

Studies on Genetic variability, Correlation and Path coefficient Analysis for Yield Contributing and Quality Traits in Marker Assisted Derived Advanced Backcross Lines of Groundnut (*Arachis hypogaea* L.)

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ABSTRACT: In the present study, 30 advanced backcross lines (BC₁F₅ and BC₂F₄) along with their parents were evaluated for 13 quantitative and quality traits in randomized block design with two replications. Yield is a polygenic and complex trait, which is significantly influenced by the environment. Direct selection for yield is less efficient, indirect selection through yield contributing traits can greatly enhance efficiency of plant breeding. The components of genetic variance revealed that phenotypic coefficient of variation (PCV) values was higher than genotypic coefficients of variation (GCV) for all the characters indicating the environment effect on genotypes. High GCV and PCV were recorded for number of pods per plant whereas, high heritability coupled with high GAM was observed in number of pods per plant, plant height, seed yield per plant and pod yield per plant. Pod yield per plant showed a positive and significant association with number of pods per plant, seed yield per plant, shelling outturn, pod length and 100 seed weight at both genotypic and phenotypic level. Path analysis revealed that seed yield per plant showed high positive direct effect whereas, shelling outturn and 100 seed weight contributed significant amount of indirect effects towards pod yield per plant.

Keywords: Groundnut, GCV, PCV, genetic advance, heritability.

INTRODUCTION

The cultivated groundnut (*Arachis hypogaea* L.), is a self-pollinated, allotetraploid ($2n = 4x = 40$) and major oilseed crop which belongs to the family Fabaceae. Groundnut is a native of South America (Brazil) and is grown in over 100 countries, between 40°N to 40° S latitude in a tropical warm climate. In India, groundnut is used as an oilseed and food crop because of its palatability. Groundnut kernels are valued as a rich source of oil (48- 50%), protein (25-28%), carbohydrates (10-20%) and provide 564 kcal of energy for every 100g of kernels (Arya *et al.*, 2016). The groundnut seed oil contains 80% of fatty acids and majorly occupies oleic acid (36-67%) and linoleic acid (15-43%) a monounsaturated fatty acid (MUFA) and polyunsaturated fatty acid (PUFA), respectively (Janila *et al.*, 2016). As groundnut is a major oilseed crop used in confectionery, there is a need to improve groundnut quality attributes. Value addition through quality enhancement will generate a large amount of foreign exchange. As a result, selection for quality features in groundnut is required in breeding programmes.

Crop improvement requires knowledge regarding the magnitude of variability and the extent to which desirable characteristics are heritable. The variability available in breeding material is crucial for the selection

of superior plant types because superior plant selection is not based solely on yield but also on yield contributing traits. The genetic makeup of the plant and the environment mostly govern the phenotypic expression of the plant character. As a result, the observed phenotypic variability must be partitioned into heritable and non-heritable components using appropriate genetic parameters such as phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were useful in the effective selection, heritability and genetic advance as percent of mean (GAM) are plant breeding tools used in determining the magnitude and direction of selection. The efficiency of selection mainly depends on the direction and magnitude of association between yield and its components. Correlation analysis provides an opportunity to study the magnitude and direction of association of yield with its components and also among various components. Correlation between two characters may be due to linkage and / or pleiotropy. If caused by linkage, an undesirable correlation can be disrupted through hybridization followed by selection in segregating generations (Ramakrishnan *et al.*, 2017). Correlation measures the level of dependence among traits, but it is often very difficult to determine the actual mutual effects among traits. Path coefficient

analysis is very important technique for partitioning the correlation coefficient in to direct and indirect effect of independent variables on dependent variable (Kumar *et al.*, 2019). Therefore, the present study estimated the genetic parameters, correlation and path coefficient analysis for 13 quantitative and quality traits.

MATERIAL AND METHODS

The present experiment was conducted during *rabi* at Regional Agricultural Research Station, Palem, Telangana State. The site of experimentation falls under a semi-arid climate and comes under Southern Telangana Zone on 16°35' latitudes, 78°1' longitude and altitude of 642 m above mean sea level. The 30 advanced backcross progenies (18 BC₁F₅ and 12 BC₂F₄) along with parents (K6, ICGV 13193 and ICGV 15033) were raised in a randomized block design with two replications. Each progeny was sown in two rows of 2.5 m length with a spacing of 30 cm between rows and 10 cm between plants with no gaps between rows. Observations were recorded in 5 randomly selected plants for 13 quantitative characters *viz.*, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod yield per plant, seed yield per plant, shelling out turn, pod length, pod width, 100 seed weight, oil and protein content, while the days to 50% flowering was recorded on whole line/ progeny basis.

Statistical analysis. The data were subjected to statistical analysis using Indostat software. The analysis of variance and their significance for all the traits were worked out as suggested by Panse and Sukhatme (1985). The genotypic and phenotypic coefficient of variation (PCV) were calculated by the formula given by Burton (1953). Heritability in broad sense (h^2) and genetic advance as percent of mean were estimated as per Allard (1960); Johnson *et al.* (1955). The correlation coefficients and path analysis were carried out by the following methods of Al-Jibouri *et al.* (1958); Dewey and Lu (1959) respectively.

RESULTS AND DISCUSSIONS

The analysis of variance showed significant differences for 13 quantitative and quality traits. It indicates presence of substantial amount of variation in experimental material under investigation. Estimates of PCV values are greater than GCV values across all traits, showing that variation was induced not only by genotypes but also by environmental effects (Table 1). The genotypic coefficient of variation (GCV) ranged from 2.48 to 21.37 and the phenotypic coefficient of variation (PCV) ranged between 3.62 to 22.6 (Fig. 1). High estimates of GCV (21.37) and PCV (22.66) were recorded in number of pods per plant indicating the presence of wide range of variation and can be further improved by simple selection process. Similar results were found in Aruna *et al.* (2019); Kumari and Sasidharan (2020); Shinde *et al.* (2019); Mandal *et al.* (2017). Heritability in a broad sense (h^2 bs) was ranged from 35.8 to 94.6 and genetic advance as percent of mean (GAM) was varied from 3.06 to 40.79 for all the characters (Fig. 2).

High heritability in a broad sense does not always imply better response to selection, because it includes non-additive genetic action. As a result, estimation of genetic advance further narrows down the response of selection. Heritability coupled with genetic advance as per cent of mean provides a very effective measure for nature of inheritance and effectiveness of selection for a particular character (Johnson *et al.* 1955) and furnished below (Table 2). High heritability accompanied with high GAM were recorded for number of pods per plant, plant height, seed yield per plant and pod yield per plant indicates these traits have been less influenced by the environment and controlled by additive gene effects and have high selection value, which can be exploited using simple selection strategies. These findings are in conformity with reports of Kumari and Sasidharan (2020); Aruna *et al.* (2019); Mandal *et al.* (2017). High heritability coupled with moderate genetic advance per mean was observed in pod length and pod width which indicates these traits were governed by both additive and non-additive gene effects and selection is less effective whereas, improvement among these traits can be achieved by breeding methods such as diallel selective mating. Similar findings were reported by Muibai *et al.* (2020); Jonah *et al.* (2012). Moderate heritability accompanied with moderate GAM were observed in protein content and number of primary branches per plant which suggest that additive gene action was involved, and there is still scope for improvement of these traits through selection. These findings are in agreement with the reports of Shukla and Rai (2014); John *et al.* (2011). Moderate heritability combines with low GAM were recorded for oil content, 100 seed weight, days to 50% flowering and shelling out turn. As a result, these characters are improved further through selection or single plant selection or inter-mating among selected individuals. These results were supported by Kumari and Sasidharan (2020); Pappammal *et al.* (2020); Aruna *et al.* (2019); Byadagi *et al.* (2018); Pattidar *et al.* (2017). High GCV (21.37) coupled with high heritability (94.6) and GAM (40.79) were observed in number of pods per plant suggested that environment had a lesser influence on the expression of these trait, and this character is governed by an additive gene action hence, selection for this trait was effective.

Correlation analysis. Yield is a complex attribute that results from the interaction of various yield components. Understanding the relationships between yield and other characters are essential in any plant breeding programme in order to make the best use of these relationships in selection of desirable characters. The effectiveness of selection is primarily determined by the direction and magnitude of the association between yield and its components when selection pressure is applied to improve any trait that is strongly correlated with yield, it also influences several other correlated characters at the same time. As a result, correlation coefficient studies allow us to understand the nature and extent of the association of yield with its components, as well as among other components. The results were discussed in present study are furnished in Table 3. Pod yield per plant showed a positive and

significant association with number of pods per plant ($rg=0.5148^{**}$, $rp=0.4232^{**}$), seed yield per plant ($rg=0.9689^{**}$, $rp=0.8460^{**}$), shelling outturn ($rg=0.7594^{**}$, $rp=0.3806^{**}$), pod length ($rg=0.4328^{**}$, $rp=0.3110^{**}$) and 100 seed weight ($rg=0.2693^{*}$, $rp=0.2943^{*}$) at both genotypic and phenotypic level but number of secondary branches per plant ($rp=0.2946^{*}$) shows positive significant relation at phenotypic only and protein content ($rg=0.2650^{*}$) showed positive significant association at genotypic only. The variation in the relation of secondary branches per plant and protein content with pod yield per plant at phenotypic and genotypic level indicates impact of the environment on these traits. The significant correlation indicates that there is strong association between various traits and positive correlation between desirable characters is favourable to the plant breeder because it helps in simultaneous improvement of both characters. These results emphasized the effectiveness of these characters in terms of their contribution towards pod yield per plant. Similar results were reported by Kumari and Sasidharan (2020); Shinde *et al.* (2019); Shendekar *et al.* (2023); Tulsi *et al.* (2017) for 100 seed weight; Chandrashekhara *et al.* (2020); Killada *et al.* (2023); Trivikrama *et al.* (2017) for number of pods per plant; Mohapatra and Khan (2020); Shinde *et al.* (2019) for shelling outturn; Mandal *et al.* (2017) for seed yield per plant; Jonah *et al.* (2012) for pod length and John *et al.* (2008) for number of secondary branches per plant; Chandrashekhara *et al.* (2020) for plant height; Kumar *et al.* (2020) for number of primary branches per plant; Shinde *et al.* (2019); Bhakal and Lal (2017) for days to 50% flowering; Mohapatra and Khan (2020); Gupta *et al.* (2015) for oil content; Krishnamurthy *et al.* (2015) for protein content and Jonah *et al.* (2012) for pod width.

Path Coefficient analysis. Path coefficient analysis is a cause-and-effect relationship and distinct from correlation coefficient by measuring the relative magnitude of direct and indirect effects of characters on

complex dependent characters such as yield. It aids breeders in determining the best and most important component traits during selection to improve yield. The present results of genotypic and phenotypic path coefficient results are furnished in Table 4 and diagrammatically represented in Fig. 3. Among various traits seed yield per plant, number of pods per plant and 100 seed weight exhibited positive direct effect and also significantly positive associated with pod yield per plant at both genotypic and phenotypic level but oil content exhibited a positive direct effect ($G=0.1791$, $P=0.0478$) on pod yield per plant and exerted a positive significant and non-significant association at genotypic and phenotypic level respectively ($rg=0.5357^{**}$, $rp=0.1353$). On the contrary, shelling percentage exhibited negative direct effect but significantly positive correlation with pod yield per plant at both genotypic and phenotypic level. The strong association might be due to the positive indirect effects through plant height and pod width both at phenotypic and genotypic level. Similar results were reported by Patel *et al.* (2021) for seed yield per plant; Alam (2014) for number of secondary branches per plant; Mandal *et al.* (2017) for number of pods per plant, shelling outturn, pod length; Mohapatra and Khan (2020) for 100 seed weight and oil content. It revealed that maximum direct effect and significant indirect contribution exhibited by seed yield per plant, as well as appreciable indirect effects exhibited by shelling outturn and 100 seed weight towards pod yield per plant. Moreover, these characters have high positive and significant association with pod yield per plant and hence, they may be regarded as the most essential yield contributing characters and appropriate importance might give to these characters while selecting for high yield in groundnut.

The high values of phenotypic residual values (0.4283) compared to genotypic residual (0.2501) might be due to the influence of other dependent variables which are not included in the study.

Table 1: Estimation of genetic parameters for 13 quantitative traits in 30 backcross lines along with parents.

Sr. No.	Traits	Mean	Range		GCV (%)	PCV (%)	h ² (bs) (%)	GAM (%)
			Minimum	Maximum				
1.	Days to 50% flowering	39.45	36.00	41.5	2.48	4.15	35.8	3.06
2.	Plant height (cm)	14.65	10.82	21.72	17.43	18.38	89.9	34.03
3.	No. of Primary branches per plant	7.22	6.00	8.80	8.40	13.88	36.6	10.46
4.	No. of Secondary branches per plant	37.97	32.90	43.20	4.97	6.09	66.7	8.36
5.	No. of Pods per Plant	12.94	8.20	18.40	21.37	22.66	94.6	40.79
6.	Pod Yield per plant (g)	9.49	6.31	11.09	13.15	15.21	74.8	23.44
7.	Seed Yield per Plant (g)	6.59	3.81	8.04	14.68	16.69	77.4	26.62
8.	Shelling out turn (%)	66.52	60.41	74.22	4.30	7.30	34.7	5.22
9.	Pod Length (mm)	24.99	21.80	27.40	5.88	6.67	77.8	10.69
10.	Pod Width (mm)	11.80	9.50	13.50	8.60	10.17	71.5	14.99
11.	100 Seed weight	40.03	35.57	42.60	2.92	4.80	37.1	3.67
12.	Oil content (%)	53.73	50.40	59.15	2.45	3.62	45.9	3.42
13.	Protein content (%)	23.26	19.35	28.25	9.14	12.38	54.5	13.90

Table 2: Different types of estimates of genetic parameters in quantitative and quality characters of advanced backcross lines of groundnut.

Sr. No.	Character	Genetic Parameter	Gene effects	Influence of environment
1.	Plant height Number of pods per plant Pod yield per plant Seed yield per plant	High heritability with high GAM	Additive	Low
2.	Pod length Pod width	High heritability with moderate GAM	Additive	Low
3.	Number of primary branches per plant Protein content	Moderate heritability with moderate GAM	Additive and non-additive	Medium
4.	100 seed weight Oil content Shelling outturn Days to 50% flowering	Moderate heritability with low GAM	Non-additive	High

Table 3: Genotypic (G) and Phenotypic (P) correlation coefficients of yield contributing and quality traits.

Character		DDF	PH	NPB/P	NSB/P	NPP	SY/P	SH%	PL	PW	100 SW	Oil content	Protein Content	Pod yield per plant
DDF	r _g	1.0000	-	0.4187**	-0.2928*	0.3953**	-0.0343	0.0390	-	-	-	-0.1790	-0.0849	-0.0062
	r _p	1.000	0.2795*	0.2611**	-0.0530	0.224	-0.0187	-0.1105	-0.5218**	0.3399**	0.3949**	-0.0985	0.0257	0.0882
PH	r _g		1.0000	-0.2644*	-	-	-	-	-	-	-	-	-	-
	r _p		1.000	0.3244**	0.3521**	0.3842**	0.3560**	-0.1480	-0.1784	0.2922*	0.0405	0.3156**	0.2713**	0.5284**
NPB/P	r _g			1.0000	0.5934**	0.0378	-0.0676	0.1689	-0.2353	-0.2115	-	-0.0205	-	-0.2359
	r _p			1.000	0.2630*	0.1663	-0.2288	-0.0916	-0.0942	-0.1764	-0.1654	-0.0563	-0.2335	-0.2355
NSB/P	r _g				1.0000	0.3186**	0.3091*	0.5829**	0.3097*	-0.3112*	-0.0518	-0.1151	-0.0885	0.2056
	r _p				1.000	0.2527*	0.2895*	0.2205	0.2803*	-0.0949	0.0834	-0.0307	-0.0991	0.2946*
NPP	r _g					1.0000	0.5363**	0.6501**	0.1953	0.0492	0.1195	0.1585	0.4455**	0.5148**
	r _p					1.000	0.4364**	0.3670**	0.1715	0.0243	0.0827	0.0849	0.3210*	0.4232**
SY/P	r _g						1.0000	0.8334**	0.3155**	-0.1160	0.2788*	0.4584**	0.2405*	0.9689**
	r _p						1.000	0.6453**	0.2487*	-0.0671	0.2102	0.1689	0.0605	0.8460**
SH%	r _g							1.0000	-0.0244	-0.3076*	0.0657	0.6984**	0.0623	0.7594**
	r _p							1.000	0.0171	-0.2999*	-0.0645	0.2695*	-0.0304	0.3806**
PL	r _g								1.0000	0.3163**	0.7066**	0.0045	0.2161	0.4328**
	r _p								1.000	0.2735*	0.3311**	0.0065	0.1392	0.3110**
PW	r _g									1.0000	0.5865**	-0.1967	0.1636	0.0840
	r _p									1.000	0.2666*	-0.1178	0.1094	0.1427
100 SW	r _g										1.0000	-0.1861	0.4188**	0.2639*
	r _p										1.000	-0.1994	0.2313	0.2943*
Oil content	r _g											1.0000	0.0453	0.5357**
	r _p											1.000	0.0853	0.1353
Protein content	r _g												1.0000	0.2650*
	r _p												1.000	0.0863

DDF: Days to 50% Flowering, PH: Plant Height (cm), NPB/P: Number of Primary Branches per Plant, NSB/P: Number of Secondary Branches per Plant, NPP: Number of Pods per Plant, PY/P: Pod Yield per Plant (g), SY/P: Seed Yield per Plant (g), SH (%): Shelling outturn (%), PL: Pod Length (mm); PW: Pod Width (mm)

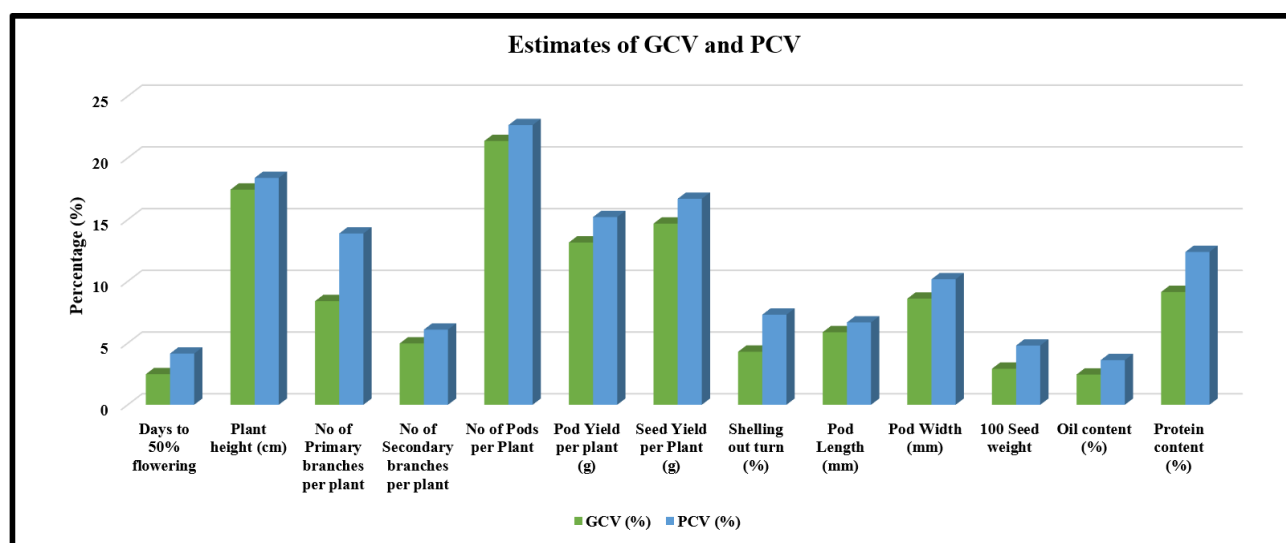


Fig. 1. Estimates of GCV (%) and PCV (%) in backcross lines along with parents.

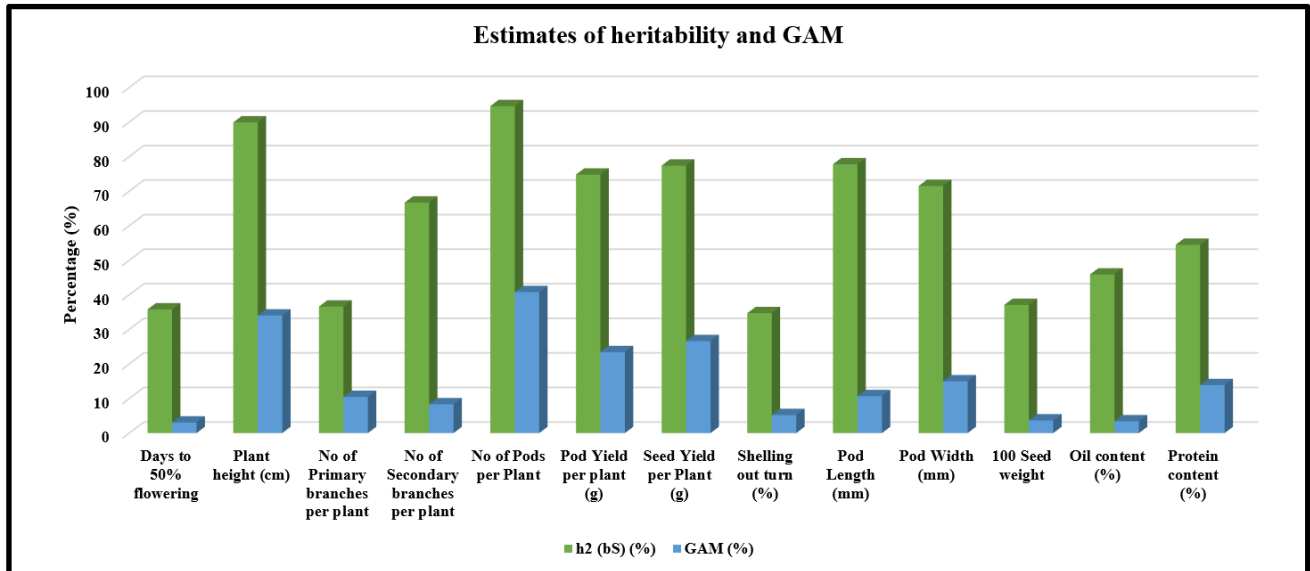


Fig. 2. Estimates of heritability and GAM in backcross lines along with parents.

Table 4: Genotypic (G) and Phenotypic (P) path coefficients of yield contributing and quality traits.

Character		DFP	PH	NPB/P	NSB/P	NPP	SY/P	SH%	PL	PW	100 SW	Oil content	Protein Content	Correlation with podyield / plant
DFP	G	-0.4800	0.1342	-0.2010	0.1405	-0.1897	0.0164	-0.0187	0.2505	0.1632	0.1896	0.0859	0.0407	-0.0062
	P	0.1007	-0.0229	0.0263	-0.0053	0.0224	-0.0019	0.0111	0.0265	0.0048	-0.0042	-0.0099	0.0027	0.0882
PH	G	0.0717	-0.2564	0.0678	0.1154	0.0988	0.1260	0.1200	0.0457	-0.0749	0.0104	0.0809	-0.0696	-0.5284**
	P	0.0288	0.1267	0.0411	0.0446	0.0487	0.0451	0.0188	0.0197	-0.0323	0.0019	0.0240	-0.0244	-0.4010**
NPB/P	G	0.1241	0.0783	0.2963	0.1758	0.0112	-0.0200	0.0500	-0.0697	0.0627	-0.1631	-0.0061	-0.1823	-0.2359
	P	0.0309	0.0384	-0.1184	-0.0311	0.0197	0.0271	0.0108	0.0112	0.0209	0.0196	0.0067	0.0276	-0.2355
NSB/P	G	0.1322	0.2033	-0.2680	0.4517	-0.1439	0.1396	-0.2633	-0.1399	0.1406	0.0234	-0.0520	0.0400	0.2056
	P	-0.0042	-0.0280	0.0209	0.0794	0.0201	0.0230	0.0175	0.0223	-0.0075	0.0066	-0.0024	-0.0079	0.2946*
NPP	G	0.1766	-0.1721	0.0169	0.1423	0.4467	0.2396	0.2904	0.0872	0.0220	0.0534	0.0708	0.1990	0.5148**
	P	0.0090	-0.0155	0.0067	0.0102	0.0403	0.0176	0.0148	0.0069	0.0010	0.0033	0.0034	0.0129	0.4232**
SY/P	G	0.0348	0.4985	0.0685	0.3135	0.5440	1.0143	0.8453	0.3201	-0.1176	0.2828	0.4649	0.2439	0.9689**
	P	-0.0157	0.2980	-0.1915	0.2423	0.3653	0.8371	0.5402	0.2082	-0.0562	0.1759	0.1414	0.0506	0.846**
SH%	G	0.0165	0.1984	0.0716	0.2471	-0.2757	-0.3533	0.4240	0.0104	0.1304	-0.0279	-0.2961	-0.0264	0.7594**
	P	0.0191	0.0256	0.0158	-0.0381	0.0634	-0.1115	0.1728	0.0030	0.0518	0.0112	-0.0466	0.0053	0.3806**
PL	G	0.0453	0.0155	0.0204	-0.0269	-0.0170	0.0274	0.0021	0.0869	0.0275	-0.0614	-0.0004	-0.0188	0.4328**
	P	0.0040	-0.0023	-0.0014	0.0042	0.0026	0.0037	0.0003	0.0150	0.0041	0.0050	0.0001	0.0021	0.3110*
PW	G	0.0304	-0.0262	0.0189	0.0279	-0.0044	0.0104	0.0276	-0.0283	0.0896	-0.0525	0.0176	-0.0147	0.0840
	P	-0.0076	0.0410	-0.0284	-0.0153	0.0039	0.0108	0.0483	0.0440	0.1609	0.0429	-0.0190	0.0176	0.1427
100 SW	G	-0.0213	0.0022	-0.0297	-0.0028	0.0065	0.0151	0.0035	0.0381	0.0317	0.0540	-0.0100	0.0226	0.2639*
	P	0.0019	-0.0007	-0.0074	0.0038	0.0037	0.0095	-0.0029	0.0149	0.0120	0.0450	-0.0090	0.0104	0.2943*
Oil content	G	0.0321	0.0565	0.0037	0.0206	0.0284	0.0821	0.1251	0.0008	-0.0352	-0.0333	0.1791	0.0081	0.5357**
	P	0.0047	0.0091	-0.0027	-0.0015	0.0041	0.0081	0.0129	0.0003	-0.0056	-0.0095	0.0478	0.0041	0.1353
Protein content	G	-0.0019	0.0061	-0.0138	0.0020	0.0100	0.0054	0.0014	0.0048	0.0037	0.0094	0.0010	0.0224	0.2650*
	P	0.0004	0.0028	0.0034	0.0015	0.0047	0.0009	0.0004	0.0021	0.0016	0.0034	-0.0013	-0.0147	0.0863 0.0863

Genotypic Residual Effect = 0.2501 Phenotypic Residual Effect = 0.4283 Direct effects are shown in bold font

DFP: Days to 50% Flowering, PH: Plant Height (cm), NPB/P: Number of Primary Branches per Plant, NSB/P: Number of Secondary Branches per Plant, NPP: Number of Pods per Plant, PY/P: Pod Yield per Plant (g), SY/P: Seed Yield per Plant (g), SH (%): Shelling outturn (%), PL: Pod Length (mm); PW: Pod Width(mm)

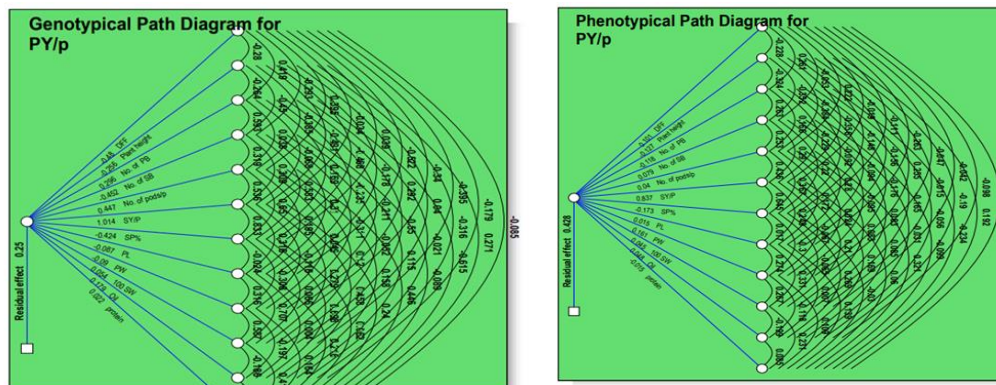


Fig. 3. Phenotypic and Genotypic path diagram for pod yield per plant.

CONCLUSIONS

From the above discussions, on variability and genetic parameters, it is evident that number of pods per plant, plant height, pod yield per plant and seed yield per plant showed high heritability coupled with high GAM which, depicts these traits are less influenced by environment and governed by additive gene effects hence, simple direct selection may be effective to improve these traits. Correlation coefficient analysis revealed that seed yield per plant showed highly positive and significant association with pod yield per plant followed by number of pods per plant, shelling out turn, pod length, number of secondary branches per plant, 100 seed weight, pod width, oil and protein content are the most essential characters, which might contribute significantly towards higher pod yield per plant. Path analysis revealed that seed yield per plant showed high positive direct effect whereas, shelling outturn and 100 seed weight contributes significant amount of indirect effects towards pod yield per plant. Hence, they may be regarded as important traits for selecting high yield in groundnut.

FUTURE SCOPE

Identifying seed yield per plant as significantly positive and direct effect on yielding in groundnut suggesting breeders to select it as the most essential yield contributing character and importance is to be given while, yield improvement in groundnut.

Conflict of Interest. None.

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