ESTIMATION OF CORRELATION AND PATH ANALYSIS FOR QUANTITATIVE TRAITS IN COWPEA (*Vigna unguiculata* (L.) Walp).

Abstract

The experiment included 20 cowpea genotypes with three replications in a Randomized Block Design. The study was carried out to estimate the genetic variability, genetic advance, correlation coefficient analysis and yield contributing traits, direct and indirect effects of yield component on yield through path analysis. The analysis of variance revealed the existence of all the traits, hence the data on all the 17 traits which showed significant differences among the entries were subjected to further statistical analysis. Maximum Genotypic coefficient of variation and Phenotypic coefficient of variation for biological yield and harvest index were recorded. At the phenotypic and genotypic levels, seed yield per plant had a high positive significant connection with Peduncle length, Number of secondary branches, Number of seeds per pod, Number of pods per plant, Biological yield, and Harvest index. Days to 50% flowering, Number of secondary branches, Number of seeds per pod, Number of pods per plant, 100 - seed weight had a significant positive effect on seed yield per plant at both the phenotypic and genotypic levels. Genotypes IC 259106, EC 58905, IC 202797, KASHI KANCHAN, IC 202803 and IC 10854 were found to be superior for seed yield per plant.

Keywords : Cowpea, Genetic variability, Correlation, Path analysis

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is the world's oldest crop. It is a member of the Papilionaceae family and the subfamily Fabaceae, with chromosome number 2n = 22. Africa is its principal source of origin. It is widely farmed and used around the world. Cowpea is consumed in a variety of forms, including long green pods as a vegetable, seeds as pulse and foliage as milch animal feed. Gujarat, West Bengal, Tamil Nadu, Andhra Pradesh, Kerala, and Orissa are the top growing states in India for cowpea. Cowpea is also known as "poor man's meat." The grain of cowpea has 57 percent carbohydrates and 21-33 percent protein and high in calcium and iron, while the leaves of cowpea contain 27 – 34 percent of protein **(Alidu *et*** ii

***al*. 2020)**. Cowpea is the most widely grown pulse in the world, accounting for 14.4 million ha with a total production of 8.9 million tonnes and productivity of 616.3 kg per ha **(FAOSTAT 2019)**. In India, the cowpea is grown in an area of about 3.9 million ha with a production of 2.21 million tones with a productivity of 625 kg per ha. During 2017 -2018 the total coverage under cowpea in Uttar Pradesh is 23.61lakh hectares with the production of around 22.34 lakh tonnes **(Anonymous, 2018**). Cowpea farmed on around 3.9 million ha in India, with a 625 kg per ha yield. The knowledge of character association i.e genotypic and phenotypic correlation between and its component character is very important for yield improvement through the selection program **(Addisu and Shumet, 2015)**. The cause-effect provides an effective means of partitioning the correlation coefficient into which direct and indirect effects of the component character on yield based on which crop improvement program can be logically confined **(Meena *et al*., 2015)**. Path analysis is an important and excellent means of studying the direct and indirect effects of interrelated components of complex traits. 3

MATERIALS AND METHODS

During *Zaid* - 2021, the current study on correlation and path analysis for yield and yield contributing character in cowpea was carried out at Naini Agricultural College, Sam Higginbottom University of Agriculture, Technology & Sciences, Prayagraj U.P. The experiment was carried out in a Randomized Block Design with 20 randomly ordered genotypes, reproduced three times and divided into 60 plots. The gross area of the experiment was 144.5 m$_2$ and the plot size was 1 × 1 m. The row-to-row spacing was 60 cm and plant to plant spacing was 30 cm. A total number of five plants from each replication were tagged and observation was taken from these tagged plants at various stages of the plant throughout the growing stages. Data were recorded for 17 characters viz, Days to 50% flowering, Days to 50% podding, Days to maturity, Petiole length, Peduncle length (cm), Number of primary branches, Number of secondary branches, Number of clusters per plant, Number of pod per cluster, Number of pods per plant, Pod length (cm), Number of seeds per pod, Plant height (cm), Harvest index, Biological yield (g) by calculating biological yield / economical yield, Seed index (g) by calculating the 100 - seed weight and Seed yield per plant (g). The mean values were computed data was analysed for analysis of variance as suggested by **(Fisher 1918)** and Coefficient of variance as suggested by **Burton and Devane (1953)**. Phenotypic and Genotypic correlation and path coefficient of variation was computed as per the method given by **Dewey and Lu (1959)**.

RESULT AND DISCUSSION

In this present investigation, the genotypic and phenotypic correlation coefficients were computed among different 17 characters (Table 2). The genotypic correlation coefficient was higher than the phenotypic correlation coefficient. Number pods per cluster, pod length, number of primary branches, number of seeds per pod, number of clusters per plant, number of pods per plant, biological yield, seed index and seed yield per plant exhibited significance both at the genotypic and phenotypic level. Therefore these above characters appeared as the greatest important associates of seed yield per plant and also very important for future aspects. Similarly, the same result was also observed by **Kanimoli *et al*. (2015)** and **Ramesh *et al*. (2001)**. At the phenotypic level, the plant height and pod length showed negative significance to seed yield, whereas at the genotypic level there is no negative significance to seed yield.

Path analysis is also an important aspect and statistical approach to separate and observed the correlation coefficient into direct and indirect effects of independent variables on the dependent 4 variables (Table 3). In these studies, the seed yield was considered as a dependent character and other characters were taken as the independent characters. The results of the present study on path analysis are presented for 17 quantitative characters of the cowpea. Path analysis revealed that the days to 50% flowering, number of secondary branches, number of seeds per pod, number of pods per plant and seed index showed a direct positive effect at both genotypic and phenotypic levels. Similar results were observed by **Suganthi and Murugan (2008) and Lingaraj (2009)**. The high indirect effects were shown by plant height, petiole length, pod length, number of primary branches and harvest index at both genotypic and phenotypic levels. By looking at the nature and the result of the correlation coefficient of variation and direct and indirect effects it can be concluded that the number of seeds per pod, number of pods per plant and seed index may be considered during selection for crop improvement. Similar results were observed by **(Patil *et al.* 2020)**. Correlation and path analysis showed that importance should be given to a number thef seeds per pod, number of pods per plant and seed index per plant because of its positive correlation and high direct positive effects at both genotypic and phenotypic levels.

CONCLUSION

The present study illustrated that among the 20 genotypes of the cowpea, the correlation coefficient revealed that the number of pods per cluster, pod length, number of primary branches, number of seed per pod, number of cluster per plant, number of pods per plant and biological yield exhibited a significant and positive correlation with seed yield both at genotypic and phenotypic levels. Days to 50% flowering, number of secondary branches, number of seeds per pod, number of pods per plant and seed index exhibited a high positive direct effect with seed yield per plant. Whereas the indirect effect of other characters through these characters towards seed yield per plant. These characters may be given due consideration during selection for crop improvement. 5

Table 1: Analysis of variance for seed yield and its contributing characters in cowpea genotypes. Mean Sum of Squares

Traits	**Treatment(df=19)**	**Replication(df=2)**	**Error(df=38)**
Days to 50% flowering	36.16**	0.42	20.26
Days to 50% pod setting	237.79**	1474	106.49
Days to maturity	132.36**	1.6	5.13
Plant Height	1936.33**	3880	1248.15
Petiole Length	2.24	14.9	1.99
Peduncle Length	24.00**	10.2	10.56
Number Pods /Cluster	0.14**	0.04	0.14
Pod Length	11.28**	6.03	6.2
Number of Primary Branches	13.47**	33.5	13.48
Number of Secondary Branches	4.87**	21.7	7.2
Number Of Seeds/Pod	3.96**	4.28	2.98
Number Of Cluster / Plant	4.38**	0.05	4.04
Number Of Pods / Plant	5.03**	0.52	6.33

Biological Yield	11338.43**	78849.7	4972.43