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 effect 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. High genetic advance as a percentage of the mean for 100 seed weight. The heritability of 100 - seed weight was found to be high. For biological yield, there was a significant genetic advance. 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 all had a significant beneficial 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, Genetic advance, 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 a 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 ii meat." The green has 84.6 percent hydration, 60.3 percent carbohydrates, 1.8% fat, and is high in vitamins and phosphorus **(Venkatesan *et al*. 2003)**. Cowpea is the most widely grown pulse in the world, accounting for 12.76 million ha with a total production of 7.56 million tonnes and productivity of 750 kg per ha **(FAO 2013)**. 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 hectare with the production of around 22.34 lakh tonnes **(Anonymous, 2018**). Cowpea are farmed on around 3.9 million ha in India, with a 625 kg per ha yield. The knowledge of chatracter association i.e genotypic and phenotypic correlation between and its component character is very important for yield improvement through the selection program **(Frasher *et al*., 1983)**. 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 **(Rao *et al*., 1997)**. Path analysis is an important and excellent means of studying the direct and indirect effects of interrelated components of complex traits. 3

MATERIAL 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 genotypes that were randomly ordered, reproduced three times, and divided into 60 plots. The gross area of the experiment is 144.5 m_2 and the plot size was 1 × 1 m. The row-to-row spacing is 60 cm and plant to plant spacing is 30 cm. The 5 competitive plants from each of the replication were tagged and observations were taken from these tagged plants at various stages of the plant through out the growing stages. Data were recorded from 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 pods per cluster, Number of cluster per plant, 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 were analysed for analysis of variance as suggested by **(Fisher 1918)** and Coefficient of variance as well as Heritability (in a broad sense), as suggested by **Burton and Devane (1953)**. The Genetic advance was obtained by the formula suggested by **Johnson *et al.* (1955)**. 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 section, the genotypic and phenotypic coefficients of variation, heritability, and genetic progress are all presented (Table- 1). All of the characters had a wide range of diversity. The phenotypic coefficient of variance was greater than the genotypic coefficient of variation for all traits studied. The phenotypic coefficient of variation (PCV) ranged from Days to 50% flowering (5.255) to Harvest index (36.978). Seed yield per plant was also found to be moderate. The genotypic coefficient of variation, which measures the level of genetic variation in a population, ranged from 0.384% to 18.703%. The traits of biological yield per plant (18.70%) and harvest index (16.40%) showed the highest genotypic coefficient. Peduncle length and pod length have moderate values. **Sapara *et al.* (2014)** discovered high PCV for pod length, while **Sapara *et al.* (2014)** and **Khanpara *et al.* (2016)** discovered moderate PCV for pod length (table -2). 4

The estimation of good heritability best way to understand the transmission of character from parents to their offspring (Falconer 1981). High heritability is observed for seed index (100 %) and seed yield per plant (88.22%) followed by days to maturity (82.56%), days to 50 % pod setting (72.6%), number of cluster per plant (70.8%). High heritability alone may not lead to any conlusion unless it will relate with the genetic advance as percent mean (Johson and Robinson, 1955). High heritability coupled with high genetic advance as percent of the mean was recorded for the seed yield per plant. This finding were accordance to **Nwosu *et al*. (2013)** and **Sapara *et al*.(2014)**. The high heritability were also reported by **Suganthi and Miurugan (2007).**

The genotypic and phenotypic correlation coefficients were computed among 17 characters in (Table -3). The number of pods per cluster, pod length, number of primary branches, number of seedss 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. Hence therefore this above character appeared as the greatest important associate 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)**.

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 variables in (Table-4). In the present study, the path analysis correlation is carried out for 17 quantitative characters of the cowpea. Path analysis revealed the days to 50% flowering, number of secondary branches, number of seeds per pod, number of pods per plant, seed index at both genotypic and phenotypic level. Similar results were observed by **Suganthi and Murugan (2008) and Lingaraj (2009)**. By looking to the nature and the result of the correlation coefficient 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 given consideration during selection for crop improvement.

CONCLUSION

The present study illustrated that among the 20 genotypes of the cowpea that phenotypic and genotypic correlations showed a positive correlation of seed yield with 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, biological yield, and seed yield per plant. Days to 50% flowering, number of secondary branches, number of seeds per pod, number of pods per plant 5 and seed index exhibited high a positive direct effect with seed yield per plant. These characters may be given due consideration during selection for crop improvement.

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
Harvest Index	351.89**	579	282.68
Seed index	15.74**	7.62	12.06
Seed yield / plant	14.74**	5.62	12.06