

Assessment of Genetic Variability, Correlation, and Path Coefficient for Yield and Its contributing traits in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]

ABSTRACT

The experimental material consisted of 155 pigeonpea genotypes sown in a Randomized Block Design (RBD) with three replications during the kharif, 2023-2024 crop season at the N. E. B. Crop Research Centre of G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. The genetic variance components, correlation, and path coefficient for seed yield and its components were estimated using these 155 pigeonpea genotypes. The highest phenotypic coefficient of variation (PCV) values (> 20%) were recorded for traits such as the number of pods per plant (26.45%), number of secondary branches per plant (22.72%), and seed yield per plant (20.27%). In contrast, the lowest PCV estimates (< 10%) were found for days to maturity (7.39%) and days to 50% flowering (6.73%). High estimates of the genotypic coefficient of variation (GCV) (> 20%) were recorded only for the number of pods per plant (23.6%). The lowest GCV estimates (< 10%) were observed for hundred seed weight (9.63%), number of seeds per pod (9.55%), plant height (9.49%), pod length (7.18%), days to maturity (6.85%), and days to 50% flowering (6.5%). The hundred seed weight showed a high positive direct effect on seed yield per plant (Genotypic = 0.58, Phenotypic = 0.47) along with a positive and significant correlation (Genotypic correlation coefficient, $r_g = 0.599$; Phenotypic correlation coefficient, $r_p = 0.485$). Based on this investigation, it is evident that exploring genetic variability, correlations, and path analyses provides a more effective approach for selecting superior cultivars for yield and related traits.

Keywords: Genetic variability; correlation; path coefficient; heritability; genetic advance, pigeonpea.

1. INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millspaugh], also known as Arhar, tur, and red gram, is an often-cross-pollinated crop with a diploid chromosome number of $2n = 2x = 22$ and a genome size of 833.07 Mb [1]. Globally, pigeonpea ranks sixth among pulses after pea, broad bean, lentil, chickpea, and common bean, cultivated over 5.4 million hectares and producing 4.49 million tons annually [2]. In India, pigeonpea is the second most significant pulse crop after chickpea, covering 4.72 million hectares and yielding 4.31 million tons annually with an average yield of 914 kg/ha, contributing 15%

to the nation's total pulse output. Pigeonpea grain is a rich source of protein (21%), carbohydrates (67%), and lipids (2.3%) [3]. With its extensive deep root system, pigeonpea enhances soil quality and structure by fixing atmospheric nitrogen. Despite its moderate to high genetic variability, pigeonpea has a lower yield potential compared to cereal crops. Seed yield in pigeonpea, a complex trait influenced by the number of pods per plant and fruiting branches per plant [4], necessitates analyzing the extent and nature of variability and the inheritance patterns of various yield-amplifying traits [5]. Current research on pigeonpea focuses on exploring its morphological and molecular diversity, identifying stable fertility restorers and maintainers, and mapping fertility restorer genes [6]. Additionally, studies address biotic and abiotic stresses affecting pigeonpea yield [7; 8]. The effectiveness of breeding programs depends significantly on the level of genetic variability available for economically important traits. Breeders utilize genetic variability components such as GCV, PCV, heritability, genetic advance, correlation, and path coefficients at various stages of crop improvement programs. Classifying variability into heritable and non-heritable components can further enhance the effect of selection. Heritability estimates are crucial as they help determine the environmental influence on genotype expression and character reliability. However, heritability estimates alone are insufficient for predicting improvement from selection; combining heritability with genetic advance is necessary to forecast the specific impact of selecting the most appropriate individuals [9]. Understanding genetic variability and trait associations is vital for selecting elite genotypes and exploiting heterosis breeding programs. While genetic variability and correlation studies provide valuable insights, they may not precisely determine the relative importance of direct and indirect influences of each component trait on grain yield. In such cases, path coefficient analysis is essential for delineating the direct and indirect effects of independent variables on the dependent variable. Correlation and path analysis are thus instrumental in identifying suitable selection criteria for improving yield. This investigation aimed to assess the genetic variability, correlation, and direct and indirect effects of different influencing characters on seed yield in pigeonpea.

2. MATERIAL AND METHODS

The present experiment was conducted during Kharif 2023-24 at experimental field area of N. E. B. Crop Research Centre of G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand in randomized complete block design with three replications. Experimental material comprised of 155 genotypes of pigeonpea. Selfed seeds of each genotype were grown in a single row of 4 m length with a spacing of 60 cm between the rows and 20 cm between the plants within rows. The observations were recorded on five randomly taken competitive plants in each genotype in each replication for ten different morphological characters, viz., number of primary branches per plant (NPB), number of secondary branches per plant (NSB), number of pods per plant (NPP), plant height (cm) (PH), pod length (cm) (PL), number of seeds per pod (NSP), days to 50% flowering (DFF), days to maturity (DM), 100 seed weight (g) (HSW), and seed yield per plant (g) (SYP). The mean data were subjected for analysis of variance [10] and various genetic parameters viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance were estimated [11; 12; 13; 14]. The procedures suggested by Fisher (1954) [15] and Al-Jibouriet *al.* (1958) [16] were used in the estimation of genotypic (r_g) and phenotypic (r_p) correlation coefficients from the phenotypic and genotypic components of variances and covariances. Path co-efficient analysis was worked out to estimate the direct and indirect effects of different traits on the yield [17].

3. RESULTS AND DISCUSSION

The boxplot for the ten traits used for the experiment is presented in **Figure 1**. The analysis of variance (ANOVA) conducted for the year 2023-24 encompassed ten distinct characters. The mean square values attributable to genotypes exhibited significant differences across all traits evaluated. This indicates substantial genetic variability within the experimental material, which is crucial for further enhancement of pigeonpea. The observed significant differences in all traits underscore the predominance of genetic variability in the experimental material, thereby confirming the appropriateness of the selected materials for this investigation. The significance of ANOVA for these traits was earlier also reported by Pandey *et al.* [18], Pal *et al.* [19], Gaur *et al.* [20] and Yadav *et al.* [21].

3.1 Genotypic coefficient of variation

Genotypic coefficient of variation (GCV) was found to be ranging between 6.5% for days to 50% flowering to 23.6% for number of pods per plant. The highest GCV was observed for number of pods per plant (23.6%) followed by number of secondary branches per plant (18.72%), seed yield per plant (17.7%) and number of primary branches per plant (13.73%). The GCV was moderate (10-20%) for number of secondary branches per plant, seed yield per plant, and number of primary branches per plant while low (<10%) in the case of hundred seed weight, number of seeds per pod, plant height, pod length, days to maturity, and days to 50% flowering (**Figure 2**).

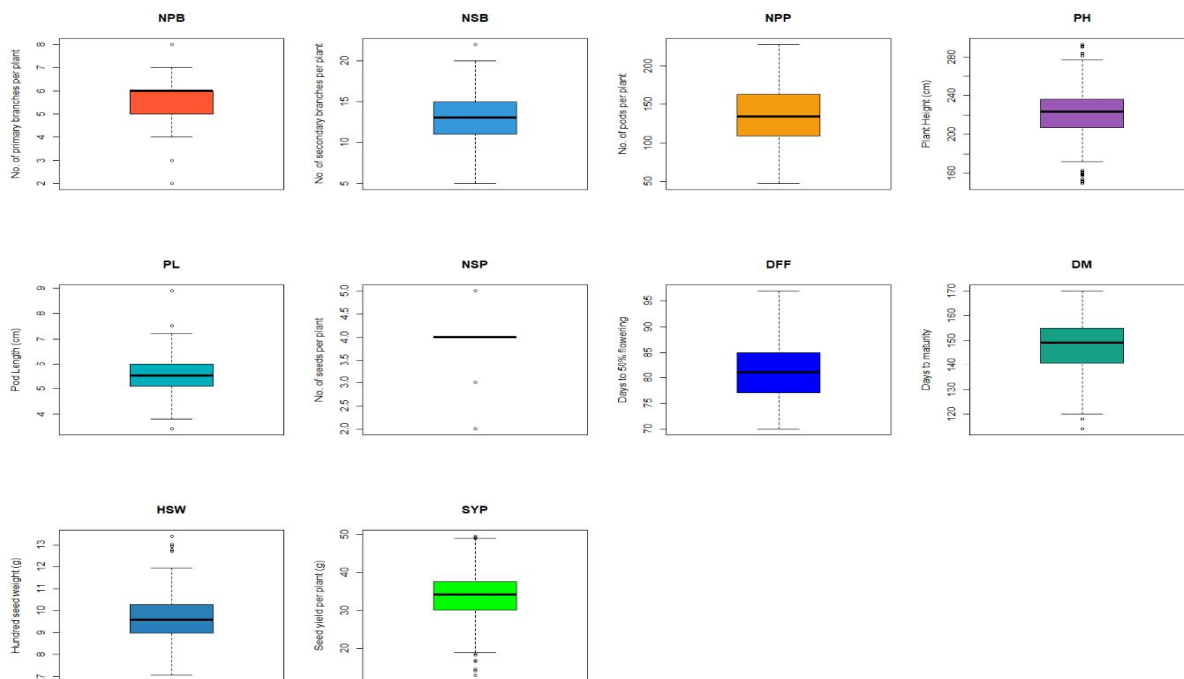


Fig. 1. Boxplot for ten quantitative traits used in the study displaying the variation in 155 genotypes across three replications.

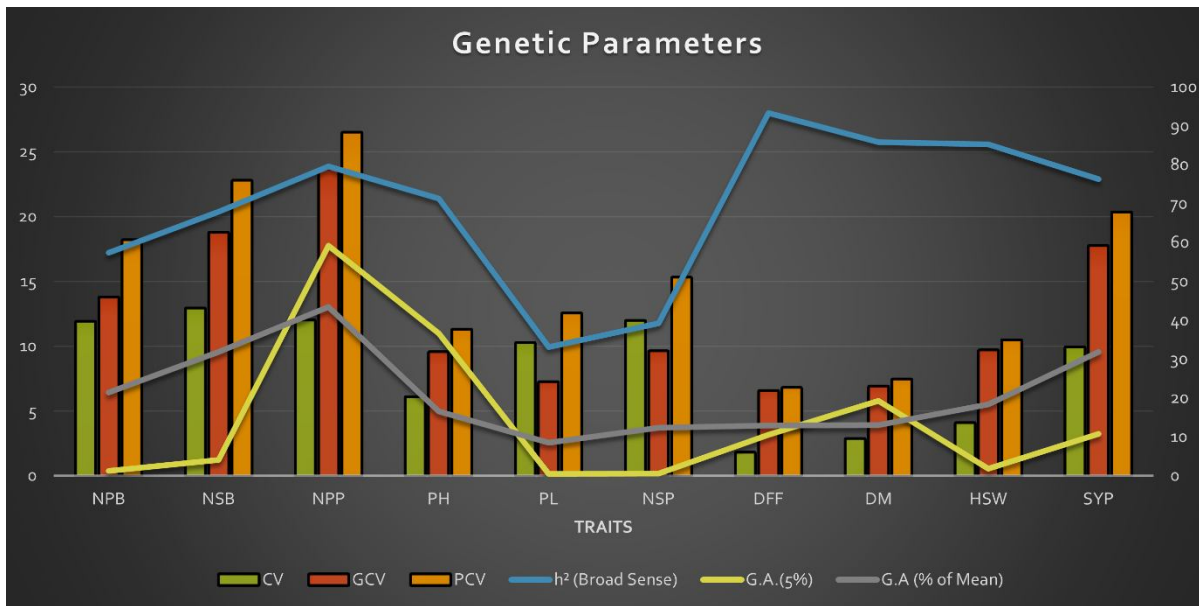


Fig. 2. Graph displaying genetic variability parameters for ten quantitative traits.

Presence of variability for different traits was also reported by Mallesh *et al.* [22] and Reddy and Jayamani [23] in cultivated pigeonpea. The expression of variable characters was found to be influenced by environment as genotypic coefficient of variation was reported to be less than respective phenotypic coefficient for all the traits. A higher estimate of PCV than the corresponding GCV estimates for different characters in pigeonpea were also reported earlier by Rangareet *et al.* [24]; Pandey *et al.* [25]; Pal *et al.* [19]; Gaur *et al.* [20], and Yadav *et al.* [21]. In the present study, high estimates of both the PCV and GCV were recorded for trait like number of pods per plant which indicated that the sufficient genetic variability existed in the experimental genotypes for this trait and that selection may be effective in bringing desirable improvements in this trait. These findings are in conformity with the earlier findings for these traits in pigeonpea by Pal *et al.* [19]; Gaur *et al.* [20], Sharma *et al.* [26]; Lakhoteet *et al.* [27]; and Yadav *et al.* [21].

3.2 Heritability and genetic advance

The analysis revealed high heritability estimates (> 60%) for several traits: days to 50% flowering (93.31%), days to maturity (85.77%), hundred seed weight (85.2%), number of pods per plant (79.61%), seed yield per plant (76.25%), plant height (71.29%), and number of secondary branches per plant (67.89%). Conversely, moderate heritability estimates (30-60%) were observed for the number of primary branches per plant (57.32%), number of seeds per plant (39.18%), and pod length (33.03%). These findings are consistent with previous reports in pigeonpea by Pal *et al.* [19]; Bisht [28]; Gaur *et al.* [20], and Yadav *et al.* [21]. High heritability suggests a strong potential for genetic improvement of these traits through selection. Additionally, high genetic advance as a percentage of the mean (>20%) was noted for the number of pods per plant (43.37%), seed yield per plant (31.84%), number of secondary branches per plant (31.78%), and number of primary branches per plant (21.41%). In contrast, low genetic advance as a percentage of the mean (<10%) was observed for pod length (8.5%). These results indicate that traits such as the number of pods per plant, seed yield per plant, number of secondary branches per plant, and primary branches per plant are predominantly influenced by additive genes, making selection an effective strategy for their improvement. The genetic advance, in conjunction with heritability

as a percentage of the mean, offers a comprehensive understanding of the inheritance patterns and the efficacy of selection for the traits of interest [14]. Comparable findings for genetic advance estimates have been reported by Sharma *et al.* [26], Lakhoteet *et al.* [27], Pal *et al.* [19], Gaur *et al.* [20], and Yadav *et al.* [21].

In the current study, the trait of the number of pods per plant exhibited higher values of genotypic coefficient of variation (GCV %), heritability, and genetic advance as a percentage of mean (GAM), indicating that this trait is predominantly influenced by additive gene action and is likely to respond to phenotypic selection. Johnson *et al.* [14] have suggested that combining heritability estimates with genetic advance as a percentage of the mean provides a more accurate prediction of the selection outcome compared to heritability alone (**Figure 1**). High genetic advance as a percentage of the mean (>20%) was observed for the number of pods per plant (43.37%), seed yield per plant (31.84%), number of secondary branches per plant (31.78%), and number of primary branches per plant (21.41%), whereas pod length exhibited low genetic advance as a percentage of the mean (<10%), specifically 8.5%. These findings imply that traits such as the number of pods per plant, seed yield per plant, number of secondary branches per plant, and number of primary branches per plant are predominantly controlled by additive genes, making selection effective for their improvement. Similar results regarding the estimates of genetic advance for various traits have been reported by Sharma *et al.* [26], Gaur *et al.* [20], and Yadav *et al.* [21]. High heritability paired with moderate genetic advance was noted for days to 50% flowering, seed yield per plant, and days to maturity. Conversely, traits like pod length, number of primary branches per plant, and number of seeds per pod showed moderate heritability with low genetic advance. The number of secondary branches per plant and hundred seed weight exhibited high heritability but low genetic advance. These results suggest that phenotypic selection for traits with low heritability and low genetic advance is ineffective due to the predominance of non-additive gene actions.

3.3 Correlation and path coefficient analysis

Correlation and path analysis were employed to estimate the nature and magnitude of associations among various traits influencing yield. These analyses facilitate the understanding of the underlying causes of associations, which can then be leveraged in the development of selection criteria for yield enhancement. Generally, the correlation analysis indicated that genotypic correlations were higher than phenotypic correlations, with the directions of genotypic and phenotypic correlations being similar for most character combinations. This trend of congruent genotypic and phenotypic correlation coefficients in both sign and magnitude has been previously reported in pigeonpea by Bisht *et al.* [28], Gaur *et al.* [20], and Yadav *et al.* [21]. Almeida *et al.* [29] also demonstrated that genetic factors contributed more to the correlations than environmental factors, resulting in higher genotypic correlations compared to phenotypic correlations. The masking and modifying effects of the environment on trait associations likely account for the lower phenotypic correlations relative to genotypic correlations [30]. Correlation coefficients among all the traits are presented in **Figure 3**.

In general, seed yield per plant exhibited a positive and significant phenotypic association with the number of secondary branches per plant, hundred seed weight, days to maturity, and days to 50% flowering. Several researchers, including Gaur *et al.* [20] and Bisht *et al.* [28], have also reported positive and significant associations between these traits and seed yield per plant. Days to maturity and seed yield per plant showed the highest significant correlations i.e. four, with the component traits at the phenotypic level. The trait days to 50% flowering exhibited a significant and positive correlation with days to maturity ($r_p = 0.683$ and $r_g = 0.749$) at both genotypic and phenotypic levels and with seed yield per plant ($r_p = 0.096$) at the phenotypic level. Plant height demonstrated a significant and positive correlation with the number of seeds per pod at both genotypic and phenotypic levels. The number of pods per plant exhibited a significant and positive

association with the number of primary branches per plant and the number of secondary branches per plant. Similar findings regarding these traits in pigeonpea have been reported by Pal *et al.* [19], Gaur *et al.* [20], Yadav *et al.* [21], Rangareet *al.* [24], and Sharma *et al.* [26]. As yield is a complex trait influenced by numerous yield-contributing traits, selection for a specific trait will also induce changes in other related contributing traits. Thus, understanding the direction and magnitude of associations among component traits is crucial for improving yield in the desired direction.



Fig. 3. Correlation heatmap displaying genotypic (upper triangle) and phenotypic (lower triangle) correlation coefficients for the ten quantitative characters. * and ** represent significance at 5% and 1% respectively.

Correlation analysis provides insight into the relationships among traits but does not distinguish between direct and indirect effects. Path coefficient analysis, on the other hand, partitions the observed correlation coefficients into direct and indirect effects of yield and its components. The concept of path coefficient was first introduced by Wright [31] and further developed by Dewey and Lu [17]. This method is used to elucidate the extent of relationships, treating seed yield per plant as the dependent variable while considering the other traits as independent variables. The results of the path coefficient analysis, detailing direct and indirect effects, are presented in Table 1. The highest positive direct effect on seed yield per plant was observed for hundred seed weight (Genotypic = 0.58, Phenotypic = 0.47), followed by the number of primary branches per plant (Genotypic = 0.14, Phenotypic = 0.10), as illustrated in Figure 4. The nearly equal magnitudes of both phenotypic and genotypic correlation coefficients and the direct effect of hundred seed weight on seed yield indicate a true relationship between these traits. Hence, direct selection for improved hundred seed weight will likely enhance seed yield. The present results indicate that, for achieving high yield, selection should prioritize primary branches per plant and hundred seed weight, which show high direct positive effects along with positive correlations. Negative direct effects on seed yield per plant were observed for the number of pods per plant, plant height, and pod length. The positive association of primary branches per plant, secondary branches per plant, days to 50% flowering, and hundred seed

weight with seed yield per plant is attributed to their positive direct effects. Similar findings have been reported by Kothimbireet *al.* [32], Singh *et al.* [5], and Yadav *et al.* [21]. The remaining traits exhibited exceptionally low direct effects on seed yield and were non-significantly associated with seed yield, except for days to maturity. The low magnitude of the direct effect of various traits has also been reported previously by Rangareet *al.* [24], Sharma *et al.* [26], Lakhoteet *al.* [27], Pandey *et al.* [18], Pal *et al.* [19], and Yadav *et al.* [21].

Table 1. Path coefficient analysis showing the direct and indirect effects of various characters on seed yield per plant at both genotypic (G) and phenotypic (P) levels in pigeonpea.

Traits		Primary branches	Secondary branches	Pods per plant	Plant height	Pod length	Seeds per pod	Days to 50% flowering	Days to maturity	100 seed weight	Correlation with SYP
Primary branches	G	0.1413	0.0131	-0.0020	-0.0004	-0.0052	-0.0023	-0.0060	-0.0062	-0.0284	0.103
	P	0.1034	0.0055	0.0004	0.0010	-0.0003	0.0012	-0.0040	-0.0032	-0.0200	0.084
Secondary branches	G	0.0228	0.0808	-0.0060	0.0002	-0.0025	0.0019	-0.0044	-0.0007	0.0612	0.153
	P	0.0090	0.0628	0.0014	-0.0003	-0.0003	-0.0011	-0.0044	0.0000	0.0393	0.106*
Pods per plant	G	0.0259	0.0439	-0.0110	-0.0001	-0.0035	0.0067	-0.0007	-0.0027	-0.0177	0.041
	P	0.0113	0.0255	0.0034	-0.0001	0.0000	0.0011	-0.0008	-0.0016	-0.0095	0.029
Plant height	G	0.0104	-0.0025	-0.0001	-0.0051	-0.0056	0.0261	-0.0040	-0.0019	0.0298	0.047
	P	0.0064	-0.0010	0.0000	0.0166	-0.0012	0.0121	-0.0031	-0.0011	0.0199	0.048
Pod length	G	0.0139	0.0038	-0.0007	-0.0005	-0.0528	0.0320	-0.0051	-0.0004	0.0135	0.003
	P	0.0015	0.0007	0.0000	0.0009	-0.0228	0.0335	-0.0029	-0.0010	-0.0062	0.004
Seeds per pod	G	-0.0032	0.0016	-0.0007	-0.0013	-0.0168	0.1006	-0.0030	0.0006	0.0553	0.133
	P	0.0015	-0.0009	0.0000	0.0025	-0.0096	0.0799	-0.0010	-0.0003	0.0142	0.086
Days to 50% flowering	G	-0.0118	-0.0049	0.0001	0.0003	0.0037	-0.0041	0.0727	0.0278	0.0280	0.111
	P	-0.0058	-0.0038	0.0000	-0.0007	0.0009	-0.0011	0.0717	0.0169	0.0181	0.096*
Days to maturity	G	-0.0237	-0.0015	0.0008	0.0003	0.0006	0.0016	0.0544	0.0371	0.1065	0.176*
	P	-0.0134	-0.0001	-0.0002	-0.0007	0.0009	-0.0010	0.0490	0.0247	0.0772	0.136**
100 seed weight	G	-0.0069	0.0085	0.0003	-0.0003	-0.0012	0.0096	0.0035	0.0068	0.5786	0.599**
	P	-0.0044	0.0052	-0.0001	0.0007	0.0003	0.0024	0.0027	0.0040	0.4743	0.485**

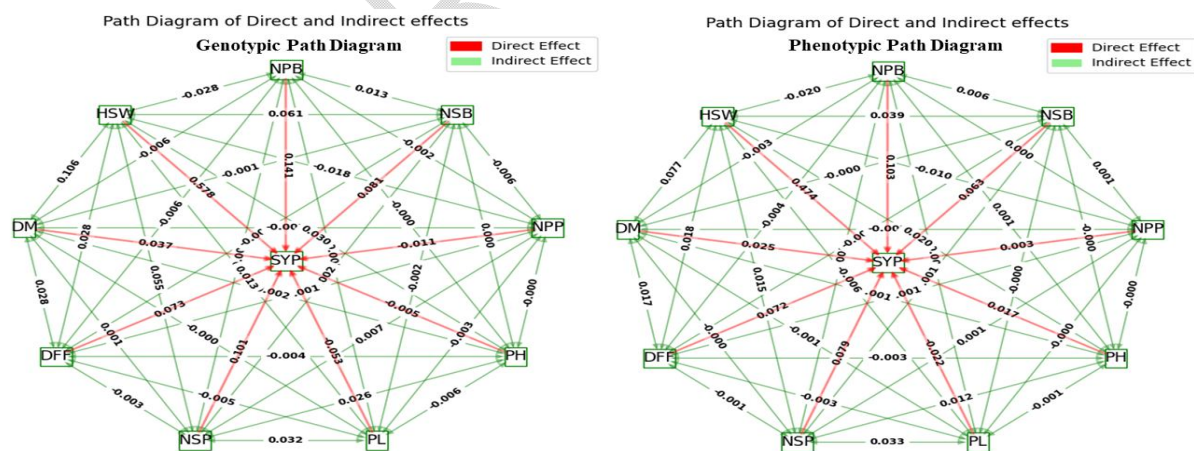


Fig. 4. Path diagram for seed yield per plant as a dependent variable and its contributing characters as independent variables for both genotypic and phenotypic levels.

4. CONCLUSION

The investigation into genetic variability parameters, correlation, and path analysis has pinpointed the number of pods per plant, secondary branches per plant, days to 50% flowering, days to maturity, and hundred seed weight as the primary yield determinants. Targeted selection for these traits is recommended to enhance seed yield in pigeonpea.

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