

Variability, Correlation and Path Analysis Studies in F₃ Generation of Cowpea [*Vigna unguiculata* (L.) Walp]

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ABSTRACT

Cowpea [*Vigna unguiculata* (L.) Walp] is most important widely adapted, stress tolerant grain legume, vegetable and fodder crop in tropical and sub-tropical regions. Two diverse parents were crossed (C-152 × V-16) and advanced to F₃ generation. The magnitude of variation, heritability, genetic advance, correlation and path co efficient analysis were estimated in a set of 194 F₃ 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 moderate phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimates were recorded for plant height (15.75% and 12.91%) and number pods per plant (16.29% and 11.42%). High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for plant height (67.13% and 21.78%) and moderate heritability and GAM was observed for number pods per plant (49.14% and 16.49 %). Path coefficient analysis revealed that seed yield was primarily influenced by number pods per plant, number seeds per pod and 100 seed weight which had maximum direct effect on seed yield per plant. Information obtained in this study suggests that traits like plant height, number pods per plant, number seeds per pod and 100 seed weight could be used as selection criteria for grain yield improvement at segregating populations of cowpea.

Keywords

Cowpea, PCV, GCV, Heritability, Genetic advance.

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Introduction

Among all the legume crops, cowpea [*Vigna unguiculata* (L.) Walp., Fabaceae (2n=2x=22)] is grown as one of the most important widely adapted, stress tolerant grain legume, vegetable and fodder crop in tropical and sub-tropical regions of Africa, Asia, Nigeria and America (Ehlers and Hall, 1997; Singh *et al.*, 1997). India and Ethiopia are recognized as primary and China as a secondary centre of origin (Vavilov, 1951). Cowpea adjusts well in a variety of cropping system and grown as catch 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 (Ayanaba and Dart, 1977). It is a very good source of high quality protein, carbohydrates, low amounts of fat, fiber, amino acids and minerals (Langyintuo *et al.*, 2003; Kabas *et al.*, 2007; Diaga, 2011). On dry weight basis, cowpea grain contains 23.4 per cent protein,

1.8 per cent fat and 60.3 per cent carbohydrates and it is rich source of calcium and iron (Gupta, 1988). Hence, it is considered as vegetable meat due to high amount of protein in grain with better biological value. Because of its smothering nature, drought tolerant characters, soil restoring properties and multi-purpose uses it is known as most versatile legume crop.

Development of cultivars with early maturity, acceptable grain quality, resistance to biotic and abiotic stress has significantly increased the yield and cultivated area (Ehlers and Hall, 1997). 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. 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.

Cowpea being a self-pollinated crop, variability existing is limited. Hence, the effort of the breeder is to evolve better yielding genotypes by exercising selection in segregating generation. In such a situation, the criteria of selecting superior plants in segregating generation have been an enigma to the plant breeder. Generally direct selection for yield is not effective due to its low heritability, hence it is desirable to adopt indirect selection of component traits for yield improvements.

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 F₃ generation derived from the cross between C-152 × V-16.

Materials and Methods

The experiment consists of the cowpea varieties *viz.*, C 152 and V-16. The variety, C-152 is a released variety from UAS, Bangalore which is agronomically superior but susceptible to Bacterial Leaf Blight (BLB) while, variety V-16, a released variety from Indian Agricultural Research Institute, New Delhi, which is resistant to BLB. In order to introgress resistance to BLB, C-152 is used as female parent and crossed with varieties V-16 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 F₁ 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 F₁s as well as using two SSR markers (CP 115/116 and CP 295) which were polymorphic between the parents of the crosses C-152 × V-16. True F₁s was selfed to obtain 192 F₂ seeds which were raised during summer 2013 by following the recommended package of practices. Seeds obtained from each individual F₂ plants were collected separately and forwarded to F₃ generation.

During *kharif* 2014, F₃ 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 (1985) and Allard (1960). Phenotypic co-efficient of variation were calculated by the formula of Burton (1952). Simple correlation coefficient was obtained using the formula suggested by Singh and Chaudhary (1985) and path co-efficient analysis was done following the method outlined by Dewey and Lu (1959).

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, 1994.

Phenotypic variance (σ^2p) = σ^2g + σ^2e (EMSS from ANOVA)

Genotypic variance (σ^2g) = MSS (G) - EMSSr

Error variance (σ^2e) = EMSS

Coefficients of variations

Phenotypic and genotypic coefficients of variability were computed as per the method suggested by Burton and De Vane, 1953.

Genotypic coefficient of variance (GCV) = $\frac{\sigma^2g}{\bar{X}} \times 100$

Phenotypic coefficient of variance (PCV) = $\frac{\sigma^2p}{\bar{X}} \times 100$

PCV and GCV values were categorized as low (0-10%), moderate (10-20%) and high (>20) values as indicated by Sivasubramanian and Menon, 1973.

Heritability

The broad sense heritability (h^2_{bs}) was estimated for all the characters as the ratio of genotypic variance to the total variance as suggested by Lush, 1945 as indicated below.

$$h^2_{bs} = \frac{\sigma^2g}{\sigma^2p} \times 100$$

Heritability was classified as suggested Robinson *et al.*, (1949) 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.*, (1955).

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

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.

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

The GAM% was categorized into low (0–10%), moderate (10.1–20%) and high (>20%) as suggested by Johnson *et al.*, (1955).

Results and Discussion

Analyses 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, 100 seed weight and seed yield per plant (Table 1). Plant height ranged from 20.90 to 50.40 cm with a mean of 32.18 cm, number of branches per plant ranged from 3.40 to 6.50 with a mean of 4.93, number of pods per plant ranged from 13.80 to 27.50 with a mean of 19.54, Number of seeds per pod ranged from 10.20 to 17.90 with a mean of 12.99, 100-seed weight ranged from 8.33 to 11.83 g with a mean of 9.91g and seed yield per plant ranged from 19.80 to 32.30 with a mean of 24.77g.

Moderate phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimates were recorded for plant height (15.75 % and 12.91%) and number pods per plant (16.29 % and 11.42%). Whereas, moderate PCV and low GCV was recorded for number of branches (15.01% and 6.66%), number seeds per pod (12.60% and 4.77%) and seed yield per plant (10.86% and 4.51%) (Tables 2 and 3).

High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for plant height (67.13% 21.78%). Moderate heritability and genetic advance as per cent of mean was observed for number

pods per plant (49.14% and 16.49 %). While low heritability and genetic advance was recorded for for number of branches (19.66% and 6.08%), number seeds per pod (14.31% and 3.72 %), 100 seed weight (25.61% and 5.11%) and seed yield per plant (17.30% and 3.96 %).

Path coefficient analysis in F₃ segregating population revealed that seed yield was primarily influenced by number pods per plant, number seeds per pod and 100 seed weight which had maximum direct effect on seed yield per plant (Table 4).

One of the ways to assess the extent of variability is examine the range, which directs the extent of phenotypic variability in respect of the trait under consideration, including genotypic, environmental and interaction components. 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. F₃ individuals of the cross C-152 × V-16 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 (Fig. 1).

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 PCV was greater than their corresponding GCV. Moderate to high GCV and PCV for the traits under investigation indicates greater scope for selection to improve upon these characters in the cross

studied. Similar results have been reported by Singh and Verma (2002), Ananda (2012), Tyagi *et al.*, (2000) and Prakash *et al.*, (2003). The trait exhibited moderate PCV and low GCV, indicating that there is less scope for

improvement of these traits through selection. While, PCV and GCV recorded was low for 100 seed weight (9.69% and 4.90%) indicating that there is no scope for improvement of these traits through selection.

Table.1 Analysis of variance for six quantitative traits in 194 F₃ progenies of cowpea

Sources of variance	df	Plant height (cm)	Number of branches	Number pods per plant	Number Seeds per pod	100 seed weight	Seed yield per plant
Replication	1	21.91	0.85	9.97	10.10	2.41	10.69
Genotypes	193	42.93**	0.66**	15.12**	3.06*	1.16**	8.49**
Error	193	8.44	0.44	5.15	2.68	0.69	5.99

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

Table.2 Estimates of genetic variability components for six quantitative traits in 194 F₃ progenies of cowpea

Sl. No	Traits	Grand Mean	Range		GCV %	PCV %	Broad sense (H)	GAM %
			Lowest	Highest				
1	Plant height (cm)	32.18	20.90	50.4	12.91	15.75	67.13	21.78
2	Number of branches	4.93	3.400	6.50	6.66	15.01	19.66	6.08
3	Number pods per plant	19.54	13.80	27.50	11.42	16.29	49.14	16.49
4	Number seeds per pod	12.99	10.20	17.90	4.77	12.60	14.31	3.72
5	100 seed weight	9.91	8.33	11.83	4.90	9.69	25.61	5.11
6	Seed yield per plant	24.77	19.80	32.30	4.51	10.86	17.30	3.96

Table.3 Estimates of phenotypic correlation coefficient analysis of seed yield and its component characters in 194 F₃ progenies of cowpea

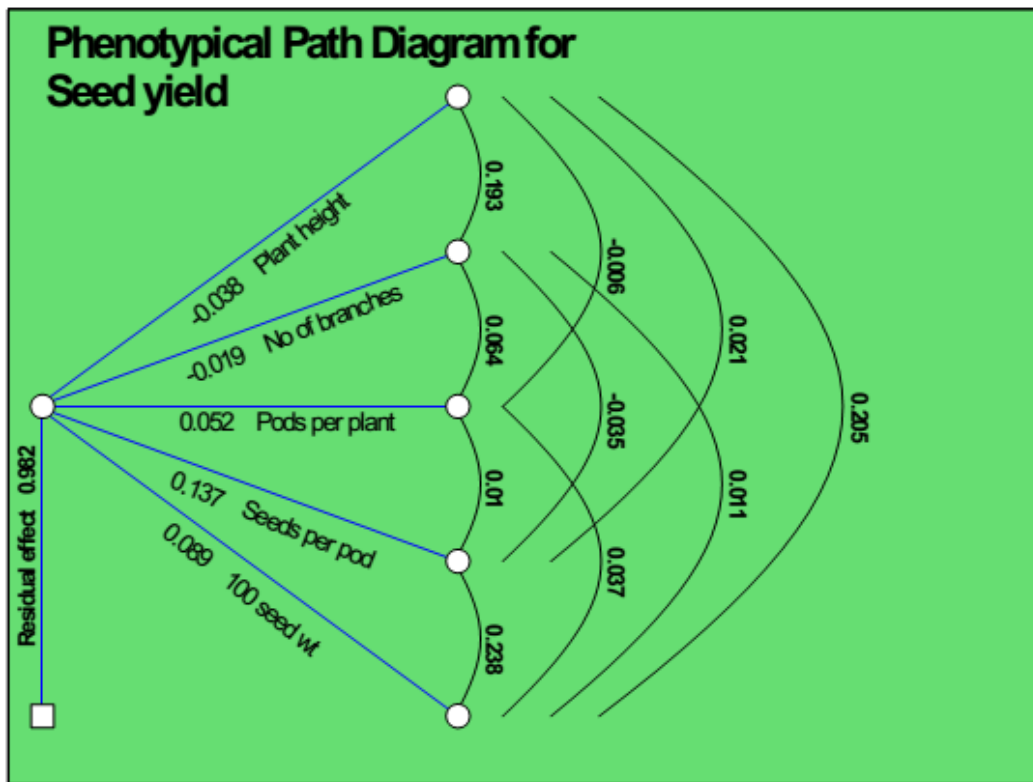
Characters	Plant height	Number of branches	Number pods per plant	Number Seeds per pod	100 seed weight	Seed yield per plant
Plant height (cm)	1.000	0.193***	-0.006	0.021	0.205***	-0.021
Number of branches		1.000	0.064	-0.035	0.011	-0.027
Number pods per plant			1.000	0.01	0.037	0.056
Number Seeds per pod				1.000	0.238***	0.158
100 seed weight					1.000	0.115
Seed yield per plant						1.000

Table.4 Phenotypic path coefficient analysis of component characters towards seed yield per plant in 194 F₃ progenies of cowpea

Characters	Plant height	Number of branches	Number pods per plant	Number Seeds per pod	100 seed weight	Seed yield per plant
Plant height (cm)	-0.038	-0.007	0.000	-0.001	-0.008	-0.021
Number of branches	-0.004	-0.019	-0.001	0.001	0.000	-0.027
Number pods per plant	0.000	0.003	0.052	0.001	0.002	0.056
Number Seeds per pod	0.003	-0.005	0.001	0.137	0.033	0.158
100 seed weight	0.018	0.001	0.003	0.021	0.089	0.115

R Square = 0.04 Residual effect = 0.982

Fig.1 Phenotypic path diagram showing the influence of five characters on seed yield per plant in 194 F₃ progenies of cowpea



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.*, (1955). 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 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. Similar kind of observations was noticed by Girish *et al.*, (2006), Suganthi and Murugan (2007), Bhadru and Navale (2012) and Vineeta Kumari *et al.*, (2003). 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 branches and 100 seed weight showed strong relationship with plant height while number seeds per pod showed strong relationship 100 seed weight suggesting that individual plant selections can be practiced in F₃ and advanced segregating generations with these characters which could precisely lead to improvement in plant height and 100 seed weight in the later generations.

The path coefficient analysis, a statistical device developed by Wright (1921) 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.

Based on results, it would be rewarding to lay emphasis on number pods per plant, number seeds per pod and 100 seed weight while developing selection strategies in cowpea. Similar results of high positive direct effect for number of pods per plant (Sawant, 1994, Vardhan and Savithamma, 1998; Anbumalarmathi *et al.*, 2005), number of seeds per pod (Subbaiah *et al.*, 2003; Anbumalarmathi *et al.*, 2005) and 100-seed weight (Siddique and Gupta, 1991; Anbumalarmathi *et al.*, 2005; Subbaiah *et al.*, 2013) 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.

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