



Correlation analysis for yield and yield contributing characters in F₂ and backcross generations of Cowpea (*Vigna unguiculata* L.)

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ABSTRACT: The present investigation was carried out to estimate genotypic and phenotypic correlation for the important yield and yield contributing characters using F₂ generations of two crosses and four backcrosses of cowpea. The experiment was conducted during *kharif* season 2020-21 at Experimental Farm, Department of Agricultural Botany, College of Agriculture, Latur. The experimental material comprised of three parents, F₂ and backcrosses. Observation were recorded on days to 50% flowering, days to maturity, number of primary branches per plant, plant height (cm), number of pods per plant, pod length (cm), number of seeds per pod, test weight (gm) and grain yield per plant (gm). In this investigation, the correlation with grain yield all nine character showed some positive and some negative correlation. The days to 50 per cent flowering, number of primary branches, number of pods per plant, number of seeds per pod, pod length (cm), and plant height (cm) and the negative correlation with only test weight (gm).

Keywords: Cowpea, yield, Correlation analysis, *Vigna unguiculata*.

I. INTRODUCTION

Cowpea [*Vigna unguiculata* (L.)Walp.] is a annual, autogamous leguminous crop belonging to family Leguminosae with a diploid chromosome number of $2n=2x=22$. It is a native to India [13], but tropical and central Africa is also considered as secondary centre of origin, where wild races are found even now [7]. Out of five subspecies, cowpea contains three cultivated species viz., *V. unguiculata*, *V. cylindrica* and *V. sequipedalis*. It is one of the most ancient, multi-seasonal, multipurpose *i.e.* food, feed, vegetable, fodder and green manure and a legume crop known to man. It is widely adopted and grown all over the world as pulse and vegetable crop. It is tropical grain legume which plays an important nutritional role in developing countries of the tropics and sub tropics, especially in Sub-Saharan Africa, Asia, Central and South America.

It has been referred to as "Poor man's meat" because of its high protein content. Dry seeds of cowpea contains high amount of quality protein (23.4%), carbohydrate (60.3%), fat (1.8%) and sufficient amount of calcium (76mg/100gm), iron (57mg/100gm) and vitamins such as thiamine (0.92mg/100g), riboflavin (0.18mg/100g) and nicotinic acid (1.9mg/100g) [1]. The crop is more tolerant to low fertility, due to its high rates of nitrogen fixation (Elawad and Hall 1987) [2], effective

symbiosis with mycorrhizae [5], and ability to adapt to soils with wide range of pH when compared to other popular grain legumes [3].

The global production of dried cowpeas exceeds 7.5 million tonnes. Africa is the biggest producer. Nigeria is the world's largest producer and consumer, accounting for 48 percent of global production and consumption. In India, the cowpea is grown in an area of about 3.9 million ha. In India, it is mostly cultivated in Haryana, Punjab, Delhi, West UP, with certain regions of Rajasthan, Kerala, Tamil Nadu, Karnataka, Gujarat, and Maharashtra states.

Cowpea is being a predominantly self-pollinated crop. The development of extra early maturing (60-70 days) and medium maturing (75-90 days), non-photosensitive lines with good grain quality and potential for dual-purpose use as (*i.e.*, food and fodder), either for use as a sole crop and as an intercrop in multiple cropping systems are the major targets of cowpea breeding programme. Grain yield is a complex and dependent character and is influenced by many other important yield contributing characters controlled by polygenes and environmental factors. The success of any selection programme in segregating generation depends on the nature and extent of correlation between independent variables with dependent variables. When highly heritable characters are associated with the important

character like yield, simultaneous selection based on these characters could be useful for improvement of yield in segregating populations.

II. MATERIAL AND METHOD

During the kharif of 2021, the current research was carried out at the Research Farm of Department of Genetics and plant Breeding, College of Agriculture, Latur. The F_2 of two crosses, GDVC-2 \times LC-1 and GC 6 \times LC-1 were obtained by selfing of F_1 involving three diverse parents *viz.*, GDVC-2, GC-6 and LC-1 during *kharif*, 2019-20. The back cross generations, BC-1 and BC-2 were obtained by crossing of F_1 of two crosses with its respective recurrent parents. Thus, seed of P_1 , P_2 , P_3 , their F_2 crosses and backcrosses were evaluated. The experimental material was tested in two replications in a Randomized Block Design (RBD) under rainfed conditions during the kharif of 2021. Line sowing was used to sow the seeds, with 45 cm row spacing and a 30 cm plant spacing, respectively. In each treatment and replication, observations were made on each plant. Days to flowering, days of maturity, plant height (cm), number of primary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 grains weight (gm), grain yield (gm). Except for the border rows, the plants were chosen from the center of the row. For all 9 yield and yield contributing characteristics utilised in the analysis, the replication means based on chosen plants were employed. The study was based on Panse and Sukhatme's proposed paradigm (1985) [9].

III. RESULTS AND DISCUSSION

A. Correlation Analysis Studies

Correlation coefficient is a statistical method, which finds the degree and direction of relationship between two or more variables. Thus correlation measures the magnitude of relationship between various characters that determines the component characters on which selection can be made for improvement in yield. It gives the mutual relationship of two or more variables. Therefore, an attempt has been made in the present study to work out relationship of different characteristics with grain yield and yield contributing component such as

1. Days to 50% flowering: The character days to 50% flowering recorded positive significant association with the traits plant height (cm) ($r_g = 0.978$, $r_p = 0.586$), number of primary branches per plant ($r_g = 0.792$, $r_p = 0.677$), number of pods per plant ($r_g = 0.984$, $r_p = 0.773$), number of seeds per pod ($r_g = 0.882$, $r_p = 0.726$), and grain yield ($r_g = 0.874$, $r_p = 0.717$) at both genotypic and phenotypic level. Positive non-significant association of days to 50 % flowering was

observed with days to maturity ($r_g = 0.313$, $r_p = 0.260$), and test weight ($r_g = 0.182$, $r_p = 0.009$) at both genotypic and phenotypic level. Whereas, it showed positive and significant association with pod length (cm) ($r_g = 0.541$) at genotypic level and positive non-significant at phenotypic level ($r_p = 0.403$).

2. Days to maturity: days to maturity had positive association with days to 50 per cent flowering ($r_g = 0.313$, $r_p = 0.260$), number of primary branches ($r_g = 0.368$, $r_p = 0.330$), number of pods per plant ($r_g = 0.343$, $r_p = 0.322$), pod length (cm) ($r_g = 0.145$, $r_p = 0.113$), number of seeds per pod ($r_g = 0.304$, $r_p = 0.270$) at both genotypic and phenotypic level. Positive and significant association was observed with grain yield ($r_g = 0.609$), at genotypic level. The negative and significant correlation with test weight (gm) ($r_g = -0.611$, $r_p = -0.545$) at genotypic and phenotypic level was recorded.

3. Plant height (cm): The character plant height showed significant positive association with days to 50 per cent flowering ($r_g = 0.978$, $r_p = 0.586$), number of pods per plant ($r_g = 0.785$, $r_p = 0.645$), number of seeds per pod ($r_g = 0.687$, $r_p = 0.586$) at both genotypic and phenotypic level. Positive non-significant association observed with number of primary branches per plant ($r_g = 0.418$, $r_p = 0.352$), pod length (cm) ($r_g = 0.359$, $r_p = 0.400$), test weight (gm) ($r_g = 0.025$, $r_p = 0.016$) at both genotypic and phenotypic basis. The negative and non-significant association observed with days to maturity ($r_g = -0.081$, $r_p = -0.071$) at both genotypic and phenotypic level.

4. Number of primary branches per plant: Number of primary branches had positive and significant association with days to 50 per cent flowering ($r_g = 0.792$, $r_p = 0.677$), number of pods per plant ($r_g = 0.785$, $r_p = 0.764$), pod length (cm) ($r_g = 0.757$, $r_p = 0.642$), number of seeds per pod ($r_g = 0.941$, $r_p = 0.710$), grain yield (gm) ($r_g = 0.785$, $r_p = 0.720$) at both level. It showed positive non-significant correlation with the days to maturity ($r_g = 0.368$, $r_p = 0.330$), plant height (cm) ($r_g = 0.418$, $r_p = 0.352$) genotypic as well as phenotypic level. With the test weight (gm) this trait showed positive significant association at genotypic level ($r_g = 0.520$)

5. Number of pods per plant: Number of pods per plant exhibited positive and significant correlation with days to 50 per cent flowering ($r_g = 0.984$, $r_p = 0.773$), plant height (cm) ($r_g = 0.785$, $r_p = 0.645$), number of primary branches per plant ($r_g = 0.785$, $r_p = 0.764$), pod length (cm) ($r_g = 0.620$, $r_p = 0.541$), number of seeds per pod ($r_g = 0.959$, $r_p = 0.759$), grain yield (gm) ($r_g = 0.998$, $r_p = 0.0.882$), at both genotypic and phenotypic level. Positive and non-significant correlation was observed with days to maturity ($r_g = 0.343$, $r_p = 0.322$), and test weight (gm) ($r_g = 0.010$, $r_p = 0.078$), at phenotypic as well as genotypic level.

Table 1: Estimates of genotypic (G) and phenotypic (P) correlations for yield and yield contributing traits in cowpea.

Sr. No.	Name of the Character		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Test weight (gm)	Grain yield (gm)
1	Days to 50% flowering	r_g	1.000	0.313	0.978**	0.792**	0.984**	0.541**	0.882**	0.182	0.874**
		r_p	1.000	0.260	0.586*	0.677**	0.773**	0.403	0.726**	0.009	0.717**
2	Days to maturity	r_g		1.000	-0.081	0.368	0.343	0.145	0.304	0.611**	0.609**
		r_p		1.000	-0.071	0.330	0.322	0.113	0.270	-0.545*	0.493
3	Plant height(cm)	r_g			1.000	0.418	0.785**	0.359	0.687**	0.025	0.738**
		r_p			1.000	0.352	0.645**	0.400	0.586*	0.016	0.387
4	Number of primary branches per plant	r_g				1.000	0.785**	0.757**	0.941**	0.520*	0.785**
		r_p				1.000	0.764**	0.642**	0.710**	0.406	0.720**
5	Number of pods per plant	r_g					1.000	0.620**	0.959**	0.010	1.006**
		r_p					1.000	0.541*	0.759**	0.078	0.882**
6	Pod length (cm)	r_g						1.000	0.943**	0.429	0.606**
		r_p						1.000	0.833**	0.311	0.342
7	Number of seeds per pod	r_g							1.000	0.278	0.964**
		r_p							1.000	0.134	0.623**
8	Test weight (gm)	r_g								1.000	-0.196
		r_p								1.000	-0.023
9	Grain yield (gm)	r_g									1.000
		r_p									1.000

6. Pod length (cm): The pod length (cm) character showed positive and significant association with the number of primary branches per plant ($r_g = 0.757$, $r_p = 0.642$), number of pods per plant ($r_g = 0.620$, $r_p = 0.541$), number of seeds per pod ($r_g = 0.943$, $r_p = 0.833$), at phenotypic as well as genotypic level. The positive and non-significant associations were observed with days to maturity ($r_g = 0.145$, $r_p = 0.113$), plant height (cm) ($r_g = 0.359$, $r_p = 0.400$), and test weight (gm) ($r_g = 0.429$, $r_p = 0.311$) showed both level. With the days to 50 per cent flowering at genotypic level correlation observed was positive and significant ($r_g = 0.541$), but at phenotypic level only positive association observed ($r_p = 0.403$). Also with grain yield (gm) at genotypic level positive and significant correlation ($r_g = 0.606$) observed but in phenotypic level only positive association showed ($r_p = 0.342$).

7. Number of seeds per pod: The character number of seeds per pod had positive and significant correlation with the days to 50 per cent flowering ($r_g = 0.882$, $r_p = 0.726$), plant height (cm) ($r_g = 0.687$, $r_p = 0.586$), number of primary branches per plant ($r_g = 0.941$, $r_p = 0.710$), number of pods per plant ($r_g = 0.959$, $r_p = 0.759$), pod length (cm) ($r_g = 0.943$, $r_p = 0.833$), grain yield (gm) ($r_g = 0.964$, $r_p = 0.623$), at the genotypic and phenotypic level. The positive and non-significant association observed with days to maturity ($r_g = 0.304$,

$r_p = 0.270$), and test weight (gm) ($r_g = 0.278$, $r_p = 0.134$), in genotypic as well as the phenotypic level.

8. Test weight (gm): Test weight trait showed positive association with the days to 50 per cent flowering ($r_g = 0.182$, $r_p = 0.009$), plant height (cm) ($r_g = 0.025$, $r_p = 0.016$), number of pods per plant ($r_g = 0.010$, $r_p = 0.078$), pod length (cm) ($r_g = 0.429$, $r_p = 0.311$), and number of seeds per pod ($r_g = 0.278$, $r_p = 0.134$), at genotypic and phenotypic both levels. The significant and negative correlation was observed with days to maturity ($r_g = -0.611$, $r_p = -0.545$) in genotypic as well as phenotypic level. With the grain yield (gm) it showed negative non-significant association ($r_g = -0.196$, $r_p = -0.023$), at both level. The positive and significant association exhibited with number of primary branches per plant at genotypic level ($r_g = 0.520$), and at phenotypic level it showed only positive correlation ($r_p = 0.406$).

9. Grain yield (gm): The grain yield (gm) character showed positive and significant correlation with days to 50 per cent flowering ($r_g = 0.874$, $r_p = 0.717$), number of primary branches per plant ($r_g = 0.785$, $r_p = 0.720$), number of pods per plant ($r_g = 0.998$, $r_p = 0.882$), and with number of seeds per pod ($r_g = 0.964$, $r_p = 0.623$), at their genotypic and phenotypic level. The grain yield (gm) showed negative and non-significant association with test weight (gm) ($r_g = -0.196$, $r_p = -0.023$), in

genotypic as well as phenotypic level. With the days to maturity positive and significant correlation observed at genotypic level ($r_g = 0.609$), and at phenotypic level positive correlation observed ($r_p = 0.493$). With plant height (cm) it showed positive and significant association at genotypic level ($r_g = 0.738$), and at phenotypic level positive relation ($r_p = 0.387$). Also with pod length (cm) it showed positive and significant association at genotypic level ($r_g = 0.606$), and at phenotypic level only observed positive correlation ($r_p = 0.342$).

The results are presented in Table 1. A study of the association of yield components with yield is useful for choosing the characters, which have a definite role in influencing the yield and may aid in selection from the breeding material. A better understanding of the contribution of such traits in building up the genetic makeup of the crop may be obtained through correlation. Genotypic correlations in general were higher than phenotypic correlations. This may be due to the relative stability of genotypes as majority of them were subjected to certain amount of selection [4]. The aim of correlation studies is primarily to know the suitability of various characters for indirect selection because selection on any particular trait may bring about undesirable changes in other associated characters. In the present investigation, correlation estimates obtained for 9 yield component characters of cowpea are discussed here. The character days to 50% flowering recorded positive significant association with the number of seeds per pod, number of pods per plant and grain yield. Similar results were obtained by Ugale *et al.* (2020). The days to maturity showed the positive non-significant association with the number of primary branches, number of pods per plant, pod length (cm), number of seeds per pod, grain yield, and the negative significant with test weight showed similar results by Thorat (2013), Aliyu and Makinde (2016) [8], Manggoel (2012) [6]. From the following analysis we can discuss the association with grain yield all nine character showed some positive and some negative correlation. The days to 50 per cent flowering, number of primary branches, number of pods per plant, number of seeds per pod, pod length (cm), and plant height (cm) and the negative correlation with only test weight (gm). This result also observed by Mnggoel *et al.* (2012), Thorat and Gadewar (2013) [11], Aliyu and Makinde (2016), Patel *et al.* (2016) [10], and Ugale *et al.* (2020) [12].

FUTURE SCOPE

The study may be useful to formulate the policies to improve upon the yield from cowpea crop on the basis of genotypic correlation and phenotypic correlation in yield and yield contributing character.

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REFERENCES

- [1]. Chatterjee BN, Bhattacharya KK. Principle and practices of grain legume production. *Oxford and IBH publishing Co. Ltd., New Delhi, 1986.*
- [2]. Elowad, H. O., & Hall, A. E. (1987). Influences of early and late nitrogen fertilization on yield and nitrogen fixation of cowpea under well-watered and dry field conditions. *Field Crops Research, 15*(3-4), 229-244.
- [3]. Fery, R. L. (1990). The cowpea: production, utilization, and research in the United States. *Horticultural Reviews, 12*, 197-222.
- [4]. Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans 1. *Agronomy journal, 47*(7), 314-318.
- [5]. Kwapata, M. B., & Hall, A. E. (1985). Effects of moisture regime and phosphorus on mycorrhizal infection, nutrient uptake, and growth of cowpeas (*Vigna unguiculata* (L.) Walp.). *Field Crops Research, 12*, 241-250.
- [6]. Manggoel, W., Uguru, M. I., Ndam, O. N., & Dasbak, M. A. (2012). Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpea [*Vigna unguiculata* (L.) Walp] accessions. *Journal of Plant Breeding and Crop Science, 4*(5), 80-86.
- [7]. Ng, N. Q., & Marechal, R. (1985). Cowpea taxonomy, origin and germplasm. *Cowpea research, production and utilization*, 11-21.
- [8]. Aliyu, O. M., & Makinde, B. O. (2016). Phenotypic analysis of seed yield and yield components in cowpea (*Vigna unguiculata* L., Walp). *Plant Breeding and Biotechnology, 4*(2), 252-261.
- [9]. Panse, V. G. & Sukhatme, P. V. (1985). Statistical methods for agricultural workers. ICAR, New Delhi, 381.
- [10]. Patel, U. V., Parmar, V. K., Patel, P. B., & Malviya, A. V. (2016). Correlation and path analysis study in cowpea (*Vigna unguiculata* (L.) WALP). *International Journal of Science, Environment and Technology, 5*(6), 3-897.
- [11]. Thorat, A., & Gadewar, R. D. (2013). Variability and correlation studies in cowpea (*Vigna unguiculata*). *International Journal for Environmental Rehabilitation and Conservation, 4*(1), 44-49.
- [12]. Ugale, S. D. & Bahl, P. N. (1980). Incorporation of germplasm from *Kabuli* to *Deshi* and *vice versa* in chickpea (*Cicer arietinum* L.). *India-Oxford and IBH. Publishing Co., New Delhi, pp.646.*
- [13]. Vavilov, N. I. (1951). *The origin, variation, immunity and breeding of cultivated plants: selected writings* (No. QK1 C55 v. 13 no. 1-6).