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Genetic variability, heritability and genetic advance studies for yield components in F₂ generation of cowpea (*Vigna unguiculata* L. Walp)

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Abstract

The present investigation was carried out to study the genetic variability, heritability, expected genetic advance for growth and yield traits in F₂ generation of 24 hybrids of cowpea. Wide range of variability was observed for all the traits except number of branches per plant and pod width. The high genotypic coefficient of variation was recorded for number of pods per plant, number of pods per cluster, mean pod weight and 100-seed weight. Higher heritability estimates coupled with high genetic advance as per cent of mean were observed for plant height, number of branches per plant, flowers per cluster, pods per cluster, per cent pod set, days to last harvest, pod length, pod weight, number of seeds per pod, 100 seed weight and pod yield per plant. Hence, selection based on these characters would be rewarding for further improvement of cowpea.

Keywords: Cowpea, PCV, GCV, heritability, genetic advance, *Vigna unguiculata*

Introduction

The cowpea *Vigna unguiculata* (L.) Walp. The crop of round utilization is an important legume crop and forms an important component of farming systems throughout the tropics and warm sub-tropics. Cowpea cultivars grown for the immature green pods which are used as vegetable are variously known as yard-long bean, asparagus bean and snake bean. Cowpea belongs to the family leguminosae; sub family fabaceae and genus *Vigna* with chromosome number, $2n = 22$. India is considered as the main *Centre of Origin*. In India, it has been known since the Vedic times. The vegetable cowpea has been subdivided into five sub species; three cultivated, *unguiculata*, *sesquipedalis* and *cylindrica* and two wild, *dekindiana* and *mensenensis*^[1]. Cowpea has been under cultivation in India from ancient times. It is known by many vernacular names like Lobia (Hindi), Barbati (Bengali), Urohi (Assami), Sonta (Garhwali), Chavati (Marathi), Alasande (Kannada) and Manpayar (Malayalam). Among legumes, cowpea is one of the most important vegetable crops grown during rainy and summer seasons. Tender pods as well as green-shelled seeds are used as vegetable and as a pulse when dried. It is also suitable for green manuring, fodder cover and catch crop. It is well adapted to stress and has excellent nutritive qualities. Cowpea, which is a high protein vegetable, suffers from alarmingly low yield, especially in south-east Asia. One of the major reasons was recognized as non-availability of improved genotype suitable for different cropping systems with greater suitability and general adaptability. Although, large amount of variability is available for almost all the traits, even then very poor productivity for green pod yield had been recorded. The yield level of cowpea is low, which is mainly due to the non-availability of desirable high yielding, disease and insect resistant varieties and poor management practices. Hence, the high yield potential and quality are the main targets for effective breeding programme in this crop. For any crop improvement programme it is essential that sufficient variability exist for economically important traits in germplasm. Many workers have repeatedly emphasized the importance of genetic diversity in selecting the parents for recombination breeding in crops. Genetic variability, heritability and genetic advance are pre-requisite for improvement of any crop for the selection of superior genotypes and improvement of any traits. Moreover, estimates of heritability indicate the extent of transmissibility of a character in advance generations which helps in selection based improvement. The present study was, therefore aimed to study variability, heritability and genetic advance between yield and its contributing traits in cowpea.

Materials and Methods

The present investigation was conducted at Horticultural Research Farm, Department of Horticulture, Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur (M.P.) during *kharif* 2014 and *kharif* 2015 and 2016. The experimental materials used in the study comprised of ten genotypes which were collected from different research institutes, eight from Indian Institute of Vegetable Research (IIVR), Varanasi, Arka Garima from IHR, Bangalore and Pusa Komal from IARI, New Delhi. Six lines and four testers were chosen for Line x Testers crossing fashion to generate 24 F₁ hybrids during *Kharif* 2014. Proper isolation of 3 m and bagging was done to check the chance of out crossing and mechanical mixture. Each plot consisted of three rows of 3.15 m long and 7 plants in each row. The spacing given was 60 cm between rows and 30 cm within a row. During *kharif* 2015 twenty-four F₁'s including parents were raised in randomized block design with three replications and true hybrid plants were confirmed based on the presence of male parent characters in the F₁s as well as using molecular markers which were polymorphic between the parents. True F₁s were selfed to obtain F₂ generation seeds and thus 24 F₂ generation hybrids with three replications were raised during *Kharif* 2016 to study variability, heritability and genetic advance among the characters. Observations were recorded on five randomly selected tagged competitive plants from each entry. The observations for sixteen characters *viz.*, plant height, number of branches per plant, days to first flowering, days to 50% flowering, number of flowers per cluster, number of pods per cluster, per cent pod set, days to first harvest, days to last harvest, pod length, pod width, pod weight, number of pods per plant, number of seeds per pod, 100 seed weight and green pod yield per plant were recorded on five plant basis in each replication. These observations were subjected to statistical analysis. The data were statistically analyzed for computation of genetic coefficients of variation and broad sense heritability was estimated as per the formula suggested by Burton [2]. The expected genetic advance was calculated by using formula as suggested by Johnson *et al.* [3].

Analysis of variance

Analysis of variance of ten parents and twenty four F₁'s was carried out as per the procedure given by Panse & Sukhatme [4]. The following linear model was used for analysis of variance

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

Table 1: The structure of analysis of variance was as follows.

Source of variation	Degrees of freedom	Sum of squares	Expected MSS
Replication	r-1	M ₁	$\sigma_e^2 + t \sigma_r^2$
Treatments	t-1	M ₂	$\sigma_e^2 + r \sigma_g^2$
Error	(r-1)(v-1)	M ₃	σ_e^2
Total	rv-1	(M ₁ +M ₂ +M ₃)	

Where

- r = Number of replications
 v = Number of genotypes (treatments)
 σ_e^2 = Error variance
 σ_g^2 = Genotypic variance

Statistical significance of variation due to genotype was tested by comparing calculated values with F-table values at one per cent and five per cent levels of probability, respectively.

Critical difference (C.D.)

In order to compare the means of various entries CD was calculated by using the formula.

$$\text{Critical difference (CD)} = \text{S.E. (d)} \times t$$

$$\text{S. E. (d)} = \sqrt{\frac{2X \text{ error MSS}}{r}}$$

Where

- t = is the table value at 5 per cent or 1 per cent probability level, respectively
 r = number of replications.

Coefficient of variation

Genotypic and phenotypic coefficients of variation were computed according to Burton & Devane [5] based on the estimates of genotypic and phenotypic variances as follows:

$$\text{PCV} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

$$\text{GCV} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where,

- GCV = Genotypic coefficient of variation
 PCV = Phenotypic coefficient of variation
 σ_g^2 = Genotypic variance
 σ_p^2 = Phenotypic variance
 \bar{X} = General mean of the character

PCV and GCV were classified as suggested by Sivasubramanian & Menon [6] and are given below.

- 0-10% : Low
 10-20% : Moderate
 20% and above : High

Heritability

Heritability in broad sense refers to the proportion of genetic variation to the total observed variance in the population. Heritability in broad sense is the ratio of genotypic variance to the phenotypic variance and is expressed in percentage.

$$h^2(b) = \frac{\text{Genotypic variance } (\sigma_g^2)}{\text{Phenotypic variance } (\sigma_p^2)} \times 100$$

The range of heritability in broad sense was classified as suggested by Johnson *et al.* [3].

- Less than 30% : Low
 30-60% : Moderate
 More than 60% : High

Genetic advance (GA)

Genetic advance is the expected genetic gain of superior individual under certain amount of selection pressure. Genetic advance for each character was worked out by adopting the formula given by Johnson *et al.* [3].

$$\text{GA} = K \times \sigma_p \times h^2(b)$$

Where,

GA = Genetic advance.

$h^2(b)$ = Heritability in broad sense.

K = Selection differential which is equal to 2.06 at 5% intensity of selection (Lush, 1940)

σ_p = Phenotypic standard deviation

below as suggested by Johnson *et al.* [3].

0- 10% - Low

10.1-20% - Moderate

>20.1% - High

Further, the genetic advance as per cent of mean was computed by using the following formula

$$\text{GA as per cent of mean} = \frac{\text{GA}}{\text{Grand mean}} \times 100$$

Genetic advance as per cent mean was categorized as given

Results and Discussion

Variability, heritability and genetic advance

The analysis of variance revealed significant differences between genotypes indicating presence of sufficient amount of variability in all the characters studied except number of branches per plant and pod width (Table 1).

Table 1: Analysis of variance for sixteen quantitative traits in cowpea

S. No.	Character	Mean sum of squares		
		Replications (df = 2)	Treatments (df = 9)	Error (df = 18)
1.	Plant height (cm)	1.783	1,920.29**	3.933
2.	Number of branches per plant	0.216	2.893*	0.986
3.	Days to first flowering	0.7285	38.148**	3.36
4.	Days to 50% flowering	0.8965	58.304**	3.344
5.	Number of flowers per cluster	0.702	3.989**	0.283
6.	Number of pods per cluster	0.001	1.147**	0.11
7.	Pod setting percentage	62.768	374.736**	17.139
8.	Days to first pod harvest	1.9355	110.774**	3.745
9.	Days to last pod harvest	0.092	521.486**	7.865
10.	Number of pods per plant	8.6075	260.484**	4.338
11.	Pod length (cm)	1.063	45.638**	1.569
12.	Pod width (cm)	0.0005	0.05*	0.01
13.	Pod weight (g)	9.704	455.635**	3.14
14.	Number of seeds per pod	0.767	6.193**	0.329
15.	100 seed weight (g)	1.5995	32.885**	0.66
16.	Marketable pod yield per plant (g)	58.173	4,852.20**	19.713

Wide range of variability was observed for number of pods per plant, pod weight and 100 seed weight indicating the scope for selection of suitable initial breeding material for further improvement. Close relationship between GCV and PCV was found in all the characters and PCV values were

slightly greater than GCV (Table 2 and Fig. 1) revealed a very little influence of environment for their expression. This was in confirmation with the results reported by many workers [7-10]. Estimates of variability, heritability and genetic advance are presented in Table 2.

Table 2: Genetic parameters of variation for green pod yield and its components in cowpea

S. No.	Parameters Characters	Mean	Range		Coefficient of variation (%)		$h^2(b)$ (%)	Genetic advance as per cent of mean
			Minimum	Maximum	Genotypic	Phenotypic		
1.	Plant height (cm)	88.047	59.80	114.00	15.616	15.812	97.5	31.769
2.	No. of branches per plant	7.801	6.25	9.27	11.303	12.073	87.7	21.800
3.	Days to first flowering	54.218	46.05	61.01	6.157	6.656	85.6	11.732
4.	Days to 50% flowering	58.870	52.00	65.41	6.149	6.680	84.7	11.658
5.	No flowers/cluster	4.375	2.97	5.43	16.047	16.929	89.8	31.333
6.	No pods/ cluster	2.913	1.76	4.03	19.670	20.545	91.7	38.794
7.	Per cent pod set	66.631	57.50	81.49	10.767	11.287	91.0	21.159
8.	Days to first harvest	64.939	57.00	71.21	5.868	6.761	75.3	10.493
9.	Days to last harvest	121.097	99.81	137.65	9.396	9.640	95.0	18.863
10.	Number of pods per plant	42.748	30.00	61.00	21.489	21.860	96.6	43.518
11.	Pod length (cm)	23.197	16.94	30.00	15.964	16.572	92.8	31.682
12.	Pod width (cm)	0.902	0.78	1.06	8.535	10.277	69.0	14.602
13.	Pod weight (g)	45.523	23.73	62.24	23.188	23.508	97.3	47.117
14.	No seeds / pod	11.444	9.34	15.22	12.348	13.038	89.7	24.090
15.	100 seed weight (g)	14.975	10.56	20.67	21.861	24.037	82.7	40.959
16.	Green pod yield/plant (g)	195.418	128.42	256.47	18.655	19.961	87.3	35.914

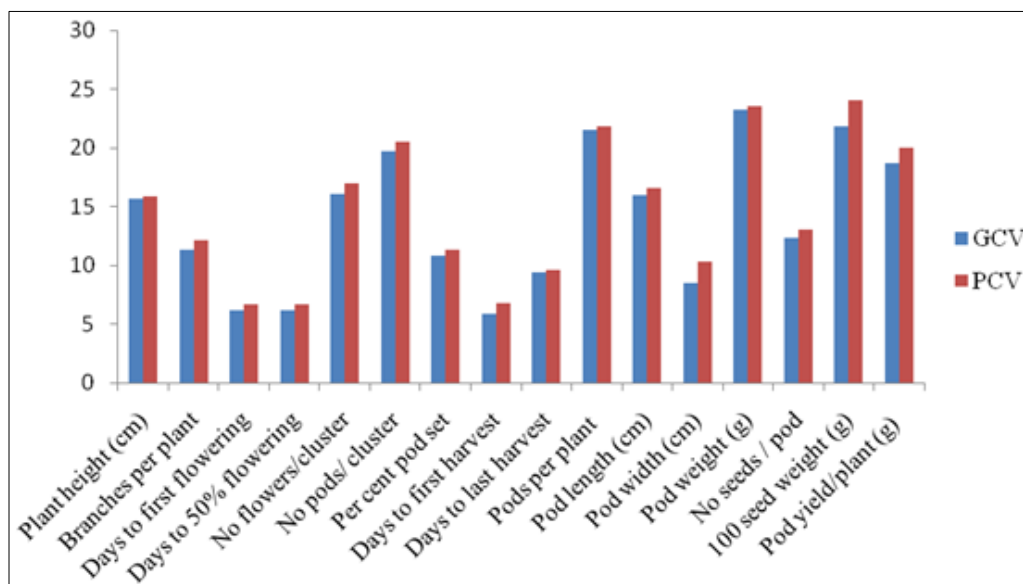


Fig 1: Phenotypic and genotypic coefficient of variation for yield components in cowpea

Among the characters studied, high PCV and GCV were observed for characters like number of pods per cluster (PCV only), number of pods per plant, pod weight and 100 seed weight indicating high variability available in the germplasm for these characters for further improvement. This was in confirmation with the results reported by Devi & Jaymani ^[11], Sabale *et al.* ^[12] for number of pods per plant and Sharma *et al.* ^[13] for pods per plant and pod weight. Moderate GCV and PCV was observed for plant height, number of branches per

plant, flowers per cluster, pods per cluster (GCV only), per cent pod set, pod length, pod width (PCV only), number of seeds per pod and pod yield per plant similar to results found by Dinesh *et al.* ^[14], Devi & Jaymani ^[11] and Sabale *et al.* ^[12] for plant height, branches per plant, pod length and seeds per pod whereas, days to first flowering, days to 50% flowering, days to first harvest, days to last harvest and pod width (GCV only) recorded low GCV and PCV which was in line with the findings of Bhagwati *et al.* ^[15].

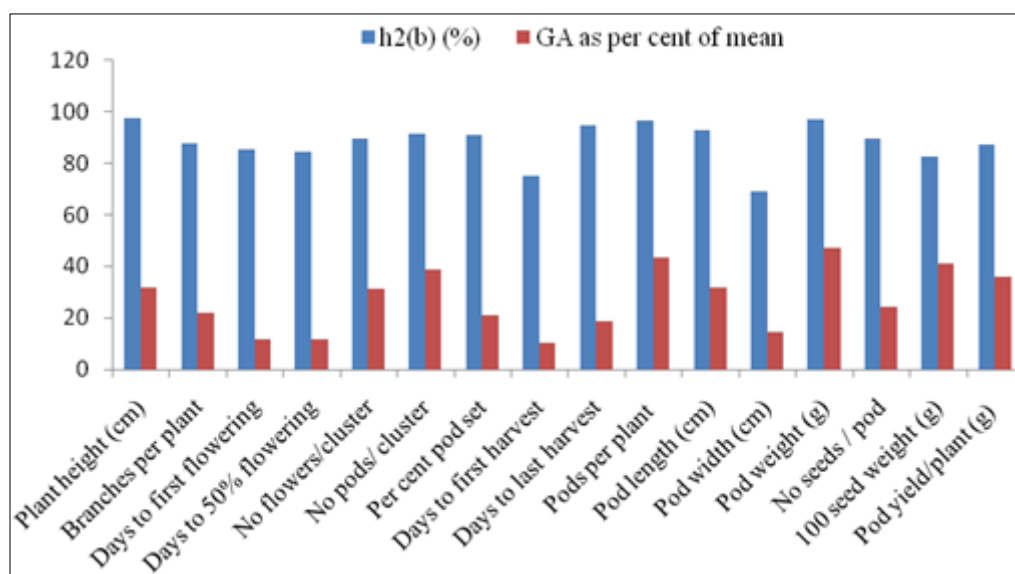


Fig 2: Heritability and genetic advance as percent of mean for yield components in cowpea

High heritability was observed for all the characters studied which were supported by Verma *et al.* ^[16] in dolichos bean, Sharma *et al.* ^[17] and Sharma *et al.* ^[13] in cowpea but, heritability being a single numerical expression on the ratio of two variances, may not lead to success if selection is based on heritability estimates alone. Therefore, high heritability coupled with high genetic advance as per cent of mean was more valuable in predicting the effect of selection ^[3]. High heritability coupled with high genetic advance as per cent of mean was reported for plant height, number of branches per plant, flowers per cluster, pods per cluster, per cent pod set, days to last harvest, pod length, pod weight, number of seeds per pod, 100 seed weight and pod yield per plant (Table 2 and

Fig. 2) which indicated that these characters were least influenced by the environmental effects and governed by additive gene action. Similar magnitude of these characters for high heritability coupled with high genetic advance as per cent of mean were reported by other workers ^[12-15, 18]. Hence, simple selection based on phenotypic characters will be rewarding for improvement of such traits. High heritability and moderate GA as per cent mean values were observed for the characters *viz.*, days to first flowering, days to 50% flowering, days to first harvesting, days to last harvesting and pod width. This indicates the influence of non additive gene action and considerable influence of environment on the expression of these traits. These traits could be exploited

through manifestation of dominance and epistatic components through heterosis breeding. Hence, the breeder should adopt suitable breeding methodology to utilize both additive and non additive gene effects simultaneously.

Conclusion

From the foregoing discussion, it can be concluded that high heritability coupled with high genetic advance as per cent of mean was reported for plant height, number of branches per plant, flowers per cluster, pods per cluster, per cent pod set, days to last harvest, pod length, pod weight, number of seeds per pod, 100 seed weight and pod yield per plant which indicated that these characters were least influenced by the environmental effects and governed by additive gene action. Hence, the genotypes which exhibited better performance for these characters can be used in future breeding programs and direct selection based on these characters would be effective in further improvement for developing high yielding varieties of cowpea.

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References

- Verdcourt B. Studies in the leguminosae-Papilionoideae for the flora of tropical East Africa. Kew. Bulletin. 1970; 24:507.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability of soybean. Agronomy J. 1955; 47:314-318.
- Al-Jibouri HA, Miller PA, Robinson HF. Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. Agronomy J. 1958; 50:633-636.
- Panse VG, Sukhatme PV. Statistical methods for Agricultural Workers 2nd Edn. ICAR, New Delhi, 1967, 361.
- Burton GW, Devane EH. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. Agronomy J. 1953; 45:478-481.
- Sivasubramanian S, Menon M. Heterosis and inbreeding depression in rice. Madras Agril J. 1973; 60:1139-1149.
- Choudhary H, Verma MK, Sofi AA. Genetic variability, heritability and genetic advance for yield components in garden pea. Pantnagar J Res. 2010; 8(2):195-197.
- Udensi O, Edu EA, Ikpeme EA, Ebiwgai JK, Ekpe DE. Biochemical evaluation and yield performance assessment of Cowpea (*Vigna unguiculata* (L.) Walp.) Landraces grown under lowland tropical conditions. Int. J Plant Breed. Gent. 2012; 6:47-53.
- Manggoel WU, Uguru MI, Ndam ON, Dasbak MA. Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpea [*Vigna unguiculata* (L.) Walp] accessions. J Pl. Breed. Crop Sci. 2012; 4(5):80-86.
- Verma AK, Jyothi KU, Rao AVD. Genetic Variability, heritability and genetic advance studies in Dolichos bean (*Lablab purpureus* L.) genotypes. Electronic J Pl Breed. 2014; 5(2):272-276.
- Devi SM, Jayamani P. Genetic variability, heritability, genetic advance studies in cowpea germplasm [*Vigna unguiculata* (L.) Walp.] Electronic J Pl Breed. 2018; 9(2):476-481.
- Sabale GR, Bhav SG, Desai SS, Dalvi MB, Pawar PR. Variability, Heritability and Genetic Advance Studies in F₂ Generation of Cowpea (*Vigna unguiculata* sub sp. *unguiculata*) Int. J Curr. Microbiol. App. Sci. 2018; 7(9):3314-3320.
- Sharma A, Mishra SP, Gour L. Heritable relationship and variability of yield and yield determinants in cow pea. Int. J Chem. Stud. 2019; 7(3):3605-3611.
- Dinesh HB, Viswanatha KP, Lohithaswa HC, Pavan R, Singh P. Genetic Variability, Correlation and Path Analysis Studies in Early Segregating Generation of Cowpea [*Vigna unguiculata* (L.) Walp]. Int. J Pure & Applied Biosci. 2017; 5(5):1389-1395.
- Bhagwati B, Meghawal DR, Sharma PP, Sharma H. To Estimate Genetic variability Parameters, Correlation and Path Coefficient in Cowpea [*Vigna unguiculata* (L.) Walp]. Int. J Curr. Microbiol. App. Sci. 2018; 7:3013-3023.
- Verma AK, Jyothi UK, Rao AVD. Variability and character association studies in dolichos bean (*Lablab purpureus* L.) genotypes. Indian J Agric. Res. 2015; 49(1):46-52.
- Sharma M, Sharma PP, Sharma H, Meghawal DR. Genetic variability in cowpea [*Vigna unguiculata* (L.) Walp.] Germplasm lines. J Pharmaco. Phytochem. 2017; 6(4):1384-1387.
- Sapara GK, Javia RM, Pokar MV. Genetic Variability, heritability and genetic advance in vegetable cowpea. Int. J Pl. Sci. 2014; 9(2):326-329.