



Study on Genetic Variability in Cowpea [*Vigna unguiculata* (L.) Walp]

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Authors' contributions

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

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ABSTRACT

Cowpea [*Vigna unguiculata* (L.) Walp] also known as a black-eyed pea or Southern pea, belongs to Fabaceae family is rich in proteins, vitamins, minerals and phosphorus. It is mainly grown for grain, pulse cum vegetable and fodder purposes. Twenty-seven genotypes of cowpea were sown in RBD with three replications and observations regarding eighteen characters were recorded at the vegetable farm, RPCAU, Pusa, Samastipur during *zaid*-2017. Analysis of variance shows that there was a significant difference among genotypes recorded among all the eighteen quantitative characters indicates the diverse genetic nature of base population. The coefficient of phenotypic variation was slightly greater than those of genotypic variation for almost all the character shows that the existing variation is mainly governed by the genotypic factor and there is little influence of environment in the expression of the character. High heritability coupled with high genetic advance

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was observed for characters like pod yield per plant, plant height, pod yield (q/ha), number of pods per plant and number of nodes on the main stem shown that the direct selection will be more effective. Genetic divergence using D^2 analysis was also carried out for all the twenty-seven genotypes and were grouped into six clusters. Cluster I was largest including of eleven genotypes whereas cluster VI was smallest consisting only one genotype. Inter-cluster D^2 values ranged from 606.11 to 1837.92. The high value of D^2 distance help breeder in selection of the parental line for initiating any hybridization programme.

Keywords: Cowpea; GCV; PCV; heritability; genetic advance and genetic divergence.

1. INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp.] is an annual legume which belongs to the family Fabaceae and native to central Africa. It is one of the important food legumes in several countries of the tropics and sub-tropics and especially in Africa, Asia, Central and South America [1]. Cowpea is grown over an area of 14 million ha with a production of 4.5 million tones and the productivity of 387 kg per ha (www.cowpea.org). India ranks second in vegetable production from 58.5 million tones in 1991-92 to 175 million tones in 2016-17 [2]. On the dry weight basis, cowpea grain contains 23.4 percent protein, 1.8 percent fat, 60.3 percent carbohydrates and it is the rich source of calcium and iron [3]. The present-day cultivars exhibit lower productivity, non-synchronous flowering and fruiting, less response to high doses of inputs like fertilizers, irrigation, tillage etc., non-suitability of the various cropping systems, lodging and shattering susceptible, long duration, complete or partial absence of genetic resistance to major insect pest and diseases like mosaic virus, rust, powdery mildew and bacterial blight that cause considerable damage and poor harvest indices. Development of cultivars with early maturity, acceptable grain quality, resistance to some important diseases and pests has significantly increased the yield and cultivated area [4].

In India, considerable germplasm is available in cowpea. Identification of superior genotypes among the existing germplasm can be a good strategy to initiate a breeding programme and also for enhancing the productivity and production of this crop. The development of an effective improvement programme depends on the existence of genetic variability. Variability depends on genetic factors, environmental factors like edaphic & climatic factor. The degree to which the variability of a quantitative character is transmitted to the progeny is referred to as heritability. It provides the valuable biometrical estimate and has been considered to be an index

of the effectiveness of selection because it helps in proportioning the total variation into heritable and environmental effects.

2. MATERIALS AND METHODS

The present investigation was carried out at vegetable research farm, Dr. RPCAU, Pusa, Samastipur, (Bihar) during *zaid*-season 2017 in Randomized Block Design with three replication. The experimental material was comprised of twenty-seven genotypes of cowpea collected from different sources, including check "Kashi Unnati". The genotypes were evaluated for following traits *viz.*, Seed germination percentage, plant height (cm), number of branches per plant, days to first flowering, first flowering node, number of nodes on main stem, peduncle length (cm), number of pods per cluster, day to first picking, pod length (cm), pod diameter (cm), average pod weight (g), number of pods per plant, number of pods per cluster, test weight (g), pod yield per plant (gm), pod yield (q/ha), pod borer infestation percentage. The plot size was 378 m² with spacing 60 cm between rows and 45 cm between plants to plant. Data regarding target traits were recorded on five randomly selected plants in each plot and mean values were calculated for statistical analysis.

2.1 Statistical Analysis

The analysis of variance (ANOVA) for all characters were carried out separately. The analysis of variance was carried out by the procedure as suggested by Panse and Sukhatme [5]. Variability present in the yield and yield contributing characters were analyzed by Burton [6]. Heritability in the broad sense was estimated as the ratio of genotypic to the phenotypic variance and was expressed in percentage as suggested by Allard. [7]. The genetic advance as Improvement in the mean genotypic value of the selected plants over the parental population was estimated by Lush

[8] and followed by Johnson et al. (1955) and Allard [7].

3. RESULTS AND DISCUSSION

The analysis of variance (Table 1.) revealed significant differences among the genotypes for all the characters under study. It indicates the presence of ample variability in the material investigated in the present study. Availability of ample variability in the material is of enormous importance for the success of any breeding programme. Mean performance of genotypes for different traits of cowpea are given in (Table 2.) and the coefficient of variance (CV) was also calculated. The lower the value of the coefficient of variation, more precise the estimate and that ranged between 2.99 to 15.27 in all the traits. The variability parameters of cowpea for twenty-seven quantitative characters are represented in (Table 3). The cowpea genotypes in this investigation showed a significant difference for all of the yield attributing characters under study. The wide range of phenotypic and genotypic variance in genotypes was observed for target traits viz., pod yield per plant, plant height, pod yield (q/h), number of pod per plant, number of nodes on main stem, number of branches per plant and peduncle length. A similar result has reported by Chetukuri et al. [9].

3.1 Genotypic and Phenotypic Coefficient of Variation (GCV and PCV)

The estimate of genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) was ranged between 4.80 to 49.59 and 7.27 to 51.41 respectively. The phenotypic coefficient of variation was slightly higher than genotypic coefficient of variation for all the traits under study. Which indicates towards least influence of environmental factors on the expression of traits viz., pod yield per plant (g), plant height (cm), pod yield (q/ha), pod borer infestation percentage, number of pods per plant, number of branches per plant, average pod weight, first flowering node, number of pods per cluster, test weight (g) and pod length (cm). The wide range of GCV and PCV defines greater variability among the genotypes and thus, better improvement is possible by selection. Several earlier workers also reported high PCV and GCV estimates for number of pods per plant, number of pods per cluster, pod weight and pod length [10], number of pods per plant, number of pods per cluster, pod weight and pod length [11] and number of seeds per pod [12]. However, traits like number of seeds per pod, days to first picking and pod diameter exhibited moderate GCV and PCV [13] while days to first flowering and plant germination percentage showed low GCV and PCV.

Table 1. Analysis of variance of 27 genotypes for eighteen characters of cowpea

Sl. No.	Characters	Mean Sum of Squares		
		Replication (d.f=2)	Treatment d.f= 26	Error d.f= 52
1	Seed germination percentage	12.9482	79.7451**	24.0581
2	Plant height (cm)	230.8033	8917.4561**	192.5840
3	Number of branches per plant	10.1111	213.2906**	9.9060
4	Days to first flowering	3.5679	55.3941**	19.4012
5	First flowering node	0.2235	1.9126**	0.0773
6	Number of nodes on main stem	33.5679	365.6135**	11.4525
7	Peduncle length (cm)	0.4129	191.1045**	1.8964
8	Number of pods per cluster	0.1378	0.8882**	0.0506
9	Day to first picking	4.0370	125.2137**	2.4088
10	Pod length (cm)	1.1481	37.5214**	0.5231
11	Pod diameter (cm)	0.0002	0.0292**	0.0015
12	Average pod weight (g)	0.0278	10.8291**	0.1496
13	Number of pods per plant	85.3296	1373.1896**	28.6661
14	Number of seeds per pod	1.3464	14.1381**	0.7607
15	Test weight (g)	0.1608	22.6497**	0.1347
16	Pod yield per plant (g)	2678.2913	68495.1016**	1119.4198
17	Pod yield (q/ha)	47.3653	6725.0288**	210.5147
18	Pod borer infestation percentage	2.5383	125.8516**	4.8834

Table 2. Mean, range and coefficient of variance of cowpea 27 genotypes for 18 quantitative characters

S. No	Characters	Mean	Range		C.V
			Minimum	Maximum	
1	Seed germination percentage	89.81 ± 2.83	80.31	98.04	5.46
2	Plant height (cm)	108.31 ± 8.01	48.33	279.67	12.81
3	Number of branches per plant	22.70 ± 1.82	9.00	42.00	13.86
4	Days to first flowering	43.49 ± 2.54	35.67	52.33	10.13
5	First flowering node	2.98 ± 0.16	1.33	4.33	9.33
6	Number of nodes on main stem	27.64 ± 1.95	10.33	53.00	12.24
7	Peduncle length (cm)	39.09 ± 0.80	23.00	56.00	3.52
8	Number of pods per cluster	2.28 ± 0.13	1.33	3.33	9.83
9	Day to first picking	51.96 ± 0.9	42.00	62.33	2.99
10	Pod length (cm)	17.75 ± 0.42	13.33	28.00	4.07
11	Pod diameter (cm)	0.82 ± 0.02	0.63	0.98	4.64
12	Average pod weight (g)	6.62 ± 0.22	4.67	12.00	5.83
13	Number of pods per plant	48.35 ± 3.09	18.51	107.79	11.07
14	Number of seeds per pod	12.64 ± 0.50	8.60	16.07	6.90
15	Test weight (g)	12.33 ± 0.21	7.23	18.50	2.98
16	Pod yield per plant (g)	302.22 ± 19.32	127.15	636.76	11.07
17	Pod yield (q/ha)	100.94 ± 8.38	35.86	200.46	14.37
18	Pod borer infestation percentage	14.46 ± 1.28	3.58	25.23	15.27

Table 3. Genetic parameters of 18 characters in cowpea

Sl. No.	Characters	σ^2_g	σ^2_p	GCV	PCV	h^2 (%)	GA	GAM
1	Seed germination percentage	18.56	42.62	4.80	7.27	43.00	5.86	6.52
2	Plant height (cm)	2908.29	3100.87	49.79	51.41	94.00	107.59	99.33
3	Number of branches per plant	67.79	77.70	36.27	38.83	87.00	15.84	69.78
4	Days to first flowering	12.00	31.40	7.96	12.88	38.00	4.41	10.14
5	First flowering node	0.61	0.69	26.24	27.85	89.00	1.52	50.93
6	Number of nodes on main stem	118.05	129.51	39.31	41.17	91.00	21.37	77.31
7	Peduncle length (cm)	63.07	64.97	20.31	20.62	97.00	16.12	41.23
8	Number of pods per cluster	0.28	0.33	23.09	25.09	85.00	1.00	43.76
9	Days to first picking	40.93	43.34	12.31	12.67	94.00	12.81	24.65
10	Pod length (cm)	12.33	12.86	19.77	20.19	96.00	7.09	39.90
11	Pod diameter (cm)	0.01	0.01	11.65	12.54	86.00	0.18	22.29
12	Average pod weight (g)	3.56	3.71	28.46	29.05	96.00	3.81	57.43
13	Number of pods per plant	448.17	476.84	43.78	45.16	94.00	42.28	87.43
14	Number of seeds per pod	4.46	5.22	16.70	18.07	85.00	4.02	31.80
15	Test weight (g)	7.50	7.64	22.20	22.40	98.00	5.59	45.33
16	Pod borer infestation %	40.32	45.21	43.88	46.47	89.00	12.35	85.38
17	Pod yield per plant (g)	22458.56	23577.98	49.59	50.81	95.00	301.30	99.69
18	Pod yield (q/ha)	2171.50	2382.02	46.16	48.35	91.00	91.65	90.80

σ^2_g = Genotypic variance, σ^2_p = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, h^2 (%) = Heritability, GA = Genetic advance;

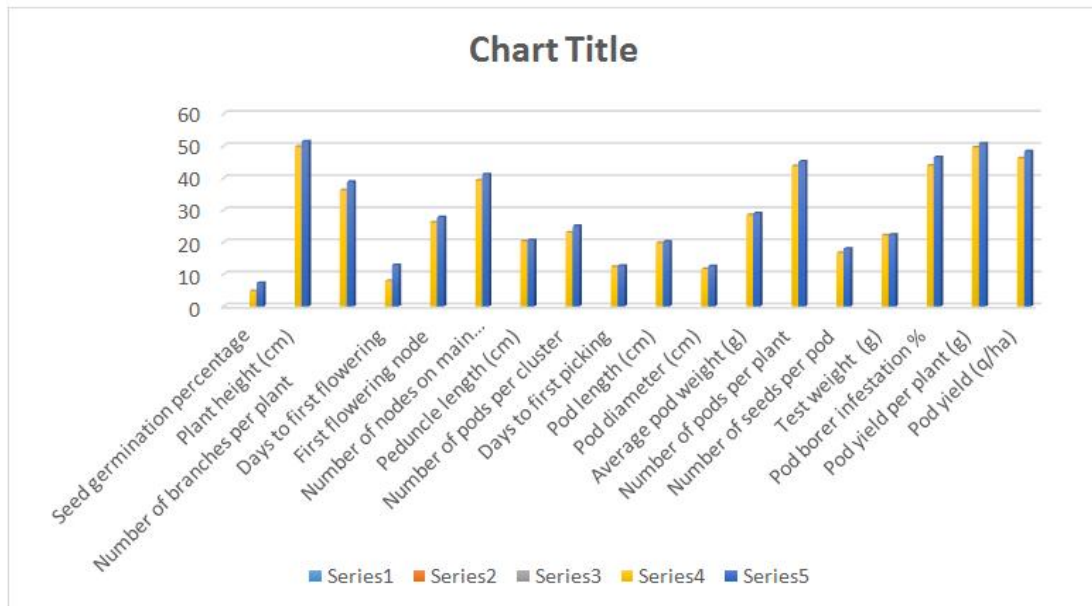


Fig. 1. Phenotypic and genotypic coefficient of variation of eighteen characters under study

3.2 Heritability and Genetic Advance

The heritability expresses the proportion of total variance that is attributed to the average effect of genes and determines the degree of resemblance between parents and its progeny. It is a good index of transmission of characters from parents to their offspring [14]. High value of heritability in a broad sense is helpful in identifying the appropriate character for selection and enabling the breeder to select superior genotypes on the basis of phenotypic expression of character. High heritability values indicates that they have number of additive factors (Panse), [15]. The coefficient of variation does not offer full scope to estimate the heritable variation. The relative amount of variation is assessed with the help of heritability estimates and genetic advance expressed as per cent of mean. In present investigation high heritability coupled with high genetic advance as per cent of mean were reported for traits such as pod yield per plant, plant height, pod yield (q/h), number of pods per plant, number of nodes on main stem, pod borer infestation percentage, first flowering node, number of branches per plant, peduncle length, number of pods per cluster, days to first picking, pod length, test weight, average pod weight, number of seeds per pod and pod diameter indicating the preponderance of additive gene action governing the inheritance of these characters and offers the best possibility of

improvement of these traits through simple selection procedures. Similar inclinations were observed by Hasan Khan et al. [16] in cowpea for number of primary branches per plant, number of pods per plant, pod length and test weight, Khanpara et al. [17] for pod yield per plant, Dinesh et al. [18] for plant height, Kumar et al. [19] for number of clusters per plant, and Diwaker et al. [20] for pod yield per hectare in their study of cowpea. Low heritability coupled with low genetic advance as per cent of mean was shown by characters like days to first picking and plant germination percentage. This indicates that the characters have the least genetic base thus, selection would be ineffective for this trait. Similar result has been reported by Girish et al., [21]. Thus, the experimental findings of this investigation will be helpful for the further breeding programme in the selection of diverse and superior genotypes as a potential donor.

3.3 Genetic Divergence (D^2)

Twenty-seven cowpea genotypes under study were grouped into six clusters mentioned in Table 4. Out of the six clusters, cluster I was largest comprising of eleven genotypes followed by cluster III with five, cluster IV with four, cluster II and V with three genotypes each and cluster VI with single genotype. Intra and inter-cluster distance were presented in Table 5. Inter-cluster between D^2 distance values ranged from 606.110

to 1837.922. Maximum intra cluster distance was observed between cluster II and cluster V (1837.922) followed by between cluster IV and cluster VI (1675.503), between cluster I and cluster V (1360.086) and between cluster II with cluster III (1277.398) and cluster IV (1231.772). The highest D^2 distance help breeder in a selection of the parental line for initiating any hybridization programme. Thus the lines from cluster V and cluster II will give the maximum variation followed by the crosses made between the lines of cluster VI and IV, between cluster V and cluster II and cluster III and cluster IV. The cluster mean (Table 6.) indicates that the cluster VI has the highest number of cluster mean for seven characters followed by cluster V having

highest cluster mean for four characters, and cluster II with the highest mean for two characters. This cluster mean analysis also suggests that the crosses between VI and IV can also give more segregants for the highest number of characters. Per cent contribution of the character towards genetic divergence (Table 7) indicates that the character test weight has the highest contribution towards the diversity followed by peduncle length and day to first picking. Thus, these characters can be further used in the identification of the parents for the hybridization programme in cowpea. These results are in accordance with the reports of Rewale et al. [22] and Kumawat and Rajee [23].

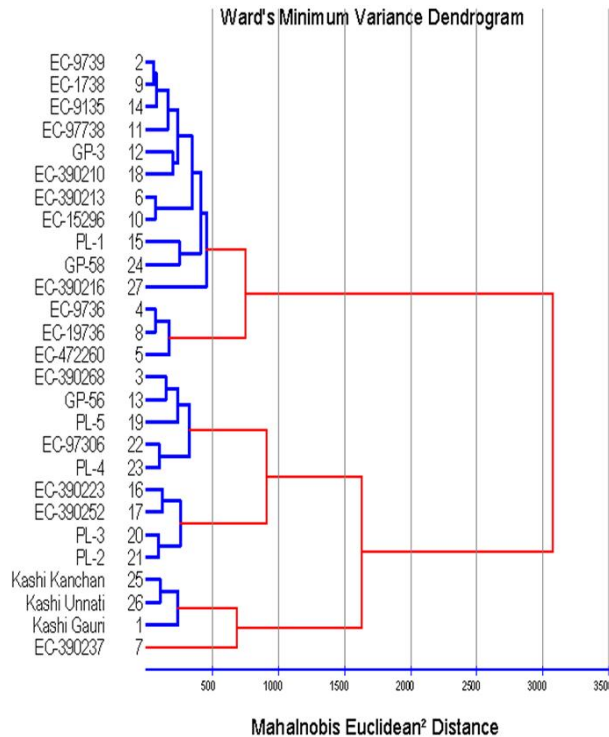


Fig. 2. Clustering pattern of 27 cowpea genotypes on the basis of D^2 statistic by Tocher method

Table 4. D^2 clustering pattern of twenty-seven cowpea genotypes

Clusters	Number of genotypes	Name of genotypes
Cluster I	11	EC-9739, EC-1738, EC-9135, EC-97738, GP-3, EC-390210, EC-390213, EC-15296, PL-1, GP-58, EC-390216
Cluster II	3	EC-9736, EC-19736, EC-472260,
Cluster III	5	EC-390265, GP-56, PL-5, EC-973P05, PL-4,
Cluster IV	4	EC-390223, EC-390252, PL-3, PL-2
Cluster V	3	Kashi Kanchan, Kashi Unnati, Kashi Gauri
Cluster VI	1	EC-390237

Table 5. Intra and inter cluster D² distance among six clusters

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
1 Cluster	453.151	606.11	962.38	650.876	1360.086	1156.628
2 Cluster		243.359	1277.398	1231.772	1837.922	1198.611
3 Cluster			405.444	688.789	917.436	1043.840
4 Cluster				311.755	1121.083	1675.503
5 Cluster					341.965	1023.190
6 Cluster						0.000

Table 7. Percent contribution of characters towards genetic divergence in cowpea genotypes

Sl. No.	Characters	Contribution %	Times Ranked 1st
1.	Seed germination percentage	0.01	0
2.	Plant height (cm)	0.57	2
3.	Number of branches per plant	0.01	0
4.	Days to first flowering	0.01	0
5.	First flowering node	1.42	5
6.	Number of nodes on main stem	0.01	0
7.	Peduncle length (cm)	15.67	55
8.	Number to pods per cluster	0.57	2
9.	Day of first picking	8.83	31
10.	Pod length (cm)	2.28	8
11.	Pod diameter (cm)	0.57	2
12.	Average pod weight (g)	1.99	7
13.	Number of pods per plant	5.7	20
14.	Number of seeds per pod	2.56	9
15.	Test weight (g)	43.87	154
16.	Pod yield per plant (g)	5.7	20
17.	Pod yield (q/ha)	2.28	8
18.	Pod borer infestation percentage	7.98	28

Table 6. Cluster mean values for eighteen characters in cowpea

	SG%	PH	BPP	DFP	FFN	NMS	PEL	PPC	DFP	PL	PD	PW	PPP	SPP	TW	PBI	YPP	YQH-I
1 Cluster	88.387	128.758	27.000	45.242	2.907	32.667	40.305	2.424	54.182	16.258	0.789	5.894	60.224	12.862	10.562	13.095	337.504	112.727
2 Cluster	90.834	90.667	21.778	47.111	3.247	26.667	54.563	2.022	54.556	14.278	0.872	6.056	43.070	12.880	11.861	14.189	234.244	81.276
3 Cluster	92.557	81.477	15.733	43.000	3.399	20.000	35.267	2.147	53.533	17.833	0.863	6.300	32.849	12.307	15.680	19.358	217.201	72.564
4 Cluster	86.223	86.417	18.583	39.917	2.164	21.750	33.150	2.117	47.000	17.917	0.779	5.542	32.756	12.650	11.075	20.765	162.873	58.181
5 Cluster	94.117	67.778	19.889	38.222	3.040	22.333	31.564	2.511	42.667	26.000	0.933	11.389	45.603	12.589	14.583	6.878	464.733	150.707
6 Cluster	90.193	279.667	38.000	46.000	3.997	53.000	44.833	2.333	59.667	19.000	0.750	8.167	81.927	11.400	14.917	3.583	613.077	193.923

4. CONCLUSION

It has been concluded that the diverse parent belonging between clusters II & V should be involved in the hybridization programme based on their merits of characters.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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