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Correlation and Path Analysis of Quantitative and Quality Traits in Short-duration Pigeonpea (*Cajanus cajan* L. Millsp.) Genotypes under Kerala Agroclimatic Conditions

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Pigeonpea (*Cajanus cajan* L. Millsp.), a vital pulse crop, faces yield improvement challenges due to the complex inheritance of productivity traits. The study aims to investigate the relationship between yield and various phenological, quantitative, and quality traits. The study was conducted during the 2023 *kharif* season at the College of Agriculture, Vellayani, evaluating thirty short-duration pigeonpea genotypes in a randomized complete block design (RCBD). Correlation analysis revealed that seed yield per plant was positively and significantly associated with number of pods

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per plant, biological yield, harvest index, primary branches, and seeds per pod, while phenol content showed a significant negative correlation. Path analysis indicated that biological yield, flowering traits, and harvest index exerted strong positive direct effects on seed yield, whereas days to bud initiation and plant height contributed negatively. These results indicate that selecting for traits like biological yield, flowering attributes, harvest index, pods per plant, and seeds per pod offers a practical and effective breeding strategy for enhancing yield in short-duration pigeonpea varieties suited to Kerala's agroclimatic conditions.

Keywords: Pigeonpea; association; correlation; path analysis.

1. INTRODUCTION

"Red gram [*Cajanus cajan* (L.) Millsp.], also known globally as pigeonpea, is a major pulse crop grown extensively in tropical and subtropical regions for its edible grains. It is recognized by various vernacular names in different parts of the world" (Saxena, 2008). The term "pigeonpea" was first documented in Barbados, where the crop was traditionally cultivated on marginal lands and its seeds served as feed for pigeons. In India, it is widely referred to as red gram, tur, or arhar, and is among the earliest legumes domesticated in the subcontinent.

"Agronomically, pigeonpea is a hardy, fast-growing, and drought-resilient crop. It is a diploid species (2n = 2x = 22) with an estimated genome size of 833.07 Mb" (Varshney *et al.*, 2012). "Belonging to the family Fabaceae, subfamily Papilionoideae, and tribe Phaseoleae, it is placed in the subtribe Cajaninae, where *Cajanus cajan* is the only cultivated species. Other related genera in the Phaseoleae tribe include *Phaseolus*, *Vigna*, and *Lablab" (Pandey et al, 2016)*.

"From a nutritional perspective, pigeonpea is an important dietary component in vegetarian populations. It is consumed both as a green vegetable and in the form of decorticated splits ("dhal"). The dry seeds contain about 20–22% protein, 67% carbohydrates, 1.9% fat, and 6.6% crude fibre. Additionally, they are rich in minerals such as calcium (120.8 mg/100 g), magnesium (122 mg/100 g), copper (1.3 mg/100 g), iron (3.9 mg/100 g), and zinc (2.3 mg/100 g)" (Saxena *et al.*, 2010). Its amino acid profile, particularly lysine, methionine, and tryptophan, complements cereal-based staples, thereby providing a balanced and protein-rich diet.

Apart from its nutritional importance, pigeonpea plays a crucial role in sustainable agriculture and rural livelihoods. The crop has multiple uses: young leaves and tops are used as animal fodder, the crop residues enrich soil fertility when incorporated as green manure, and the woody stems serve as firewood, thatching, and basket material. Its deep root system, coupled with symbiotic association with *Bradyrhizobium* spp., facilitates biological nitrogen fixation, thereby enhancing soil productivity. These attributes make pigeonpea vital in smallholder farming systems and in addressing food and nutrition security challenges under erratic rainfall and changing climatic conditions.

Globally, pigeonpea is cultivated predominantly in the Kharif season, either as a sole crop or in association with cereals and legumes. "Its ability to thrive in low-input and stress-prone environments has increased its importance as a climate-resilient crop" (Mula, 2012). "India remains the leading producer, where pigeonpea is the second most important pulse after chickpea. Presently, it is cultivated on about 4.06 million hectares, producing 3.31 million tonnes annually, with an average productivity of 814 kg/ha" (FAOSTAT, 2023). Major pigeonpea-growing states include Maharashtra, Karnataka, Madhya Pradesh, Uttar Pradesh, and Gujarat. Even though red gram is a staple food in Kerala, very little of it is grown commercially.

Pigeonpea is a vital pulse crop, particularly in subsistence farming systems. However, despite substantial research efforts, its productivity remains relatively low. Grain yield in pigeonpea is a complex quantitative trait, governed by polygenes and strongly influenced by environmental factors. Therefore, yield per se is not a reliable selection criterion for genetic improvement. Understanding the nature and extent of correlation coefficients among yield components enables breeders to identify traits that warrant greater emphasis during selection and to develop suitable criteria for simultaneous improvement of seed yield and associated attributes. In addition to yield-related traits, quality traits such as protein, methionine, phenol, and tannin were evaluated due to their impact on nutritional value and seed quality. Protein and methionine contribute to dietary amino acid balance, while phenol and tannin influence antioxidant properties and digestibility. Including these traits allows identification of genotypes with both high productivity and superior nutritional quality, aiding in the breeding of improved short-duration pigeonpea cultivars (Yadav *et al.*, 2024).

Nevertheless, when several characters are interrelated, correlation analysis alone does not clearly reveal which traits directly contribute to yield and which act indirectly through other attributes. Path coefficient analysis is used as a potent biometrical approach to overcome this constraint. By separating the link into direct and indirect impacts, it makes it easier to comprehend how each character contributes to yield.

In this context, the study was undertaken to assess the association among quantitative and quality traits, their direct effects on grain yield, and their indirect contributions through interrelated characters in short-duration pigeonpea genotypes under the agro-climatic conditions of Kerala.

2. MATERIALS AND METHODS

2.1 Experimental Site

The study was carried out at the College of Agriculture, Vellayani, Thiruvananthapuram, Kerala, during the *kharif* season of 2023 (June–September). The experimental site is located in the humid tropics of southern Kerala.

2.2 Experimental Material

Thirty short-duration pigeonpea (*Cajanus cajan* L. Millsp.) genotypes were used in the study. These included ICPL 11249, ICPL 11256, ICPL 11259, ICPL 11263, ICPL 11273, ICPL 20338, ICPL 20340, ICPL 20341, ICPL 11242, ICPL 11279, ICPL 11296, ICPL 11298, ICPL 11300, ICPL 11318, ICPL 11326, ICPL 20326, ICPL 20327, ICPL 20328, ICPL 20329, ICPL 20333, ICPL 11255, ICPL 11301, MN5, ICPL 22045, ICPL 22077, ICPL 22084, ICPL 22110, ICPL 22081, APK 1, and Pusa Arhar 16. All ICPL lines were obtained from ICRISAT, Hyderabad, whereas APK 1 and Pusa Arhar 16 were originated from TNAU, Coimbatore, and IARI, New Delhi, respectively.

2.3 Experimental Design and Layout

The study employed a randomized complete block design (RCBD) with three replications to evaluate the genotypes. Each genotype was planted in two 3-meter rows, spaced 40 cm apart, with 20 cm between plants within rows. Standard agronomic practices for pigeonpea cultivation were followed to ensure optimal crop growth.

2.4 Data Collection

Observations were recorded on sixteen traits:

- **Phenological traits:** days to flower bud initiation, days to flower initiation, days to 50% flowering, and days to physiological maturity (recorded on a plot basis).
- **Quantitative traits:** plant height (cm), number of primary branches per plant, number of seeds per pod, number of pods per plant, seed yield per plant (g), 100-seed weight (g), biological yield (g), and harvest index (%).
- **Quality traits:** protein content (%), phenol content (mg/g), tannin content (mg/g), and methionine content (mg/g).

Five randomly chosen plants per replication were used to gather data for quantitative and quality attributes.

2.5 Statistical Analysis

According to Fisher (1954) and Al-Jibouri et al. (1958), variance and covariance components were used to estimate genotypic and phenotypic correlation coefficients. Using the Wright (1921) and Dewey and Lu (1959) methods, path coefficient analysis was used to separate the association into direct and indirect effects.

3. RESULTS AND DISCUSSION

3.1 Correlation Analysis

For seed yield and related variables, Tables 1 and 2 display the genotypic and phenotypic correlation coefficients. Seed yield per plant exhibited significant and positive associations with several traits, including days to flower bud initiation (r_g=0.676; r_p=0.631), days to flower initiation (r_g=0.649; r_p=0.545), days to 50% flowering (r_g=0.673; r_p=0.554), plant height (r_g=0.509; r_p=0.444), number of primary branches per plant (r_g=0.488; r_p=0.478), number of pods per plant (r_g=0.795; r_p=0.752), number of seeds per pod (r_g=0.412; r_p=0.376), biological yield (r_g=0.877; r_p=0.803), harvest index (r_g=0.315; r_p=0.315), protein content (r_g=0.364; r_p=0.246), tannin content (r_g=0.215; r_p=0.208), methionine content (r_g=0.245; r_p=0.238) and days to physiological maturity (r_g=0.817; r_p=0.624). Similar findings were reported by Merentoshi (2020) for days to 50 percent flowering, days to maturity, primary branches per plant, plant height and number of pods per plant; Burhade *et al.* (2025) for harvest index; Kandarkar *et al.* (2020) for number of seeds per pod. The association with 100-seed weight was positive but not significant (r_g=0.2; r_p=0.186). Similar finding was reported by Hemavathy *et al.* (2019) this trait. In contrast, phenol content showed a significant negative correlation with seed yield per plant (r_g= -0.238; r_p= -0.219).

At the genotypic level, several noteworthy associations were observed. Days to physiological maturity was positively correlated with all traits except phenol (r_g= -0.587) and tannin (r_g= -0.021) content. Methionine content exhibited positive correlations with most traits but showed negative associations with days to flower initiation (r_g= -0.08), harvest index (r_g= -0.204), tannin content (r_g= -0.314) and days to physiological maturity (r_g= -0.021).Tannin content was positively associated with most characters except number of seeds per pod (r_g= -0.109), 100-seed weight (r_g= -0.003), methionine content (r_g= -0.314) and days to physiological maturity (r_g= -0.021).

Phenol content had negative associations with most traits, except for number of primary branches (r_g= 0.021), protein content (r_g= 0.043), tannin content (r_g= 0.075) and methionine content (r_g= 0.053). Protein content was positively correlated with all traits except number of primary branches per plant (r_g= -0.119) and harvest index (r_g= -0.066). Similarly, 100-seed weight showed positive correlations with most traits but had negative associations with number of pods per plant (r_g= -0.085), phenol content (r_g= -0.250) and tannin content (r_g= -0.003).

Harvest index showed positive correlations with most characters but was negatively related to number of seeds per pod (r_g= -0.08), biological yield (r_g= -0.091), protein content (r_g= -0.066), phenol content (r_g= -0.092) and methionine content (r_g= -0.204). Number of seeds per pod was positively associated with all traits except harvest index (r_g= -0.08), phenol content (r_g= -0.149) and tannin content (r_g= -0.109). Likewise, number of pods per plant had positive associations with most traits, except 100-seed weight (r_g= -0.085) and phenol content (r_g= -0.152).

While there was a minor negative correlation with days to 50% flowering (r_g=-0.006), plant height (r_g=-0.013), and protein content (r_g=-0.119), the number of primary branches per plant was favourably linked with the majority of the characteristics. Plant height and days to 50% flowering exhibited positive associations with most traits, except number of primary branches (r_g= -0.013 and r_g= -0.006, respectively) and phenol content (r_g= -0.131 and r_g= -0.512, respectively). Days to flower initiation was positively correlated with all characters except phenol content (r_g= -0.521) and methionine content (r_g= -0.08). Similarly, days to flower bud initiation had positive correlations with most traits but a strong negative association with phenol content (r_g= -0.531).

Overall, genotypic correlations were greater than phenotypic ones, suggesting that environmental influences decreased the manifestation of these connections at the phenotypic level whereas genetic factors primarily govern them.

According to the correlation analysis, a number of characteristics, including the number of pods per plant, biological yield, harvest index, number of major branches per plant, and number of seeds per pod, were significantly and favourably correlated with seed production per plant. These traits exhibited strong genotypic and phenotypic associations with yield, indicating their pivotal role in determining productivity. Therefore, selection based on pods per plant, biological yield, harvest index, primary branches, and seeds per pod would provide a more reliable approach for identifying and developing high-yielding pigeonpea genotypes.

3.2 Path Coefficient Analysis

Path coefficient analysis was utilized to dissect the genotypic correlations between seed yield and its contributing traits, partitioning them into direct and indirect effects. Specifically, seed yield per plant was treated as the dependent variable, while other traits were considered independent variables, allowing for a nuanced understanding of their relationships and contributions to seed yield The estimates of direct and indirect effects of these traits on seed yield are presented in Table 3, and the corresponding genotypic path diagram is illustrated in Fig. 1.

Table 1. Estimation of genotypic correlation coefficient in pigeon pea

	Genotypic correlation matrix															
	DFBI	**DFI**	**DFF**	**PH**	**NPB**	**NPPP**	**NSPP**	**BY**	**HI**	**TW**	**Protein**	**Phenol**	**Tannin**	**Methionine**	**DM**	**SYPP**
DFBI	1	0.967**	0.871**	0.570**	0.136	0.460**	0.376**	0.600**	0.13	0.441**	0.626**	-0.531**	0.132	0.09	0.812**	0.676**
DFI		1	0.967**	0.624**	0.018	0.421**	0.251*	0.524**	0.148	0.351**	0.669**	-0.521**	0.127	-0.008	0.877**	0.649**
DFF			1	0.676**	-0.006	0.446**	0.203	0.503**	0.205	0.056	0.559**	-0.512**	0.112	0.002	0.960**	0.673**
PH				1	-0.013	0.545**	0.345**	0.545**	0.183	0.152	0.506**	-0.131	0.062	0.134	0.587**	0.509**
NPB					1	0.572**	0.398**	0.437**	0.204	0.14	-0.119	0.021	0.179	0.053	0.078	0.488**
NPPP						1	0.308*	0.758**	0.224*	-0.085	0.12	-0.152	0.268*	0.03	0.519**	0.795**
NSPP							1	0.499**	-0.08	0.419**	0.349**	-0.149	-0.109	0.177	0.328*	0.412**
BY								1	-0.091	0.209*	0.430**	-0.145	0.126	0.307*	0.647**	0.877**
HI									1	0.084	-0.066	-0.092	0.317*	-0.204	0.121	0.315*
TW										1	0.300*	-0.250*	-0.003	0.315*	0.066	0.2
Protein											1	0.043	0.066	0.151	0.350**	0.364**
Phenol												1	0.075	0.053	-0.587**	-0.238*
Tannin													1	-0.314*	-0.021	0.215*
Methionine														1	0.192	0.245*
DM															1	0.817**
SYPP																1

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

Note: DFBI- Days to flower bud initiation, DFI- Days to flower initiation, DFF- Days to 50 % flowering, PH- Plant height (cm), NPB- Number of primary branches per plant, NPPP- Number of pods per plant, NSPP- Number of seeds per pod, SYPP- Seed yield per plant (g), BY- Biological yield (g), HI- Harvest index (%), TW- 100 seed weight (g), Protein- Total protein content (%), Phenol- Total phenol content (mg/g), Tannin- Total tannin content (mg/g), Methionine- Total methionine content (mg/g) and DM- Days to physiological maturity

Table 2. Estimation of phenotypic correlation coefficient in pigeon pea

Phenotypic correlation matrix																
	DFBI	**DFI**	**DFF**	**PH**	**NPB**	**NPPP**	**NSPP**	**BY**	**HI**	**TW**	**Protein**	**Phenol**	**Tannin**	**Methionine**	**DM**	**SYPP**
DFBI	1	0.887**	0.722**	0.520**	0.115	0.421**	0.325*	0.526**	0.125	0.346**	0.480**	-0.511**	0.115	0.092	0.687**	0.631**
DFI		1	0.832**	0.522**	-0.002	0.345**	0.219*	0.434**	0.104	0.198	0.421**	-0.455**	0.102	0.005	0.750**	0.545**
DFF			1	0.431**	0.003	0.349**	0.163	0.391**	0.174	0.133	0.390**	-0.415**	0.08	0.009	0.780**	0.554**
PH				1	-0.009	0.481**	0.265*	0.467**	0.097	0.071	0.377**	-0.122	0.056	0.123	0.442**	0.444**
NPB					1	0.550**	0.353**	0.401**	0.2	0.1	-0.131	0.021	0.175	0.052	0.069	0.478**
NPPP						1	0.269*	0.693**	0.196	-0.057	0.086	-0.145	0.261*	0.034	0.395**	0.752**
NSPP							1	0.433**	-0.055	0.325*	0.247*	-0.133	-0.101	0.156	0.221*	0.376**
BY								1	-0.183	0.162	0.326*	-0.125	0.124	0.284*	0.471**	0.806**
HI									1	0.074	-0.082	-0.084	0.273*	-0.181	0.08	0.315*
TW										1	0.253*	-0.191	-0.015	0.239*	0.092	0.186
Protein											1	0.029	0.055	0.12	0.269*	0.246*
Phenol												1	0.08	0.053	-0.497**	-0.219*
Tannin													1	-0.313*	-0.042	0.208*
Methionine														1	0.161	0.238*
DM															1	0.624**
SYPP																1

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

Note: DFBI- Days to flower bud initiation, DFI- Days to flower initiation, DFF- Days to 50 % flowering, PH- Plant height (cm), NPB- Number of primary branches per plant, NPPP- Number of pods per plant, NSPP- Number of seeds per pod, SYPP- Seed yield per plant (g), BY- Biological yield (g), HI- Harvest index (%), TW- 100 seed weight (g), Protein- Total protein content (%), Phenol- Total phenol content (mg/g), Tannin- Total tannin content (mg/g), Methionine- Total methionine content (mg/g) and DM- Days to physiological maturity

Table 3. Direct and indirect effect of associated traits on seed yield per plant at genotypic level

	Genotypic path matrix															
	DFBI	**DFI**	**DFF**	**PH**	**NPB**	**NPPP**	**NSPP**	**BY**	**HI**	**TW**	**Protein**	**Phenol**	**Tannin**	**Methionine**	**DM**	**Correlation with SYPP**
DFBI	**-0.48**	-0.464	-0.418	-0.274	-0.065	-0.221	-0.181	-0.288	-0.063	-0.212	-0.301	0.255	-0.064	-0.043	-0.39	0.676**
DFI	0.555	**0.574**	0.581	0.358	0.01	0.242	0.145	0.301	0.085	0.201	0.384	-0.299	0.073	-0.005	0.503	0.649**
DFF	0.418	0.485	**0.48**	0.324	-0.003	0.214	0.098	0.241	0.098	0.027	0.268	-0.246	0.054	0.001	0.461	0.673**
PH	-0.261	-0.286	-0.31	**-0.458**	0.006	-0.25	-0.158	-0.25	-0.084	-0.07	-0.232	0.06	-0.029	-0.061	-0.269	0.509**
NPB	-0.019	-0.003	0.001	0.002	**-0.14**	-0.08	-0.056	-0.061	-0.029	-0.02	0.017	-0.003	-0.025	-0.008	-0.011	0.488**
NPPP	0.114	0.105	0.111	0.135	0.142	**0.248**	0.077	0.188	0.056	-0.021	0.03	-0.038	0.067	0.008	0.129	0.795**
NSPP	0.07	0.047	0.038	0.064	0.074	0.058	**0.186**	0.093	-0.015	0.078	0.065	-0.028	-0.021	0.033	0.061	0.412**
BY	0.474	0.414	0.397	0.431	0.345	0.599	0.394	**0.789**	-0.072	0.165	0.339	-0.114	0.1	0.242	0.511	0.877**
HI	0.05	0.056	0.078	0.07	0.078	0.086	-0.031	-0.035	**0.38**	0.032	-0.025	-0.035	0.121	-0.078	0.046	0.315*
TW	0.037	0.029	0.005	0.013	0.012	-0.007	0.035	0.018	0.007	**0.083**	0.025	-0.021	-0.001	0.026	0.006	0.2
Protein	-0.132	-0.141	-0.118	-0.106	0.025	-0.026	-0.074	-0.09	0.014	-0.063	**-0.21**	-0.009	-0.014	-0.032	-0.074	0.364**
Phenol	-0.099	-0.097	-0.095	-0.025	0.004	-0.029	-0.028	-0.027	-0.017	-0.047	0.008	**0.186**	0.014	0.01	-0.109	-0.238*
Tannin	-0.002	-0.002	-0.002	-0.001	-0.002	-0.003	0.002	-0.002	-0.004	0	-0.001	-0.001	**-0.011**	0.004	0.001	0.215*
Methionine	0.015	-0.002	0.001	0.022	0.009	0.005	0.029	0.05	-0.033	0.052	0.025	0.009	-0.051	**0.163**	0.031	0.245*
DM	-0.063	-0.068	-0.074	-0.046	-0.006	-0.04	-0.026	-0.05	-0.01	-0.005	-0.027	0.046	0.002	-0.015	**-0.077**	0.817**

Note: DFBI- Days to flower bud initiation, DFI- Days to flower initiation, DFF- Days to 50 % flowering, PH- Plant height (cm), NPB- Number of primary branches per plant, NPPP- Number of pods per plant, NSPP- Number of seeds per pod, SYPP- Seed yield per plant (g), BY- Biological yield (g), HI- Harvest index (%), TW- 100 seed weight (g), Protein- Total protein content (%), Phenol- Total phenol content (mg/g), Tannin- Total tannin content (mg/g), Methionine- Total methionine content (mg/g) and DM- Days to physiological maturity

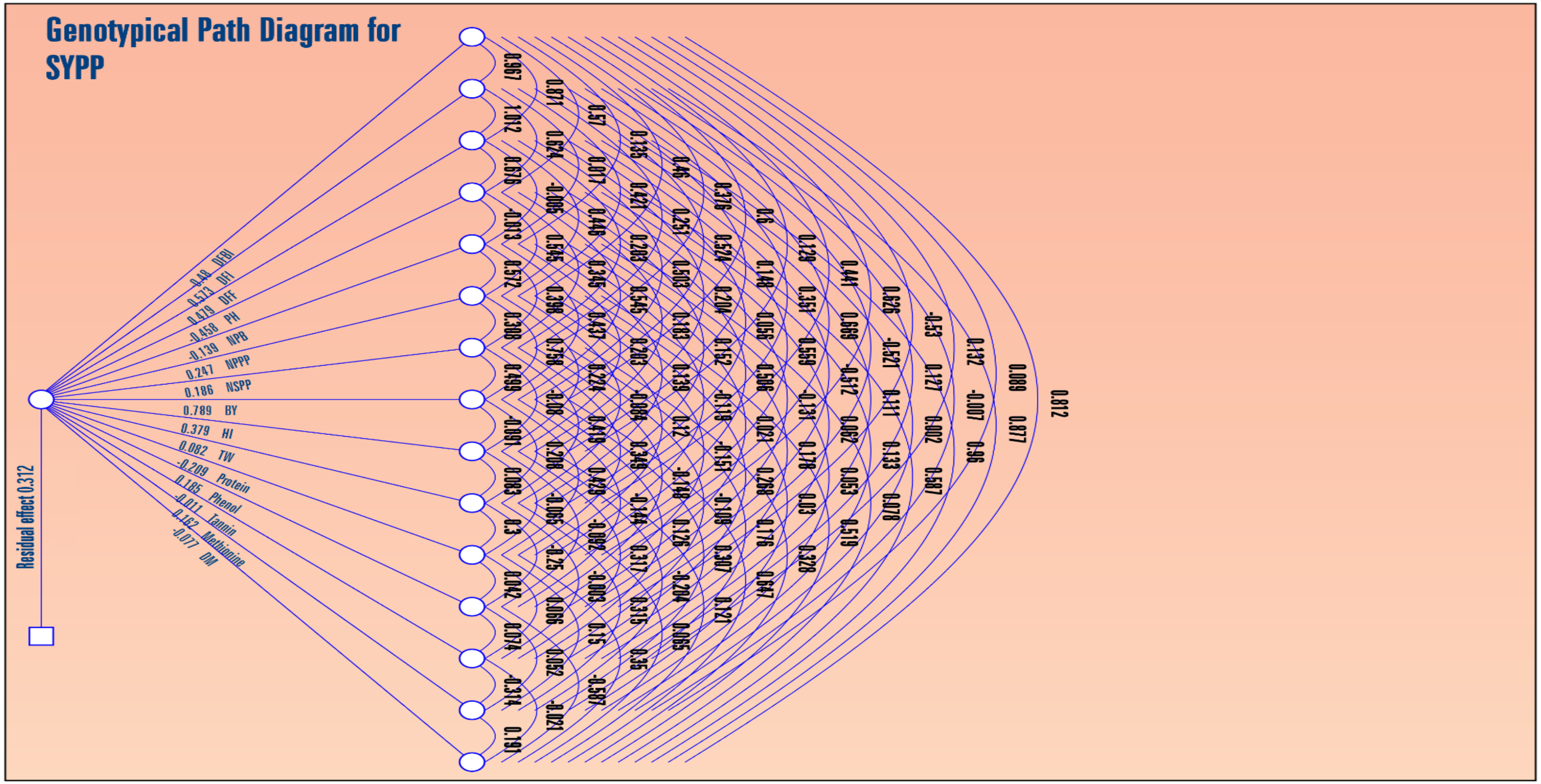

Fig. 1. Genotypic path diagram showing the direct and indirect effect of different characters on seed yield/plant along with residual effect

Biological yield (0.789) had the most significant positive direct impact on seed yield, followed by days to flower initiation (0.574), days to 50% flowering (0.480), and harvest index (0.380), consistent with findings by Pandey et al. (2016) and Akshaya et al. (2023). Protein content (0.248) contributed moderately, while traits like number of seeds per pod (0.186), phenol content (0.186), and methionine content (0.163) had relatively low positive effects. In contrast, 100-seed weight (0.083) had a negligible positive influence, aligning with reports by Chisa et al. (2021) and Tharageshwari and Hemavathy (2020).

In contrast, days to flower bud initiation (-0.480) and plant height (-0.458) had substantial negative direct impacts on yield, consistent with Kandarkar et al.'s (2020) findings for plant height. Protein content (-0.210) and number of primary branches per plant (-0.140) also negatively affected yield, with the latter's effect being relatively low, aligning with Lakhote et al.'s (2015) report on vegetable-type pigeonpea. Meanwhile, days to physiological maturity (-0.077) and tannin content (-0.011) had negligible negative effects.

Days to 50% flowering had the highest positive indirect impact on seed yield through several traits, particularly days to flower initiation (0.485), followed by days to physiological maturity (0.461), days to flower bud initiation (0.418), plant height (0.324), protein content (0.268), biological yield (0.241), and number of pods per plant (0.214). Conversely, it had negative indirect effects via phenol content (-0.246) and number of primary branches per plant (-0.003).

Biological yield had maximum positive indirect effect on seed yield via., number of pods per plant (0.599) followed by days to physiological maturity (0.511), days to flower bud initiation (0.474), plant height (0.431), days to flower initiation (0.414), days to 50% flowering (0.397), number of seeds per pod (0.394), number of primary branches (0.345), protein content (0.339), methionine content (0.242) and 100-seed weight (0.165) whereas negative indirect effect on seed yield via., phenol content (-0.114) and harvest index (-0.072).

The path analysis revealed that biological yield, days to flower initiation, days to 50% flowering, and harvest index were the key traits directly influencing seed yield in pigeonpea, emerging as crucial determinants of crop productivity and highlighting potential targets for selection in breeding programs In addition, traits such as days to 50% flowering and biological yield exerted substantial indirect effects on yield through their associations with flowering traits, plant height, pods per plant, and protein content. In contrast, traits such as days to flower bud initiation, plant height, and number of primary branches per plant had detrimental effects on yield, exerting either direct or indirect negative influences.

4. CONCLUSION

The present investigation on thirty short-duration pigeonpea genotypes grown in kerala revealed that seed yield per plant exhibited significant and positive associations with several yield-contributing traits, particularly number of pods per plant, biological yield, harvest index, number of primary branches per plant, and number of seeds per pod. Genotypic correlations were generally stronger than phenotypic ones, indicating that these associations were predominantly governed by genetic factors, though influenced to some extent by the environment.

Path coefficient analysis confirmed that biological yield, days to flower initiation, days to 50% flowering, and harvest index had significant positive direct impacts on seed yield, making them ideal selection criteria for enhancing yield potential. Conversely, traits like days to flower bud initiation, plant height, and number of primary branches per plant showed negative direct effects, indicating limited value in direct selection for yield enhancement.

Overall, the findings emphasize that improvement in pigeonpea productivity can be effectively achieved by prioritizing genotypes with higher biological yield, favorable flowering traits, and better harvest index, while simultaneously considering pods per plant and seeds per pod. These results provide useful insights for breeders in formulating effective selection strategies and in developing high-yielding, short-duration pigeonpea cultivars suitable for diverse agro-climatic conditions.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

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