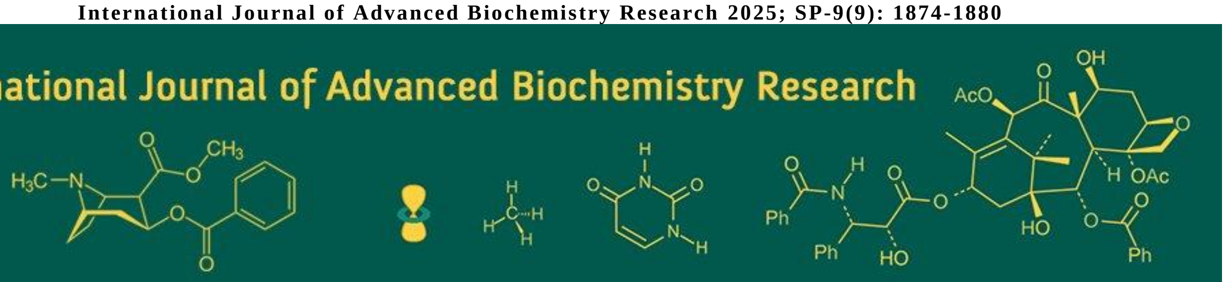
International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2025): 5.29
IJABR 2025; SP-9(9): 1874-1880
www.biochemjournal.com
Received: 20-08-2025
Accepted: 21-09-2025

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Correlation and path analysis studies in F_3 generation of cowpea [*Vigna unguiculata* (L.) Walp.]

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DOI: https://www.doi.org/10.33545/26174693.2025.v9.i9Sx.5784

Abstract

The present investigation was undertaken to analyze the association between yield and yield-attributing traits and to assess their direct and indirect effects on seed yield in cowpea (*Vigna unguiculata* (L.) Walp.). A total of 72 F_3 lines along with five checks were evaluated during *Rabi* 2024-25 in an Augmented Block Design at the College of Agriculture, Dapoli. Correlation analysis at both genotypic and phenotypic levels revealed that seed yield per plant had significant and positive associations with number of branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, test weight, and harvest index. Path coefficient analysis, also carried out at both genotypic and phenotypic levels, indicated that number of pods per plant, harvest index, and number of clusters per plant exerted the highest positive direct effects on seed yield. These traits can be effectively targeted in selection strategies to improve seed yield in cowpea breeding programs. The strong genotypic correlations and direct effects suggest the predominance of additive gene action. Thus, early generation selection based on these key traits would accelerate the development of high-yielding cowpea genotypes with desirable agronomic profiles.

Keywords: Cowpea, correlation, path analysis and yield attributes

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is an important pulse crop grown widely in India and other tropical regions for its nutritional value, adaptability, and role in sustainable agriculture. It is a rich source of protein, minerals, and dietary fiber making it an essential component in the diets of rural and urban populations. In addition to its nutritional benefits, cowpea improves soil fertility through nitrogen fixation and is well suited for cultivation in drought-prone and low-input environments.

In regions like the Konkan, cowpea is commonly cultivated during the *rabi* season in rice fallows, offering a profitable option to farmers. However, the genetic improvement of cowpea has been relatively limited due to the use of narrow genetic base and lack of systematic selection for complex traits such as seed yield. Seed yield is influenced by several interrelated plant characters, which makes its direct improvement a challenging task.

To improve seed yield effectively, it is important to understand the relationships between yield and its contributing traits. Correlation analysis helps in identifying the strength and direction of association among traits, while path coefficient analysis provides a clearer picture by separating these associations into direct and indirect effects. This approach helps in identifying the most important traits that directly contribute to yield and can be used for effective selection in early segregating generations.

The present investigation was undertaken in the F_3 generation of cowpea to assess the association between seed yield and related quantitative traits at both genotypic and phenotypic levels and to determine the direct and indirect contributions of these traits through path coefficient analysis. The study aims to identify key characters that can be used as selection criteria for the development of high-yielding cowpea genotypes.

Materials and Methods

The present investigation was conducted during *Rabi* 2024-25 at the Educational and Research Farm, Department of Agricultural Botany, College of Agriculture, Dapoli, District

Ratnagiri, Maharashtra. The experimental material for the present study comprised 72 F_3 generation lines of cowpea, developed at the Department of Agricultural Botany, College of Agriculture, Dapoli. These 72 F_3 lines, along with five check varieties, were evaluated using an Augmented Block Design (ABD) comprising four blocks. Each block contained 18 lines and all five checks, which were repeated across the blocks for comparison. Each entry was sown in two rows, with a spacing of 30 cm between rows and 30 cm between plants. Each row contained 15 plants, making a total of 30 plants per line.

Cultural Practices

The crop was grown under uniform agronomic conditions. Land preparation was done through standard tillage practices to ensure a fine tilth. Fertilizers were applied at the rate of 25 kg nitrogen and 50 kg phosphorus (P_2O_5) per hectare. Half the nitrogen dose was applied at sowing, and the remaining half was applied 30 days after sowing. Recommended plant protection measures and irrigation were provided as required to ensure healthy crop growth.

Statistical Analysis

- Genotypic and phenotypic correlation coefficients were calculated to estimate the degree of association between seed yield per plant and other quantitative traits using the method suggested by Johnson *et al*. (1955) [8].
- Path coefficient analysis was performed following the method of Dewey and Lu (1959) [2] to partition the correlation coefficients into direct and indirect effects, with seed yield per plant considered as the dependent variable. The residual effect was also computed to account for the unexplained variation in seed yield.
- For interpreting the magnitude of direct and indirect effects from path analysis, the classification proposed by Lenka and Mishra (1973) was followed:
- **Negligible**: 0.00 - 0.09
- **Low**: 0.10 - 0.19
- **Moderate**: 0.20 - 0.29
- **High**: 0.30 - 0.99
- **Very High**: >1.00

Results and Discussion

Correlation analysis

Phenotypic Correlation Coefficient

Seed yield per plant showed highly significant positive correlation with test weight (0.346), number of pods per cluster (0.387), number of seeds per pod (0.444), number of branches per plant (0.453), number of clusters per plant (0.625), number of pods per plant (0.670) and harvest index (0.958). It had significant positive correlation with pod length (0.273). It showed non-significant positive correlation with days to maturity (0.039), iron content (0.045), days to 50% flowering (0.051) and days to first flowering (0.060). Seed yield per plant showed non-significant negative correlation with plant height (-0.155) and protein content (-0.059). The similar results were observed by Sogalad *et al.* (2022) [16] and Gawande *et al.* (2024) [6] for number of clusters per plant, number of pods per plant, number of pods per cluster, number of seeds per pod, pod length, test weight and harvest index.

Number of branches per plant exhibited highly significant positive correlation with number of pods per cluster (0.296), number of seeds per pod (0.300), seed yield per plant (0.453), number of clusters per plant (0.489), harvest index (0.492) and number of pods per plant (0.571). Number of clusters per plant showed highly significant positive correlation with harvest index (0.593), seed yield per plant (0.625) and number of pods per plant (0.822). Number of pods per cluster showed highly significant positive correlation with Seed yield per plant (0.387), harvest index (0.398) and number of pods per plant (0.415). Number of pods per plant showed highly significant positive correlation with harvest index (0.642) and seed yield per plant (0.670). Harvest index exhibited highly significant positive correlation with seed yield per plant (0.958). Protein content had non-significant negative correlation with iron content (-0.063) and seed yield per plant (-0.059). Iron content had non-significant positive correlation with seed yield per plant (0.045).

Genotypic Correlation Coefficient

Seed yield per plant exhibited highly significant positive correlation with pod length (0.383), test weight (0.432), number of seeds per pod (0.553), number of pods per cluster (0.565), number of branches per plant (0.620), number of clusters per plant (0.715), number of pods per plant (0.901) and harvest index (0.996). It had non-significant positive correlation with iron content (0.031), days to 50 per cent flowering (0.085), days to first flowering (0.093), days to maturity (0.101) and non-significant negative correlation with protein content (-0.076) and plant height (-0.197). The similar results were observed by Sogalad *et al.* (2022) [16] and Gawande *et al.* (2024) [6] for number of clusters per plant, number of pods per plant, number of pods per cluster, number of seeds per pod, pod length, test weight and harvest index.

Number of branches per plant exhibited highly significant positive correlation with number of seeds per pod (0.346), pod length (0.356), number of pods per cluster (0.445), number of clusters per plant (0.522), harvest index (0.599), seed yield per plant (0.620) and number of pods per plant (0.828). Number of clusters per plant showed highly significant positive correlation with pod length (0.328), harvest index (0.672), seed yield per plant (0.715) and number of pods per plant (0.975). Number of pods per cluster showed highly significant positive correlation with number of seeds per pod (0.313), test weight (0.332), number of pods per plant (0.369), harvest index (0.544) and seed yield per plant (0.565). Number of pods per plant showed highly significant positive correlation with harvest index (0.806), seed yield per plant (0.901) Harvest index exhibited highly significant positive correlation with seed yield per plant (0.996). Protein content had non-significant negative correlation with seed yield per plant (-0.076). Iron content had non-significant positive correlation with seed yield per plant (0.031).

Path coefficient analysis

Phenotypic Path Coefficient Analysis

At the phenotypic level, harvest index exerted the highest positive direct effect on seed yield per plant, with a value of 0.9195, indicating that this trait contributed substantially and directly to yield. Number of clusters per plant and number of pods per plant also showed positive direct effects, with values of 0.0894 and 0.0457 respectively, although their contributions were relatively lower. Similar results were reported by Bhagwati *et al.* (2017) [1], Patil *et al.*

(2021) [15] and Gawande *et al.* (2024) [6]. Protein content (0.0184), test weight (0.0146), days to first flowering (0.0143), days to maturity (0.0322), and number of pods per cluster (0.0143) recorded negligible but positive direct effects on seed yield per plant. The similar results were obtained by Jogdhande *et al.* (2017) [7], Patil *et al.* (2021) [15] and Pareet *et al.* (2022) [14]. Negative direct effects were observed for days to 50% flowering (-0.0540), number of branches per plant (-0.0513), pod length (-0.0323), number of seeds per pod (-0.0388), plant height (-0.03), and iron content (-0.0023) suggesting that these traits had minimal direct contributions to seed yield at the phenotypic level. The result was in conformation with reports of Dinesh *et al.* (2017) [3] and Sogalad *et al.* (2022) [16].

Overall, harvest index emerged as the most influential trait contributing directly to yield, while most other traits contributed through indirect effects.

Genotypic Path Coefficient Analysis

At the genotypic level, harvest index recorded the highest positive direct effect on seed yield per plant, with a value of 0.6245, followed by days to maturity (0.4649) and number of clusters per plant (0.3288) on seed yield per plant. Bhagwati *et al*. (2017) [1], Pareet *et al.* (2022) [14] and Gawande *et al.* (2024) [6] observed similar results in cowpea for positive direct effect on seed yield per plant. Days to 50 per cent flowering (0.133), number of branches per plant (0.1322) and protein content (0.143) had low positive direct effect. Similar results were reported by Jogdhande *et al.* (2017) [7] and Lonare *et al.* (2024). Number of pods per cluster (0.0291), number of pods per plant (0.0244), pod length (0.0461), number of seeds per pod (0.0212) and test weight (0.076) had negligible positive direct effect on seed yield per plant. Patil *et al.* (2021) [15], Pareet *et al.* (2022) [14] and Gawande *et al.* (2024) [6] observed similar results for seed yield per plant. Plant height (-0.1272) and iron content (-0.1873) had low negative direct effect on seed yield per plant. Similar results were reported by Jogdhande *et al.* (2017) [7] for plant height on seed yield per plant. Days to first flowering had high negative direct effect (-0.6976). Pareet *et al.* (2022) [14] observed similar negative direct effect of days to first flowering on seed yield per plant.

This analysis indicates that days to maturity, harvest index, and number of clusters per plant had the strongest direct contributions to seed yield per plant at the genotypic level, and should be considered as important selection criteria in cowpea improvement programs.

Table 1: Estimates of phenotypic correlation coefficient between different characters in cowpea.

Traits	D1	D50	DM	NBPP	NCPP	NPPC	NPPP	PH	PL	NSPP	TW	HI	PC	IC	SYPP
D1	1	0.790**	0.720**	0.126	0.210	0.047	0.212	-0.084	-0.041	-0.033	-0.053	0.040	0.094	0.015	0.060
D50		1	0.838**	0.163	0.189	0.028	0.168	0.012	-0.004	-0.033	-0.031	0.054	0.112	0.104	0.051
DM			1	0.147	0.124	0.032	0.097	-0.005	0.029	0.032	-0.003	0.042	0.048	0.196	0.039
NBPP				1	0.489**	0.296**	0.571**	-0.013	0.158	0.300**	0.091	0.492**	-0.164	0.101	0.453**
NCPP					1	0.119	0.822**	0.066	0.168	0.233*	0.116	0.593**	-0.071	0.211	0.625**
NPPC						1	0.415**	-0.058	0.183	0.203	0.216	0.398**	0.013	0.045	0.387**
NPPP							1	-0.019	0.158	0.188	0.113	0.642**	-0.051	0.149	0.670**
PH								1	-0.119	-0.176	-0.212	-0.145	0.070	0.135	-0.155
PL									1	0.593**	0.138	0.332**	0.108	0.069	0.273*
NSPP										1	0.049	0.515**	0.107	-0.022	0.444**
TW											1	0.341**	-0.091	-0.192	0.346**
HI												1	-0.071	0.060	0.958**
PC													1	-0.063	-0.059
IC														1	0.045
SYPP															1

*Significant at 5% level **Significant at 1% level

Table 2: Estimates of genotypic correlation coefficient between different characters in cowpea

Traits	D1	D50	DM	NBPP	NCPP	NPPC	NPPP	PH	PL	NSPP	TW	HI	PC	IC	SYPP
D1	1	0.956**	0.887**	0.235*	0.272*	-0.048	0.206	-0.125	0.153	0.072	0.023	0.126	0.175	0.016	0.093
D50		1	0.784**	0.189	0.297**	0.035	0.253*	0.078	-0.142	0.012	0.104	0.055	0.041	0.119	0.085
DM			1	0.161	0.126	0.009	0.107	-0.105	-0.015	0.007	0.008	0.131	0.040	0.260*	0.101
NBPP				1	0.522**	0.445**	0.828**	0.002	0.356**	0.346**	0.023	0.599**	-0.205	0.123	0.620**
NCPP					1	0.166	0.975**	0.036	0.328**	0.244*	0.054	0.672**	-0.070	0.266*	0.715**
NPPC						1	0.369**	-0.058	0.247*	0.313**	0.332**	0.544**	-0.006	0.097	0.565**
NPPP							1	-0.012	0.197	0.277*	0.148	0.806**	-0.009	0.180	0.901**
PH								1	-0.145	-0.224	-0.249*	-0.132	0.120	0.175	-0.197
PL									1	0.947**	0.416**	0.395**	-0.010	0.070	0.383**
NSPP										1	-0.077	0.571**	0.066	-0.015	0.553**
TW											1	0.386**	-0.059	-0.205	0.432**
HI												1	-0.095	0.038	0.996**
PC													1	-0.044	-0.076
IC														1	0.031
SYPP															1

*Significant at 5% level **Significant at 1% level

Table 3: Path analysis for different characters at phenotypic level in cowpea

Traits	D1	D50	DM	NBPP	NCPP	NPPC	NPPP	PH	PL	NSPP	TW	HI	PC	IC
D1	0.0143	0.0113	0.0103	0.0018	0.003	0.0007	0.003	-0.0012	-0.0006	-0.0005	-0.0007	0.0006	0.0013	0.0002
D50	-0.0427	-0.054	-0.0452	-0.0088	-0.0102	-0.0015	-0.0091	-0.0007	0.0002	0.0018	0.0017	-0.0029	-0.006	-0.0056
DM	0.0232	0.0269	0.0322	0.0047	0.004	0.001	0.0031	-0.0001	0.0009	0.001	-0.0001	0.0014	0.0015	0.0063
NBPP	-0.0065	-0.0083	-0.0075	-0.0513	-0.0251	-0.0152	-0.0293	0.0007	-0.0081	-0.0154	-0.0047	-0.0253	0.0084	-0.0052
NCPP	0.0187	0.0169	0.0111	0.0437	0.0894	0.0106	0.0734	0.0059	0.015	0.0208	0.0104	0.053	-0.0063	0.0189
NPPC	0.0008	0.0005	0.0005	0.0048	0.0019	0.0163	0.0067	-0.0009	0.003	0.0033	0.0035	0.0065	0.0002	0.0007
NPPP	0.0097	0.0077	0.0044	0.0261	0.0375	0.0189	0.0457	-0.0009	0.0072	0.0086	0.0052	0.0293	-0.0023	0.0068
PH	0.0025	-0.0004	0.0001	0.0004	-0.002	0.0017	0.0006	-0.03	0.0036	0.0053	0.0064	0.0043	-0.0021	-0.004
PL	0.0013	0.0001	-0.0009	-0.0051	-0.0054	-0.0059	-0.0051	0.0038	-0.0323	-0.0192	-0.0045	-0.0107	-0.0035	-0.0022
NSPP	0.0013	0.0013	-0.0012	-0.0116	-0.009	-0.0079	-0.0073	0.0068	-0.023	-0.0388	-0.0019	-0.02	-0.0041	0.0009
TW	-0.0008	-0.0005	0.0001	0.0013	0.0017	0.0032	0.0017	-0.0031	0.002	0.0007	0.0146	0.005	-0.0013	-0.0028
HI	0.0368	0.0494	0.0388	0.4526	0.5451	0.3658	0.5905	-0.1332	0.3051	0.4733	0.3133	0.9195	-0.0649	0.0549
PC	0.0017	0.0021	0.0009	-0.003	-0.0013	0.0002	-0.0009	0.0013	0.002	0.002	-0.0017	-0.0013	0.0184	-0.0012
IC	-0.0003	-0.0024	-0.0045	-0.0023	-0.0049	-0.001	-0.0034	-0.0031	-0.0016	0.0005	0.0044	-0.0014	0.0014	-0.023
SYPP	0.060	0.051	0.039	0.453**	0.625**	0.387**	0.670**	-0.155	0.273*	0.444**	0.346**	0.958**	-0.059	0.045

The residual effect of path analysis at phenotypic level was found be about 0.262

Table 4: Path analysis for different characters at genotypic level in Cowpea.

Traits	D1	D50	DM	NBPP	NCPP	NPPC	NPPP	PH	PL	NSPP	TW	HI	PC	IC
D1	-0.6976	-0.6669	-0.6188	-0.1641	-0.1896	0.0331	-0.1439	0.0873	-0.1064	-0.0501	-0.0158	-0.0881	-0.1223	-0.0113
D50	0.1271	0.133	0.1371	0.0251	0.0395	0.0047	0.0336	0.0103	-0.0189	0.0016	0.0138	0.0073	0.0055	0.0158
DM	0.4124	0.4793	0.4649	0.0746	0.0587	0.0043	0.0497	-0.0489	-0.0071	0.0031	0.0037	0.061	0.0187	0.1209
NBPP	0.0311	0.0249	0.0212	0.1322	0.069	0.0588	0.1095	0.0001	0.047	0.0458	0.003	0.0792	-0.027	0.0163
NCPP	0.0894	0.0976	0.0416	0.1717	0.3288	0.0547	0.3207	0.012	0.1079	0.0803	0.0176	0.2211	-0.0231	0.0873
NPPC	-0.0014	0.001	0.0003	0.0129	0.0048	0.0291	0.0107	-0.0017	0.0072	0.0091	0.0096	0.0158	-0.0002	0.0028
NPPP	0.005	0.0062	0.0026	0.0202	0.0238	0.009	0.0244	-0.0003	0.0048	0.0068	0.0036	0.0197	-0.0002	0.0044
PH	0.0159	-0.0099	0.0134	0.0001	-0.0046	0.0074	0.0015	-0.1272	0.0184	0.0285	0.0317	0.0168	-0.0153	-0.0223
PL	0.007	-0.0066	-0.0007	0.0164	0.0151	0.0114	0.0091	-0.0067	0.0461	0.0437	0.0192	0.0182	-0.0005	0.0032
NSPP	0.0015	0.0003	0.0001	0.0073	0.0052	0.0066	0.0059	-0.0047	0.0201	0.0212	-0.0016	0.0121	0.0014	-0.0003
TW	0.0017	0.0079	0.0006	0.0017	0.0041	0.0252	0.0112	-0.0189	0.0316	-0.0058	0.076	0.0293	-0.0045	-0.0156
HI	0.0789	0.0345	0.0819	0.3741	0.4199	0.3399	0.5032	-0.0825	0.2468	0.3567	0.2408	0.6245	-0.0594	0.0235
PC	0.0251	0.0059	0.0057	-0.0292	-0.01	-0.0008	-0.0013	0.0172	-0.0015	0.0094	-0.0084	-0.0136	0.143	-0.0064
IC	-0.003	-0.0223	-0.0487	-0.0231	-0.0497	-0.0182	-0.0337	-0.0328	-0.0131	0.0028	0.0383	-0.007	0.0083	-0.1873
SYPP	0.093	0.085	0.101	0.620**	0.715**	0.565**	0.901**	-0.197	0.383**	0.553**	0.432**	0.996**	-0.076	0.031

The residual effect of path analysis at genotypic level was found be about 0.184

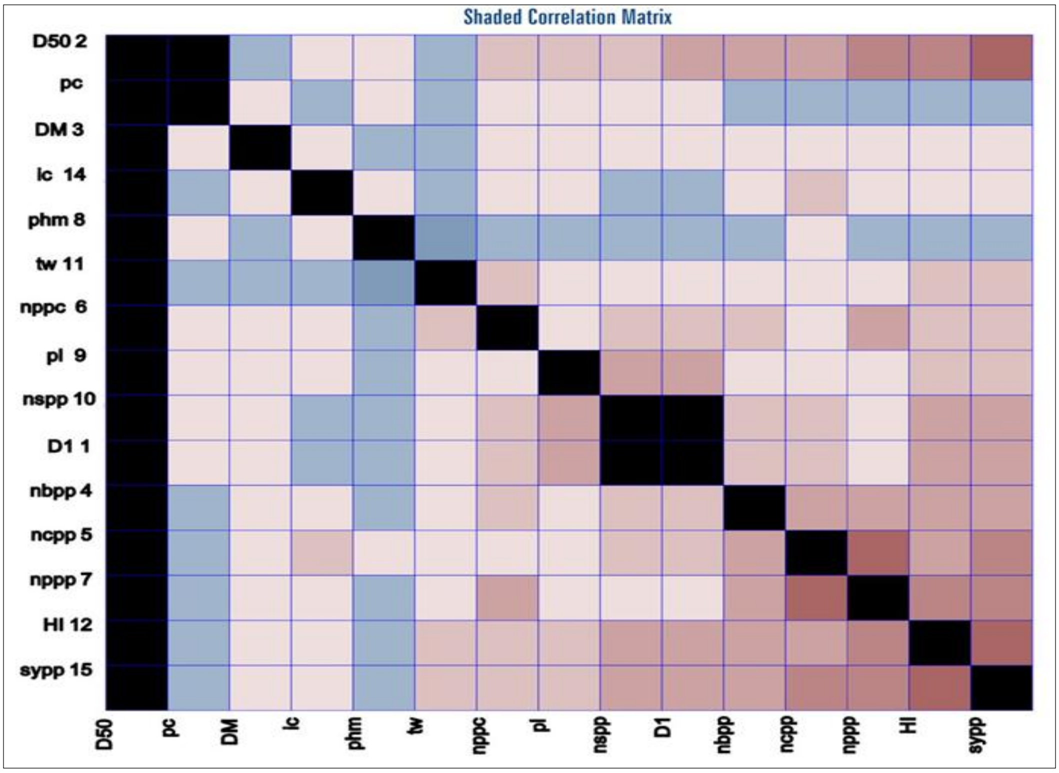

Fig 1: Shaded phenotypic correlation

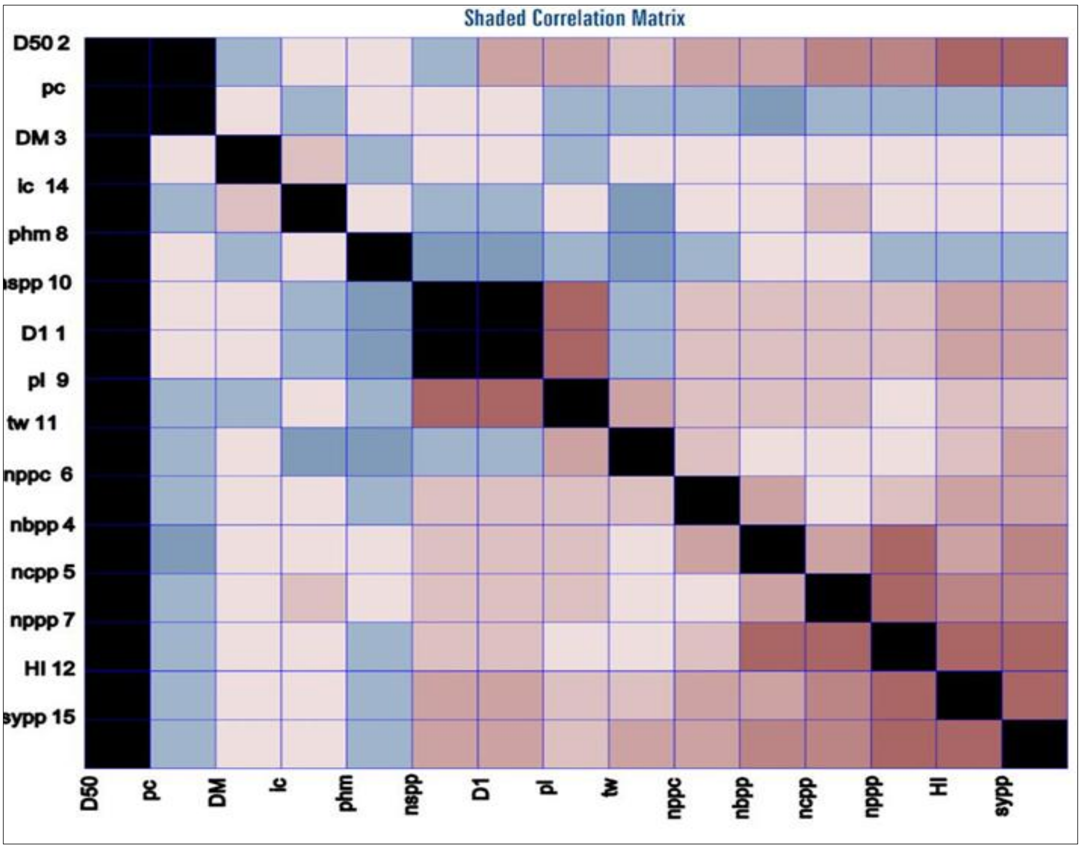

Fig 2: Shaded genotypic correlation matrix

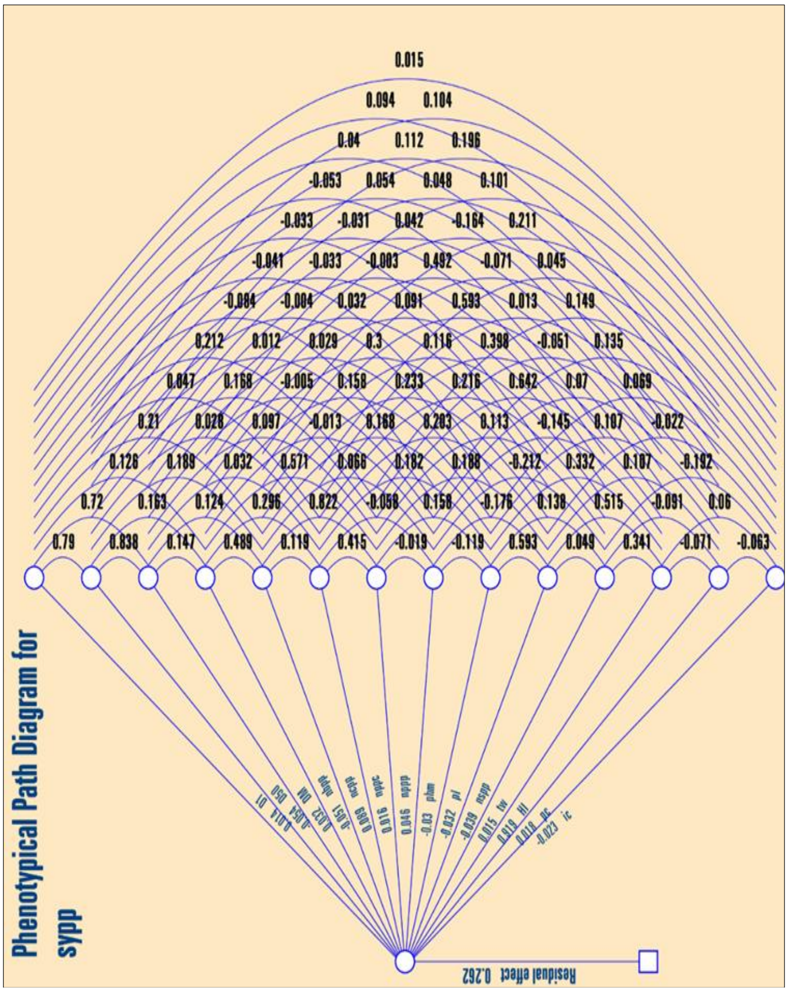

Fig 3: Phenotypic path diagram

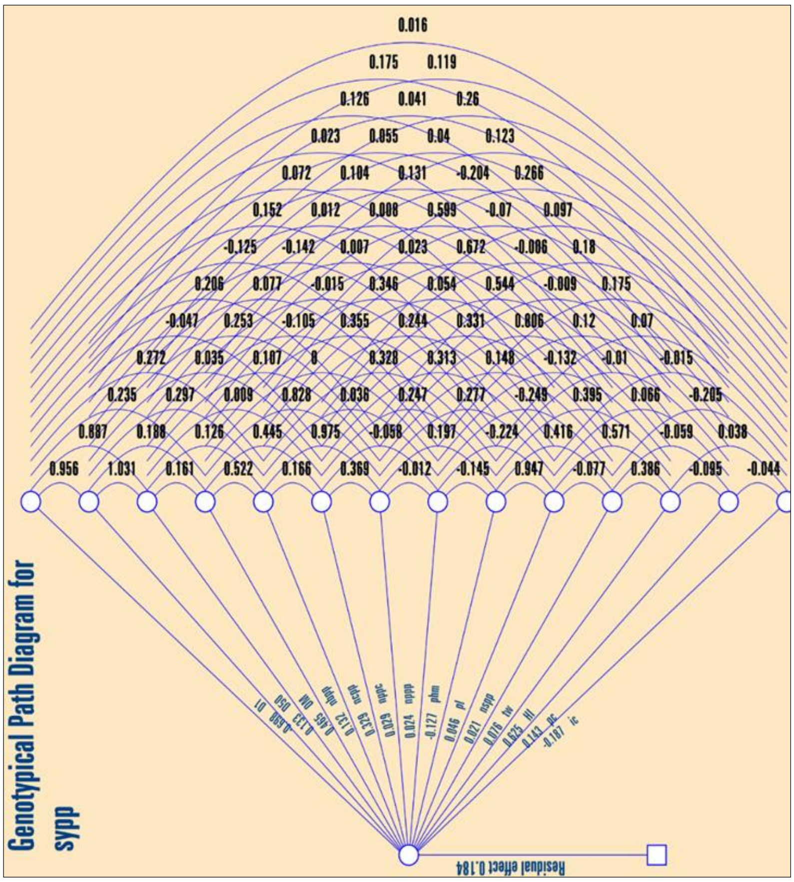

Fig 4: Genotypic path diagram

Conclusion

From this study, it can be concluded that seed yield per plant was positively and significantly associated with number of branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, test weight, and harvest index at both genotypic and phenotypic levels. These traits play a crucial role in yield determination and can be considered important for selection. Path analysis revealed that harvest index, number of clusters per plant, and pods per plant had high positive direct effects at the phenotypic level. At the genotypic level, harvest index, days to maturity and clusters per plant showed high direct effects on seed yield. Therefore, these traits should be prioritized as key selection criteria for improving seed yield in cowpea breeding programs. The results also suggest that selection based on both correlation and path analysis can enhance breeding efficiency. The strong genetic associations observed in this study indicate that early generation selection for these traits can lead to substantial genetic improvement. Overall, these findings provide a useful basis for identifying superior genotypes and designing effective yield improvement strategies in cowpea.

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