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Genetic variability, correlation and path coefficient analysis for yield traits in groundnut (*Arachis hypogaea* L.)

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Abstract

Groundnut (*Arachis hypogaea* L.) is one of the most important oilseed crops, it is valued for its edible oil, protein, and nutritional quality. The present study was done to check genetic variability, correlation, path coefficient analysis, and genetic divergence, among 24 groundnut genotypes during the kharif seasons of 2024 and 2025, at the Agricultural Farm, Rani Lakshmi Bai Central Agricultural University, Jhansi. The trial was carried out in a randomized complete block design with four replications. In general, significant differences among the genotypes were found for all traits. Higher genotypic and phenotypic coefficients of variation, together with high heritability, coupled with high genetic advance were observed for pod yield per plant, hundred seed weight, total number of pods per plant, seed weight, seed length, and pod length. This overall pattern suggests additive gene action so direct selection is likely to work well for these characters. Correlation outcomes showed that pod yield per plant had a significant positive relationship with total number of pods per plant, pod length, pod width, seed length, seed weight, shelling percentage, and hundred seed weight. The path coefficient study further indicated that pod length, seed length, and total number of pods per plant had high positive direct effects on pod yield. Mahalanobis D² analysis placed the 24 genotypes into four separate clusters, indicating fairly large genetic diversity within the material tested. Overall, the results imply that parents which are genetically diverse and also show superior performance for key yield related traits can be used effectively in hybridization programmes to generate high-yielding groundnut varieties, with better productivity.

Keywords: Genetic variability, heritability, genetic advance, D² analysis

Introduction

Groundnut (*Arachis hypogaea* L.) is an essential and profitable oilseed crop also known as King of Oilseeds. It has a chromosome number ($2n = 4x = 40$) and is a self-pollinated crop with cleistogamous flowers and belongs to family Fabaceae. Groundnut supplies oil, protein, dietary fibre, vitamins B-complex, vitamin E, and minerals including iron, zinc, potassium, and magnesium (Mondal *et al.*, 2018) ^[11]. Groundnut also contains trace minerals such as selenium, manganese, and copper, along with antioxidant polyphenolic materials such as flavonoids and resveratrol, which help keep cellular functioning normal. Globally groundnut is cultivated in area of 359.84 lakh hectares and total production reaches 770.69 lakh tonnes, while the average productivity stands at 2109.47 kg ha⁻¹. In India, groundnut occupies 53.51 lakh hectares, producing 120.91 lakh tonnes, and the average productivity is around 2260 kg ha⁻¹ during 2025-26 (upag.gov.in, 2025-26). The crop was grown on 4.87 lakh hectares in Bundelkhand, with total production of 3.61 lakh tonnes, crop together has average productivity of 1580 kg ha⁻¹ in 2022-23 (desagri.gov.in, 2022-23).

Groundnut (*Arachis hypogaea* L.) has huge economic value as a major oilseed, and also as a food legume crop but it has narrow genetic base. Because of that, there is a need for a systematic characterization and screening of the existing germplasm, for agronomically relevant traits, and ability to cope with the biotic and abiotic stresses (Reddy *et al.*, 2023) ^[14]. The overall success of any breeding programme depends a lot on finding better genotypes, through evaluating genetic variability and the amount of diversity that exists in the breeding material.

Measuring the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV) gives useful insight into how much variation is actually available for each trait. Heritability, along with genetic advance, also plays a role in anticipating how well selection might work in practice. Correlation analysis measures the strength of the relationship between yield, and its component traits. In path coefficient analysis, the correlation coefficients are split into direct and indirect effects, which highlight the traits that are required to enhance the yield. So, the current study was carried out to estimate the genetic variability, to look into the association among pod yield and its component traits, and to figure out the direct along with indirect effects of these traits on pod yield. In the end, it should offer practical knowledge that can support future groundnut improvement programmes (BIRTHAL *et al.*, 2010) [2].

Materials and Methods

This study was carried out during kharif season of 2024 at the agricultural Farm, RLBCAU, Jhansi. The experiment was arranged in a randomized complete block design, with four replications. The experimental material consisted of 20 genotypes and 4 checks of groundnut (Table 1). Usual recommended package of practices was followed for crop establishment. The observations were taken from five randomly chosen competitive plants for each genotype in each replication, except days to 50% flowering which was noted on plot basis.

Later, the data was handled for statistical analysis, and the analysis of variance (ANOVA) was computed. Based on that, the following genetic parameters were worked out for the traits that showed significant mean square effects due to genotypes. Phenotypic and genotypic variances were obtained based on the formula explained by Johnson *et al.* (1955) [7]. The phenotypic coefficient of variation and genotypic coefficient of variation were estimated by following Burton (1952) [3]. Broad sense heritability was computed in percent using the approach given by Allard (1960) [1]. The expected genetic advance from selecting five percent of the superior progeny was calculated with the help of Allard (1960) [1]. The genotypic correlation coefficient was determined using the formula recommended by Hazel *et al.* (1943) [6]. For correlation significance, the coefficient was tested against the 'r' value reported by Fischer and Yates (1963) [5]. Further, path coefficient analysis was done by employing the correlation coefficients to understand the direct along with indirect impacts of these variables on yield as suggested by Wright (1921) [20] and demonstrated by Dewey and Lu (1959) [4].

Result and Discussion

Genetic variability

The analysis of genetic variability showed variation among the groundnut genotypes for all the characters that were observed (Table 2). PYQPH, recorded the top mean value 23.99 g, and ranged from 8.80-57.20 g. In the same way, broad ranges were observed for PH (24.28-61.70 cm), TNOB (4.99-29.40), TNOP (8.20-33.20), SPP (1.4-2.6), PL (19.88-37.76 mm), PW (1.08-19.52 mm), SL (3.27-27.94), SW (0.13-14.12 g), SP (48.09-73.54) and HSW (29.67-90.81 g), which indicate substantial genetic diversity present for those traits, overall. This study is in agreement with Reddy *et al.*, (2025) [15], Kumari *et al.*, (2023) [9], Saiteja *et al.*, (2023) [16].

The phenotypic coefficient of variation (PCV) was only slightly higher than the genotypic coefficient of variation (GCV) for all traits, showed that the environment does not interfere too much with how these characters are expressed. The strongest GCV and PCV values were noted for PYQPH (44.71% and 45.03%), TNOB (31.81% and 41.05%), SW (29.58% and 32.76%), TNOP (25.03% and 27.44%), HSW (24.72% and 25.96%), and SP (24.21% and 27.51%). On the other hand, SPP had the smallest GCV at 4.92% and PCV at 8.64%, meaning this particular trait has narrow genetic variability, comparatively.

PYQPH showed the highest heritability (98.6%) followed by PL (96.0%), SP (94.3%), HSW (90.6%), TNOP (83.2%), SW (81.6%), SL (77.5%), PH (70.5%), and PW (70.0%). On the other hand, TNOB (60.0%) had moderate heritability and SPP (32.5%), recorded the smallest heritability.

Highest GAM value was recorded for, PYQPH (91.45%) followed by SW (55.04%), TNOB (50.77%), HSW (48.47%) and TNOP (47.02%). SL (43.90%), PL (31.00%), PH (29.17%), PW (28.16%), SP (16.95%) and SPP (5.79%) showed lowest GAM value. When heritability is coupled with genetic advance, the highest combination observed in PYQPH, HSW, TNOP, SW, SL, and PL showed that additive gene action is predominant in all these traits. But for SPP it was different, it had low h^2 (32.5%) and also low GAM (5.79%) indicating involvement of non-additive gene action. The present investigation is in agreement with Reddy *et al.*, (2025) [15], Kumari *et al.*, (2023) [9], Saiteja *et al.*, (2023) [16], Mallepogu *et al.*, (2025) [10].

Correlation analysis

Phenotypic and genotypic correlation coefficients (Table 3) showed that PYQPH had positive and highly significant phenotypic and genotypic correlation with TNOP ($r_p = 0.975^{**}$, $r_g = 0.889^{**}$), PL ($r_p = 0.990^{**}$, $r_g = 0.964^{**}$), PW ($r_p = 0.910^{**}$, $r_g = 0.856^{**}$), SL ($r_p = 0.908^{**}$, $r_g = 0.866^{**}$), SW ($r_p = 0.918^{**}$, $r_g = 0.914^{**}$), SP ($r_p = 0.903^{**}$, $r_g = 0.878^{**}$), and HSW ($r_p = 0.986^{**}$, $r_g = 0.931^{**}$). At the same time PYQPH was only positively related but not statistically significant with PH, phenotypic correlation (0.239) but significant genotypic correlation with (PH) (0.201*) and non-significant for TNOB. But there was a very small negative association also spotted with SPP (-0.019, -0.005). PH in turn, gave significant positive correlations with TNOB ($r_p = 0.815^{**}$, $r_g = 0.667^{**}$), SP ($r_p = 0.413^*$, $r_g = 0.345^{**}$), TNOP ($r_g = 0.234^*$), PL ($r_g = 0.253^*$), PW ($r_g = 0.230^*$), and HSW ($r_g = 0.270^{**}$). Meanwhile TNOB had significant positive associations with TNOP ($r_g = 0.202^*$), PL ($r_g = 0.229^*$), SP ($r_g = 0.259^*$), and HSW ($r_g = 0.230^*$). For yield contributing traits, TNOP exhibited highly significant positive correlations with PL ($r_p = 0.993^{**}$, $r_g = 0.902^{**}$), PW ($r_p = 0.959^{**}$, $r_g = 0.792^{**}$), SL ($r_p = 0.939^{**}$, $r_g = 0.765^{**}$), SW ($r_p = 0.990^{**}$, $r_g = 0.831^{**}$), SP ($r_p = 0.995^{**}$, $r_g = 0.899^{**}$), and HSW ($r_p = 0.996^{**}$, $r_g = 0.901^{**}$). Similarly, PL also showed highly significant positive correlations with PW ($r_p = 0.924^{**}$, $r_g = 0.865^{**}$), SL ($r_p = 0.947^{**}$, $r_g = 0.859^{**}$), SW ($r_p = 0.994^{**}$, $r_g = 0.915^{**}$), SP ($r_p = 0.941^{**}$, $r_g = 0.915^{**}$), and HSW ($r_p = 0.904^{**}$, $r_g = 0.940^{**}$). And, PW was highly and positively correlated with SL ($r_p = 0.961^{**}$, $r_g = 0.813^{**}$), SW ($r_p = .902^{**}$, $r_g = 0.904^{**}$), SP ($r_p = 0.913^{**}$, $r_g = 0.840^{**}$), and HSW ($r_p = 0.949^{**}$, $r_g = 0.795^{**}$). Overall, among SL, SW, SP, and HSW, positive correlations were also significant at both phenotypic and genotypic levels. In general, the

magnitude of rg was usually higher than the rp across most trait pairings, so the correlation looks like they are mainly governed by genetic factors, with less impact from the environment. So, the strong positive correlation pattern involving PYQPH with TNOP, PL, PW, SL, SW, SP and HSW means these traits could work as suitable selection yardsticks for improving yield in groundnut. Zaman *et al.*, (2012) ^[22], Kumar *et al.*, (2014) ^[8] and Shoba *et al.*, (2012) ^[17] finds similar results in their investigation.

Path coefficient analysis

Genotypic and phenotypic path coefficient (Table 4a and 4b) analyses showed differences in how large the direct and indirect effects of the studied traits are on PYQPH. At the genotypic level, the highest positive direct effect on PYQPH was contributed by SL (0.95484), then TNOP (0.57900), PL (0.37160), PH (0.11099), PW (0.05699), SPP (0.03559) and, finally DT50% (0.02566). Meanwhile the negative direct effects for SW (-0.42652), SP (-0.29591), HSW (-0.24896) and TNOB (-0.02460). The residual effect stayed at 0.0326 which showed that most of the variability in PYQPH is covered by the traits.

At the phenotypic level, PL (0.59288) had the highest positive direct effect on PYQPH, and after that HSW (0.25090), TNOP (0.08767), PW (0.08531), SW (0.08200), SL (0.04401), TNOB (0.00308), and DT50% (0.00088). Negative direct effects were noticed for SP (-0.13423), PH (-0.03403) and SPP (-0.00969). In addition, many yields related traits gave large positive indirect effects through PL, emphasizing its influence on PYQPH when conditions are phenotypic. The residual effect was 0.0551, pointing towards the selected characters accounting for a big share of the phenotypic variation in PYQPH. Patel *et al.*, (2021) ^[12], Tirkey *et al.*, (2021) ^[18] found similar results as the present

study.

Genetic divergence analysis

Using Mahalanobis D² statistics, 20 groundnut genotypes with 4 checks were grouped into four clusters, by Tocher's method (Table 5). Cluster I was the largest, with 18 genotypes (2, 12, 1, 17, 10, 21, 4, 7, 13, 15, 23, 24, 20, 16, 3, 8, 6, and 9), then Cluster II had only three (11, 19, and 22). Cluster III held two genotypes (5 and 18) and Cluster IV was more like a solo cluster, only genotype 14. This spread across clusters suggests that there is quite a lot of genetic diversity.

Looking at the mean intra-cluster D² distance (Table 6), it went from 0.00 up to 103.80. Cluster III showed the highest intra-cluster value (103.80), and after that Cluster I (56.87), while Cluster II came next (38.03). Cluster IV, since it had just one genotype, naturally had an intra-cluster distance of 0.00. The fact that Cluster III had the larger intra-cluster distance means the genotypes inside it are more genetically diversity.

For the mean inter-cluster D² distance, the range was 139.48 to 1722.22. The largest inter-cluster distance was between Clusters III and IV (1722.22), then Clusters I and III (1131.45) and finally Clusters II and IV (645.71). So, in general, these clusters are quite genetically far apart. Meanwhile the smallest inter-cluster distance came from Clusters I and IV (139.48), then Clusters I and II (288.43), and then Clusters II and III (371.96). This pattern implies the genetic relation between Clusters I, II, and IV are somewhat less distant compared with the other pairings. The present finding is in agreement with the results of Zaman *et al.*, (2010) ^[21], Vivekananda *et al.*, (2015) ^[19], Raghuvanshi *et al.*, (2016) ^[13].

Table 1: Mean performance of genotypes combination for 12 characters in Groundnut [*Arachis hypogaea* (L)]

Genotype No.	Genotype	DT50%	PH	TNOB	TNOP	SPP	PL	PW	SL	SW	SP	HSW	PYQPH
1	TG82	26.5	53.33	20.60	21.65	2.00	28.71	11.69	12.87	6.86	65.38	52.21	25.87
2	TG83	27	49.93	15.55	20.85	2.15	27.74	11.29	12.68	6.68	65.32	51.09	24.37
3	TG86	25	53.90	18.80	15.34	2.25	24.68	9.72	11.21	5.45	59.56	37.80	16.70
4	TG87	25.25	47.50	15.95	18.55	1.90	26.14	10.56	12.24	6.17	62.88	46.47	20.20
5	TG88	26	46.83	16.50	27.90	1.75	36.17	14.65	21.12	11.66	71.01	74.30	46.13
6	TG92	28	28.50	5.9975	14.09	2.00	23.64	9.43	10.57	5.02	55.49	34.88	15.06
7	TG93	27	31.10	5.195	18.71	1.80	26.20	10.56	12.16	6.26	62.62	46.22	20.40
8	TG90	26	31.26	5.995	15.09	1.95	24.17	9.60	10.94	5.34	58.23	36.60	16.13
9	TG84	27	25.58	5.995	13.01	1.95	22.66	9.08	10.18	4.84	53.55	32.86	13.33
10	TG89	26	45.70	20.80	18.97	1.95	26.80	10.76	12.35	6.42	63.20	48.72	23.00
11	TAG24	28	46.45	19.20	25.20	1.95	33.02	13.06	14.52	8.26	68.51	61.08	35.60
12	JL 776	26.5	45.65	11.10	20.37	1.90	27.39	11.06	12.56	6.69	64.72	50.76	24.10
13	CGM1	27	52.73	18.85	17.56	2.00	25.42	10.36	11.93	5.89	61.60	43.78	18.97
14	RLBGN1	27.25	46.95	16.35	10.15	1.70	21.71	6.81	8.29	3.36	51.33	32.03	10.07
15	RLBGN2	26	46.25	14.50	16.61	1.80	25.17	10.08	11.80	5.75	61.34	42.96	18.07
16	RLBGN3	25.75	50.00	13.85	14.99	1.85	24.42	9.63	11.12	5.33	58.33	37.50	16.20
17	RLBGN4	26.5	51.35	10.15	21.92	1.95	29.29	12.16	13.06	7.47	66.64	54.67	26.43
18	RLBGN5	27.25	42.73	15.20	30.30	1.95	37.19	15.21	23.13	12.24	71.61	73.95	55.00
19	RLBGN6	27	46.23	13.55	26.53	1.95	34.37	13.32	16.32	9.02	69.61	64.03	38.17
20	RLBGN7	27.25	43.42	20.95	15.48	1.95	24.29	9.73	11.12	5.38	58.32	38.61	17.20
21	TAG73	25.75	43.04	15.35	23.30	2.05	29.85	12.34	13.07	7.58	67.37	55.35	29.20
22	TG37A	27	45.23	17.05	23.75	2.05	31.92	12.75	13.53	7.92	67.96	59.39	30.77
23	GIRNAR2	27	39.45	15.20	20.30	2.00	24.76	9.95	11.50	5.50	60.49	39.64	17.70
24	K6	26.75	39.58	9.83	16.15	1.95	24.89	9.96	11.64	5.59	60.46	39.61	17.10

DT50% = Days to 50% flowering; PH = Plant height; TNOB = Total number of branches per plant; TNOP = Total number of pods per plant; SPP = Seeds per pod; PL = Pod length; PW = Pod width; SL = Seed length; SW = Seed weight; SP = Shelling percentage; HSW = Hundred seed weight; PYQPH = Pod yield quintal per hectare.

Table 2: Range, Heritability, Genetic Advance, Genotypic and Phenotypic Coefficient of variation for 12 characters in Groundnut [*Arachis hypogaea* (L.)]

Trait	Mean	Range	SEm	CD (5%)	GCV (%)	PCV (%)	h ² (BS)	GA	GAM (%)
PYQPH	23.99	8.80-57.20	0.641	1.808	44.71	45.03	98.6	21.94	91.45
PH	43.86	24.28-61.70	2.393	6.751	16.86	20.09	70.5	12.79	29.17
TNOB	14.27	4.99-29.40	1.852	5.224	31.81	41.05	60	7.25	50.77
TNOP	19.45	8.20-33.20	1.095	3.089	25.03	27.44	83.2	9.14	47.02
SPP	1.95	1.40-2.60	0.069	0.195	4.92	8.64	32.5	0.113	5.79
PL	27.52	19.88-37.76	0.430	1.212	15.36	15.67	96	8.53	31.00
PW	10.99	1.08-19.52	0.589	1.661	16.34	19.54	70	3.09	28.16
SL	12.91	3.27-27.94	0.843	2.379	24.21	27.51	77.5	5.67	43.90
SW	6.69	0.13-14.12	0.471	1.328	29.58	32.76	81.6	3.68	55.04
SP	62.73	48.09-73.54	0.652	1.840	8.47	8.72	94.3	10.63	16.95
HSW	48.10	29.67-90.81	1.913	5.396	24.72	25.96	90.6	23.31	48.47

Table 3: Genotypic and Phenotypic correlation among 12 characters in Groundnut [*Arachis hypogaea* (L.)]

S. No.	Character		DT50%	PYQPH	PH	TNOB	TNOP	SPP	PL	PW	SL	SW	SP	HSW
			1.000	0.051	-0.205*	0.016	0.033	-0.060	0.045	-0.005	-0.012	-0.002	-0.016	0.046
1	PYQPH	r _p		1.000	0.239	0.268	0.975**	-0.019	0.990**	0.910**	0.908**	0.918**	0.903**	0.986**
		r _g		1.000	0.201*	0.192	0.889**	-0.005	0.964**	0.856**	0.866**	0.914**	0.878**	0.931**
2	PH	r _p			1.000	0.815**	0.298	0.172	0.289	0.255	0.176	0.214	0.413*	0.346
		r _g			1.000	0.667**	0.234*	0.164	0.253*	0.230*	0.165	0.199	0.345**	0.270**
3	TNOB	r _p				1.000	0.299	0.221	0.277	0.242	0.192	0.212	0.322	0.312
		r _g				1.000	0.202*	0.175	0.229*	0.179	0.164	0.167	0.259*	0.230*
4	TNOP	r _p					1.000	0.107	0.993**	0.959**	0.939**	0.990**	0.995**	0.996**
		r _g					1.000	0.078	0.902**	0.792**	0.765**	0.831**	0.899**	0.901**
5	SPP	r _p						1.000	0.013	0.089	-0.127	-0.059	0.159	-0.034
		r _g						1.000	0.013	0.130	-0.011	0.030	0.096	-0.019
6	PL	r _p							1.000	0.924**	0.947**	0.994**	0.941**	0.904**
		r _g							1.000	0.865**	0.859**	0.915**	0.915**	0.940**
7	PW	r _p								1.000	0.961**	0.902**	0.913**	0.949**
		r _g								1.000	0.813**	0.904**	0.840**	0.795**
8	SL	r _p									1.000	0.994**	0.848**	0.953**
		r _g									1.000	0.949**	0.758**	0.819**
9	SW	r _p										1.000	0.924**	0.909**
		r _g										1.000	0.841**	0.864**
10	SP	r _p											1.000	0.970**
		r _g											1.000	0.914**
11	HSW	r _p												1.000
		r _g												1.000

DT50% = Days to 50% flowering; PH = Plant height; TNOB = Total number of branches per plant; TNOP = Total number of pods per plant; SPP = Seeds per pod; PL = Pod length; PW = Pod width; SL = Seed length; SW = Seed weight; SP = Shelling percentage; HSW = Hundred seed weight; PYQPH = Pod yield quintal per hectare.

Table 4(a): Genotypic path for 12 characters in Groundnut [*Arachis hypogaea* (L.)]

Trait	DT50%	PH	TNOB	TNOP	SPP	PL	PW	SL	SW	SP	HSW
DT50%	0.02566	-0.09414	0.01388	0.13696	-0.00767	0.10364	0.01029	0.17612	-0.06455	0.03409	-0.03163
PH	-0.02176	0.11099	-0.02004	0.17240	0.00613	0.10743	0.01451	0.16845	-0.09108	-0.12217	-0.08614
TNOB	-0.01447	0.09043	-0.02460	0.17295	0.00788	0.10276	0.01378	0.18300	-0.09041	-0.09533	-0.07776
TNOP	0.00607	0.03305	-0.00735	0.57900	0.00380	0.36887	0.06033	0.89609	-0.42241	-0.29427	-0.24804
SPP	-0.00553	0.01912	-0.00545	0.06190	0.03559	0.00499	0.00508	-0.12092	0.02503	-0.04703	0.00836
PL	0.00716	0.03209	-0.00680	0.57473	0.00048	0.37160	0.05837	0.90413	-0.42379	-0.27850	-0.24998
PW	0.00463	0.02826	-0.00595	0.61288	0.00317	0.38060	0.05699	0.91761	-0.42739	-0.29972	-0.26119
SL	0.00473	0.01958	-0.00471	0.54337	-0.00451	0.35187	0.05477	0.95484	-0.42383	-0.25097	-0.23714
SW	0.00388	0.02370	-0.00521	0.57342	-0.00209	0.36922	0.05711	0.94882	-0.42652	-0.27330	-0.25109
SP	-0.00296	0.04582	-0.00792	0.57580	0.00566	0.34974	0.05772	0.80984	-0.39393	-0.29591	-0.24139
HSW	0.00326	0.03840	-0.00768	0.57685	-0.00119	0.37312	0.05979	0.90951	-0.43017	-0.28691	-0.24896

Table 4(b): Phenotypic path for 12 characters in Groundnut [*Arachis hypogaea* (L)]

Character	DT50%	PH	TNOB	TNOP	SPP	PL	PW	SL	SW	SP	HSW
DT50%	0.00088	0.00697	0.00005	0.00291	0.00061	0.02674	-0.00041	-0.00052	-0.00020	0.00207	0.01152
PH	-0.00018	-0.03403	0.00205	0.02049	-0.00161	0.14982	0.01962	0.00728	0.01631	-0.04627	0.06762
TNOB	0.00001	-0.02270	0.00308	0.01774	-0.00171	0.13595	0.01524	0.00722	0.01373	-0.03474	0.05768
TNOP	0.00003	-0.00795	0.00062	0.08767	-0.00076	0.53489	0.06759	0.03368	0.06815	-0.12065	0.22603
SPP	-0.00005	-0.00560	0.00054	0.00684	-0.00969	0.00735	0.01086	-0.00044	0.00244	-0.01298	-0.00477
PL	0.00004	-0.00860	0.00071	0.07910	-0.00012	0.59288	0.07381	0.03779	0.07501	-0.12278	0.23587
PW	0.00000	-0.00783	0.00055	0.06946	-0.00125	0.51296	0.08531	0.03576	0.07407	-0.11270	0.19956
SL	-0.00001	-0.00563	0.00051	0.06709	0.00010	0.50916	0.06932	0.04401	0.07783	-0.10175	0.20549
SW	0.00000	-0.00677	0.00052	0.07287	-0.00029	0.54242	0.07706	0.04177	0.08200	-0.11284	0.21675
SP	-0.00001	-0.01173	0.00080	0.07880	-0.00095	0.54231	0.07162	0.03336	0.06892	-0.13423	0.22922
HSW	0.00004	-0.00917	0.00071	0.07898	0.00019	0.55736	0.06785	0.03604	0.07083	-0.12264	0.25090

Table 5: Estimation of average Inter and Intra Cluster distance in Groundnut [*Arachis hypogaea* (L)]

Cluster	Number of Genotypes	Genotype Numbers
I	18	2, 12, 1, 17, 10, 21, 4, 7, 13, 15, 23, 24, 20, 16, 3, 8, 6, 9
II	3	11, 19, 22
III	2	5, 18
IV	1	14

Table 6: Cluster mean for 12 characters in Groundnut [*Arachis hypogaea* (L)]

Cluster	I	II	III	IV
I	56.87	288.43	1131.45	139.48
II	288.43	38.03	371.96	645.71
III	1131.45	371.96	103.80	1722.22
IV	139.48	645.71	1722.22	0.00

Conclusion

This present investigation showed wide, genetic variability among 24 groundnut genotypes for pod yield and the traits that come with it, so that overall, there is a real scope for genetic improvement via selection. Genotypes RLBGN5, TG88, RLBGN6, TAG24 and TG37A did well in pod yield per plant, and they also looked good for several yield contributing characters, so they can be considered useful genetic resources for future breeding programmes. Heritability coupled with high genetic advance for pod yield per plant, hundred seed weight, total number of pods per plant, seed weight, seed length, and pod length, indicated that additive gene action is playing the major role, and this also suggests that direct selection on these phenotypes would be beneficial. Then correlation and path coefficient analyses highlighted total number of pods per plant, pod length, seed length, pod width, seed weight, shelling percentage, and hundred seed weight as the main selection criteria to improve pod yield, but pod length, seed length, and total number of pods per plant gave the highest positive direct effects, sort of the strongest push. Using Mahalanobis D^2 , the genotypes were divided into four separate clusters, and the largest inter cluster distance was between Clusters III and IV, which clearly points toward wide genetic divergence. So, genetically divergent and high performing genotypes like RLBGN5 and TG88 from Cluster III with RLBGN1 from Cluster IV, or from Cluster II, like TAG24, RLBGN6, and TG37A, are expected to create broad genetic variability and also desirable recombinants. In the end these genotypes may help in developing new high yielding groundnut varieties, with better yield traits overall.

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