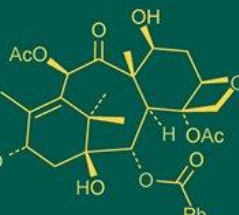
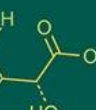
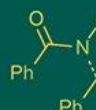


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Trait association direct and indirect effects of yield-attributing traits on pod yield in advanced breeding lines of Groundnut (*Arachis hypogaea* L.)

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Abstract

Groundnut (*Arachis hypogaea* L.) is an important oilseed crop where improvement of pod yield depends on selection of key yield contributing trait. The present investigation was conducted during *rabi* 2025-26 at RARS, Palem, using 96 groundnut genotypes including six commercial checks in an alpha lattice design with two replications. Analysis of variance (ANOVA), indicated significant genetic variability for all the characters studied and highlighting the scope for genetic improvement. Genotypic correlation analysis revealed that pod yield per plant was positively and significantly associated with number of primary branches per plant ($r = 0.294^{**}$), number of pods per plant ($r = 0.990^{**}$), seed yield per plant ($r = 0.994^{**}$), germination percentage ($r = 0.560^{**}$), shelling percentage ($r = 0.421^{**}$) and duration of fresh seed dormancy ($r = 0.330^{**}$). Significant negative association were observed with the late leaf spot score at 90 DAS ($r = -0.282^{**}$). Path coefficient analysis indicated that seed yield per plant had the highest positive direct effect on pod yield at both the genotypic (6.790) and phenotypic (1.041) levels. The residual effects were low (0.1999 at genotypic and 0.1691 at phenotypic levels, indicating that the selected traits accounted for most of the variation in pod yield. The study suggests that simultaneous selection for seed yield per plant, number of pods per plant, germination percentage, shelling percentage and optimum fresh seed dormancy would be effective for developing high-yielding groundnut cultivars with improved tolerance to late leaf spot and enhanced adaptability.

Keywords: *Arachis hypogaea* L., Pod yield, Seed yield, Correlation analysis, Path coefficient analysis, Genetic variability, Yield contributing traits, Late leaf spot, Germination percentage, Shelling percentage, Leaf bud borer and fresh seed dormancy

Introduction

Groundnut (*Arachis hypogaea* L.) is one of the most important oilseed and food legume crop cultivated worldwide. It is a self-pollinated allotetraploid species ($2n = 4x = 40$) belonging to the family Fabaceae and is believed to have originated in South America, particularly Brazil and adjoining regions (Bertioli *et al.*, 2019) ^[2]. The kernels are rich in oil (40-56%), protein (20-30%), carbohydrates (10-20%) and essential micronutrients such as vitamin E, niacin, folate, magnesium, phosphorus, calcium, zinc and iron (Arya *et al.*, 2016) ^[1].

In India, groundnut is one of the principal oilseed crops cultivated under both rainfed and irrigated ecosystems. Gujarat, Rajasthan, Andhra Pradesh, Telangana, Karnataka and Tamil Nadu are major groundnut growing states contributing significantly to national production. In Telangana, groundnut is predominantly cultivated during the *rabi* season under irrigated conditions and the crop occupies a substantial area in districts such as Nagarkurnool, Wanaparthy, Gadwal and Nalgonda. Despite improvements in cultivation practices and varietal development, the productivity of groundnut remains lower than its realizable potential due to the occurrence of several biotic and abiotic stresses. Among these, foliar fungal disease like late leaf spot (LLS), caused by *Nothopassalora personata* (formerly *Phaeoisariopsis personata*), is considered one of the most destructive foliar fungal diseases worldwide (Sudini *et al.* 2015) ^[19], insect pest like groundnut leaf bud borer (*Anarsia ephippias*) was economically important pest causing severe damage to foliage, terminal buds and reproductive structures (Wightman and Rao, 1993) ^[20] and among physiological constraints fresh seed dormancy plays a crucial role in preventing pre harvest sprouting, which otherwise adversely affects seed viability, pod quality, oil composition and market

value. Previous studies have shown that fresh seed dormancy is largely governed by major genes with significant influence of environmental factors (Khedikar *et al.* 2018) ^[11]. A dormancy period of about 15-20 days is considered optimum for balancing protection against *in situ* germination and ensuring rapid seed germination during subsequent sowing.

Understanding the interrelationship among traits is essential for effective crop improvement. Correlation analysis provides information regarding the magnitude and direction of association among characters, while path coefficient analysis partitions correlation into direct and indirect effects, thereby identifying traits contributing substantially towards pod yield. Since pod yield is a complex quantitative trait governed by several interacting component characters, indirect selection through associated traits often improves breeding efficiency.

Keeping these aspects in view, the present investigation was undertaken to evaluate 90 advanced breeding lines along with six commercial checks viz., Kadiri-6, K1812, Vishista, Gimar-4, TAG-24 and GJG-32 for yield and yield attributing traits, foliar fungal disease resistance, fresh seed dormancy and leaf bud borer tolerance under field conditions.

Materials and Methods

Ninety advanced breeding lines along with six commercial checks like Kadiri-6, K-1812, TAG-24, GJG-32, Gimar-4 and Vishista, were evaluated in an alpha lattice design with two replications. Each line was sown in five rows of 5 m length, 30 cm between rows and 10 cm between plants at the AICRP Groundnut Centre, Regional Agricultural Research Station (RARS), Palem, Nagarkurnool, Telangana, during the *rabi*, 2025-26. The experimental site has a semi-arid climate and is located at 16°51' N latitude, 78°25' E longitude and 642 m above mean sea level in the Southern Telangana Zone (STZ).

Observations were recorded for all yield related traits like germination percentage, days to 50 per cent flowering, number of primary branches per plant, number of pods per plant, days to maturity, pod yield per plant (g), seed yield per plant (g), shelling percentage, late leaf spot score at 90 DAS, leaf bud borer incidence at 60 DAS (%), Intensity of fresh seed dormancy (%) at 7 DAS and duration of fresh seed dormancy (days) for each genotype.

Observations recorded

1. Germination percentage: It was recorded by counting the number of seeds that germinated on the observation date and was expressed as a percentage of the total number of seeds sown using the following formula:

$$\text{Germination Percentage (\%)} = \frac{\text{Number of germinated seeds}}{\text{Total number of seeds}} \times 100$$

2. Days to 50 per cent flowering: The number of days from the date of sowing to the day on which 50 per cent of the plants in a plot produced at least one open flower.

3. Number of primary branches per plant: Branches arising directly from the main stem were counted on five randomly selected competitive plants in each genotype at maturity and the average value was recorded.

4. Number of pods per plant: The total number of mature pods harvested from each of the five randomly selected competitive plants was counted and the average number was recorded.

5. Days to maturity: It was recorded as the number of days from sowing until approximately 75-80 per cent of the pods attained physiological maturity, as indicated by darkening of the inner shell surface.

6. Pod yield per plant (g): After harvesting and drying, pods from each of the five selected competitive plants were weighed individually using an electronic balance. The average pod weight was expressed in grams per plant.

7. Seed yield per plant (g): Seeds obtained after shelling the pods harvested from each of the five selected plants were weighed and the average seed weight per plant was recorded in grams.

8. Shelling percentage: It was calculated as the proportion of seed weight to pod weight and expressed as a percentage using the following formula:

$$\text{Shelling percentage (\%)} = \frac{\text{Seed yield}}{\text{Pod yield}} \times 100$$

9. Late leaf spot score at 90 DAS: Late leaf spot disease was assessed at 90 days after sowing (DAS) using the standard 9-point disease rating scale developed by Subrahmanyam *et al.* (1995) ^[15], where lower scores indicate higher levels of resistance.

10. Leaf bud borer incidence at 60 DAS: Leaf bud borer incidence was recorded at 60 DAS by estimating the percentage of leaf damage caused by *Anarsia ephippias*. Observations were recorded from 35 randomly selected plants of each genotype and the mean percentage of leaf damage was calculated.

11. Intensity of fresh seed dormancy (%) at 7 DAS: Fresh seed dormancy intensity was assessed seven days after sowing freshly harvested seeds. It was calculated as the percentage of seeds that failed to germinate using the following formula:

$$\text{Intensity of fresh seed dormancy (\%)} = 100 - \text{Germination (\%)}$$

12. Duration of fresh seed dormancy (days): It was recorded as the number of days required for freshly harvested seeds of each genotype to attain approximately 75 per cent germination under laboratory conditions.

The experimental data were subjected to analysis of variance (ANOVA) for an alpha lattice design as described by Patterson and Williams (1976) ^[16] using R statistical software with the agricolae package (de Mendiburu, 2023) ^[6] to test the significance of genotypic differences among the groundnut genotypes. Genotypic and phenotypic correlation coefficients among different pairs of traits were estimated following the procedure described by Falconer and Mackay (1996) ^[17]. The estimated correlation coefficients were further partitioned into direct and indirect

effects through path coefficient analysis as proposed by Wright (1921) ^[21] and elaborated by Dewey and Lu (1959) ^[5]. Correlation and path coefficient analyses were carried out using INDOSTAT software.

Results and Discussion

Analysis of variance

Analysis of variance revealed significant genetic variability among the 96 groundnut genotypes for most of the traits studied. At 1% level, highly significant differences were observed for the majority of traits, while days to 50% flowering and number of primary branches per plant were significant at the 5% level and days to maturity was non-significant. Replication effects were non-significant for all traits, indicating uniform experimental conditions. Significant treatment effects and block effects for a few traits confirmed substantial genetic variability and the effectiveness of the alpha lattice design in accounting for environmental variation.

Genotypic correlation analysis

The genotypic correlation coefficients among yield and yield-attributing traits are presented in Table 2. Pod yield per plant exhibited significant positive associations with the number of primary branches per plant ($r = 0.294^{**}$), seed yield per plant ($r = 0.994^{***}$), number of pods per plant ($r = 0.990^{***}$), germination percentage ($r = 0.560^{***}$), shelling percentage ($r = 0.421^{***}$) and duration of fresh seed dormancy ($r = 0.330$). In contrast, pod yield exhibited a significant negative association with late leaf spot score at 90 DAS ($r = -0.282^{**}$), whereas its associations with days to 50 per cent flowering ($r = -0.041$), plant height ($r = -0.114$), days to maturity ($r = -0.105$) and leaf bud borer incidence at 60 DAS ($r = -0.048$) were non-significant. Among the component traits, number of pods per plant showed a very strong positive association with seed yield per plant ($r = 0.988^{***}$), shelling percentage ($r = 0.394^{***}$) and duration of fresh seed dormancy ($r = 0.343^{***}$), but a significant negative association with late leaf spot score ($r = -0.279^{**}$). Similarly, seed yield per plant was positively associated with shelling percentage ($r = 0.481^{***}$) and duration of fresh seed dormancy ($r = 0.342^{***}$). Overall, the results indicated that seed yield per plant, number of pods per plant, germination percentage, shelling percentage and duration of fresh seed dormancy were the major traits positively associated with pod yield and can be effectively utilized as selection criteria in groundnut breeding programmes. Similar results were reported by Madhuri *et al.* (2022) ^[12], Reddy *et al.* (2023) ^[14] and Sravanti *et al.* (2024) ^[18].

Path coefficient analysis

Genotypic and phenotypic path coefficient analyses revealed that seed yield per plant exerted the highest positive direct effect on pod yield at both genotypic (6.7890) and phenotypic (1.0410) levels, indicating its major contribution to yield improvement. At the genotypic level, bud borer incidence at 60 DAS (0.2670), duration of fresh seed dormancy (0.1690) and plant height (0.0750) also showed positive direct effects. In contrast, number of pods per plant (-5.3990), shelling percentage (-0.5510) and days to maturity (-0.2950) exhibited negative direct effects. However, the strong positive correlation of number of pods per plant with pod yield ($r = 1.0143$) was mainly due to substantial positive indirect effects through plant height and number of primary branches per plant. At the phenotypic level, most traits exhibited negative direct effects except seed yield per plant and days to maturity. The low residual effects at the genotypic (0.1999) and phenotypic (0.1691) levels indicated that the studied traits explained about 96.0% and 97.1% of the variation in pod yield, respectively. Overall, path coefficient analysis identified seed yield per plant as the most important direct selection criterion for improving pod yield in groundnut. Similar results were reported by Madhuri *et al.* (2022) ^[12], Reddy *et al.* (2023) ^[14] and Sravanti *et al.* (2024) ^[18].

Conclusion

The present investigation revealed significant genetic variability among the 96 groundnut genotypes, indicating ample scope for genetic improvement. Pod yield per plant showed strong positive associations with number of primary branches per plant ($r = 0.294^{**}$), number of pods per plant ($r = 0.990^{**}$), seed yield per plant ($r = 0.994^{**}$), germination percentage ($r = 0.560^{**}$), shelling percentage ($r = 0.421^{**}$) and duration of fresh seed dormancy ($r = 0.330^{**}$). Significant negative association was observed with late leaf spot score at 90 DAS ($r = -0.282^{**}$). Path coefficient analysis identified seed yield per plant as the major direct contributor to pod yield with the highest positive direct effect at both genotypic (6.789) and phenotypic (1.041) levels. The low residual effects (0.1999 and 0.1691) indicated that the studied traits explained 96.0% and 97.1% of the variation in pod yield, respectively. Therefore, seed yield per plant, number of pods per plant, germination percentage, shelling percentage and duration of fresh seed dormancy can be used as effective selection criteria for improving pod yield in groundnut breeding programmes.

Competing Interests

The authors have declared that no competing interests exist.

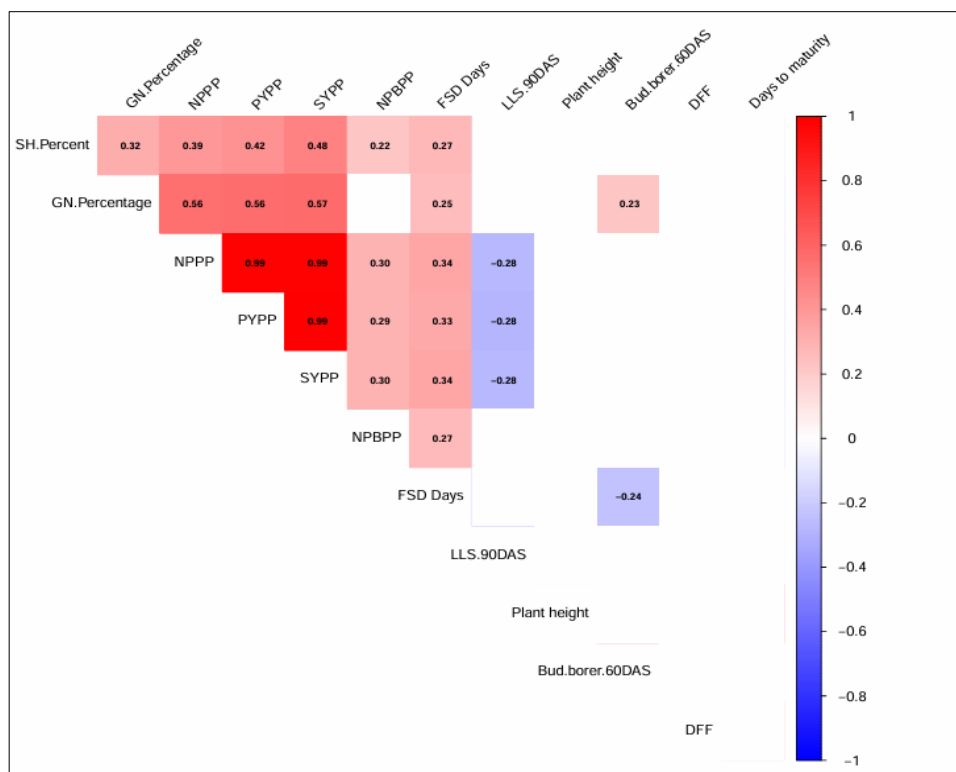


Fig 1: Genotypic correlation heatmap

Table 1: Analysis of variance (ANOVA) for yield, and yield attributing traits in Groundnut

Sl. No.	Trait	Replication (DF=1)	Treatment (Genotype) (DF=95)	Block (DF=14)	Error (DF=81)
1	Germination percentage	7.425	44.627**	17.857**	6.326
2	Days to 50% flowering	0.422	2.920*	2.742	2.737
3	Plant height	206.483	15.641**	6.971	5.924
4	No. of primary branches per plant	28.985	45.353*	69.371	44.694
5	No. of pods per plant	2.083	5.995**	0.328**	0.136
6	Days to maturity	25.521	56.895	40.691	44.775
7	Pod yield per plant	6.417	5.942**	0.296*	0.129
8	Seed yield per plant	4.113	3.256**	0.134*	0.067
9	Shelling percentage	4.963	1.612**	0.236	0.392
10	Late leaf spot at 90 DAS	1.505	5.287**	1.115	0.721
11	Bud borer incidence at 60 DAS	10.757	217.203**	5.255	8.475
12	Intensity of FSD at 7 DAS	29.904	722.848**	34.339	27.897
13	FSD duration	0.630	35.086**	0.422	0.691

*= Significant at 5%, **= Significant at 1%

DF= Degrees of freedom, DAS: Days after sowing, FSD: Fresh seed dormancy.

Table 2: Genotypic and phenotypic correlation coefficients among yield and yield contributing traits of 96 genotypes in groundnut

Traits	GN%	DFF	PH	NPBPP	NPPP	DM	SYPP	SH%	LLS (90 DAS)	Bud borer (60 DAS)	FSD Days	PYPP
GN%	1.000	-0.071	0.007	0.197	0.556 **	-0.080	0.570 **	0.315**	-0.105	0.226*	0.252*	0.560 **
DFF		1.000	0.165	-0.071	-0.037	0.091	-0.047	-0.017	0.066	-0.009	0.055	-0.041
PH			1.000	0.014	-0.099	0.181	-0.108	-0.044	-0.007	0.189	-0.032	-0.114
NPBPP				1.000	0.298**	-0.080	0.299**	0.223*	-0.106	0.001	0.267**	0.294**
NPPP					1.000	-0.090	0.988 **	0.394 **	-0.279**	-0.026	0.343 **	0.990 **
DM						1.000	-0.092	-0.030	-0.015	-0.003	-0.006	-0.105
SYPP							1.000	0.481 **	-0.277**	-0.055	0.342 **	0.994 **
SH								1.000	-0.094	-0.157	0.270**	0.421 **
LLS.90 DAS									1.000	-0.025	-0.150	-0.282**
Bud borer 60 DAS										1.000	-0.237*	-0.048
FSD Days											1.000	0.330**
PYPP												1.000

*= Significant at 5%, **= Significant at 1%

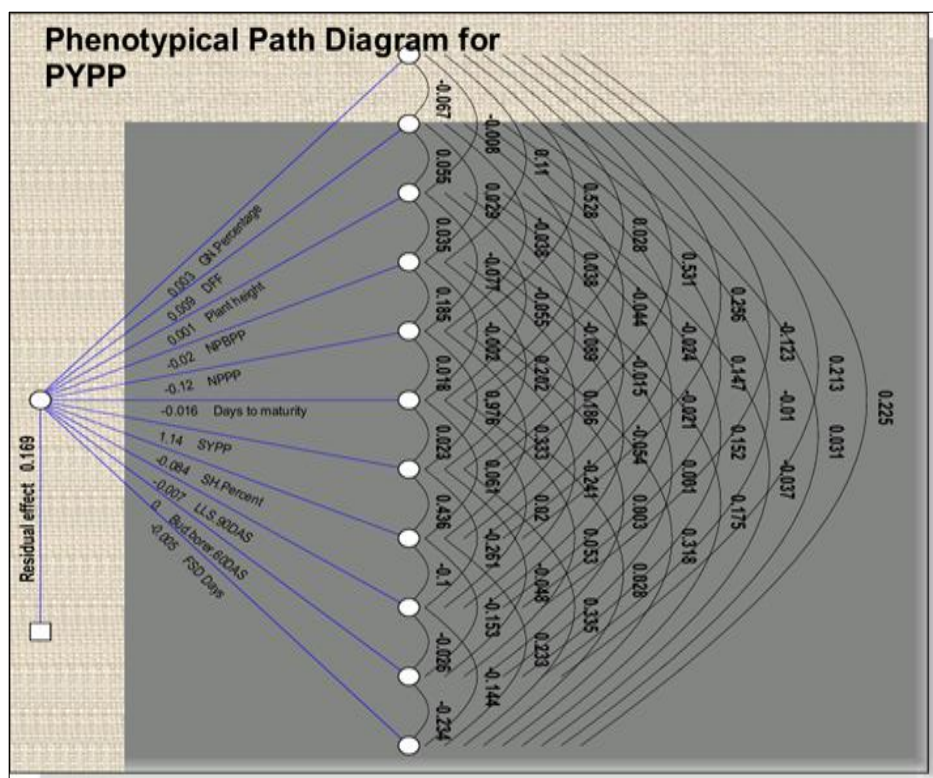
GN%: Germination percentage, rg: genotypic correlation, rp: phenotypic correlation, DFF: Days to 50% flowering, PH: Plant height, NPBPP: No. of. Primary branches per plant, NPPP: No. of. Pods per plant, DM: Days to maturity, PYPP: Pod yield per plant, SYPP: Seed yield per plant, SH%: Shelling out turn%, LLS90: Late leaf spot score at 90 days after sowing, BB60: Bud borer incidence at 60 days after sowing, FSDD: Fresh seed dormancy duration.

Table 3: Genotypic and phenotypic path coefficient analysis showing direct and indirect effects of component traits on pod yield per plant (PYPP)

Trait	G/P	GN%	DFF	PH	NPBPP	NPPP	DM	SYPP	SH%	LLS 90 DAS	Bud B 60 DAS	FSDD	r with PYPP
GN%	G	0.098	-0.003	0.001	-0.010	0.006	0.003	0.006	0.004	-0.001	0.002	0.003	0.616
	P	-0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.007	0.557
DFF	G	0.018	-0.064	-0.076	-0.183	0.009	0.055	0.013	0.003	0.015	0.006	-0.018	-0.213
	P	0.001	-0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.069
PH	G	0.003	0.09	0.075	0.016	-0.009	-0.019	-0.012	-0.008	0.002	0.021	-0.002	-0.173
	P	0.001	0.001	-0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	-0.002	0.134
NPBPP	G	-0.071	0.198	0.015	0.069	-0.093	0.027	-0.089	-0.049	0.04	0.001	-0.081	-1.437
	P	-0.001	0.001	0.001	-0.003	-0.001	0.001	-0.001	-0.001	0.001	0.001	0.006	0.482
NPPP	G	-3.353	0.716	0.642	7.272	-5.399	-0.281	-5.377	-2.465	1.550	0.053	-1.819	1.014
	P	-0.003	0.001	-0.001	-0.003	-0.005	0.001	-0.005	-0.002	0.001	0.001	0.010	0.987
DM	G	-0.102	0.257	0.075	-0.115	-0.015	-0.295	-0.025	-0.035	-0.046	-0.062	-0.009	0.093
	P	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	-0.100
SYPP	G	4.234	-1.421	-1.038	-8.776	6.762	0.581	6.790	3.601	-2.047	-0.389	2.372	1.007
	P	0.582	0.069	0.137	0.509	1.023	-0.099	1.041	0.462	-0.271	-0.271	0.010	0.996
SH%	G	-0.223	0.029	0.061	0.393	-0.251	-0.066	-0.292	-0.551	0.047	0.091	-0.177	0.496
	P	-0.023	0.001	-0.002	-0.022	-0.031	-0.001	-0.040	-0.089	0.009	0.009	0.007	0.371
LLS 90 DAS	G	-0.014	-0.039	0.004	0.098	-0.049	0.026	-0.051	-0.015	0.170	-0.004	-0.027	-0.304
	P	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	-0.003	0.001	-0.004	-0.264
Bud B 60 DAS	G	0.065	-0.024	0.074	-0.001	-0.003	0.056	-0.015	-0.044	-0.007	0.267	-0.064	-0.057
	P	0.002	-0.002	0.001	0.001	0.001	-0.001	0.001	-0.001	-0.001	0.001	-0.005	-0.041
FSDD	G	0.049	0.048	-0.004	-0.199	0.057	0.005	0.059	0.054	-0.027	-0.04	0.169	0.346
	P	0.007	0.003	-0.002	0.006	0.010	0.001	0.010	0.007	-0.004	-0.004	-0.005	0.316

Genotypic Residual Effect = 0.1999 Phenotypic Residual Effect = 0.1691 Direct effects are shown in bold font

G: Genotypic value, P: Phenotypic value, GN%: Germination percentage, PH: plant height, DFF: Days to 50% flowering, PH: Plant height, NPBPP: No. of. Primary branches per plant, NPPP: No. of. Pods per plant, DM: Days to maturity, SYPP: Seed yield per plant, SH%: Shelling out turn%, DAS: Days after sowing, LLS 90 DAS: Late leaf spot score at 90 DAS, Bud B 60 DAS: Bud borer incidence at 60 DAS, FSDD: Duration of fresh seed dormancy, r with PYPP: Correlation with Pod yield per plant.

**Fig 2:** Phenotypic path diagram with PYPP

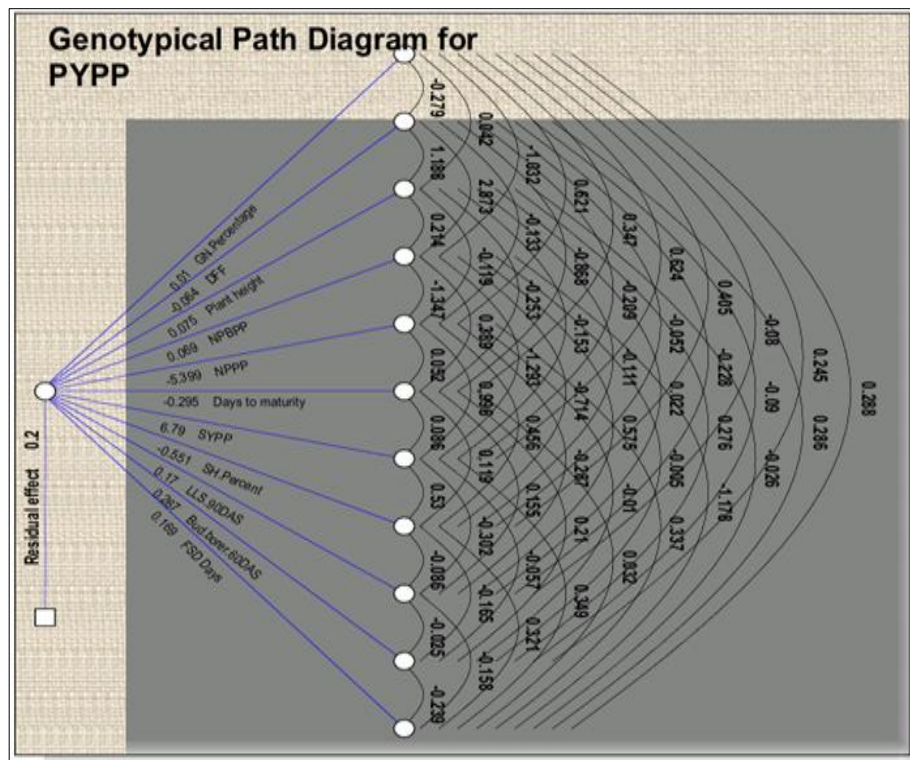


Fig 3: Genotypic path diagram with PYPP

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