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Genetic Variability Studies in Advanced Stabilized Lines of Cowpea (*Vigna unguiculata* (L.) Walp.)

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ABSTRACT

The success of any crop improvement programs depends upon the genetic variability and heritability of desirable traits. Thirty genotypes along with two checks (DC 15 and DCS 47-1) were evaluated for genetic variability and other related parameters in respect of eight quantitative characters during Kharif 2016. Analysis of variance revealed highly significant differences among genotypes for all the characters studied. Considerably high range of variation was observed for characters viz., seed yield, days to fifty per cent flowering, plant height and number of pods per plant. High PCV and GCV values were recorded for the traits seed yield and number of pods per plant. Plant height showed moderate PCV and GCV values whereas, remaining traits exhibited low to moderate PCV and GCV values. High heritability coupled with high GAM was exhibited by seed yield, number of pods per plant and plant height. Characters such as days to fifty percent flowering and days to maturity showed high heritability and low GAM. Moderate heritability with moderate GAM was recorded by number of seeds per pod and hundred seed weight. However, pod length recorded moderate heritability and low GAM.

Key words: *Genetic variability, Heritability, Genetic advance, GCV, PCV.*

INTRODUCTION

Cowpea is an important food legume crop of the world, originated in central Africa, botanically known as *Vigna unguiculata* (L.) Walp belonging to the order *Rosale*, family *Leguminosae*, sub family *Fabaceae* and the genus *Vigna* consisting of 169 species. Cytologically it is a diploid species with somatic chromosome number of 2n = 22[18].It is also called as lobia, black-eyed pea and southern bean, grown as pulse crop, vegetable, fodder, cover crop, catch crop. Globally, Cowpea is cultivated over an area of 11.31 million hectares with a production of 5.7 million tonnes and productivity of 505.3 kg ha^{-1} [5]. Even though cowpea is minor pulse crop of India, it is grown in an area of 3.9 million hectares with a production of 2.21 million tonnes and 625 kg ha^{-1} productivity. Karnataka accounts 12 per cent of area under pulses in the country.

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Cowpea stands fourth in Karnataka among all pulses with an area of 0.89 lakh hectares with a production of 0.36 lakh tonnes with average productivity of 426 kg ha^{-1} [3]. The productivity potential of cowpea in Karnataka is low as compared to the national productivity. It is a major staple component of the human diet in many developing countries, nutritionally on an average cowpea seeds contain about 25 per cent of protein, making it extremely valuable in areas where many people cannot afford proteinacious food such as meat and fish[9] hence, it is often regarded as vegetable meat and poor man's meat. Further, tender pods are also be used as vegetable. Apart from this, the green and dry haulms are used as a nutritious livestock feed.

Cowpea is relatively drought tolerant and warm weather crop, it is well adapted to dry regions of the tropics where other food legumes do not thrive well[1]. As a legume, cowpea plays an important role in maintaining the soil fertility and sustainability in the production from different cropping systems.

Lack of sufficient genetic variability for economically important characters is one of the reasons attributed for insignificant progress in crop improvement. A systemic collection of natural variability has not been made and therefore, limited genetic variability is available in cowpea. Further, in India cowpea improvement has been restricted only in collection of limited numbers of germplasm and hybridization between randomly chosen parental lines with narrow genetic base. Hence, there is a need of collection, maintenance and evaluation of different genotypes for genetic variability of economically important traits for genetic improvement of cowpea.

Before any selection programme, it is essential to have knowledge about the magnitude of variability for the characters, which needs to improve to develop high yielding varieties. The magnitude of genetic variance denotes how much of the variability of the characters is heritable and how much genetic advance can be achieved. Hence, the assessment of genetic variability, estimation of heritability and genetic advance are important for successful selection programme to evolve high yielding varieties.

In this context, the present investigation was undertaken to estimate the variability, heritability, genetic advance and other related parameters for yield and its attributes in cowpea.

MATERIAL AND METHODS

The present experiment was carried out using thirty genotypes along with two checks (DC 15 and DCS 47-1) at Botanical garden, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad (Karantaka) during *Kharif* 2016 in a Randomized Complete Block Design with two replications. Of the thirty genotypes 25 were superior advanced stabilized lines (F_5, F_6, F_7, F_9, F_{10} and BC_1F_6 generations) and 5 were germplasm lines superior in terms of yield *per se* which were evaluated during summer 2016. The details of the genotype used for the study are presented in Table 1. Each entry was raised in three rows of three meter length with the spacing of 45 cm between the rows and 15 cm between the plants. Five plants were tagged randomly for recording observations from each entry in each replication and the data on eight traits *viz.*, days to fifty per cent flowering, days to maturity, plant height, pod length, number of seeds per pod, number of pods per plant, hundred seed weight and seed yield were analyzed. Both genotypic and phenotypic coefficients of variability were computed as per the procedure proposed by Burton and Devane[4]. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were classified as suggested by Sivasubramanian and Menon[15] that are, low (< 10 %), moderate (10 - 20 %) and high (> 20 %). Broad sense heritability was estimated as suggested by Hanson *et al.* [6] and expressed as percentage. The heritability percentage was classified as low (0-30%), moderate (30–60%) and high (> 60%) by Robinson *et al.*[11]. Genetic advance was determined by using the formula given by Johnson *et al.* [7] and genetic advance over mean was calculated and categorized as low up to 10 per cent, 10 to 30 per cent consider as a moderate and more than 20 per cent noticed as a high[7].

RESULT AND DISCUSSION

The analysis of variance revealed statistically significant mean sum of squares due to the genotypes (Table 2) confirmed the existence of significant genetic variability among the genotypes with respect to all the characters studied. This indicated that, the breeding material chosen for the study are significantly different and diverse for different traits. Genetic variability is the basic knowledge needed in every breeding programme to improve the crops by adopting appropriate method of selection. In this regard, the present study was attempted to estimate genetic variability components *viz.*, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability percentage and genetic advances over the mean for various characters associated with grain yield. Statistical analysis revealed the presence of considerable level of genetic variability for all the characters under this study (Table 3).

One of the ways in which the variability is assessed is through a simple approach of examining the range of variation. In the present study the genotypes revealed considerable variation for characters *viz.*, days to fifty per cent flowering (48-60 days), plant height (23.67-42.60 cm), number of pods per plant (8.00-21.50) and seed yield (542-2157kg ha^{-1}) exhibited higher variation. These differences may be attributed to their diverse genetic makeup and the environmental interactions. The high range of values indicated the good scope for selection of suitable basic material for breeders for further improvement.

However, the range in mean values does not reflect the total variance in the material studied. Hence actual variance has to be estimated for the characters to know the extent of existing variability. The knowledge of variance alone will not suffice unless the variance is partitioned into phenotypic and genotypic coefficient of variation, which is more reliable for effective selection. High values of these parameters indicate wider variability and vice versa. Similarly, a narrow difference between the PCV and GCV implies lesser influence of environmental on these traits.

Accordingly, high PCV (> 20 %) values were recorded by seed yield (29.00) and number of pods per plant (21.06). However, moderate PCV (10 - 20 %) was observed for the trait plant height (15.12), pod length (10.86) and number of seeds per pod (11.64). But days to fifty percent flowering (5.63), days to maturity (5.03) and hundred seed weight (9.82) recorded low PCV (< 10 %). Similarly for GCV, seed yield (23.07) and number of pods per plant (20.38) recorded higher, whereas plant height showed moderate (13.40) and remaining traits viz., days to fifty percent flowering (4.62) , days to maturity (3.96), pod length (6.92) and number of seeds per pod (7.72) and hundred seed weight (7.03) shown less GCV.

Traits seed yield and number of pods per plant were recorded higher PCV and GCV this indicates the substantial variability existing for these traits and also indicating greater scope for selection of these traits for better expression. Similarly higher PCV and GCV were also reported by Tigga *et al.*[17], Olayiwola and Soremi[10] and Aliyu and Makinde[2] for seed yield and Olayiwola and Soremi[10], Sapara *et al.* [12] and Khanpara *et al.* [8] for number of pods per plant. Further, the characters *viz.,* pod length, number of seeds per pod and seed yield exhibited the considerable differences between GCV and PCV indicating the influence of environment in the expression of these traits and selection based on phenotypic observations may not be very effective for these traits since these characters were more sensitive to environmental changes. Similar findings were reported by Sarath and Reshma[13].

The coefficient of variation indicates the magnitude of variability existing for various traits, but does not give any information about the heritable portion of it. The estimation of heritability however indicates the effectiveness with which selection of genotypes can be based on their phenotypic performance but fail to indicate the amount of progress expected from selection. Therefore, heritability estimates appear to be more meaningful when accompanied by estimates of genetic advance.

In the present investigation, the heritability in broad sense estimates were high for seed yield (63.29), days to fifty percent flowering (67.41), days to maturity (61.90), plant height (78.53) and number of pods per plant (93.63). Whereas, pod length (40.62), number of seeds per pod (44.03) and hundred seed weight (51.34) showed moderate heritability. Genetic advance as per cent of mean (GAM) is more reliable index for understanding the effectiveness of selection in improving the traits because the estimates are derived by involvement of heritability, phenotypic standard deviation and intensity of selection. Thus, genetic advance along with heritability provides clear picture regarding the effectiveness of selection for improving the plant character. The estimates of genetic advance as per cent over mean (GAM) recorded high for seed yield (37.81), number of pods per plant (40.64) and plant height (24.46). Moderate genetic advance as per cent over mean was recorded for number of seeds per pod (10.56) and hundred seed weight (10.39) and low GAM for days to fifty percent flowering (7.81), days to maturity (6.42) and pod length (9.09).

High heritability coupled with high genetic advance was exhibited by number of pods per plant, seed yield and plant height it is indicative of presence of additive gene action and selection based on phenotypic value could be more reliable[7]. Hence, one can practice the selection. Since, the large number of genotypes are involved in this investigation the heritability and genetic advance were high. These results are in conformity with the reports of earlier workers, Olayiwola and soremi[10] and Sunita[16] for number of pods per plant and seed yield while, Sapara *et al.*[12] and Tudu *et al.*[19] for plant height. Characters such as days to fifty percent flowering and days to maturity showed high heritability and low genetic advance as per cent over mean. This indicates less influence of environment but prevalence of non additive gene action for which simple selection will be less effective. Tudu *et al.*[19] and Khanpara *et al.*[8] also reported similar values of heritability and genetic advance for days to fifty percent flowering and Sharma *et al.*[14] for days to maturity. Moderate heritability with moderate genetic advance as per cent over mean was recorded by number of seeds per pod and hundred seed weight. Both additive and non additive gene actions are prevailing in these traits and these traits have considerable influence of environment and hence these two traits are not amenable for simple phenotypic selection. Moderate heritability coupled with moderate genetic advance as per cent mean for these traits were also reported earlier by Vishwanathreddy[20].

In general, on the basis of overall consideration for genetic variability parameters it may be concluded that the direct selection for seed yield and number of pods per plant in the breeding material of present study is effective for yield improvement because of high variability, heritability and genetic advance which are the key factors for any selection programme to achieve better results.

Table 1: List of superior thirty promising advanced stabilized lines and germplasm lines considered for variability and stability studies

Sl. No	Genotype	Sl. No	Genotype
1	C 152 × IC 202864 (F_{10})	16	IC 202823 × IC 219550 (F_7)
2	DC15 × DCS 47-1-1(F_6)	17	C 152 × IC 257425 (F_6)
3	IC97838 (Germplasm)	18	IC249133 (Germplasm)
4	DC 15 × DCS 47-1-2 (F_6)	19	IC259106 (Germplasm)
5	DCS 47-1 × DC 15-1 (F_6)	20	Bailhongal local × C 152 (BC_1F_6)
6	C 152 × IC 202863 (F_{10})	21	GC 3 × IC 202718 (F_5)
7	V 118 × Goa local (F_7)	22	C 152 × IC 202872 (F_7)
8	Bailhongal local × IC 202710 (BC_1F_6)	23	DCS 47-1 × DC 15-2 (F_6)
9	DC 15 × Goa local (F_6)	24	V 118 × IC 257425-2 (F_9)
10	V 118 × IC 257425-1 (F_9)	25	C 152 × Goa local (F_7)
11	V 118 × IC 257437 (F_7)	26	DC 15 × CPD 118 (F_6)
12	DC 15 × C 152 (F_6)	27	C 152 × IC 202711 (F_6)
13	C 152 × IC 257425 (F_9)	28	C 152 × Goa local (F_5)
14	C 152 × IC 202860 (F_6)	29	IC257445 (Germplasm)
15	GC 3 × CPD 115 (F_6)	30	IC202702 (Germplasm)
Checks			
1	DC 15- A new high yielding and early maturing variety released for cultivation for southern states of India and also notified.	2	DCS 47-1- A high yielding variety released for South India and notified.

Table 2: Analysis of variance for yield and yield attributes in thirty two cowpea genotypes

Source	*d. f.*	Days to fifty per cent flowering	Days to maturity	Plant height (cm)	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Hundred seed weight (g)	Seed yield (kg ha^{-1})
Genotype	31	15.70**	23.03**	47.50**	24.07**	4.10**	4.04**	1.96**	260415.20**
Replication	1	6.25	0.01	1.29	0.14	1.56	0.81	1.58	9644.43
Error	31	3.06	5.42	5.71	0.78	1.73	1.57	0.63	58546.14
S.EM		1.24	1.65	1.69	0.63	0.93	0.89	0.56	171.09
CD (5 %)		3.57	4.75	4.87	1.81	2.68	2.56	1.61	493.49
CD (1 %)		4.80	6.39	6.56	2.43	3.61	3.44	2.17	663.96
CV		3.21	3.11	7.01	5.29	8.37	8.71	6.85	17.57

* - Significant at 5% probability level ** - Significant at 1% probability level

Table 3: Mean, range and genotypic variability parameters for yield and yield attributes in thirty two cowpea genotypes

Character	Mean	Range	GCV (%)	PCV (%)	h^2 (bs)	GAM
Seed yield (kg ha^{-1})	1377	542-2157	23.07	29.00	63.29	37.81
Days to fifty per cent flowering	54.44	48-60	4.62	5.63	67.41	7.81
Days to maturity	74.97	67-82	3.96	5.03	61.90	6.42
Plant height (cm)	34.12	23.67-42.60	13.40	15.12	78.53	24.46
Number of pods per plant	16.96	8.00-21.50	20.38	21.06	93.69	40.64
Pod length (cm)	15.74	11.92-17.92	6.92	10.86	40.62	9.09
Number of seeds per pod	14.50	11.10-16.90	7.72	11.64	44.03	10.56
Hundred seed weight (g)	11.72	9.85-14.45	7.03	9.82	51.34	10.39

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