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GENETIC VARIABILITY AND CORRELATION STUDY AMONG ADVANCED BREEDING LINES OF GROUNDNUT (*ARACHIS HYPOGAEA* L.)

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ABSTRACT

A field experiment was conducted during *kharif* 2024 at ZAHRS, Hiriyur, Karnataka India to assess genetic variability and correlation study in advanced breeding lines of groundnut along with four checks. Analysis of variance (ANOVA) revealed that there is a significant difference among genotypes for most traits indicating substantial genetic variability. Plant height showed high heritability coupled with considerable genetic advance highlighting the role of additive gene action. Similarly, number of mature pods per plant, test weight and pod yield per plant recorded high heritability estimates with substantial genetic advance as percent of mean indicating these traits can be effectively improved through selection. Moderate to high genotypic (GCV) and phenotypic coefficients of variation (PCV) were observed for traits like number of branches, number of mature pods per plant and pod yield per plant reflecting wide variability among genotypes. ANOVA also showed significant treatment mean squares for plant height and number of mature pods per plant further confirming variability. Correlation studies revealed that kernel yield, pod yield and test weight were positively and strongly associated suggesting simultaneous improvement is feasible. Pod yield exhibited a perfect positive correlation with kernel yield ($r = 1.00$) and a strong correlation with test weight ($r = 0.62$) while kernel yield was also positively correlated with test weight ($r = 0.62$) indicating these yield components contribute substantially to overall productivity. The study thus highlights the rich genetic base present in the evaluated groundnut material and underscores that selection emphasizing kernel yield, pod yield and test weight could effectively enhance seed yield providing valuable direction for future breeding programs aimed at yield improvement.

***Keywords* :** GCV, PCV, ANOVA.

Introduction

Groundnut being the important source of edible oil and vegetable protein, the productivity of the crop is increasingly threatened by soil salinity, a growing abiotic stress that is being exacerbated by factors such as climate change, improper irrigation practices and seawater intrusion (Shrivastava and Kumar, 2015). The presence of genetic variability for various traits is crucial for any crop improvement program. Assessing the variability for salt tolerance, yield, and yield components were taken in normal field condition and is crucial for selecting the desired genotypes for breeding. In plant breeding, it is essential to examine the associations between yield and yield-related traits for efficient selection. Selection based on highly heritable, simply inherited traits is often more effective and reliable than direct selection for yield itself. A comprehensive understanding of the relationships among different yield components and their interdependencies is vital for formulating effective breeding strategies aimed at improving yield (Prabhu *et al.*, 2016).

Materials and Methods

The present investigation on 'Genetic Variability and Correlation Study among Advanced Breeding Lines of Groundnut (*Arachis hypogaea* L.)' was carried out to achieve the set of objectives. The details of material used and techniques adopted in the present study for recording of observations, analysis and interpretation of data are briefly presented in this chapter.The present investigation was conducted in ZAHRS, Hiriyur, 2024-25. The experimental material comprised 200 advanced breeding lines of groundnut obtained from IIGR, Junagadh, Gujarat and four checks, namely Kadiri Lepakshi, TMV-2, GPBD-4 and Dh-256 from ZAHRS, Hiriyur which are presented in Table 1.

Method of sampling and recording observations

Three randomly selected plants in all the genotypes were used for taking the observations on below mentioned characters. The average of observations recorded on the three plants was considered for statistical analysis. The characters observed for eliciting the information are described below.

Observations recorded

Days to fifty per cent flowering

The number of days taken from the date of sowing to fifty *per cent* of the plants to flower was recorded for each genotype.

Days to physiological maturity

The number of days taken from the date of sowing to physiological maturity of the plants was recorded for each genotype.

Plant height (cm)

The plant height was recorded as the height of the main axis from ground level to apical leaflet.

Number of branches per plant

The total number of primary branches borne on the main axis in each plant was counted.

Number of mature pods per plant

Total number of mature pods produced in each plant was counted.

Pod yield per plant (g)

The weight of total pods per plant obtained after optimum drying of the plants was recorded.

Kernel yield per plant (g)

The weight of the total kernels obtained from pods per plant was recorded.

Shelling percentage

A random sample of pods from each genotype was drawn and its weight was recorded. Then, the quantity of kernels recovered after shelling the same sample of pods was recorded. The shelling percentage was calculated with the help of following formula:

$$\text{Shelling percentage} = \frac{\text{Kernel yield}}{\text{Pod yield}} \times 100$$

Test weight (g)

A random sample of 100 filled seeds (avoiding shrivelled and broken ones) was drawn and its weight was recorded in grams to get 100 kernel weight.

Statistical Analysis

The mean of observations recorded from three randomly selected plants was used for statistical analysis. Variability and correlation parameters were computed using R software.

Results and Discussion

Genetic variability parameters for yield and yield attributing traits

The mean values of all considered traits, of 200 genotypes were subjected to statistical analysis in R software, to check whether the used population were exhibiting variability or not.

Variation in advanced breeding lines may be due to either genetic or environmental differences. Genetic variability is the presence of variation among individuals, due to differences in the genetic composition and its presence is a key prerequisite for any crop improvement. The genetic variability parameters *viz.*, mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (h^2) and genetic advance as *per cent* of mean(GAM) for all the nine characters are mentioned in Table 2 and 3.

A high heritability value of 74.33 *per cent* coupled with medium genetic advance as *per cent* of mean (14.28) and overall trait mean value of 33.50 with a range of 25 to 42 days were recorded for days to 50 *per cent* flowering. The phenotypic and genotypic coefficients of variability for this trait were low with values 9.31 and 8.03*per cent*, respectively.

Days to physiological maturity recorded a range from 98 to 119 days with an overall mean of 108.5 days. This trait exhibited a low phenotypic and genotypic coefficient of variability of 6.56 and 6.44 *per cent*, respectively. A high heritability of 96.22 *per cent* and a moderate genetic advance as *per cent* of mean of 13.02 *per cent* was recorded for this trait.

The plant height at maturity was in the range of 32.23 to 60.66 cm with a mean of 44.73 cm. A moderate genotypic and phenotypic coefficient of variability of 11.10 and 11.28 *per cent*, respectively, were recorded for this trait. A high heritability of 96.82*per cent* coupled with high genetic advance as *per cent* of mean of 22.54 *per cent* was recorded for this trait.

Number of primary branches per plant ranged from 3.12 to 8.53 with a mean value of 5.81. The estimates of GCV and PCV were moderate with values 21.71 and 28.66*per cent*, respectively. Moderate heritability (57.39) coupled with high genetic advance as *per cent*of mean (33.93 %) was recorded for this character.

The mean number of pods per plant was 20.50 ranging from 13.07 to 29.07. A high heritability of 90.48*per cent* was observed with a high genetic advance as *per cent*of mean of 27.05*per cent*. Moderate phenotypic and genotypic coefficients of variability were observed for this trait (14.49 and 13.78%, respectively).

The moderate PCV (16.96%) and GCV (15.66%) were estimated for pod yield per plant. The heritability was high with a value of 85.28 *per cent* coupled with high genetic advance as *per cent* of mean (29.83%). Pod yield per plant ranged from 11.30 to 24.05 g with a mean of 17.68 g.

Kernel yield per plant varied from 7.68 to 16.11 g with a mean of 12.28 g. Moderate values of GCV (13.69%) and PCV (16.89%) were recorded for this trait. High heritability (65.69 %) combined with high genetic advance as *per cent* of mean (22.89%) were observed. The shelling percentage varied from 53.25 to 86.43 with a mean of 68.78. Moderate values of GCV (13.43) and PCV (13.58) were also recorded for this character. High heritability coupled with high genetic advance as *per cent*of mean (97.81and 27.40%, respectively) were also recorded.

Test weight exhibited considerable variation and ranged from 35.66 g to 71.46 g with a mean of 53.73 g. The moderate estimates of GCV and PCV (12.09 and 12.52%) were recorded, respectively. Further, this trait exhibited high heritability (93.33%) combined with high genetic advance as *per cent* of mean (24.10%).

Phenotypic correlation coefficient analysis for yield and yield attributing traits

Correlation studies provides a clear idea of character association which is generally due to pleiotropy, linkage, physiological association in development and biochemical pathways. Correlation analysis is very essential to know the mutual relationship between two variables as it measures the degree of closeness and the linear relationship between two variables. The correlation for nine traits of groundnut advanced breeding lines were recorded to draw the conclusion about the association present among them (Table 4)

Days to 50*per cent* flowering showed a strong and significant positive correlation with days to physiological maturity (0.42), shelling percentage (0.14) and a weak positive association with number of branches per plant (0.04), pod yield per plant (0.08) and kernel yield per plant (0.06). Its association with plant height (–0.01) was weak and negative, while with number of mature pods per plant (–0.13) and test weight (–0.13), it was also negative and significant.

Days to physiological maturity was positively correlated with days to 50 *per cent* flowering (0.42) and shelling percentage (0.17), while weak positive association with plant height (0.02), number of primary branches per plant (0.03), and pod yield per plant (0.01). It showed weak and negative association with kernel yield per plant (–0.02) and strong negative association with number of mature pods per plant (–0.17) and test weight (–0.17).Plant height showed weak and non-significant associations with days to 50*per cent* flowering (–0.01), days to physiological maturity (0.02), number of branches per plant (0.01) and number of mature pods per plant (0.02). Its correlation with pod yield per plant (–0.03), kernel yield per plant (–0.04), shelling percentage (–0.09) and test weight (–0.03), were negligible. Number of branches per plant showed weak positive correlation with days to 50 *per cent* flowering (0.04), days to physiological maturity (0.03), plant height (0.01), number of mature pods per plant (0.08), pod yield per plant (0.02), kernel yield per plant (0.03) and shelling percentage (0.09). Its correlation with test weight (0.01) weak and positive, with none of the associations being significant.

Number of mature pods per plant recorded a significant positive correlation with pod yield per plant (0.14) and test weight (0.72), while showing weak positive association with kernel yield per plant (0.12) and shelling percentage (0.06). It showed significant negative association with days to 50*per cent* flowering (–0.13) and days to physiological maturity (–0.17), whereas the correlation with plant height (0.02) was negligible.

Pod yield per plant showed a strong and highly significant positive correlation with kernel yield per plant (0.95) and shelling percentage (0.86), while also positive and significant with number of mature pods per plant (0.14) and test weight (0.18). Its association with days to 50 *per cent* flowering (0.08) and days to physiological maturity (0.01) was weak and non-significant, and correlation with plant height (–0.03) was weak and negative.

Kernel yield per plant was strongly and positively correlated with pod yield per plant (0.95) and shelling percentage (0.81). It also showed a weak but positive correlation with test weight (0.15) and number of mature pods per plant (0.12). Correlation with days to 50 *per cent* flowering (0.06) was weak and positive, while with days to physiological maturity (–0.02) and plant height (–0.04) was weak and negative.

Shelling percentage exhibited strong and highly significant positive correlation with pod yield per plant (0.86) and kernel yield per plant (0.81). It also showed positive associations with days to 50*per cent* flowering (0.14), days to physiological maturity (0.17), number of branches per plant (0.09), number of mature pods per plant (0.06), and test weight (0.10). Its correlation with plant height (–0.09) was weak and negative.

Test weight showed a highly significant positive correlation with number of mature pods per plant (0.72), as well as weak but positive association with pod yield per plant (0.18), kernel yield per plant (0.15), and shelling percentage (0.10). Its association with number of branches per plant (0.01) were negligible. Test weight saw negatively correlated with days to 50 *per cent* flowering (-0.13), days to physiological maturity (-0.17) and plant height (-0.03).

Genetic variability parameters for yield and yield attributing traits

The assessment of genetic variability is crucial for formulating effective breeding strategies as it determines the potential for improvement of traits through selection. In the present study, all evaluated traits exhibited differences in the magnitude of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as *percent* of mean (GAM) indicating varied levels of genetic control and environmental influence.

For all measured traits, PCV values were marginally higher than GCV values implying a minor but consistent influence of environmental factors on trait expression. The highest variability was observed for number of branches per plant followed by pod yield per plant and kernel yield per plant. Such high estimates indicate ample scope for improvement through phenotypic selection. Conversely, traits like days to 50*per cent* flowering and days to physiological maturity showed low GCV and PCV reflecting a broad genetic base and greater stability under the test conditions. Similar trends have been documented by Abubakar *et al.* (2024) and Suthar (2023) suggesting that traits with high variability respond better to selection pressure.

Heritability estimates were predominantly high across traits, with the highest recorded for shelling percentage, plant height, days to physiological maturity and test weight. High heritability suggests that these traits are primarily governed by additive gene action and less affected by the environment, making them amenable for direct selection. Moderate heritability for number of branches per plant suggests moderate genetic control possibly due to the combined influence of additive and non-additive genetic effects as supported by findings from Rathod *et al.* (2023).

High GAM values were observed for number of branches per plant, number of mature pods per plant, shelling percentage and pod yield per plant indicating the possibility of substantial genetic gains through selection. Traits such as days to 50*per cent* flowering and days to physiological maturity recorded medium GAM, while plant height, kernel yield per plant and test weight showed high GAM, reinforcing their potential for improvement in early segregating generations. The combination of high heritability and high GAM for these traits confirms that they are under additive genetic control similarly reported by Rajput *et al.* (2024) and Sushmitha *et al.* (2024).

The observed variability patterns suggest that traits like number of branches per plant, number of mature pods per plant, shelling percentage, pod yield per plant and test weight which exhibit high heritability coupled with high GAM should be prioritized for direct phenotypic selection. For traits with high heritability but lower GAM such as days to physiological maturity, selection may need to be practiced over multiple generations or integrated with other breeding approaches like recurrent selection. The variability observed among genotypes indicates a rich genetic base that can be effectively exploited to develop superior groundnut varieties with improved yield.

Phenotypic correlation analysis for yield and yield attributing traits

Yield is a complex quantitative trait influenced by environmental factors and various yield components making genotype selection based solely on yield less effective. Understanding the interactions among different traits is crucial in plant breeding. The direction and strength of associations between yield and its component traits as well as the relationships among those traits influence the efficiency of selection. However, if a correlation arises mainly due to a trait's indirect effect on other components, breeders should focus on selecting the specific trait that is likely to enhance yield through its indirect impact. Therefore, correlation coefficients are valuable for improving the primary trait of interest through the indirect selection of secondary related traits.

When a trait is used for indirect selection has high heritability, significant genetic advance and a positive correlation with yield, the resulting yield response is highly beneficial. Consequently, correlation analysis becomes a valuable tool for breeders helping them to design effective breeding strategies for genetic improvement.

Days to 50*per cent* flowering exhibited positive correlations with days to physiological maturity and shelling percentage, but negative associations with number of mature pods per plant and test weight. This suggests that late-flowering genotypes tend to extend reproductive duration, thereby achieving better kernel recovery, though often at the cost of reduced pod number and seed size. Similar findings were observed by Korale *et al.* (2022), who reported that prolonged flowering duration was associated with improved assimilate partitioning but slightly reduced seed weight in groundnut. Recent studies by Reddy *et al.* (2023) also confirmed that phenological traits such as flowering and maturity strongly influence yield adaptability under multi-environment trials.

Days to physiological maturity showed positive correlation with shelling percentage but negative with number of mature pods per plant and kernel yield per plant. This indicates that prolonged maturity supports kernel filling and shelling but reduces kernel yield efficiency. Shendekar *et al.* (2023) also reported that maturity traits influenced yield indirectly via pod yield and shelling percentage, aligning with the present results.

Plant height had negligible correlation with yield traits, suggesting it is not an effective selection trait for productivity. Kolekar *et al.* (2017) observed similar weak associations between plant height and kernel yield, highlighting its limited role in yield improvement.

Number of branches per plant showed weak, positive but non-significant correlations with yield traits, confirming its minor influence on productivity. Parmar *et al.* (2013) also found branching to have negligible associations with pod and kernel yield, in agreement with the present findings

Number of mature pods per plant showed strong positive correlations with pod yield per plant and test weight but negative associations with days to 50 per cent flowering and days to maturity. This indicates that, genotypes with higher pod numbers yield more and produce bold seeds. Gampa *et al.* (2020) reported similar relationships, where pod number was positively associated with pod yield and test weight.

Pod yield per plant exhibited the strongest positive correlation with kernel yield per plant and shelling percentage, confirming it as the most reliable yield component. Rajanna *et al.* (2024) also identified pod yield as the primary determinant of kernel yield in groundnut, which agrees with these results.

Kernel yield per plant was strongly correlated with pod yield per plant and shelling percentage, while its association with plant height and days to maturity was negligible. This confirms that kernel yield is mainly determined by pod yield and shelling percentage. Reddy *et al.* (2023) also demonstrated that kernel yield depends largely on pod yield and shelling efficiency under different environments.

Shelling percentage exhibited strong positive correlations with pod yield per plant and kernel yield per plant, highlighting its role as both a yield and quality trait. Shendekar *et al.* (2023) similarly reported shelling percentage as a major direct and indirect contributor to kernel productivity, consistent with the present study.

Test weight was positively correlated with number of mature pods per plant, pod yield per plant, and kernel yield per plant but negatively with days to 50 *per cent* flowering and days to maturity. This shows that bold seeds contribute to yield improvement, while delayed phenology reduces seed size. Vekariya *et al.* (2010) also reported test weight to be positively associated with yield but negatively related to late maturity, supporting the present results.

Table 1: List of genotypes used in the present investigation

Sl. No.	Genotypes	Sl. No.	Genotypes	Sl. No.	Genotypes
1	NRCG 6909	31	NRCG 8219	61	NRCG 11131
2	NRCG 10329	32	NRCG 11444	62	NRCG 235
3	NRCG 11554	33	NRCG 10572	63	NRCG 210
4	NRCG 12278	34	NRCG 13378	64	NRCG 14102
5	NRCG 10339	35	NRCG 10575	65	NRCG 16234
6	NRCG 10630	36	NRCG 13363	66	NRCG 16074

7	NRCG 14045	37	NRCG 10269	67	NRCG 10556
8	NRCG 121	38	NRCG 12294	68	NRCG 9386
9	NRCG 14075	39	NRCG 14588	69	NRCG 3522
10	NRCG 8231	40	NRCG 6728	70	NRCG 150
11	NRCG 9272	41	NRCG 9375	71	NRCG 14034
12	NRCG 10812	42	NRCG 14069	72	NRCG 10398
13	NRCG 10334	43	NRCG 10262	73	NRCG 14434
14	NRCG 8218	44	NRCG 8358	74	NRCG 16237
15	NRCG 228	45	NRCG 8211	75	NRCG 14096
16	NRCG 12217	46	NRCG 10341	76	NRCG 8167
17	NRCG 10753	47	NRCG 9863	77	NRCG 13586
18	NRCG 10277	48	NRCG 10335	78	NRCG 13746
19	NRCG 4341	49	NRCG 14016	79	NRCG 10348
20	NRCG14493	50	NRCG 10519	80	NRCG 13583
21	NRCG 14098	51	NRCG 10983	81	NRCG 12291
22	NRCG 10576	52	NRCG 10649	82	NRCG 6937
23	NRCG 6912	53	NRCG 10417	83	NRCG 10338
24	NRCG 13924	54	NRCG 14094	84	NRCG 6388
25	NRCG 9406	55	NRCG 8323	85	NRCG 6775
26	NRCG 9333	56	NRCG 11577	86	NRCG 237
27	NRCG 6734	57	NRCG 10292	87	NRCG 11568
28	NRCG 14049	58	NRCG 10981	88	NRCG 14004
29	NRCG 13384	59	NRCG 14036	89	NRCG 14586
30	NRCG 10332	60	NRCG 135	90	NRCG 11567
91	NRCG 6800	125	NRCG 11574	159	NRCG 10638
92	NRCG 12379	126	NRCG 10379	160	NRCG 13971
93	NRCG 6860	127	NRCG 10273	161	NRCG 11649
94	NRCG 11112	128	NRCG 9331	162	NRCG 10287
95	NRCG 13965	129	NRCG 10275	163	NRCG 13960
96	NRCG 7096	130	NRCG 14674	164	NRCG 10574
97	NRCG 14060	131	NRCG 14521	165	NRCG 9259
98	NRCG 8457	132	NRCG 14631	166	NRCG 10285
99	NRCG 12200	133	NRCG 8199	167	NRCG 14064
100	NRCG 13985	134	NRCG 10269	168	NRCG 8198
101	NRCG 8397	135	NRCG 7086	169	NRCG 10330
102	NRCG 14079	136	NRCG 6774	170	NRCG 3706
103	NRCG 10567	137	NRCG 10633	171	NRCG 14138
104	NRCG 14588	138	NRCG 10469	172	NRCG 12201
105	NRCG 14062	139	NRCG 201	173	NRCG 10523
106	NRCG 12679	140	NRCG 10371	174	NRCG 6655
107	NRCG 6236	141	NRCG 1376	175	NRCG 13981
108	NRCG 6784	142	NRCG 8222	176	NRCG 10286
109	NRCG 14067	143	NRCG 14089	177	NRCG 10406
110	NRCG 12239	144	NRCG 14074	178	NRCG 5114
111	NRCG 10648	145	NRCG 10412	179	NRCG 10340
112	NRCG 14072	146	NRCG 13379	180	NRCG 8230
113	NRCG 11127	147	NRCG 10558	181	NRCG 10637
114	NRCG 8213	148	NRCG 14608	182	NRCG 10566
115	NRCG 11445	149	NRCG 6547	183	NRCG 11120
116	NRCG 14605	150	NRCG 11119	184	NRCG 11147
117	NRCG 8216	151	NRCG 9279	185	NRCG 10471
118	NRCG 8183	152	NRCG 16233	186	NRCG 9336
119	NRCG 14643	153	NRCG 12352	187	NRCG 13535
120	NRCG 10267	154	NRCG 133	188	NRCG 8204
121	NRCG 10474	155	NRCG 9869	189	NRCG 219
122	NRCG 14018	156	NRCG 9388	190	NRCG 3491
123	NRCG 6230	157	NRCG 13936	191	NRCG 10545

124	NRCG 14065	158	NRCG 8343	192	NRCG 10402
193	NRCG 10403	196	NRCG 14039	199	NRCG 10619
194	NRCG 12483	197	NRCG 12380	200	NRCG 11203
195	NRCG 14606	198	NRCG 13591		
The source for all above mentioned 200 advanced breeding lines of groundnut is, Indian Institute of Groundnut Research (IIGR, Junagadh, Gujarat).					

Table 2: Analysis of variance for yield and yield attributing traits in groundnutadvanced breeding lines

Source of variation	**Degrees of freedom**	**Days to fifty *percent* flowering**	**Days to physiological maturity**	**Plant height (cm)**	**Number of primary branches**	**Number of mature pods per plant**	**Pod yield per plant(g)**	**Kernel yield per plant (g)**	**Shelling percentage**	**Test weight (g)**
Treatment (ignoring Blocks)	203	8.62**	71.06**	32.32**	3.08**	9.04**	10.74**	4.99**	90.71*	46.54**
Treatment: Check	3	3.16**	0.69	491.89**	18.17**	16.69**	55.61**	15.77**	89.92**	121.65**
Treatment: Test	199	6.39**	47.22**	25.46**	2.85**	8.82**	10.04**	4.72**	91.17*	45.23**
Treatment: Test vs. Check	1	36.06**	121.86**	18.60**	4.20*	29.77**	16.50**	26.31**	0.47	80.70**
Block (eliminating Treatments)	9	4.00	2.75	0.97	0.23	1.23	0.71	0.50	50.61	52.04
Residuals	27	1.64	1.78	0.81	1.28	0.84	1.29	0.63	53.06	3.02

*Significant at P = 0.05, ** Significant at P = 0.01 probability levels

Table 3: Mean, range and genetic variability parameters for yield and yield attributing traits in advanced breeding lines of groundnut

Traits	**Range**		**Mean**	**Co-efficient of variation (%)**		**h^2_{bs} (%)**	**GAM (%)**
	Min.	**Max.**		**GCV**	**PCV**		
Days to fifty *percent* flowering	25.00	42.00	33.5	8.03	9.31	74.33	14.28
Days to physiological maturity	98	119.00	108.5	6.44	6.56	96.22	13.02
Plant height (cm)	32.23	60.66	44.73	11.10	11.28	96.82	22.54
Number of primary branches	3.12	8.53	5.81	21.71	28.66	57.39	33.93
Number of mature pods per plant	13.07	29.07	20.50	13.78	14.49	90.48	27.05
Pod yield per plant(g)	11.30	24.05	17.68	15.66	16.96	85.28	29.83
Kernel yield per plant (g)	7.86	16.11	12.28	13.69	16.89	65.69	22.89
Shelling percentage	53.25	86.43	68.78	13.43	13.58	97.81	27.40
Test weight (g)	35.66	71.46	53.73	12.09	12.52	93.33	24.10

Table4: Phenotypic correlation coefficients for yield and yield attributing traits in groundnut advanced breeding lines

Traits	**DFF**	**DPM**	**PH**	**NB**	**NMPP**	**PYPP**	**SP**	**TW**	**KYPP**
DFF	1.00								
DPM	0.42**	1.00							
PH	-0.01	0.02	1.00						
NB	0.04	0.03	0.01	1.00					
NMPP	-0.13*	-0.17**	0.02	0.08	1.00				
PYPP	0.08	0.01	-0.03	0.02	0.14*	1.00			
SP	0.14*	0.17**	-0.09	0.09	0.06	0.86**	1.00		
TW	-0.13*	-0.17*	-0.03	0.01	0.72**	0.18**	0.10	1.00	
KYPP	0.06	-0.02	-0.04	0.03	0.12	0.95**	0.81*	0.15*	1.00

*Significant at P = 0.05, ** Significant at P = 0.01 probability levels

Where, DFF: Days to 50 *per cent* flowering, DPM: Days to physiological maturity, PH: Plant height, NB: Number of branches per plant,

NMPP: Number of mature pods per plant, PYPP: Pod yield per plant, SP: Shelling percentage, TW: Test weight, KYPP: Kernel yield per plant.

Conclusion

The study established that, groundnut harbors a broad spectrum of genetic variability for yield and yield-related traits, which can be effectively harnessed in breeding programmes. Significant variability observed for various yield traits highlights the genetic richness of the material under study. High heritability coupled with high genetic advance in key traits such as pod yield per plant, kernel yield per plant, shelling percentage and test weight confirmed the predominance of additive gene action, indicating that these traits can be improved effectively through simple phenotypic selection.

The association and path analysis provided deeper insights into the interrelationships of traits influencing yield. Pod yield per plant emerged as the most decisive factor determining kernel yield, supported by strong direct and indirect contributions from shelling percentage and test weight. This finding reinforced the importance of prioritizing these component traits in yield improvement programmes. In contrast, traits such as plant height, number of branches and phenological attributes contributed minimally to yield, suggesting limited scope for direct selection based on these characters.

In summary, pod yield per plant, shelling percentage, kernel yield per plant and test weight were identified as the most reliable selection criteria for yield improvement under field investigation.

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