

Character Association and Path Coefficient Analysis for Yield and its Contributing Traits in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]

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ABSTRACT: Seed yield in pigeonpea is a complex and highly variable trait, controlled by several genes. The study of genetic association of the yield with other morphological characters may help to devise improved selection indices for yield improvement. Correlation coupled with path-coefficient analysis is a powerful tool to examine the character associations and their final effect on yield. The present study was undertaken with 75 pigeonpea genotypes using augmented randomized complete block design to ascertain the associations among yield and component characters and their effects by path analysis in pigeonpea during Kharif, 2020. Character association studies revealed that the number of pods per plant (NPP), 100 seed weight (HSW), and the number of seeds per pod (NSP) were strongly and positively associated with seed yield (Yield). Path coefficient analysis revealed that the number of pods per plant (NPP) had a high positive direct effect on seed yield (Yield), and therefore the number of pods per plant (NPP) may serve basis of selection for yield in pigeonpea.

Keywords: Pigeonpea, Correlation coefficient, Path coefficient, Morphological characters.

INTRODUCTION

Pigeonpea or red gram [*Cajanus cajan* (L.) Mills.] originated and domesticated in the Indian subcontinent (van der Maesen, 1990). After chickpea, it is India's second most significant legume. It is a major source of protein (~22%) to poor people and is very popular among small and marginal farmers due to low input and multiple uses as each part of the plant provides subsistence economic return to the farmers in form of food, fodder or firewood. Globally, it is being cultivated in tropical and subtropical countries of South Asia, Eastern Africa, and Central America. India alone (77%) is the major contributor to pigeonpea production worldwide followed by Malawi (11%), Myanmar (8%), Kenya (2%), and the United Republic of Tanzania (2%). According to FAO statistics (2019), worldwide pigeonpea is cultivated in about 4.5 million hectares area yielding approximately 3.68 million tons with an average yield of 832 kg/ha. Despite the substantial area under pigeonpea, productivity across the world is very low and stagnant as compared to other cereals. This low productivity can be attributed to the lack of effective selection indices for yield improvement while selecting parents for varietal development. Yield is a polygenic

character and is the outcome of the direct or indirect association of several component characters. It is significantly impacted by the environment and has a low heritability in general (Luz *et al.*, 2011; Mukherjee *et al.*, 2016; Pal *et al.*, 2018). Since direct selection for yield is less efficient, improvement in contributing traits is imperative. Knowledge of the extent and nature of association among yield and yield contributing traits are important for efficient selection for yield improvement (Meena *et al.*, 2017; Verma *et al.*, 2018; Baye *et al.*, 2020; Gaur *et al.*, 2020). Thus through correlation and path coefficient analysis, it would be possible to elucidate the most important characters that would aid in achieving progress under selection (Mani *et al.*, 1997; Zaman *et al.*, 2011). Because the component characters are interconnected, the change in one character influences the expression of other characters (Singh & Choudhury 1977). Therefore, correlation studies are critical in any selection programme since they reveal the degree and direction of the relationship between two or more contributing traits. The information from correlation analysis aids in the selection of characters for which selection will be rewarding in improving overall yield (Aparna and Deo, 2021). If two characters are found positively correlated,

improvement in one character will simultaneously improve the other character, and selection for that character will be rewarding in yield improvement. At molecular level, coupling phase linkage between genes leads to positive correlation whereas negative correlation is the consequence of repulsion phase linkage (Nadarajan and Gunasekaran 2008). Although correlation estimates help determine the components of complex traits, one cannot completely rely on correlation estimates since they do not illustrate the relative contribution of causal factors to seed yield, moreover, component characters themselves are interrelated and often affect their direct relationship with seed yield. Therefore, a simple correlation study is insufficient to fully comprehend the proportional relevance of each component character in determining grain yield (Dewey and Lu, 1959). Path coefficient analysis proposed by Wright (1921) and first applied to plant selection by Dewey and Lu in (1959), could provide a better insight into the contributing characters and their association with yield. The path coefficient is a standardized partial regression coefficient that assesses the cause-effect relationship as well as allows partitioning of the correlation coefficient into direct and indirect effects. Path analysis unfolds the nature of the association between component traits and yield, it reveals whether the association is due to their direct effect on yield or is a consequence of their indirect effect via some other character (Gautam *et al.*, 2021). In this way, correlation and path analysis helps in identifying traits on which selection pressure ought to be given for enhancing yield. Keeping the above facts in view, the present investigation was, therefore, undertaken to estimate association among different morphological traits and to assess their direct and indirect effects on seed yield of pigeonpea to develop suitable selection criteria for future pigeonpea breeding programs.

MATERIALS AND METHODS

Experimental material: Seventy pigeonpea genotypes along with five checks, *viz.* UPAS 120, PARAS, PUSA 992, AL 201, and PA 421 were used in the present investigation.

Description of Experimental site: All the 70 genotypes and five checks were evaluated at Norman E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand during *Kharif*, 2020. Pantnagar is located ~275 km northeast of New Delhi with an altitude of 243.84 m above mean sea level. This comes in the *Tarai* region of the Himalayas, in the foothills of the Shivalik range of mountains. The Pantnagar climate is humid to subtropical, with average minimum and maximum temperatures of 19°C and 36°C, respectively, and a mean annual rainfall of 1700 mm. The soil type is sandy clay loam, having a pH of 7.2, and the water table is high.

Experimental design and management: Considering each genotype as one treatment, the experiment was laid out in augmented randomized complete block design (Federer, 1956, 1961; Federer and Raghavrao,

1975) with ten blocks. Each block is planted with twelve genotypes including five checks. Each genotype was planted in a single 4 m long row. The row to row distance of 60 cm and plant to plant distance of 15 cm was maintained. The recommended packages of agronomic practices relevant to the crop were followed throughout the crop period.

Data collection: Data were recorded on five randomly selected plants on yield and its contributing traits *viz.*, plant height (cm) (PH), number of primary branches per plant (NPB), number of secondary branches per plant (NSB), number of pods per plant (NPP), number of seeds per pod (NSP), 100 seed weight (g) (HSW), and seed yield per plant (g) (Yield). However, data on days to 50% flowering (DFF) and days to maturity (DM) was recorded on a whole plot basis. The mean values computed from the observations for each block were utilized for statistical analysis.

Data analysis: Correlation analysis was performed following Pearson's method using R statistical software version 4.1.1 (R Development Core Team, 2020). The correlation matrix and heat map were generated by using the *Metan* package (Olivoto & Lucio, 2020) in R software. The estimation of correlation coefficients was done using the formula given by Searle (1961). The direct and indirect effects of each character for the dependent variable were computed with the help of path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). Seed yield was considered as the dependent variable and other yield components as the independent variables. Path analysis was carried out using *Indostat* software version 9.2.

RESULTS AND DISCUSSION

Correlation coefficient analysis

The knowledge of the degree of association among yield and its contributing traits *i.e.* correlation has great importance because it allows simultaneous improvement in yield and its component traits. The present investigation of the relationship between seed yield and associated traits helps to reveal their significance in pigeonpea breeding programs. The estimates of Pearson's correlations among nine studied characters are presented in Table 1. The correlation heatmap (Fig. 1) shows correlations in terms of color intensity, with dark red representing a high positive correlation (+1) and dark blue representing a strong negative correlation (-1). The seed yield exhibited a strong positive association with all of the investigated characters *viz.*, DFF (0.237*), DM (0.441***), NPB (0.367**), NSB (0.257*), PH (0.479***), NPP (0.985***), NSP (0.468***), and HSW (g) (0.799***). This showed that there was an inherent positive association among the characters, indicating that any improvement in these component traits may bring desirable change in the yield, and hence these characters may be useful for serving as a basis of selection for high yield. Similar trends for correlation between yield and different yield components were also reported earlier by Linge *et al.*, (2010); Prasad *et al.*, (2013); Saroj *et al.*, (2013); Meena *et al.*, (2017); Pal *et al.*, (2018); Verma *et al.*, (2018); Gaur *et al.*, (2020);

Sharma *et al.*, (2021) in pigeonpea. Inter-character correlation showed many significant positive associations between other yield contributing traits. DFF revealed a significant positive correlation with DM (0.358*) and NSP (0.3157**). DM showed a significant positive correlation with DFF (0.358*), NPB (0.2868*), NPP (0.425***), and HSW (g) (0.408***). NPB registered a significant positive correlation with DM (0.2868*), NPP (0.335**). NSB revealed a significant positive association with NPP (0.230*). PH (cm) exhibits a significant positive association with NPP (0.481***) and HSW (g) (0.331**). NPP showed

a positive correlation with PH (0.481***), DM (0.425***), NPB (0.335**), NSB (0.230*), and HSW (g) (0.788***). NSP was found to have a significant positive correlation with DFF (0.3157**). HSW (g) showed a positive significant association with DM (0.408***), PH (cm) (0.331**), and NPP (0.788***). These findings are in perfect agreement with the earlier findings of Sharma *et al.*, (2012); Vohra *et al.*, (2015); Singh *et al.*, (2016); Meena *et al.*, (2017); Pal *et al.* (2018); Chandirakala & Subbaraman (2010); Sodavadiya *et al.* (2009).

Table 1: Pearson's correlation coefficients for seed yield and agro-morphological characters.

Traits	DFD	DM	NPB	NSB	PH	NPP	NSP	100SW	Yield
DFD	1.0000	0.358**	0.0254	-0.0723	0.1465	0.216	0.3157**	0.132	0.237*
DM		1.0000	0.2868*	0.1681	0.1804	0.425***	0.2186	0.408***	0.441***
NPB			1.0000	0.1930	0.1849	0.335**	0.2053	0.223	0.367**
NSB				1.0000	0.0326	0.230*	0.0564	0.140	0.257*
PH					1.0000	0.481***	0.0772	0.331**	0.479***
NPP						1.0000	0.4316	0.788***	0.985***
NSP							1.0000	0.446	0.468***
100SW								1.0000	0.799***
YIELD									1.0000

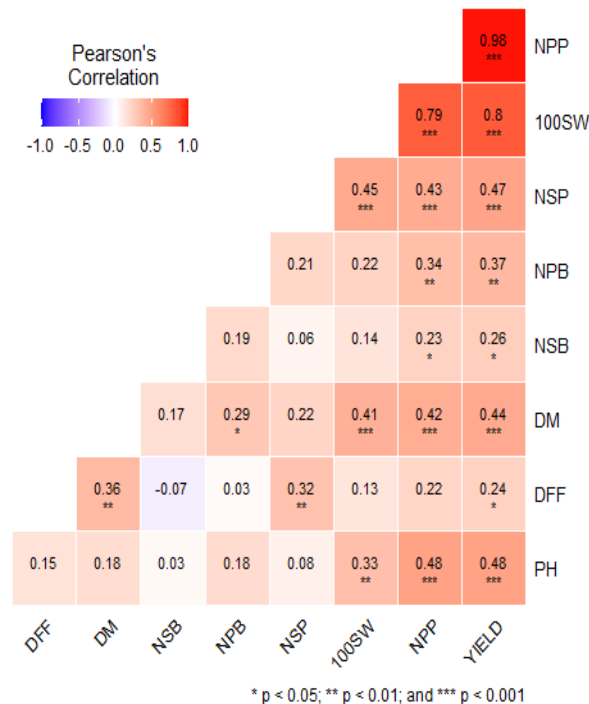


Fig. 1. A heatmap of Pearson's correlation coefficients among characters with red color denoting positive correlation while blue color representing a negative correlation coefficient.

Path coefficient analysis: In the present study path coefficient analysis was carried out considering the seed yield as the dependent character and yield attributes as the independent characters. The outcomes of path coefficient analysis are presented in Table 2. It is evident from the table that NPP had the highest positive direct effect on Yield (0.8824) followed by HSW (0.0617). The direct effect of DM, DFF, PH can be neglected due to very weak value. It is also evident from the table that NPP not only had high direct effect

on Yield (0.8824), it also exhibited high positive association with Yield (0.985***). It further indicated that these two characters are truly associated with each other since the direct effect and correlation of NSP are almost equal in magnitude and therefore an improvement in NSP will certainly bring an improvement in Yield. Similar findings were also reported by Saroj *et al.*, (2013); Verma *et al.*, (2018); Gaur *et al.*, (2020).

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