CHARACTER ASSOCIATION AND PATH CO-EFFICIENT ANALYSIS FOR YIELD AND ITS ATTRIBUTES IN COWPEA [*Vigna unguiculata* (L.) Walp.]

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ABSTRACT

Character association and path co-efficient analysis were carried out using 25 genotypes of cowpea for 10 yield attributing traits. Character association analysis revealed that the characters number of pods plant[-1], number of clusters plant[-1], number of branches plant[-1], 100 seed weight, days to 50 per cent flowering and days to maturity exhibited significant and positive association with seed yield plant[-1] indicating that selection based on these characters would bring about simultaneous improvement of the yield. Path co-efficient analysis revealed that number of pods plant[-1] exhibited the highest positive direct effect on seed yield plant[-1] followed by 100 seed weight, number of clusters plant[-1], days to maturity, plant height, pod length, number of seeds pod[-1] and number of branches plant[-1] indicating that direct selection of these characters would be rewarding for improvement of the yield.

INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp.] is an annual, autogamous leguminous crop belonging to family *Leguminoseae* with a diploid chromosome number of 2n = 22. Cowpea is considered as one of the oldest legumes and referred as "Poor man's meat" as its seeds have high protein content making it extremely valuable in areas where many people cannot afford proteinaceous food like meat and fish. On dry weight basis, cowpea grain contains 23.4 per cent protein, 1.8 per cent fat, 60.3 per cent carbohydrates and is a good source of vitamins and phosphorus (Gupta *et al.,* 2019).

Cowpea is an early, multi seasonal and multipurpose crop. It has multifarious uses like fodder, cover crop and green manure and provides high quality protein in the form of vegetable and pulse to human diet. All parts of cowpea are used as food and fodder. It is mostly cultivated as sole crop and mix-crop in India and also an ideal crop for soil and water conservation because of its fast growing and ground covering ability. It adjusts well in a variety of cropping system and also grown as catch crop and green manure crop as it fixes about 240 kg ha^{-1} atmospheric nitrogen and leaves about 60 to 70 kg nitrogen for succeeding crop (Panchta *et al*., 2020).

In India, cowpea is grown almost in all states, but the largest cultivating states are Gujarat, West Bengal, Tamil Nadu, Andhra Pradesh, Kerala and Orissa (Detroja *et al.,* 2020)*.* In Andhra Pradesh, it is grown in an area of 0.13 lakh hectares with a production of 0.06 lakh tonnes and with a productivity of 487 kg ha^{-1} (Directorate of Economics and Statistics, Ministry of Agriculture and Farmers Welfare (DAC and FW), Government of India, 2019-20).

Knowledge on the interrelationship between the different morphological and yield contributing traits is necessary for drawing out sound breeding programmes for any crop. Seed yield, being a complex quantitative trait, is governed by a large number of genes and is greatly influenced by environmental fluctuations, therefore, selection of elite genotypes based on yield as such is not effective. Under such circumstances, a breeder has to find out some other characters which contribute to yield. Therefore, knowledge of association of characters with seed yield and among themselves and their direct and indirect effects upon the yield is very helpful and provides an effective measure in crop improvement programme of cowpea. Hence, the objective of the present study is to determine the correlation and path analysis to understand the degree and direction of association of different yield component traits with the seed yield in cowpea.

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MATERIAL AND METHODS

The present investigation was carried out with 25 diverse genotypes during *Rabi,* 2020, irrigated dry conditions, at Regional Agricultural Research Station (RARS), Tirupati. The total rainfall received during crop growth period was 304 mm and the total number of rainy days were 18 under the influence of North East Monsoon and no irrigation was given during the crop growth period. The experimental site is situated at an altitude of 189.2 m above MSL, 13˚N latitude and 79˚E longitude geographically.

The data was recorded on ten randomly selected plants taken from each replication for days to 50 per cent flowering, days to maturity, plant height (cm), number of branches plant[-1], number of clusters plant[-1], number of pods plant[-1], pod length (cm), number of seeds pod[-1], 100 seed weight (g) and seed yield plant[-1] (g). The data collected on 10 yield and yield attributing traits was used to study the association and path analysis. Genotypic and phenotypic correlation coefficients were calculated using the method given by Johnson *et al.* (1955b). Path co-efficient analysis was carried out by the procedure originally proposed by Wright (1921), which was subsequently elaborated by Dewey and Lu (1959) to estimate the direct and indirect effects of the individual characters on yield.

RESULTS AND DISCUSSION

The phenotypic and genotypic correlation co-efficients were estimated to assess the direction and magnitude of association existing among seed yield and its attributes, which are presented in Table 1. It was found that genotypic correlation co-efficients were higher than that of phenotypic correlation co-efficients in the present study, which indicated higher degree of correlation between two characters at genotypic levels and the magnitude of phenotypic correlation co-efficient decreased due to environment effect.

The phenotypic and genotypic correlation studies between yield and yield component trait pairs among 25 genotypes revealed that, number of pods plant[-1] ($r_p = 0.748^{**}$ and $r_g = 0.774^{**}$), number of clusters plant[-1] ($r_p = 0.739^{**}$ and $r_g = 0.833^{**}$), number of branches plant[-1] ($r_p = 0.666^{**}$ and $r_g = 0.755^{**}$), 100 seed weight ($r_p = 0.463^{**}$ and $r_g = 0.535^{**}$), days to 50 per cent flowering ($r_p = 0.393^{**}$ and $r_g = 0.463^{**}$) and days to maturity ($r_p = 0.365^{**}$ and r_g

$= 0.415^{**}$) recorded significant and positive association with seed yield plant[-1].These results were in confirmity with Chaudhary *et al.* (2020) and Vijayakumar *et al.* (2020) for number of clusters plant[-1] and number of pods plant[-1]; Chaudhary *et al.* (2020), Nagalakshmi *et al.* (2020) and Shanko *et al.* (2014) for number of branches plant[-1]; Vijayakumar *et al.* (2020) for 100 seed weight and Nagalakshmi *et al.* (2020) for days to 50 per cent flowering and days to maturity. The presence of a significant positive association between seed yield plant[-1] and most of its component traits indicates that the situation is favourable from a breeding standpoint, implying that selecting for one trait may result in correlated responses for improvement of other traits that are positively associated with seed yield plant[-1].

On contrary, number of seeds pod[-1] ($r_p = -0.122$ and $r_g = -0.099$) and plant height ($r_p = -0.206$ and $r_g = -0.235^*$) had a negative and non-significant association with seed yield plant[-1]. Further, pod length ($r_p = 0.175$ and $r_g = 0.180$) recorded positive and non-significant association with seed yield plant[-1]. The negative association of plant height and number of seeds pod[-1] with seed yield plant[-1] was in accordance with Panchta *et al.* (2020) for plant height; Sharma *et al.* (2017) and Shanko *et al.* (2014) for number of seeds pod[-1].

For developing an efficient breeding strategy, in addition to identification of yield attributing traits showing positive and significant association with grain yield, the information about the association of yield attributes with each other is also essential. Interrelationship between yield characters revealed that days to 50 per cent flowering had significant positive association with days to maturity, number of branches plant[-1], number of clusters plant[-1], pod length, number of seeds pod[-1] and 100 seed weight; days to maturity with number of branches plant[-1], number of clusters plant[-1], pod length, number of seeds pod[-1] and 100 seed weight; plant height with number of seeds pod[-1]; number of branches plant[-1] with number of clusters plant[-1], number of pods plant [-1], pod length and 100 seed weight; number of clusters plant[-1] with number of pods plant[-1] and 100 seed weight; pod length with number of seeds pod[-1] and 100 seed weight indicating the interdependency of these characters. Therefore, the genotypes with these characters could be considered during selection for improving the respective characters which simultaneously improves seed yield plant[-1].

Table 1. Phenotypic (r_p) and genotypic (r_g) correlation co-efficients of yield attributes with seedyield in cowpea

Characters		DM	PH	BPP	CPP	PPP	PL	SPP	100 SW	SYPP
DFF	r_p	0.920**	0.062	0.431**	0.319**	0.076	0.624**	0.500**	0.414**	0.393**
	r_g	0.945**	0.075	0.473**	0.360**	0.074	0.721**	0.625**	0.492**	0.463**
DM	r_p		-0.082	0.365**	0.257*	-0.033	0.714**	0.481**	0.543**	0.365**
	r_g		-0.088	0.390**	0.286*	-0.050	0.786**	0.593**	0.609**	0.415**
PH	r_p			-0.336**	-0.226*	-0.121	-0.163	0.317**	-0.537**	-0.206
	r_g			-0.375**	-0.274*	-0.117	-0.165	0.408**	-0.622***	-0.235**
BPP	r_p				0.716**	0.526**	0.310**	-0.057	0.505**	0.666**
	r_g				0.827**	0.557**	0.350**	-0.074	0.586**	0.755**
CPP	r_p					0.726**	0.057	-0.121	0.254*	0.739**
	r_g					0.796**	0.023	-0.219	0.319**	0.833**
PPP	r_p						-0.259*	-0.383**	0.019	0.748**
	r_g						-0.328**	-0.462**	0.032	0.774**
PL	r_p							0.511**	0.610**	0.175
	r_g							0.619**	0.670**	0.180
SPP	r_p								0.069	-0.122
	r_g								0.134	-0.099
100 SW	r_p									0.463**
	r_g									0.535**

*, ** Significant at 5% and 1% level, respectively

DFF : Days to 50% flowering   DM : Days to maturity   PH : Plant height   BPP : Number of branches plant[-1]

CPP : Number of clusters plant[-1]   PPP : Number of pods plant[-1]   PL : Pod length   100 SW : 100 Seed weight

SYPP : Seed yield plant[-1]

Table 2. Phenotypic (P) and genotypic (G) path co-efficients for seed yield and yield attributing characters in cowpea

Characters		DFF	DM	PH	BPP	CPP	PPP	PL	SPP	100 SW	SYPP
DFF	P	-0.096	0.186	0.009	0.005	0.052	0.050	0.014	0.008	0.165	0.393**
	G	-0.278	0.247	0.020	-0.024	0.094	0.050	-0.007	0.069	0.292	0.463**
DM	P	-0.088	0.202	-0.012	0.005	0.042	-0.022	0.016	0.008	0.217	0.365**
	G	-0.263	0.261	-0.023	-0.020	0.075	-0.034	-0.008	0.065	0.361	0.415**
PH	P	-0.006	-0.017	0.149	-0.004	-0.037	-0.080	-0.004	0.005	-0.214	-0.206
	G	-0.021	-0.023	0.264	0.019	-0.072	-0.080	0.002	0.045	-0.369	-0.235**
BPP	P	-0.041	0.074	-0.050	0.013	0.116	0.348	0.007	-0.001	0.202	0.666**
	G	-0.131	0.102	-0.099	-0.050	0.217	0.381	-0.004	-0.008	0.347	0.755**
CPP	P	-0.031	0.052	-0.034	0.009	0.162	0.479	0.001	-0.002	0.101	0.739**
	G	-0.100	0.075	-0.073	-0.042	0.262	0.546	0.000	-0.024	0.189	0.833**
PPP	P	-0.007	-0.007	-0.018	0.007	0.118	0.660	-0.006	-0.006	0.008	0.748**
	G	-0.020	-0.013	-0.031	-0.028	0.209	0.685	0.003	-0.051	0.019	0.774**
PL	P	-0.060	0.144	-0.024	0.004	0.009	-0.171	0.022	0.008	0.244	0.175
	G	-0.200	0.205	-0.044	-0.018	0.006	-0.225	-0.010	0.068	0.397	0.180
SPP	P	-0.048	0.097	0.047	-0.001	-0.020	-0.253	0.011	0.016	0.028	-0.122
	G	-0.174	0.155	0.108	0.004	-0.057	-0.316	-0.006	0.110	0.079	-0.099
100 SW	P	-0.040	0.109	-0.080	0.006	0.041	0.013	0.013	0.001	0.399	0.463**
	G	-0.137	0.159	-0.164	-0.030	0.084	0.022	-0.007	0.015	0.593	0.535**

*, ** Significant at 5% and 1% level, respectively
Phenotypic residual effect: 0.431 and Genotypic residual effect: 0.259

DFF : Days to 50% flowering
CPP : Number of clusters plant[-1]
SYPP : Seed yield plant[-1]

DM : Days to maturity
PPP : Number of pods plant[-1]

PH : Plant height
PL : Pod length

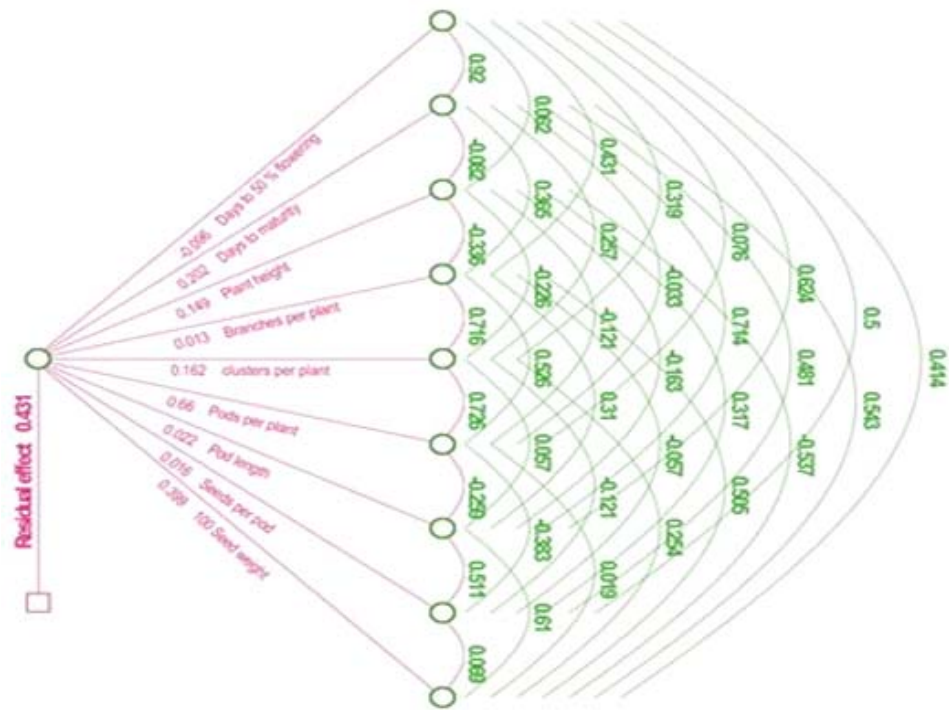BPP : Number of branches plant[-1]
100 SW : 100 Seed weight

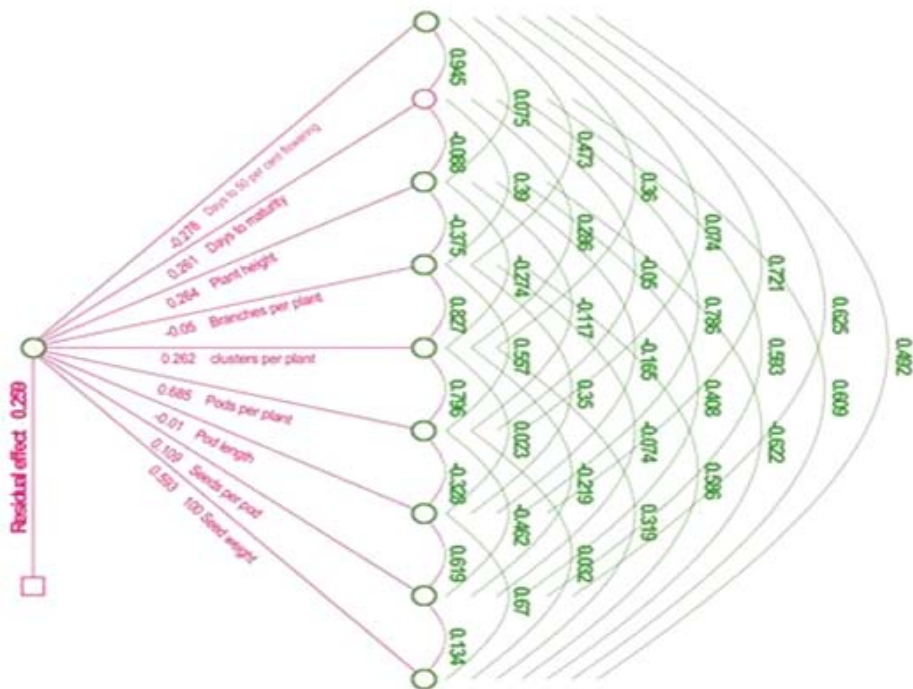**Figure 1. Phenotypic path diagram of yield and yield attributing character in cowpea.**

Figure 2. Genotypic path diagram of yield and yield attributing character in cowpea.

On the basis of correlation studies, it is suggested that more emphasis should be given on number of pods plant[-1], number of clusters plant[-1], number of branches plant[-1], 100 seed weight, days to 50 per cent flowering and days to maturity for improvement of seed yield in cowpea as these characters showed strong correlation with seed yield plant[-1].

Correlation alone can only reveals the direction and magnitude of the association between any two characters but the path coefficient analysis helps in partitioning the correlation into direct and indirect effects of various yield components on yield Therefore, correlation studies coupled with path coefficient analysis are a powerful tool to study the character association and their final impact on yield, which helps the selection procedure accordingly. The path co-efficient analysis of yield and yield attributes was analyzed and provided in Table 2. The phenotypic and genotypic path diagram of yield attributing characters is presented in Figure 1 and Figure 2, respectively. In the present study, it was noted that the characters number of pods plant[-1] (P = 0.660 and G = 0.685), 100 seed weight (P = 0.399 and G = 0.593), days to maturity (P = 0.202 and G = 0.261), number of clusters plant[-1] (P = 0.162 and G = 0.262), plant height (P = 0.149 and G = 0.264), number of seeds pod[-1] (P = 0.016 and G = 0.110), pod length (P = 0.022 and G = -0.010) and number of branches plant[-1] (P = 0.013 and G = -0.050) had positive direct effect on seed yield plant[-1] indicating that direct selection of these characters would be rewarding for improvement of yield.

Conversely, negative direct effect on seed yield plant[-1] was exhibited by days to 50 per cent flowering (P = -0.096 and G = -0.278) but its association with seed yield plant[-1] was found to be positive and significant which could be attributed to the indirect influence of days to maturity, 100 seed weight, number of pods plant[-1], number of clusters plant[-1], pod length, plant height, number of seeds pod[-1] and number of branches plant[-1] resulting in mutual cancellation of their negative effects. The negative direct effect of days to 50 per cent flowering on seed yield plant[-1] was in accordance with Panchta *et al.* (2020), Sharan *et al.* (2017), Khandait *et al.* (2016) and Nawab *et al.* (2008).

The phenotypic residual effect was 0.431, while genotypic residual effect was 0.259 indicating that the characters included in the present study are contributing 60 per cent of variability pertaining to the dependent variable *i.e.* seed yield plant[-1]. Hence, along with the characters under the consideration, some additional characters *viz.,* dry matter content, biological yield, harvest index, pod weight, pod yield plant[-1] and number of pods cluster[-1] which may also contribute to yield should also be included in future breeding programme.

Considering the nature and magnitude of character association and their direct and indirect effects, it can be concluded that the simultaneous improvement of seed yield plant[-1] is possible through the improvement of number of pods plant[-1], number of clusters plant[-1], number of branches plant[-1], 100 seed weight, days to 50 per cent flowering and days to maturity which also had positive direct effects on seed yield plant[-1]. It is therefore, suggested that preference should be given to these traits in the selection programme to improve seed yield in cowpea.

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