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Study of Genetic Variability Parameters in F_2 Generation of Interspecific Hybrids in Cowpea

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ABSTRACT

A genetic variability study is carried out with 25 F_2 interspecific hybrids of cowpea and their fourteen parents and analysis of variance revealed significant differences among the segregants tested for all the fourteen characters, justifying the selection of genotypes for the study. The genotypes exhibits considerable amount of genetic variation for all the characters and it indicated the good scope for selection of suitable basic material for further improvement. Phenotypic coefficient of variation (PCV) was greater in magnitude over respective genotypic coefficient of variation (GCV) for all the character under study. The estimate of PCV and GCV were high for plant height and green pod yield per plant. High heritability and genetic advance as percent of mean (GAM) was observed for plant height, green pod yield per plant, seed yield per plant, pod length and number of pods per plant. These characters are governed by additive gene action and these characters should go for direct selection for development of better generations in future.

Key words: *cowpea, Interspecific hybrid, Variability, Heritability, Genetic advance*

INTRODUCTION

Cowpea (*Vigna unguiculata* (L). Walp) 2n=22 is one of the most widely adapted; drought-tolerant, versatile, and nutritious grain legumes or pulse crop. It is used as dry seed or green pod as vegetable or as forage crop. Estimation of genetic variability parameters is the foremost step to be adopted in the source population, if the breeding program is aimed at improving economically important traits. For any crop improvement programme, evaluation of germplasm to assess the existing variability is the first step. Greater the variability present in the initial material better would be the chances for evolving desired types. A clear understanding of variability of various characters of the breeding materials is an asset to the plant breeder for selecting superior genotypes on the basis of their phenotypic expression. In this regards estimates of genotypic and phenotypic variance for various quantitative characters along with heritability and genetic advance expected by selection for yield and its components are useful in designing an effective breeding programme. Yield is a complex character influenced by various components towards yield.

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MATERIAL AND METHODS

The present study comprised a set of selected 25 F_2 interspecific hybrids and their 14 parents. These were sown during *Rabi* 2016-17 in Randomized Block Design, with a spacing of about 45 x 30 cm in three replication and standard agronomic practices were followed. Five plants selected at random were tagged from each genotype and observations on fourteen quantitative characters (plant height, number of primary branches per plant, days to first flowering, days to maturity, pod length, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, green pod yield per plant, dry pod yield per plant, hundred seed yield, harvest index and seed yield per plant) were recorded on these plants.

Genetic variability parameter *viz.*, mean, variance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation $(GCV)^2$, heritability (h^2) and Genetic advance $(GA)^3$, among characters were calculated by following the standard procedures with the help of INDOSTST software's.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the all the F_2 interspecific hybrids and their parents and it indicated the presence of sufficient variability for these characters (table 1). One of the main ways of observing variability is through examining the range of variation for each character considered.

In the present study the genotypes exhibited considerable amount of variation for fourteen characters viz., (plant height, number of primary branches per plant, days to first flowering, days to maturity, pod length, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, green pod yield per plant, dry pod yield per plant, hundred seed yield, harvest index and seed yield per plant (Table 2). Khan *et al*[4], recorded higher range for most of these characters, which was in accordance to the present study. The high range of values indicated the good scope for selection of suitable basic material for breeders for further improvement.

The mean values for each character play an important role in selection. In case of days to first flowering and days to maturity lower mean values enabled identification of several short duration segregants. The lower mean value for these characters were observed in Konkan safed x Konkan wali (52.33 days) and Konkan safed x Arka garima (77.67 days) respectively out of the 25 cross combination. But minimum days to first flowering was showed by Konkan sadabahar (47.67 days) the parental population. Genetic variability is a basic information needed for the breeders to improve the crops by adopting appropriate method of selection based on variability that exist in the material. So, it is necessary to partition the total variability into heritable and non-heritable components *viz.*, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and further to compute heritability and genetic advances for various metric traits.

Comparison of variability between two traits is possible with coefficient of variation as it is free of units. As expected, the PCV values were greater than the GCV values for all the characters indicating considerable influence of environment on the expression of these characters under field conditions (Table 2). The difference between PCV and GCV was more for plant height, number of primary branches per plant and number of seeds per pod, indicating a major role of environment in these characters The genotypic coefficient of variation helps in assessing the genetic reliability of the different characters and enables to compare the magnitude of variation. It was found that the characters plant height (67.12%) and green pod yield per plant (40.22%) exhibited maximum phenotypic coefficient of variation whereas least magnitude of phenotypic coefficient of variation for days to first flowering (8.99%) and number of seeds per pod (13.09%). Highest value of genotypic coefficient of

variation was registered for plant height (65.29%) and green pod yield per plant (39.89%). The character days to first flowering (8.35%) followed by number of seeds per pod (11.40%) showed minimum value of GCV. These results are in agreement with Salimath *et al.*[5], Kurer *et al*. in cowpea and Gondhalekar in Lablab bean.

High estimate of heritability in broad sense was observed for all the characters under study. Heritability estimates was highest for green pod yield per plant (98.42%) followed by dry pod yield per plant (97.71%), harvest index (97.31%), pod length (97.18%), seed yield per plant (97.10%), number of pods per plant (96.38%), number of clusters per plant (96.21%), plant height (94.62%). Heritability estimate for other ranges between 88.39% to 75.93%. Similar results were reported by Vidya *et al*.[8] for green and dry pod yield in cowpea, Archana Thorat and Gadewar[1], and Saroj *et al.*[6], in Pigeon pea.

Genetic advance is a measure of expected progress under selection scheme. It gives the magnitude of improvement per cycle in the base population by selection. The estimate of genetic advance as per cent of mean ranged from days to first flowering (15.97%) to plant height (130.83%). Plant height (117.29%), pod length (72.89%), seed yield per plant (73.01%) and number of pods per plant (70.06%) showed higher estimate of genetic advance as per cent mean which clearly indicated the role of selection for improvement of these character. Days to first flowering (15.97%), number of seeds per pod (20.47%) and days to maturity (24.10%) exhibited minimum genetic advance as per cent of mean. High genetic advance as per cent of mean was recorded in pod length and seed yield per plant by Khan *et al.*[4], in cowpea and pods per plant by Salimath *et al.*[5].

Heritability alone provides no information on amount of genetic progress that would result from the selection. High heritability estimates along with high genetic advance was noticed in plant height (94.62%, 117.29) and green pod yield per plant (98.42%, 93.03). The high heritability coupled with genetic advance reveals the presence of lesser environmental influence and prevalence of additive gene action in their expression. Hence green yield per plant can be improved by selection in further generation. Similar result was reported by Khan *et al.*[4]. High heritability with low genetic advance for number of pods per cluster, number of primary branches per plant and hundred seed weight indicating these characters may be controlled by non-additive gene action. Similar results were recorded by Salimath *et al*.[5] for hundred seed weight and for pod length and number of primary branches per plant by Saroj *et al.*[6].

Table 1: Analysis of variance for fourteen quantitative characters

Source of variation	df	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}
Replication	2	19.44	0.1132	1.564	65.444	0.730	0.157	0.014	0.462	2.198	7.365	5.755	0.119	0.809	1.151
Genotypes	38	10473.29*	4.2716*	76.631*	500.833*	123.602*	7.384*	0.520*	63.844*	543.878*	6249.449*	1829.516*	10.955*	420.867*	140.61*
Error	76	194.90	0.288	3.853	25.084	1.186	0.705	0.028	0.827	6.728	33.239	14.154	0.459	3.836	1.388

*indicate 5 % level of significance.

X_1= plant height, X_2= No. of primary branches per plant, X_3= days to first flowering, X_4= =days to maturity, X_5= pod length, X_6= No. of seeds per pod, X_7= No. of pods per cluster, X_8= No. of clusters per plant, X_9= No. of pods per plant, X_{10}= green pod yield per plant, X_{11}= dry pod yield per plant, X_{12}= hundred seed weight, X_{13}= harvest index, X_{14}= seed yield per plant.

Table 2: Estimation of genetic variability parameters for fourteen characters

Sr. No.	characters	PCV (%)	GCV (%)	h^2	GAM
1	**Plant height (cm)**	67.12	65.29	94.62	130.83
2	**Number of primary branches per plant**	32.65	29.59	82.13	55.24
3	**Days to first flowering**	8.99	8.35	86.29	15.97
4	**Days to maturity**	13.55	12.29	86.34	24.10
5	**Pod length (cm)**	36.41	35.89	97.18	72.89
6	**Number of seeds per pod**	13.09	11.40	75.93	20.47
7	**Number of pods per cluster**	19.83	18.30	85.23	34.81
8	**Number of clusters per plant**	27.24	26.72	96.21	53.98
9	**Number of pods per plant**	35.29	34.64	96.38	70.06
10	**Green pod yield per plant (g)**	40.22	39.89	98.42	81.54
11	**Dry pod yield per plant**	33.30	32.92	97.71	67.03
12	**100 seed weight**	15.21	14.29	88.39	27.69
13	**Harvest index (%)**	30.78	30.37	97.31	61.71
14	**Seed yield per plant (g)**	36.50	35.97	97.10	73.01

CONCLUSION AND RECOMMENDATION

Wide range of variability was exist among the genotypes studied for the different quantitative characters, which could be used for systematic exploitation in segregants of cowpea. Induced variability indicated that significant improvement can be achieved by hybridization followed by appropriate selection methods. High heritability with high genetic advance as percentage of mean was observed for green pod yield per plant, seed yield per plant, dry pod yield per plant, pod length and number of pods per plant. It indicates additive gene action and made it suitable for direct selection. The progenies Pusa phalguni x DPL-YB-5, ACP-1264 x UBA-1, ACP-109 x DPL-YB-5, PCP-97102 x UBA-1 and Pusa dophasali x Arka garima are observed as best performers in the studied population as these had highest seed yield per plant and also maximum yield attributing characters. The cross ACP-1264 x UBA-1 had the maximum green pod yield per plant followed by V-585 x UBA-1 (195.79g) and PCP-97100 x Konkan wali (192.37g). These crosses can be advance to F_3 generation for selection of promising cultivar in future.

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