

CORRELATION AND PATH ANALYSIS IN COWPEA (*Vigna unguiculata* (L.) Walp)

RM. NAGALAKSHMI^{1*}, R. USHA KUMARI² AND R. ANANDA KUMAR²

¹Centre for plant breeding and genetics, Tamilnadu Agricultural university, Coimbatore, Tamilnadu - 641003, INDIA.

²Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai - 625 104, Tamilnadu
e-mail:rmnagalakshmi@gmail.com

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*Corresponding author

ABSTRACT

Knowledge on the relationship between yield and yield related characters is essential for designing any plant breeding programme. With this aim, a study was conducted in cowpea (*Vigna unguiculata* (L.) Walp) to estimate the correlation coefficients among 12 quantitative characters and to analyse the direct and indirect effects of these characters on seed yield by path coefficient analysis in 66 genotypes collected from various agroclimatic zones of India. The study revealed that seed yield was positively and significantly correlated with number of pods per plant (0.40), peduncle length (0.38), number of clusters per plant (0.31), number of seeds per pod (0.29), number of leaves per plant (0.28), number of branches per plant (0.27) and days to 50% flowering (0.19). 100 seed weight (-0.44) and pod length (-0.1) were negatively correlated with seed yield. Number of seeds per pod (0.34), peduncle length (0.26), plant height (0.23), number of branches per plant (0.15), number of clusters per plant (0.12), number of pods per plant (0.12) and days to 50% flowering (0.07) exerted a direct positive association with seed yield. The results of correlation and path analysis suggests that seeds per pod, pod length and number of branches per plant are the important characters for selection in cowpea.

INTRODUCTION

Cowpea is one among the important pulse crops in the world. It is an essential component of cropping systems in the drier regions and marginal areas of the tropical world (Fabunmi *et al.*, 2012). Cowpea is of major importance to the livelihood of millions of people in less developed countries (Agbicodo *et al.*, 2009). With over 25% of protein in its seeds, cowpea is a major source of protein, minerals and vitamins in the daily diet and hence called vegetable meat (Ibrahim *et al.*, 2010). It has the ability to fix atmospheric nitrogen through its nodules and it grows well in soils with 85% soil and less than 0.2% organic matter.

The ultimate aim of plant breeding is to achieve a higher level of seed yield in many cases, which is a complex trait. Yield is governed by many number of genes and results due to the interaction of morphological, physiological and biochemical factors with the environment (Mir *et al.*, 2012). It has been generally accepted that correlation between different characters represents a coordination of physiological processes, which is often achieved through gene linkages. The complex nature of seed yield is largely influenced by number of component traits. Hence information on the strength and direction of association of these component characters with seed yield and also inter association among them would be very useful in formulating an effective and viable breeding programme for improvement of seed yield (Jogdhande *et al.*, 2017; Manisha *et al.*, 2018). Character association studies are of great significance in the process of selection by which simultaneous improvement of more than one character is possible.

Genotypic correlation enables the breeders to assess the pattern of inherent relationship between various traits since it is based on the heritable part. (Singh *et al.*, 2014). In general, the reduction in magnitude of phenotypic correlation from that of genotypic correlation is due to the influence of environment. Simple correlation will not provide any reliable basis for selection themselves, so partitioning it into direct and indirect components through path analysis becomes essential (Choudhary *et al.*, 2005; Sawarkar *et al.*, 2014; Muchero *et al.*, 2008).

Adequate information on the direction and strength of relation between yield and yield related characters will help to design an effective breeding programme. With this objective, current research was conducted to study the relation between 12 quantitative characters among 66 genotypes of cowpea collected from different agroclimatic zones of India, the results of which can be used in future breeding programmes.

MATERIALS AND METHODS

Description of study area

The experiment was conducted at the research block, Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai.

Experimental material

A total of sixty six germplasm entries of diverse origin were used for the present study. 22 genotypes were obtained from Regional Research Station, Vamban, 21 genotypes from Central Arid Zone Research Institute, Jodhpur, eight from Agricultural College and Research Institute, Madurai, six from Kerala

Agricultural University, Vellayani, four from Tamilnadu Agricultural University, Coimbatore, three from ARS, Durgapura and two from National Bureau of Plant Genetic Resources, Delhi were used for the present study.

Experimental design and procedure

The crop was raised in Randomized Block Design with two replications under irrigated conditions. Each entry was raised in two rows of 3 m length spaced at 30 cm between rows and 20 cm between plants in each replication. Data was collected from the plants in the two rows.

Data collection

The observations were recorded on three randomly selected plants in each replication and the average was worked out and used for statistical analysis. The random plants of all the plots in each replication were labelled for recording the observations. The pre and post-harvest observations in respect of plant characters were recorded on the labelled plants. The following twelve quantitative characters were studied, days to 50% flowering, plant height (cm), number of branches per plant, Number of leaves per plant, Petiole length (cm), Peduncle length (cm), Number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and grain yield per plant (g).

Data analysis

Correlation analysis

With the observed data, the variance and covariance were calculated. The genotypic and phenotypic variances were calculated using the formula suggested by Johnson *et al.* (1955) and Comstock and Robinson (1952). The genotypic and phenotypic correlations was calculated using the method suggested by Miller *et al.* (1958) using the following formula

$$\text{The phenotypic correlation coefficient } r_{pxy} = \frac{\text{cov}_{pxy}}{\sqrt{\sigma^2_{p_x} \times \sigma^2_{p_y}}}$$

where,

r_{pxy} = phenotypic correlation coefficient between the traits x and y.

COV_{pxy} = phenotypic covariance between the traits x and y.

$\sigma^2_{p_x}$ = phenotypic variance of the trait x.

$\sigma^2_{p_y}$ = phenotypic variance of the trait y.

$$\text{The genotypic correlation coefficient } r_{gxy} = \frac{\text{COV}_{gxy}}{\sqrt{\sigma^2_{g_x} \times \sigma^2_{g_y}}}$$

where,

r_{gxy} = genotypic correlation coefficient between the traits x and y.

COV_{gxy} = genotypic covariance between the traits x and y.

$\sigma^2_{g_x}$ = genotypic variance of the trait x.

$\sigma^2_{g_y}$ = genotypic variance of the trait y.

significance of correlation was tested using t statistic at n-2 degrees of freedom

Path analysis

The relative influence of twelve components on yield by themselves (direct effects) and through other traits (indirect effects) was evaluated by the method of path coefficient analysis as suggested by Dewey and Lu. (1959). The simple correlation coefficients already estimated at genotypic level were utilized for this purpose. By keeping yield as dependent variable and other thirteen traits as independent variables, simultaneous equations which express the basic relationship between path coefficients were solved to estimate the direct and indirect effects. The direct and indirect effects were classified based on the scale given by Lenka and Misra (1973).

More than 1.0	Very high
0.30 to 0.99	High
0.20 to 0.29	Moderate
0.10 to 0.19	Low
0.00 to 0.09	Negligible

RESULTS AND DISCUSSION

Correlation analysis

The inter relationship among the twelve characters were estimated through correlation coefficients both at genotypic and phenotypic levels and the same is presented in Table 1. In the present study genotypic correlation coefficients were higher than phenotypic correlation coefficients indicating the presence of strong inherent association among the traits (Adetiloye *et al.*, 2017).

Association of yield components with grain yield

Grain yield per plant had high significant positive association with number of pods per plant followed by peduncle length, number of seeds per pod, number of branches per plant, number of clusters per plant, number of leaves per plant, days to 50% flowering. Similar findings were reported by Renukadevi and Subbalakshmi. (2006), Mangoel *et al.* (2012), Bhagwai *et al.* (2017), Kalambe *et al.* (2019) for number of primary branches, number of pods per plant, peduncle length, number of seeds per pod. Singh and Verma. (2002), Parmer *et al.* (2003), Lokesh *et al.* (2017), Lopes *et al.* (2017), Ribeiro *et al.* (2017), Paghadar *et al.* (2019) reported similar results for number of leaves per plant and days to 50% flowering. Grain yield per plant recorded significant negative correlation with 100 seed weight and pod length. Similar results were given by Jogdhande *et al.* (2017), Kumar *et al.* (2017), Patel *et al.* (2018) and Waghmare *et al.* (2019).

Hence, these characters namely numbers of pods per plant, number of branches per plant, number of leaves per plant, peduncle length, number of clusters per plant and number of seeds per pod have to be given importance during selection to improve the yield potential of the crop. Among these characters, number of clusters per plant and peduncle length had high correlation with seed yield.

Inter correlation among yield components

Days to 50% flowering exhibited high positive and significant correlation with plant height, pod length, number of branches per plant, peduncle length and number of leaves per plant. Days to 50% flowering exhibited significant negative

Table 1: Genotypic and phenotypic (in bold) correlation coefficients between different traits

S. No	Characters	Days to 50% flowering	Plant height	Number of branches per plant	Number of leaves per plant	Petiole length	Peduncle length	Number of clusters per plant	Number of pods per plant	Pod length	Number of seeds per pod	100 seed weight	Grain yield per plant
1	Days to 50% flowering	G	0.35**	0.22*	0.21*	0.19	0.21*	0.10**	0.10**	0.27*	-0.03**	-0.19**	0.19**
		P	0.34	0.16	0.2	0.14	0.2	0.08	0.1	0.26	-0.01	-0.19	0.19
2	Plant height (cm)	G		0.17	0.05	-0.06	0.13	0.14	-0.14	0.84**	-0.01	0.14	0.02
		P		0.15	0.06	-0.04	0.123	-0.127	-0.14	0.82	-0.01	0.13	0.01
3	Number of branches per plant	G			0.54**	0.007	0.27*	0.26*	0.27*	-0.01	-0.02	-0.34**	0.35**
		P			0.44	0.07	0.23	0.2	0.26	-0.02	0.05	-0.27	0.27
4	Number of leaves per plant	G				-0.15**	0.32**	0.23*	0.41**	-0.13	0.04	-0.36**	0.28**
		P				-0.13	0.31	0.222	0.404	-0.13	0.03	-0.35	0.28
5	Petiole length (cm)	G					-0.15**	-0.03	-0.02	-0.11	0.08	-0.24*	0.06
		P					-0.115	-0.02	-0.02	-0.09	0.1	-0.21	0.02
6	Peduncle length (cm)	G						0.28	0.43**	0.08	-0.01	-0.14	0.40**
		P						0.26	0.42	0.08	0.01	0.12	0.38
7	Number of clusters per plant	G							0.71**	-0.12	0.05	-0.15	0.34**
		P							0.67	-0.11	-0.01	-0.14	0.31
8	Number of pods per plant	G								-0.26*	-0.02	-0.31**	0.41**
		P								-0.25	-0.01	0	0.4
9	Pod length (cm)	G									0.02	0.28*	-0.11
		P									0.028	0.27	-0.1
10	Number of seeds per pod	G										-0.31**	0.37**
		P										-0.25	0.29
11	100 seed weight (g)	G											-0.45**
		P											-0.44

* Significance at 5% level; ** Significance at 1% level

Table 2 : Direct and indirect effects of yield components as partitioned by path analysis

S. No	Characters	Days to 50% flowering	Plant height	Number of branches per plant	Number of leaves per plant	Petiole length	Peduncle length	Number of clusters per plant	Number of pods per plant	Pod length	Number of seeds per pod	100 seed weight	Grain yield per plant
1	Days to 50% flowering	0.07	0.08	0.03	-0.02	-0.002	0.05	0.01	0.012	-0.074	-0.011	0.036	0.19
2	Plant height (cm)	0.026	0.23	0.028	-0.006	0.0008	0.035	-0.016	-0.016	-0.228	-0.005	-0.026	0.2
3	Number of branches per plant	0.016	0.04	0.158	-0.057	-0.0009	0.073	0.03	0.032	0.005	-0.007	0.064	0.35
4	Number of leaves per plant	0.015	0.01	0.085	-0.1	0.002	0.08	0.02	0.047	0.036	0.013	0.067	0.28
5	Petiole length (cm)	0.01	-0.014	0.001	0.016	-0.012	-0.039	-0.003	-0.003	0.03	0.029	0.046	0.06
6	Peduncle length (cm)	0.015	0.03	0.044	-0.034	0.001	0.262	0.032	0.05	-0.023	-0.003	0.027	0.4
7	Number of clusters per plant	0.007	-0.03	0.041	-0.024	0.0004	0.074	0.116	0.081	0.035	0.017	0.028	0.34
8	Number of pods per plant	0.007	-0.03	0.044	-0.043	0.0003	0.115	0.082	0.115	0.071	-0.007	0.057	0.41
9	Pod length (cm)	0.02	0.195	-0.003	0.014	0.001	0.022	-0.015	-0.03	-0.271	0.009	-0.053	-0.11
10	Number of seeds per pod	-0.002	-0.003	-0.003	-0.004	-0.001	-0.003	0.005	-0.002	-0.007	0.342	0.057	0.37
11	100 seed weight (g)	-0.014	0.033	-0.054	-0.038	0.003	-0.038	-0.017	-0.035	-0.077	-0.106	-0.185	0.45

Residual effect = 0.246

correlation with 100 seed weight and number of seeds per pod. Similar results were given by Mangoel *et al.* (2012) and Waghmare *et al.* (2019). Plant height exhibited high positive and significant association with pod length, Number of branches per plant, 100 seed weight, peduncle length and number of leaves per plant. Number of branches per plant exhibited positive and significant association with number of leaves per plant, peduncle length, number of pods per plant and number of clusters per plant. Similar results were given by Dinesh *et al.* (2017), Santos *et al.* (2014) and Paghader *et al.* (2019).

Number of leaves per plant exhibited high positive significant correlation with number of pods per plant, peduncle length and number of clusters per plant. Petiole length showed positive correlation with number of seeds per pod. Peduncle length recorded significant positive correlation with number of pods per plant, Number of clusters per plant and pod length. significant and positive genotypic correlation was found between number of clusters per plant and number of pods per plant. Parmer *et al.* (2003) and Lokesh *et al.* (2017) reported similar results.

Number of pods per plant exhibited significant negative correlation with 100 seed weight and pod length. Pod length showed significant positive correlation and number of seeds per pod exhibited significant negative correlation with 100 seed weight. Similar results were reported by Patel *et al.* (2018) and Waghmare *et al.* (2019).

Path coefficient analysis

The genotypic correlation coefficient of seed yield with its component traits is further partitioned into direct and indirect effects. The results of path analysis showing the direct and indirect effects of all the eleven characters on seed yield are furnished in

Table 2.

Direct effects

The dependent variable taken into consideration for path analysis was seed yield per plant. Among the eleven characters analyzed, seven characters showed positive direct effect and the remaining four characters showed negative direct effects on seed yield per plant. The highest positive direct effect was

registered by number of seeds per pod, followed by peduncle length, plant height, number of branches per plant, number of clusters per plant, number of pods per plant and low positive direct effect was registered by number of days to 50% flowering. Negative direct effect was recorded through pod length, 100 seed weight, number of leaves per plant and petiole length. Similar results were reported by Mangoel *et al.* (2012), Bhagwati *et al.* (2017) and Kalambe *et al.* (2019)

Indirect effects

Positive negligible indirect effect was recorded by days to 50% flowering on seed yield through number of plant height. Plant height showed moderate indirect negative effect through pod length. Number of leaves per plant, Petiole length, Peduncle length, 100 seed weight and Number of clusters per plant recorded negligible positive indirect effect through number of branches per plant, 100 seed weight, number of pods per plant, pod length, days to 50% flowering, plant height and number of seeds per pod. Lopes *et al.* (2017), Ribeiro *et al.* (2017) and Paghadar *et al.* (2019) reported similar results.

Number of pods per plant, pod length, number of seeds per pod recorded low positive indirect effect through peduncle length, number of clusters per plant, pod length, 100 seed weight, number of branches per plant, days to 50% flowering and petiole length. Similar results were given by Kumar *et al.* (2017).

Though the characters, number of seeds per pod, peduncle length, pods per plant, number of branches per plant contributed more to the grain yield, path analysis shows that seeds per pod, pod length and number of branches per plant had direct effect on yield. So, selection based on seeds per pod, pod length and number of branches per plant will give productive results.

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