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Research Article

Genetic Variability, Correlation and Path Analysis Studies in Early Segregating Generation of Cowpea [*Vigna unguiculata* (L.) Walp]

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ABSTRACT

Cowpea [Vigna unguiculata (L.) Walp] is grown as one of the most important multipurpose grain legume extensively cultivated in arid, semi-arid and subtropics. Two genetically diverse parents (C-152 × V-57817) were crossed and advanced to F_3 generation. The magnitude of variation, heritability, genetic advance, association of component characters and path co efficient analysis were estimated in a set of 200 F_3 progenies. Grain yield is complex and is determined by several component traits. The traits having high heritability and significant positive correlation with the grain yield can be utilized for indirect selection for genetic improvement. A high phenotypic coefficient of variation (PCV) and moderate genotypic coefficient of variation (GCV) estimates were recorded for plant height (20.48 % and 19.50 %) and number pods per plant (20.80% and 17.41%). High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for plant height (90.66% and 38.25%) and number of pods per plant (70.06% and 30.02%). Path coefficient analysis in F_3 segregating population revealed that seed yield was primarily influenced by number of pods per plant and 100 seed weight which had maximum direct effect on seed yield per plant. Results suggests that traits like number pods per plant and 100 seeds weight could be used as selection criteria for grain yield improvement in segregating populations of cowpea.

Key words: *Cowpea, PCV, GCV, Heritability, Genetic advance*

INTRODUCTION

Among all the legume crops, cowpea [*Vigna unguiculata* (L.) Walp., Fabaceae (2n=2x=22)] is grown as one of the most important multipurpose grain legume extensively cultivated in arid, semi-arid and subtropics[10,20]. India and Ethiopia are recognized as primary and China as a secondary centre of origin[29]. Cowpea is photo insensitive in nature and can be cultivated throughout the year. Cowpea fits well in different cropping system as it is relatively drought tolerant.

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It is also grown as catch crop, mulch crop, inter crop, mixed crop and green manure crop. Also as an excellent forage crop due to its heavy vegetative growth which covers the ground so well that it checks the soil erosion. Green manure crop as it fix atmospheric nitrogen into the soil by symbiotic bacteria to a range of 70-240 kg per ha of nitrogen per year[4]. It is a very good source of high quality protein, carbohydrates, low amounts of fat, fiber, amino acids and minerals[9,13,14].Genetic variability for economic traits is pre-requisite for any successful breeding programme. Systemic collections of natural variability have not been made and therefore, limited genetic variability is available in cowpea. In India, cowpea improvement has been restricted only in assembling of limited numbers of germplasm and hybridization between randomly chosen parental lines with narrow genetic base.

Development of cultivars with early maturity, acceptable grain quality, resistance to biotic and abiotic stress has significantly increased the yield and cultivated area[10]. Yield being a complex trait, is influenced by other important yield contributing traits controlled by polygenes and also environmental factors. An understanding of genetic variability for economic traits is pre-requisite for any successful breeding programme through effective selection under genetic gain. Systemic collections of natural variability have not been made and therefore, limited genetic variability is available in cowpea.

Selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Heritability indicates the relative degree to which a character is transmitted from parent to offspring. The magnitude of such estimates suggests the extent to which improvement is possible through selection. The success of any selection programme in segregating generations depends on the nature and extent of correlations between independent variables with dependent variables like yield and simultaneous selection can be carried out for more than one character to achieve the required improvement in seed yield.Study of correlation in combination with path coefficient analysis which will partition the correlation value in to direct and indirect effects of component traits is very much helpful for implementation of any selection programme. In the present study, variability, genotypic correlation coefficients, phenotypic correlation coefficient and path coefficient values in respect of six quantitative traits are estimated from the F_3 generation derived from the cross between C-152 × V-57817.

MATERIALS AND METHODS

The experiment consists of the cowpea varieties *viz*., C 152 and V-57817. The variety, C-152 is a released variety from UAS, Bangalore which is agronomically superior but susceptible to cowpea mosaic virus (CpMV) while, variety V-57817, a released variety from Indian Agricultural Research Institute, New Delhi, which is resistant to CpMV. In order to introgress resistance to CpMV, C-152 is used as female parent and crossed with varieties V-57817 during summer 2012 at the Department of Genetics and Plant Breeding, College of Agriculture, V. C. Farm, Mandya, University of Agricultural Sciences (UAS), Bangalore, India. The F_1 hybrid is sown along with their parents during *Kharif* 2012, and true hybrid plants were confirmed based on the presence of male parent characters in the F_1s as well as using two SSR markers (CP115/116 and EX43) which were polymorphic between the parents of the crosses C-152 × V-57817. True F_1s was selfed to obtain 200 F_2 seeds which were raised during summer 2013 by following the recommended package of practices. Seeds obtained from each individual F_2 plants were collected separately and forwarded to F_3 generation. During *kharif* 2014, F_3 were sown in two rows in two replications under natural field conditions at Department of Genetics and Plant Breeding, College of Agriculture, V. C. Farm, Mandya. Observations were recorded at physiological maturity on the yield and its attributes like, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per pod, 100 seeds weight (gm) and seed yield per plant (gm). Heritability and genetic advance were measured as suggested by Singh and Chaudhary[22] and Allard[1]. Phenotypic co-efficient of variation were calculated by the formula of Burton[6]. Simple correlation coefficient was obtained using the formula suggested by Singh and Chaudhary[22] and path co-efficient analysis was done following the method outlined by Dewey and Lu[8].In order to assess and estimate the variability among the genotypes, the statistical analysis was carried out using WINDOSTAT 8.1 package. Phenotypic and genotypic components of variance estimated by applying the formula as suggested by Snedecor and Cochran[24].

$$\text{Phenotypic variance } (\sigma^2p) = \sigma^2g + \sigma^2e \text{ (EMSS from ANOVA)}$$

$$\text{Genotypic variance } (\sigma^2g) = \text{MSS (G) - EMSSr}$$

$$\text{Error variance } (\sigma^2e) = \text{EMSS}$$

Coefficients of variations: Phenotypic and genotypic coefficients of variability were computed as per the method suggested by Burton and De Vane[6].

$$\text{Genotypic coefficient of variance (GCV)} = \frac{\sigma^2 g}{\overline{X}} \text{ x } 100$$

$$\text{Phenotypic coefficient of variance (PCV)} = \frac{\sigma^2 p}{\overline{X}} \text{ x } 100$$

PCV and GCV values were categorized as low (0-10%), moderate (10-20%) and high (>20) values as indicated by Sivasubramanian and Menon[23].

Heritability: The broad sense heritability (h^2bs) was estimated for all the characters as the ratio of genotypic variance to the total variance as suggested by Lush[15], as indicated below.

$$h^2\text{bs} = \frac{\sigma^2 g}{\sigma^2 p} \text{ X } 100$$

Heritability was classified as suggested Robinson *et al*[17]. into low (0-30%), moderate (30.1-60%) and high (>60%).

Genetic advance (GA)

It was predicted by using the formula provided by Johnson *et al*[12].

$$\text{GA} = h^2_{(bs)} \times \sigma^2 p \times k$$

Where, $h^2_{(bs)}$ = Heritability in broad sense, σ^2p = Phenotypic standard deviation of the trait, k = Standard selection differential which is 2.06 at 5 per cent selection intensity

Genetic advance as per cent mean (GAM):

It was calculated by the following formula.

$$\text{GAM (\%)} = \frac{\text{GA}}{\overline{X}} \text{ X } 100$$

The GAM% was categorized into low (0–10%), moderate (10.1–20%) and high (>20%) as suggested by Johnson *et al*[12].

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant mean of squares due to genotypes for all traits *viz*., plant height (cm), number of branches, number of pods per plant, number of seeds per pod and seed yield per plant except for 100 seed weight (Table 1). Highly significant mean squares indicated substantial variability among the genotypes as indicated by analysis of variance which indicate the scope for selection of desirable genetic material for further improvement. F_3 individuals of the cross C-152 × V-57817 exhibited widespread variation for all the traits studied. The estimates of range provide clues about the occurrence of genotypes with extreme expression which varied with the trait. Plant height ranged from 31.40 to 86.00 cm with a mean of 50.03 cm, number of branches per plant ranged from 3.80 to 8.20 with a mean of 5.66, number of pods per plant ranged from 12.50 to 31.80 with a mean of 20.55, number of seeds per pod ranged from 7.70 to 16.60 with a mean of 13.28, 100-seed weight ranged from 8.58 to 59.25g with a mean of 11.55 g and seed yield per plant ranged from 17.13 to 33.76 with a mean of 25.37g (Table 2). Knowledge on relative contribution of genetic and non-genetic sources on the quantitative trait variability is useful in formulating appropriate selection strategies to breed improved cultivars. The estimates of GCV and PCV which reflect average inter-genotype differences are more useful tools to understand variability among the genotypes. In general phenotypic coefficient of variability was greater than their corresponding genotypic coefficient of variability. The estimates of GCV and PCV were presented in table 2 indicates that high phenotypic coefficient of variation (PCV) and moderate genotypic coefficient of variation (GCV) estimates were recorded for plant height (20.48 % and 19.50 %) and number pods per plant (20.80% and 17.41%). While, high phenotypic coefficient of variation (PCV) and low genotypic coefficient of variation (GCV) estimates were recorded for 100-seed weight (47.80% and 9.11%). Moderate phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimates were recorded for number of branches (18.05% and 10.71%). This indicates greater scope for selection to improve upon these characters in the cross studied. Similar results have been reported by Singh and Verma[21], Ananda[2], Tyagi *et al.*[27] and Prakash *et al.*[16] Whereas, moderate PCV and low GCV was recorded for number seeds per pod (11.63% and 9.59%) and seed yield per plant (12.48% and 8.88%). The trait exhibited moderate PCV and low GCV, indicating that there is less scope for improvement of these traits through selection.The broad-sense heritability reported in the present study provide only a broad idea about the extent to which the traits are heritable and assessing the degree to which the traits are fixable require development and evaluation of carefully planned experimental populations. Heritability estimates along with genetic advance would be more valuable in predicting the success in selecting the best individuals Johnson *et al.*[12]. Therefore, it is vital to consider the predicted genetic advance along with heritability estimate as a tool in the selection programme for enhanced efficacy in the selection.High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for plant height (90.66% and 38.25%) and number of pods per plant (70.06% and 30.02%) (Table 2). Whereas, high heritability coupled with moderate genetic advance as per cent of mean (GAM) was observed for number of seeds per pod (68.01% and 16.29%). Moderate heritability and genetic advance as per cent of mean was observed for number of branches (35.20% and 13.09%) and seed yield per plant (50.60% and 13.01%). While, low heritability and genetic advance as per cent of mean was recorded for 100 seed weight (3.64% and 3.58%). These observations were in accordance with Girish *et al.*[11], Suganthi and Murugan[26] Bhadru and Navale[5] and Vineeta Kumari *et al.*[30].

High heritability coupled with high genetic advance as per cent of mean for the above said trait indicated that the trait is under the control of additive gene action and directional phenotypic selection for these traits in segregating populations could be effective for desired genetic improvement. These traits could further be improved by applying pedigree selection. Moderate heritability coupled with moderate and low genetic advance which is being observed in the present study showed considerable influence of environment apart from non-additive gene action. Therefore, pedigree selection or population improvement programs bring about desired improvement.In crop improvement programmes, it would be essential to have simultaneous selection of more than one character, especially in the case of complex character like yield, which is influenced by many other contributing traits. Correlation of characters serves as a measure and forms the basis of selection as it gives direction and magnitude of relationship between the characters studied. Selection for yield will be effective, only when it is considered along with yield attributes rather than relying on yield alone. When a breeder applies selection pressure for a trait, it also brings about a simultaneous change in all associated characters with it.

Number of pods per plant showed strong relationship with number of seeds per pod (Table 3) suggesting that individual plant selections can be practiced in F_3 and advanced segregating generations with these characters which could precisely lead to improvement in number of pods per plant and number of seeds per pod in the later generations. The path coefficient analysis, a statistical device developed by Wright[31] takes into account the cause and effect relation between the variables which is unique in partitioning the association into direct and indirect effects through other independent variables. The path coefficient analysis also measures the relative importance of causal factors involved.Path coefficient analysis in F_3 segregating population revealed that seed yield was primarily influenced by number of pods per plant and 100 seed weight which had maximum direct effect on seed yield per plant (Table 4 and Fig 1). Hence, it would be rewarding to lay emphasis on number pods per plant, and 100 seed weight while developing selection strategies in cowpea. Similar results of high positive direct effect for number of pods per plant[3,18,28] and 100-seed weight[3,19,25] were reported by earlier workers. Considering correlation and path coefficient analysis for the characters under study with positive correlation on grain yield per plant included number of pods per plant, number of seeds per pod and 100- seeds weight. These traits could be considered as critical criteria for yield improvement in segregating generations of cowpea during selection of breeding lines.

Table 1: Analysis of variance for six quantitative traits in 157 F_3 progenies of cowpea

Sources of variance	df	Plant height (cm)	Number of branches	Number of pods per plant	Number of seeds per pod	100 seed weight	Seed yield per plant
Replication	1	0.10	2.39	2.72	2.73	33.60	13.31
Genotypes	156	200.14**	1.41**	31.07**	4.01**	31.61	15.10**
Error	156	9.81	0.68	5.47	0.76	29.39	4.95

*Significant at P≤ 0.05 level, ** Significant at P≤ 0.01 level.

Table 2: Estimates of genetic variability components for six quantitative traits in 157 F_3 progenies of cowpea

Sl. No	Traits	Grand Mean	Range		GCV %	PCV %	Broad sense (H)	GAM %
			Lowest	Highest				
1	**Plant height (cm)**	50.03	31.40	86.00	19.50	20.48	90.66	38.25
2	**Number of branches**	5.66	3.80	8.20	10.71	18.05	35.20	13.09
3	**Number of pods per plant**	20.55	12.50	31.80	17.41	20.80	70.06	30.02
4	**Number of seeds per pod**	13.28	7.70	16.60	9.59	11.63	68.01	16.29
5	**100 seed weight**	11.55	8.58	59.25	9.11	47.80	3.64	3.58
6	**Seed yield per plant**	25.37	17.13	33.76	8.88	12.48	50.60	13.01

Table 3: Estimates of phenotypic correlation coefficient analysis of seed yield and its component characters in 157 F_3 progenies of cowpea

Characters	Plant height	Number of branches	Number of pods per plant	Number of seeds per pod	100 seed weight	Seed yield per plant
Plant height (cm)	1.000	0.080	-0.066	-0.020	0.000	-0.052
Number of branches		1.000	0.081	0.002	0.095	-0.001
Number of pods per plant			1.000	0.134*	0.044	0.032
Number of seeds per pod				1.000	-0.035	-0.027
100 seed weight					1.000	0.023
Seed yield per plant						1.000

Table 4: Phenotypic path coefficient analysis of component characters towards seed yield per plant in 157 F_3 progenies of cowpea

Characters	Plant height	Number of branches	Number of pods per plant	Number of seeds per pod	100 seed weight	Seed yield per plant
Plant height (cm)	**-0.050**	-0.004	0.003	0.001	0.000	-0.052
Number of branches	0.000	**-0.001**	0.000	0.000	0.000	-0.001
Number of pods per plant	-0.002	0.003	**0.032**	0.004	0.001	0.032
Number of seeds per pod	0.001	0.000	-0.004	**-0.032**	0.001	-0.027
100 seed weight	0.000	0.002	0.001	-0.001	**0.020**	0.023

R Square = 0.005 Residual effect = 0.998

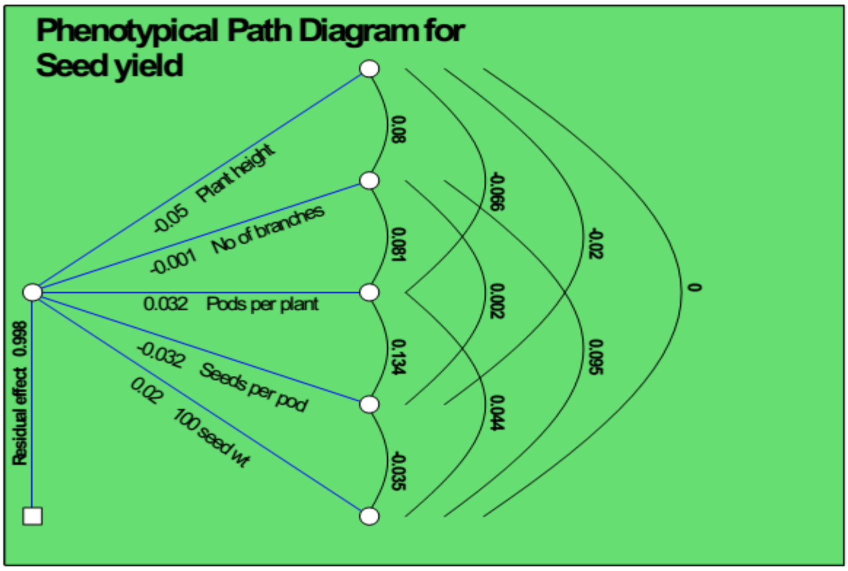

Fig 1: Phenotypic path diagram showing the influence of five characters on seed yield per plant in 157 F_3 progenies of cowpea

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