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

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Abstract

The present investigation was undertaken to analyse the association and perform path analysis in forty-two cowpea [*Vigna unguiculata* (L.) Walp.] genotypes which were evaluated in Randomised Block Design with two replication during *Rabi* 2024-25 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 plant height at maturity, number of branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, test weight, and harvest index. Path coefficient analysis, also carried out at both genotypic and phenotypic levels, indicated that test weight, number of pods per plant, number of seeds per pod, number of branches per plant, number of pods per cluster exerted the 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.] 2n=22 is a vital multipurpose legume cultivated worldwide for food, fodder, vegetables and soil fertility enhancement., It is drought-tolerant and widely grown in arid and semi-arid regions (Fatokun *et al.* 2018; Goufo *et al.* 2017) [3, 6]. It is predominantly a self-pollinated crop, belonging to family Fabaceae and sub family Faboideae (Horn and Shimelis, 2020) [7], tribe Phaseoleae and genus Vigna. West and Central Africa is recognized as the primary centre of origin of cowpea (Vavilov, 1951) [19], where maximum diversity of landraces and cultivated cowpeas is present (Padulosi and Ng, 1997) [10] while India is regarded as a secondary center of origin (Pant, 1982) [11] and is one of the earliest regions to use cowpea as a vital protein source for both humans and livestock (Steele, 1972) [15].

India is the largest producer, processor, importer and consumer of pulses in the world. During 2023-24 total area under pulse cultivation in India was 275.05 lakh hectares, with a production of 242.46 lakh tonnes and an average productivity of 881 kg/ha (MoAFW 2025) [9]. In India, cowpea is primarily grown in states such as Uttar Pradesh, Punjab, Haryana, Rajasthan, Madhya Pradesh, and Maharashtra. According to the Food and Agriculture Organization (FAO), global cowpea production in 2022 was approximately 9.775 million metric tons, cultivated over an area of 15.91 million hectares (FAOSTAT, 2023) [4].

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 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 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 of 42 cowpea genotypes, comprising 40 local genotypes collected from the different district of Maharashtra along with 2 checks of cowpea, reflecting the rich germplasm diversity. The experiment was conducted in Randomised Block Design (RBD) with two replications. The genotypes were evaluated for following traits *viz*., days to first flowering, days to 50% flowering, days to maturity, plant height at maturity(cm),number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, pod length (cm),test weight(g),seed yield per plant(g) and protein content (%).Each plot has size of 3.0 m x1.2 m with 4 rows per genotype and each row contains 10 plants, so there were total of 80 plants of each genotype in 2 replication. The data were recorded from five randomly selected plant from each entry in each replication and mean values were calculated for stastical analysis.

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.

Results and Discussion

Correlation analysis

Phenotypic Correlation Coefficient

Seed yield per plant showed highly significant positive correlation with harvest index (0.759), test weight (0.597), number of pods per plant (0.513) while positive significant with pod length (0.414), plant height at maturity (0.341), number of pods per cluster (0.395), number of clusters per plant (0.323) number of branches per plant (0.220). It showed non-significant positive correlation with number of seeds per pod (0.203), protein content (0.015). Seed yield per plant showed negative non-significant correlation with days to first flowering (-0.175), days to 50% flowering (-0.021) and days to maturity (-0.018). Similar result of seed yield per with days to first flowering reported by Chaudhary *et al.* (2020) [1]. Sogalad *et al.* (2022) [14] reported similar result for days to 50% flowering, days to maturity, number of clusters per plant and number of pods per cluster. Similar finding for number of seeds per pod, harvest index and test weight reported by Tambitkar *et al.* (2020) [16].

Number of branches per plant had positive significant correlation with number of clusters per plant (0.358), number of pods per cluster (0.355), number of pods per plant (0.415), harvest index (0.235) and seed yield per plant (0.220). Number of clusters per plant had highly significant positive correlation with number of pods per plant (0.666) while positive significant correlation with number of pods per cluster (0.291), harvest index (0.298) and seed yield per plant (0.323). Number of pods per cluster had highly significant positive correlation with number of pods per plant (0.795). Number of pods per plant had highly significant positive correlation with harvest index (0.571) and seed yield per plant (0.513). Number of seeds per pod showed positive significant correlation pod length (0.262), Pod length had positive significant correlation with test weight (0.529) and seed yield per plant (0.414), Test weight showed highly significant positive correlation with seed yield per plant (0.597), Harvest index had highly significant positive correlation with seed yield per plant (0.759). Protein content reported positive non-significant correlation with seed yield per plant (0.015)

Genotypic Correlation Coefficient

Highly significant and positive correlation of seed yield per plant observed with harvest index (0.742), test weight (0.707) while positive significant with number of pods per plant (0.495), pod length (0.430), plant height at maturity (0.355), number of pods per cluster (0.40), number of clusters per plant (0.451) and number of branches per plant (0.244). It had positive non-significant correlation with number of seeds per pod (0.269), protein content (0.009), days to maturity (0.001). It showed negative non-significant correlation with days to first flowering (-0.177) and days to 50% flowering (-0.022).Highly significant positive correlation of seed yield per plant with its contributing character (number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, test weight) reported by Sogalad *et al.* (2022) [14] while its negative non-significant correlation with days to maturity reported by Reddy *et al.* (2022) [13].

Number of branches per plant showed positive significant correlation with number of clusters per plant (0.426), number of pods per cluster (0.430), seed yield per plant (0.244), number of pods per plant (0.431) and harvest index (0.284). Number of clusters per plan**t** showed highly significant positive correlation with number of pods per plant (0.913) while positive signification correlation with number of pods per cluster (0.494), harvest index (0.467) and seed yield per plant (0.451). Number of pods per cluster showed highly significant positive correlation with number of pods per plant (0.896) while positive significant with harvest index (0.484) and seed yield per plant (0.403). Number of pods per plant showed positive significant correlation with harvest index (0.557) and seed yield per plant (0.495). Number of seeds per pod showed positive non-significant correlation with pod length (0.202), harvest index (0.176) and seed yield per plant (0.269). Pod length had positive significant correlation with test weight (0.606) and seed yield per plant (0.430). Test weight showed highly significant positive correlation with seed yield per plant (0.707). Harvest index had positive highly significant correlation with seed yield per plant (0.742). Protein content showed positive non-significant correlation with seed yield per plant (0.0093).

Path coefficient analysis

Phenotypic Path Coefficient Analysis

At the phenotypic level, test weight (0.5178) and harvest index (0.4219) exerted the highest positive direct effect on seed yield per plant, indicating that these traits contributed substantially and directly to yield. Number of pods per plant (0.3678), plant height at maturity (0.2510), number of seeds per pod (0.1227) also showed positive direct effect though of relatively smaller magnitude. number of clusters per plant (0.0108), protein content (0.0105) and number of pods per clusters (0.0070) had negligible positive direct effect on seed yield per plant (Table 3). Similar result of test weight and harvest index were reported by Pareet *et al.* (2022) [12].

Negative direct effect was observed for days to 50% flowering (-0.0419), days to maturity (-0.0163) and pod length (-0.0111).

Overall, test weight and harvest index emerged as the most influential trait contributing directly to yield, while most other traits contributed through indirect effects. Fig no.3 illustrate the phenotypic path diagram for seed yield per plant, depicting the direct and indirect effects of various contributing trait.

Genotypic Path Coefficient Analysis

At the genotypic level, Test weigh recorded the highest positive direct effect on seed yield per plant with a value of 1.4602 followed by number of pods per plant (1.0810), number of seeds per pod (0.6536), days to first flowering (0.5513). Chaudhary *et al.* (2020) [1] and Teppavari *et al.* (2023) [17] reported similar positive direct effect of number of pods per plant. Number of branches per plant (0.2861), number of pods per cluster (0.2798), days to 50% flowering (0.2413) and pod length (0. 1702) had moderate positive direct effect on seed yield per plant. Gawande *et al.* (2024) [5] observed similar results in cowpea for positive direct effect on seed yield per plant.

Harvest index (-0.7975), days to maturity (-0.5707), plant height at maturity (-0.5616), protein content (-0.1084) and number of clusters of plant (-0. 0549) reported negative direct effect on seed yield per plant. Similar result of number of clusters per plant, plant height at maturity and harvest index were reported by Tirkey *et al.* (2022) [18]. Findings of Sogalad *et al.* (2022) [14] were in confirmation with days to maturity.

This analysis indicates that test weight, number of pods per plant and number of seeds per pod exerted the prominent positive direct effect on seed yield per plant at genotypic level. Therefore, these characters emerge as the key selection criteria for enhancing seed yield per plant in cowpea. Fig no.4 demonstrate genotypic path diagram for seed yield per plant, highlighting the direct and indirect effect of contributing trait.

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

Traits	DFF	DFPF	DTM	PHT	NBPP	NCPP	NPPC	NPPP	NSPP	PL	TW	HI	PC	SYPP
DFF	1	0.767**	0.705**	0.203	-0.154	-0.117	-0.392**	-0.350**	-0.168	-0.058	0.104	-0.242*	0.045	-0.175
DFPF		1	0.895**	0.288**	-0.114	-0.177	-0.221*	-0.229*	-0.193	0.131	0.208	-0.108	-0.025	-0.021
DTM			1	0.292**	-0.004	-0.152	-0.141	-0.195	-0.335**	0.116	0.222*	-0.122	-0.076	-0.018
PHT				1	-0.064	-0.037	-0.005	-0.008	0.204	0.516**	0.315**	-0.178	-0.000	0.341**
NBPP					1	0.358**	0.355**	0.415**	0.005	-0.076	-0.108	0.235*	-0.144	0.220*
NCPP						1	0.291**	0.666**	0.073	-0.153	-0.158	0.298**	-0.049	0.323**
NPPC							1	0.795**	0.067	-0.067	-0.208	0.464**	-0.109	0.395**
NPPP								1	0.041	-0.108	-0.250*	0.571**	-0.164	0.513**
NSPP									1	0.262*	-0.062	0.096	-0.156	0.203
PL										1	0.529**	0.097	0.135	0.414**
TW											1	0.284**	0.242*	0.597**
HI												1	-0.087	0.759**
PC													1	0.015
SYPP														1

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

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

Traits	DFF	DFPF	DTM	PHT	NBPP	NCPP	NPPC	NPPP	NSPP	PL	TW	HI	PC	SYPP
DFF	1	0.839**	0.803**	0.219*	-0.187	-0.228*	-0.432**	-0.360**	-0.203	-0.040	0.093	-0.265*	0.057	-0.177
DFPF		1	0.932**	0.301**	-0.099	-0.200	-0.255*	-0.242*	-0.182	0.158	0.215*	-0.127	-0.028	-0.022
DTM			1	0.308**	0.049	-0.152	-0.136	-0.161	-0.313**	0.159	0.223*	-0.133	-0.123	0.001
PHT				1	-0.046	-0.059	0.005	-0.002	0.272*	0.554**	0.326**	-0.203	-0.003	0.355**
NBPP					1	0.426**	0.430**	0.431**	-0.169	-0.149	-0.091	0.284**	-0.192	0.244*
NCPP						1	0.494**	0.913**	0.031	-0.185	-0.222*	0.467**	-0.190	0.451**
NPPC							1	0.896**	-0.088	-0.106	-0.187	0.484**	-0.162	0.403**
NPPP								1	-0.033	-0.205	-0.186	0.557**	-0.245*	0.495**
NSPP									1	0.202	-0.043	0.176	-0.231*	0.269
PL										1	0.606**	0.092	0.125	0.430**
TW											1	0.405**	0.289**	0.707**
HI												1	-0.105	0.742**
PC													1	0.009
SYPP														1

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

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

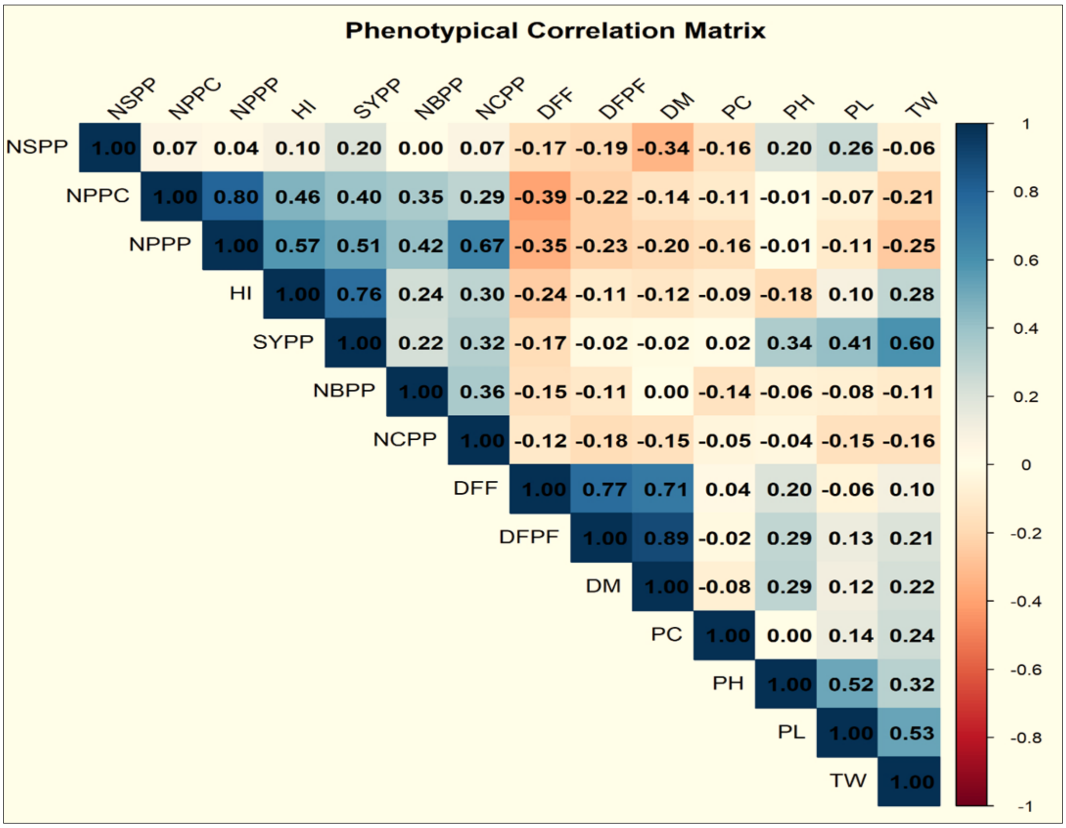
Traits	DFF	DFPF	DTM	PHT	NBPP	NCPP	NPPC	NPPP	NSPP	PL	TW	HI	PC
DFF	0.0235	0.0180	0.0166	0.0048	-0.0036	-0.0028	-0.0092	-0.0082	-0.0040	-0.0014	0.0025	-0.0057	0.0011
DFPF	-0.0321	-0.0419	-0.0375	-0.0121	0.0048	0.0074	0.0092	0.0096	0.0081	-0.0055	-0.0087	0.0045	0.0010
DTM	-0.0115	-0.0146	-0.0163	-0.0048	0.0001	0.0025	0.0023	0.0032	0.0055	-0.0019	-0.0036	0.0020	0.0012
PHT	0.0510	0.0722	0.0733	0.2510	-0.0161	-0.0093	-0.0013	-0.0021	0.0513	0.1295	0.0791	-0.0448	0.0001
NBPP	-0.0053	-0.0039	-0.0001	-0.0022	0.0344	0.0123	0.0122	0.0143	-0.0002	-0.0026	-0.0037	0.0081	-0.0050
NCPP	-0.0013	-0.0019	-0.0016	-0.0004	0.0039	0.0108	0.0032	0.0072	0.0008	-0.0017	-0.0017	0.0032	-0.0005
NPPC	-0.0028	-0.0016	-0.0010	0.0001	0.0025	0.0021	0.0070	0.0056	-0.0005	-0.0005	-0.0015	0.0033	-0.0008
NPPP	-0.1289	-0.0841	-0.0717	-0.0031	0.1528	0.2450	0.2924	0.3678	0.0150	-0.0396	-0.0921	0.2101	-0.0603
NSPP	-0.0207	-0.0236	-0.0411	0.0251	-0.0006	0.0090	-0.0083	0.0050	0.1227	0.0322	-0.0076	0.0117	-0.0191
PL	0.0006	-0.0015	-0.0013	-0.0057	0.0008	0.0017	0.0007	0.0012	-0.0029	-0.0111	-0.0059	-0.0011	-0.0015
TW	0.0540	0.1077	0.1151	0.1631	-0.0562	-0.0816	-0.1075	-0.1296	-0.0319	0.2741	0.5178	0.1470	0.1254
HI	-0.1021	-0.0455	-0.0513	-0.0752	0.0992	0.1258	0.1958	0.2409	0.0403	0.0408	0.1198	0.4219	-0.0366
PC	0.0005	-0.0003	-0.0008	0.0001	-0.0015	-0.0005	-0.0011	-0.0017	-0.0016	0.0014	0.0025	-0.0009	0.0105

The residual effect of path analysis at phenotypic level was found be about 0.255

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

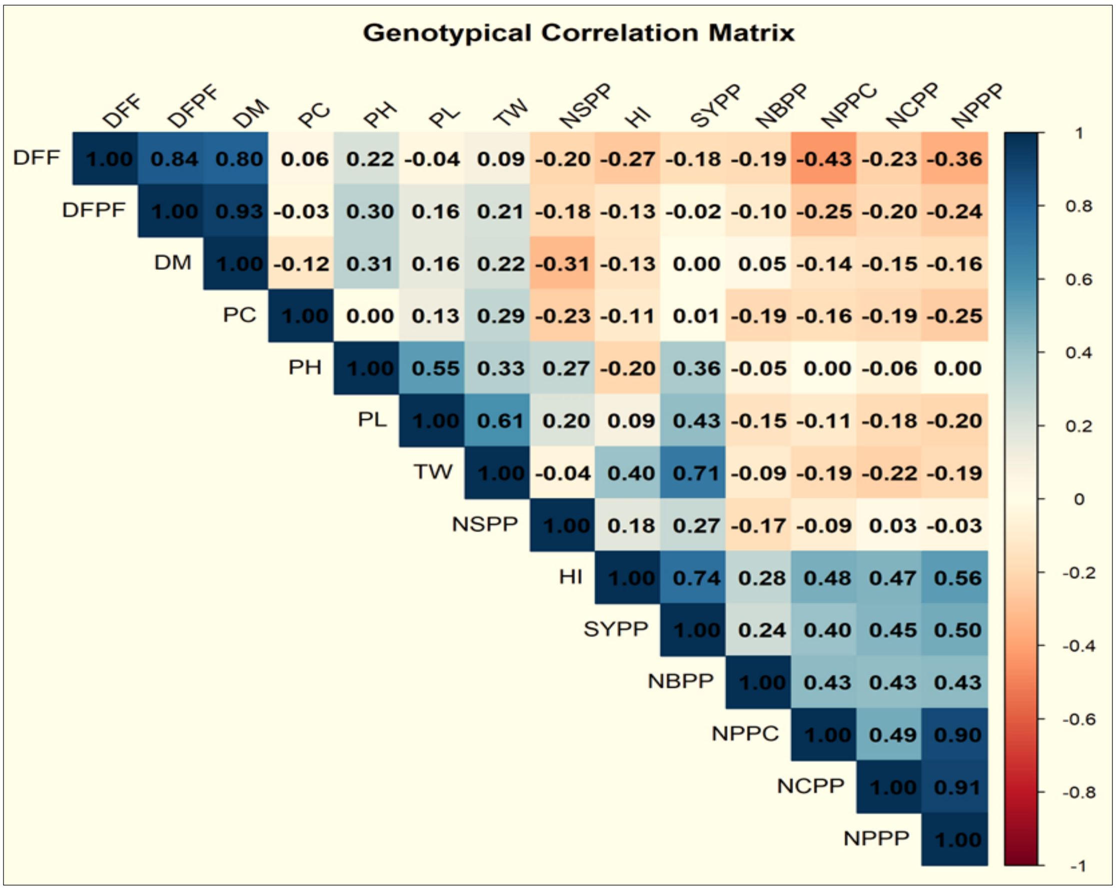
Traits	DFF	DFPF	DTM	PHT	NBPP	NCPP	NPPC	NPPP	NSPP	PL	TW	HI	PC
DFF	0.5513	0.4623	0.4429	0.1205	-0.1031	-0.1257	-0.2381	-0.1983	-0.1121	-0.0221	0.0513	-0.1462	0.0312
DFPF	0.2024	0.2413	0.2248	0.0725	-0.0239	-0.0481	-0.0614	-0.0585	-0.0439	0.0380	0.0518	-0.0306	-0.0067
DTM	-0.4585	-0.5316	-0.5707	-0.1761	-0.0280	0.0865	0.0777	0.0921	0.1785	-0.0908	-0.1272	0.0758	0.0704
PHT	-0.1228	-0.1688	-0.1733	-0.5616	0.0260	0.0332	-0.0028	0.0013	-0.1530	-0.3114	-0.1831	0.1141	0.0018
NBPP	-0.0535	-0.0284	0.0140	-0.0132	0.2861	0.1218	0.1232	0.1232	-0.0484	-0.0427	-0.0262	0.0812	-0.0549
NCPP	0.0125	0.0109	0.0083	0.0032	-0.0234	-0.0549	-0.0271	-0.0501	-0.0017	0.0101	0.0122	-0.0256	0.0104
NPPC	-0.1208	-0.0712	-0.0381	0.0014	0.1205	0.1383	0.2798	0.2506	-0.0247	-0.0297	-0.0523	0.1353	-0.0454
NPPP	-0.3888	-0.2619	-0.1745	-0.0025	0.4655	0.9865	0.9682	1.0810	-0.0362	-0.2214	-0.2012	0.6024	-0.2651
NSPP	-0.1329	-0.1189	-0.2044	0.1780	-0.1106	0.0205	-0.0577	-0.0219	0.6536	0.1320	-0.0279	0.1147	-0.1512
PL	-0.0068	0.0268	0.0271	0.0944	-0.0254	-0.0315	-0.0181	-0.0349	0.0344	0.1702	0.1031	0.0156	0.0213
TW	0.1359	0.3135	0.3255	0.4762	-0.1336	-0.3242	-0.2729	-0.2718	-0.0624	0.8844	1.4602	0.5912	0.4215
HI	0.2115	0.1013	0.1060	0.1621	-0.2264	-0.3725	-0.3858	-0.4444	-0.1400	-0.0732	-0.3229	-0.7975	0.0842
PC	-0.0061	0.0030	0.0134	0.0004	0.0208	0.0206	0.0176	0.0266	0.0251	-0.0136	-0.0313	0.0114	-0.1084

The residual effect of path analysis at genotypic level was found be about 0.284



	NSPP	NPPC	NPPP	HI	SYPP	NBPP	NCPP	DFF	DFPF	DM	PC	PH	PL	TW
NSPP	1.00	0.07	0.04	0.10	0.20	0.00	0.07	-0.17	-0.19	-0.34	-0.16	0.20	0.26	-0.06
NPPC		1.00	0.80	0.46	0.40	0.35	0.29	-0.39	-0.22	-0.14	-0.11	-0.01	-0.07	-0.21
NPPP			1.00	0.57	0.51	0.42	0.67	-0.35	-0.23	-0.20	-0.16	-0.01	-0.11	-0.25
HI				1.00	0.76	0.24	0.30	-0.24	-0.11	-0.12	-0.09	-0.18	0.10	0.28
SYPP					1.00	0.22	0.32	-0.17	-0.02	-0.02	0.02	0.34	0.41	0.60
NBPP						1.00	0.36	-0.15	-0.11	0.00	-0.14	-0.06	-0.08	-0.11
NCPP							1.00	-0.12	-0.18	-0.15	-0.05	-0.04	-0.15	-0.16
DFF								1.00	0.77	0.71	0.04	0.20	-0.06	0.10
DFPF									1.00	0.89	-0.02	0.29	0.13	0.21
DM										1.00	-0.08	0.29	0.12	0.22
PC											1.00	0.00	0.14	0.24
PH												1.00	0.52	0.32
PL													1.00	0.53
TW														1.00

Fig 1: Phenotypical Correlation Matrix



	DFF	DFPF	DM	PC	PH	PL	TW	NSPP	HI	SYPP	NBPP	NPPC	NCPP	NPPP
DFF	1.00	0.84	0.80	0.06	0.22	-0.04	0.09	-0.20	-0.27	-0.18	-0.19	-0.43	-0.23	-0.36
DFPF		1.00	0.93	-0.03	0.30	0.16	0.21	-0.18	-0.13	-0.02	-0.10	-0.25	-0.20	-0.24
DM			1.00	-0.12	0.31	0.16	0.22	-0.31	-0.13	0.00	0.05	-0.14	-0.15	-0.16
PC				1.00	0.00	0.13	0.29	-0.23	-0.11	0.01	-0.19	-0.16	-0.19	-0.25
PH					1.00	0.55	0.33	0.27	-0.20	0.36	-0.05	0.00	-0.06	0.00
PL						1.00	0.61	0.20	0.09	0.43	-0.15	-0.11	-0.18	-0.20
TW							1.00	-0.04	0.40	0.71	-0.09	-0.19	-0.22	-0.19
NSPP								1.00	0.18	0.27	-0.17	-0.09	0.03	-0.03
HI									1.00	0.74	0.28	0.48	0.47	0.56
SYPP										1.00	0.24	0.40	0.45	0.50
NBPP											1.00	0.43	0.43	0.43
NPPC												1.00	0.49	0.90
NCPP													1.00	0.91
NPPP														1.00

Fig 2: Genotypical Correlation Matrix

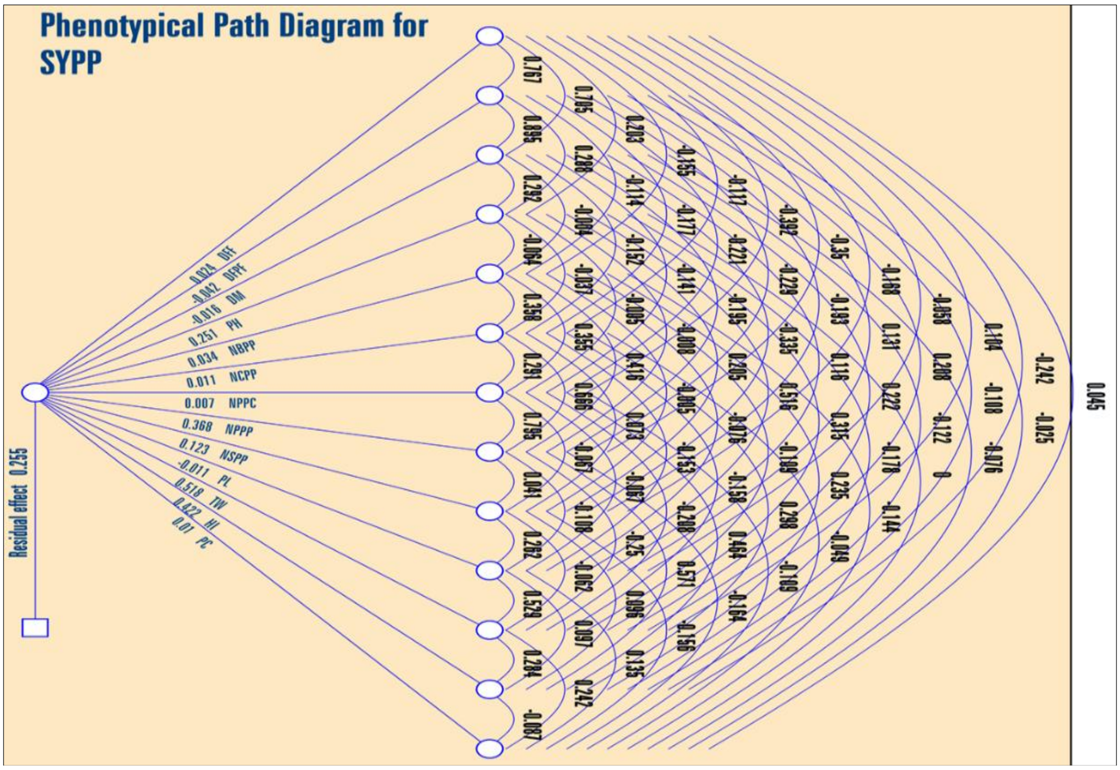


Fig 3: Phenotypical Path Diagram for SYPP

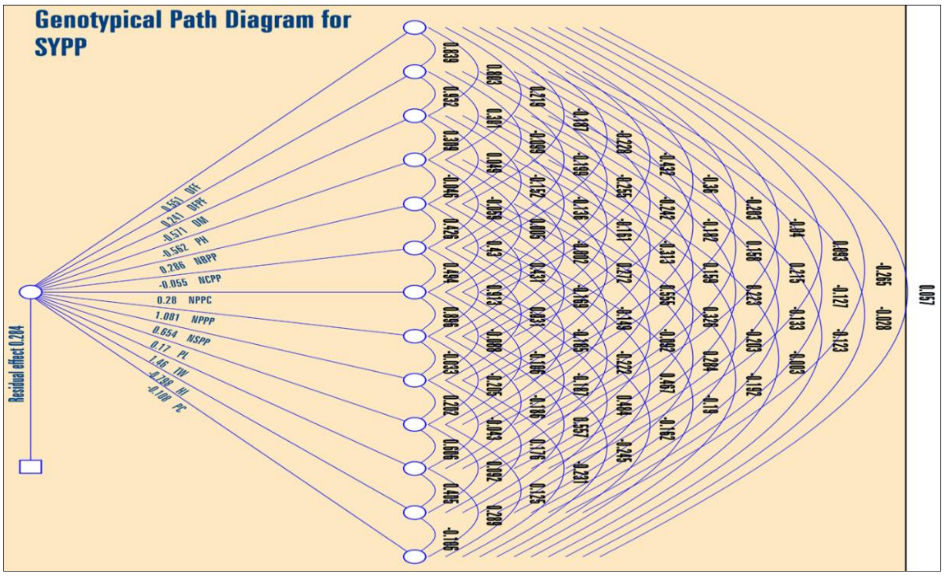


Fig 4: Genotypical Path Diagram for SYPP

Conclusion

From this study, it can be concluded that seed yield per plant can be enhanced through simultaneous selection for traits such as number of branches per plant, number of pods per cluster, number of pods per plant, pod length and test weight. These traits exhibited significant positive and direct effect on seed yield per plant at both genotypic and phenotypic level, indicating their potential utility in yield improvement. It is desirable to give more weightage to these characters during selection programme.

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