	24.59
2	Days to maturity	152.59**	68.66	94.66	85.69	8.10	8.74	85.71	13.23	15.44
3	Leaf length (cm)	3.96**	7.20	11.50	8.93	11.61	15.08	59.28	1.64	18.41
4	Leaf width (cm)	2.74**	4.94	8.29	6.25	14.30	17.12	69.76	1.53	24.61
5	Number of nodes on main stem	37.09**	8.26	20.53	14.06	24.45	26.07	87.98	6.64	47.25
6	Number of main branches	7.63**	7.46	13.03	9.51	15.60	18.90	68.17	2.52	26.54
7	Number of pods per plant	88.89**	7.06	27.33	15.66	34.42	35.39	94.58	10.80	68.96
8	Pod length (cm)	15.19**	9.62	20.36	13.04	16.62	18.45	81.13	4.02	30.84
9	Number of seeds per pod	7.66**	7.80	13.66	10.70	14.17	16.32	75.41	2.71	25.35
10	Test weight (g)	17.52**	7.23	17.53	12.02	20.01	20.25	97.60	4.89	40.72
11	Seed yield per plant (g)	77.78**	7.92	24.89	15.78	31.82	33.08	92.53	9.95	63.06
12	Protein (%)	2.20**	17.16	20.89	19.77	4.06	4.82	71.16	1.39	7.06
13	Tannin (mg/100 gm)	0.008**	0.45	0.71	0.62	8.14	9.41	74.83	0.09	14.50
14	CHO (%)	116.15**	41.30	49.50	44.88	4.37	4.50	94.17	3.92	8.74
15	Fat (%)	11.79**	3.43	7.34	5.91	15.00	15.92	88.78	1.72	29.12
16	Lignin (%)	2.45**	0.37	1.97	1.08	37.23	41.27	81.37	0.74	69.18
17	Starch (%)	0.52**	38.58	44.38	40.89	3.14	3.26	92.85	2.55	6.24
18	Host preference Mechanism of pulse beetle	5.08**	6.33	29.00	18.22	33.94	34.54	96.54	12.52	68.70

33.08), lignin content (37.23, 41.27) and host preference mechanism (33.94, 34.54) where as the traits days to maturity (8.10, 8.74), protein content (4.06, 4.82), tannin content (8.14, 9.41), carbohydrate (4.37, 4.50) and starch content (4.37, 4.50) recorded low PCV and GCV. Moderate PCV and GCV were recorded in days to 50 per cent flowering (13.24, 14.69), leaf length (11.61, 15.08), leaf width (14.30, 17.12), the number of main branches (15.60, 18.90), pod length (16.62, 18.45), seeds per pod (14.17, 16.32) and content of fat (15.00, 15.92).

The wide differences between GCV and PCV values were observed in lignin content (4.04%) followed by leaf length (3.47) and the number of main branches (3.3), while host preference mechanism (0.6) and starch content (0.12) had less differences between PCV and GCV. The value genotypic coefficient of variation was lower than the phenotypic coefficient of variation for all traits which inferring that all the traits were impacted by environmental components (**Table 2**).

Manjudevi and Jayamani (2018) reported that GCV was lower than the PCV values for plant height, the number of primary branches per plant, days to flowering, the number of racemes per plant, peduncle length, the number of pods per plant, the number of clusters per plant, the number of pods per cluster, days to maturity, pod length, the number of seeds per pod, 100 seed weight and single plant yield. High PCV and GCV were observed in lignin content, the number of pods per plant, host preference mechanism, the number of nodes on main stem, test weight, pod length and the number of main branches which indicates that simple selection procedures may be followed to improve these characters. Similar findings were reported earlier by Singh *et al.* (2018) for the number of pods per plant and seed yield per plant, Manjudevi and Jayamani (2018) for 100 seed weight, Anbuselvam (2000) for the number of branches and Kalaiyarasai and Palanisamy (2000) for pod length.

The range of heritability (b.s.) was observed from 59.28 to 97.60 per cent. In the case of leaf length (59.28%) medium heritability was found. High heritability was observed in the number of main branches (68.17%), leaf width (69.76%), protein (71.16%), tannin (74.83%), seeds per pod (75.41%), length of pod (81.13%), days to

50% flowering (81.24%), lignin (81.37%), days to maturity (85.71%), nodes on main stem (87.98%), fat per cent (88.78%), seed yield per plant (92.53%), starch per cent (92.85 %), carbohydrate (94.17%), the number of pods per plant (94.58%), host preference mechanism of pulse beetle (96.54%) and test weight (97.60%) which showed less influence of environment for expression of these characters. Similar results were given by Venkatesan *et al.* (2003), Nwosu *et al.* (2013) and Shanko *et al.* (2014) for pods per plant, 100 seed weight and seed yield/plant. (**Table 2**).

High heritability and genetic advance as per cent of mean were recorded in the number of days to 50% flowering (81.24, 24.59), width of leaf (69.76, 24.61), nodes on main stem (87.98, 47.25) main branches (68.17, 26.54), pods/plant (94.58, 68.96), length of pod (81.13, 30.84), seeds per pod (75.41, 25.35), 100 seed weight (97.60, 40.72), yield of seed/plant (92.53, 63.06), fat content (88.78, 29.12), lignin content (81.37,69.18) and host preference mechanism of pulse beetle (96.54, 68.70) which indicates these traits were controlled by additive gene effects follow simple selection method for further improvement.

On the contradictory, the traits days to maturity (85.71, 15.44), leaf length (59.28, 18.41), protein (71.16, 7.06), tannin (74.83, 14.50), carbohydrate (94.17, 8.74) and starch (92.85, 6.24) showed low heritability with low genetic advance are governed by non-additive gene action, such trait can be improved by hybridization followed by simple selection. Similar findings were reported by Shanko *et al.* (2014) for seed yield per plant and pods per plant, Bhadru and Navale (2012) for days to maturity, Koraddi and Basavaraja (2019) reported for days to 50 per cent flowering, the number of pods per plant, test weight and seed yield per plant and Nehru and Manjunath (2001) for test weight & the number of pods per plant.

The determined values of D^2 ranged from 9.60 to 20.38. The maximum inter cluster distance was found between clusters III and IV (4.51), followed by clusters II and III (4.18) and clusters I and IV (3.78) whereas, a minimum inter cluster distance was found between clusters I and II (3.58). Considering the intra-cluster distance, cluster III had maximum intra cluster distance (3.46) whereas, intra-cluster distance was not found in the cluster IV due to solitary cluster (**Table 3**).

The cluster I showed the least value, whereas among clusters III & IV we can see the highest value having genotypes PCP-1126, Phule Vithai, PMCP-1002, Phule Rukmini, PMCP-1021, Phule Pandhari, CP-17-1, CP-16 and CP-26 (**Table 4**). Thitry-three genotypes were grouped into four clusters. Cluster I had the largest with sixteen genotypes, followed by clusters II and III with eight genotypes each, while cluster IV was solitary.

Rao (1952) narrated the Tocher's method which is used here to form cluster. Thirty-three genotypes were distributed in four clusers. Out of four clusters sixteen genotypes are found in cluster I, eight genotypes are found in clusters II and III while cluster IV was solitary. A similar study was found by Sulnathi *et al.* (2007) and Lovely *et al.* (2017).

Among the clusters III and IV (4.51), the highest inter cluster was followed by clusters II and III (4.18) and clusters I and IV (3.78), while clusters I and II (3.58) showed lower inter cluster distance. Cluster III was observed with the highest intra-cluster value (3.46), due

Table 3. D^2 values of cowpea for average intra and inter cluster

Clusters	I	II	III	IV
I	9.60	12.82	13.97	14.29
II		10.37	17.48	13.68
III			12.04	20.38
IV				0.00

Table 4. Various clusters distributed for 33 cowpea genotypes

Cluster	Number of genotypes	Name of the genotypes
I	16	CP-20, CP-15, CP-13, PCP-1809, PCP-1814, PCP-1110, PCP-1115, PMCP-1008, PCP-1116, PCP-1805, PMCP-1005, CP-17, CP-8, CP-7, CP-18, CP-6.
II	8	CP-2-1, CP-9-1, CP-5, CP-19, PCP-1810, PCP-1124, PCP-1123, CP-25.
III	8	PCP-1126, Phule Vithai, PMCP-1002, Phule Rukmini, PMCP-1021, Phule Pandhari, CP-17-1, CP-16.
IV	1	CP-26.

Table. 5 Mean performance of 4 clusters for 18 characters in cowpea

Cluster	Days to 50% flowering	Days to maturity	Leaf length (cm)	Leaf width (cm)	Number of nodes on main stem	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)	Protein (%)	Tannin (mg/100 gm)	CHO (%)	Fat (%)	Lignin (%)	Starch (%)	Host pre. mechanism
I	57.19	84.54	8.90	6.28	14.40	9.20	15.94	13.52	10.77	11.96	16.12	19.89	0.64	45.57	6.20	1.15	41.45	22.40
II	56.38	84.21	8.86	6.44	14.25	9.74	12.73	13.28	10.42	14.78	15.39	20.00	0.61	43.00	5.25	0.73	40.21	14.42
III	55.21	90.25	9.20	6.18	13.79	10.00	18.82	11.81	10.83	9.19	16.13	19.49	0.61	45.10	5.82	1.34	40.05	14.54
IV	53.67	79.67	7.93	4.94	9.30	8.60	9.40	13.40	11.13	13.67	10.97	18.32	0.65	47.26	7.30	0.77	44.38	11.30

to solitary intra cluster distance not seen in cluster IV. Similar interpretations of the study with Bhandari and Verma (2007) for the intra cluster distance.

On the basis of mean performance of the cluster with 18 traits, resulted in the vast range of variability present among the clusters. Test weight, number of pods per plant and yield of seed per plant provide highest values for the calculation of GCV and PCV. All traits showed higher heritability resulted in effect of environment on traits except leat length. The traits *viz*., maturity days, length of leaf, tannin, starch, protein and carbohydrate can be improved by hybridization which shows non-additive gene action with low genetic advance and high or low heritability on the contradictory base.

The GCV and PCV both were observed to be high for the number of pods per plant, lignin content, test weight and seed yield per plant. Thus, these characters provide a good source of variation and hence they are useful in crop improvement programme in cowpea.

High heritability estimates along with high genetic advance were obtained for several characters. The character test weight showed the highest heritability followed by host preference mechanism. The character number of days to 50% flowering showed the highest genetic advance followed by the character number of days to maturity. This suggests that the characters were governed by additive gene action and selection will be effective. Therefore, it can be concluded that environmental effects are the least on the characters studied. Therefore, there is scope for improvement of these characters having high heritability in the breeding programme.

The number of days to 50% flowering, the number of nodes of main stem, pod length and host preference mechanism showed the highest mean for cluster I, whereas cluster IV shows the lowest mean for flowering, maturity, length of leaf, width of leaf, the number of nodes on main stem, the number of main branches, pods per plant, yield per plant, protein content and host preference mechanism of pulse beetle, while highest in cluster IV for the number of seeds/pod, tannin, carbohydrate, fat and starch content **(Table 5).** The highest mean of cluster observed for cluster III for maturity datys, leaf length, the number of branches, pods/plant, yield per plant and lignin, while the lowest for pod length, test weight, tannin and starch content. Cluster II showed the highest cluster mean for leaf width, test weight and protein content while lower to no. of seeds per pod, tannin, carbohydrate, fat and lignin content. The genotype CP-26 was mono-genotypic, which indicated wide diversity from the remaining. Thus, this genotype has an entirely different genetic markup from the others.

Based on D^2 analysis, 33 genotypes were grouped in four clusters with a wide range of divergence between them. D^2 analysis revealed that, there was a wide

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diversity between the genotypes with D^2 values ranging from 9.60 to 20.38. The highest D^2 value was observed between clusters III and IV. The maximum cluster mean for carbohydrate content was observed in the genotype of cluster IV, followed by starch content in the genotype of cluster IV, while the number of pods per plant and seed yield per plant in genotypes of cluster III. On the basis of divergence classes studied the genotypes *viz.,* PMCP-1021, CP-20, CP-25, CP-26, CP-7, CP-2-1, CP-15, CP-9-1, CP-17, CP-2-1, PCP-1809, PCP-1124, PCP-1123, Phule Rukmini and Phule Pandhari can be used for the further breeding programme.

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