



Variability and Association Analysis in Groundnut Germplasm Lines for Yield and Yield Attributing Traits

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ABSTRACT

Background: The present study was conducted using groundnut germplasm lines obtained from ICRISAT, Hyderabad to analyse the genetic variability and association among 93 groundnut germplasm lines along with 5 checks for yield and yield attributing traits.

Methods: An experiment was done to study 14 quantitative traits in 98 groundnut genotypes for yield and yield components. Data analyse for variability and correlation were done using R studio version 4.4.2 software.

Result: The traits of plant fresh weight, 100 pod weight, 100 seed weight, plant dry weight, kernel color, kernel shape, 100 shell weight and shelling percentage had high PCV and GCV. Shelling percentage had negative correlation with plant fresh weight, 100 pod weight, plant dry weight and 100 shell weight and it is positively correlates with the number of primary branches. These traits may be utilized as selection indices to improve yield in the groundnut breeding program.

Key words: Association analysis, Germplasm lines, Groundnut, Variability.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is a part of the Papilionaceae subfamily within the Fabaceae family (Kulheri *et al.*, 2022 and Suchitra, 2022). Groundnut is the "king of oilseed crops" due to its high protein and oil content (Menge *et al.*, 2018 and Meena, 2021). It is among the most significant oilseed crops that are cultivated worldwide in semi-arid and subtropical climates (Ibrahim *et al.*, 2024). Groundnut ranks as the fifth most cultivated oilseed crop worldwide, occupying approximately 27.9 million hectares and producing 47 million tons annually with an average productivity of 1676 kg/ha. India ranks second after China in production. Groundnut global cultivation spans across 4.96 million hectares, yielding 10.03 million tons with a productivity of 1616 kg/ha (FAOSTAT, 2023).

Groundnut is a predominantly self-pollinated crop and is having less variation. Also it is an unpredictable legume due to the geotropic orientation of the pods. The available variability is being exhausted due to vicious breeding cycle of selection-hybridization-selection. Hence, it is necessary to access the extent of genetic variability available in the groundnut germplasm to have a successful crop improvement program.

Groundnut is primarily cultivated as a rainfed crop in various countries around the world. Yield tends to be low and unstable under rain-dependent conditions due to erratic rainfall and frequent droughts during the growing season. This instability is intensified by the poor adaptation of improved varieties and the impact of drought stress varies based on its intensity, duration, growth stage and the specific genotype. Drought stress during critical reproductive phases, such as flowering and pod filling, significantly affects yield. However, tolerant groundnut varieties can achieve considerably better yields due to

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physiological and biochemical changes that occur in response to drought stress. This understanding is crucial for effective peanut breeding programs. Yield and quality in peanuts can be significantly influenced by environmental conditions.

Due to its allotetraploid nature, groundnuts had relatively low genetic variation. Therefore, to improve groundnut yield, breeding programmes should enrich genetic variability. Genetic variations are pivotal in crop improvement schemes. The presence and extent of the variations enable the selection of new genotypes with diverse traits. Heritability measures the specific traits which is inherited by offspring. Creating and utilizing diversity through appropriate breeding practices is the first step for genetic improvement.

The evaluation of genetic variation and the extent of transmission of desirable traits is deciding the successful breeding program. To separate the total variability into heritable and non-heritable factors, it is necessary to observe the different plant traits and its relationship with each other traits.

Additive gene activity and selection conditions are responsible for traits with high heritability and genetic gain. To improve groundnut production, breeding program must identify component traits that affect productivity. To make seed selection and increase pod yield, it is needed to know the degree of genetic variation, as well as how traits are inherited (Chauhan *et al.*, 2022).

Any successful crop breeding programme, depends on the amount of variability in the source population. Generally genetic variability is estimated at variance level. But, the coefficient of variation is free from units and is comparable with any other trait. Hence, in the present inquiry the coefficient of variation at phenotypic and genotypic levels were estimated. Heritability was estimated to quantify the extent of genetic variation available in the reference population for the traits of interest. Genetic gains that are harvestable were also quantified the traits with high heritability coupled with high genetic gain were identified and to utilize in the current plant breeding programme.

MATERIALS AND METHODS

Five check varieties and ninety-three test genotypes obtained from ICRISAT, Hyderabad (Table 1), were used in the experiment. During Kharif 2024, these genotypes were sown in an augmented design in SRM College of Agricultural Sciences. Four blocks were used to repeat each check. The spacing adopted was 30 × 10 cm. The crop was raised in two rows plot of 3m length. Recommended agronomic practices and need based plant protection measures were judiciously followed under irrigated conditions. Observations were recorded on 14 morphometric traits viz., days to 50% flowering (DFF), plant height at maturity (PH), number of primary branches (NPB), number of secondary branches (NSB), leaf size (LS), flowers on main axils (FMA), plant fresh weight (PFW), plant dry weight (PDW), 100 pod weight (HPW), 100 seed weight (HSW), kernel color (KC), kernel shape (KS), shelling percentage (SP) and 100 shell weight (HSW) were included for the analysis. Six plants were selected at random for each entry in each replication and their data were recorded. Biometric genetic analyses were performed by following the standard procedure, outlined by Burton (1952). The data were analysed using R software version 4.2.2.

RESULTS AND DISCUSSION

The availability with sufficient diversity is an essential objective for any crop breeding program since it allows for selection based on predetermined goals. The estimates of the genetic variability parameters for the 98 genotypes in each of the 14 observable traits are presented in Table 2.

The traits under this investigation are influenced by several genes. They are also significantly impacted by environmental factors. GCV is preferable since PCV considers environmental influences. It calculates the amount of total variability that is heritable (Allard, 1960). However, selection requires additional information than solely the genotypic coefficient of variation. GCV illustrates the possible genetic advantages of selection using heritability estimates (Burton, 1952). Genetic variability, heritability and selection intensity are therefore necessary for genetic advancement. GCV and PCV differed the least for the majority of characters studied (Thakur *et al.*, 2013; Rao *et al.*, 2014).

There was significant phenotypic and genotypic variation for every trait examined in the experiment, which included 98 germplasm lines. Low GCV and PCV indicated that the days to 50% flowering trait was not suitable for selection. Strong environmental influence on these traits is shown from the low GCV. A narrow genetic base for this trait is suggested by this study, which is consistent with earlier research on groundnut variability that similarly found low GCV and PCV for days to 50% flowering, according to Kadam (2016) and Vasanthi *et al.* (2015).

A high phenotypic coefficient of variation (PCV) and a modest genotypic coefficient of variation (GCV) for leaf size and the number of primary branches may suggest that these traits are influenced by the environment. The number of secondary branches, on the other hand, had low GCV and moderate PCV. Characteristics such as shelling %, kernel color, kernel shape, 100 shell weight, 100 pod weight, 100 seed weight, plant fresh weight and plant dry weight all showed significant PCV and GCV. Similar patterns of variations in shelling percentage were observed by Vinithashri *et al.* (2019), Mitra *et al.* (2021) and Zaman *et al.* (2011).

Heritability and genetic advance as per cent of mean

Estimates of heritability illustrate the inheritance patterns of traits. Developing selection strategies is aided by genetic advancement. There is little genetic advancement and heritability in the number of secondary branches. Non-additive gene action is indicated by this trait. According to Nath and Alam (2002), phenotypic selection for these traits will not be very successful.

There is considerable genetic advancement and moderate heritability for characteristics such as plant dry weight and the flowers on main axis. The number of major branches and days to 50% flowering indicate a moderate level of genetic advance with high heredity. Shukla and Rai (2014), Yadav *et al.* (2023) and Poojitha *et al.* (2024) all reported similar results.

Several traits showed high genetic advance and high heritability. Plant height, leaf size, plant fresh weight, plant dry weight, 100 pod weight, 100 seed weight, kernel color, kernel shape, shelling percentage and 100 shell weight indicated these high genetic advance with high heritability. According to Mitra *et al.* (2021), a substantial additive variance in 100 pod weight is indicated by a stronger genetic advance with high heritability. Plant height at maturity, number of flowers on the

Table 1: List of 98 groundnut genotypes assessed for yield and associated traits.

S. no	Genotypes	Accession number	Source	S. no	Genotypes	Accession number	Source
1	G1	ICG44	ICRISAT	50	G51	ICG68	ICRISAT
2	G2	ICG22	ICRISAT	51	G52	ICG52	ICRISAT
3	G3	ICG95	ICRISAT	52	G53	ICG62	ICRISAT
4	G4	ICG47	ICRISAT	53	G54	ICG70	ICRISAT
5	G5	ICG98	ICRISAT	54	G55	ICG15	ICRISAT
6	G6	ICG73	ICRISAT	55	G56	ICG63	ICRISAT
7	G7	ICG77	ICRISAT	56	G57	ICG80	ICRISAT
8	G8	ICG46	ICRISAT	57	G58	ICG82	ICRISAT
9	G9	ICG5	ICRISAT	58	G59	ICG90	ICRISAT
10	G10	ICG25	ICRISAT	59	G60	ICG61	ICRISAT
11	G11	ICG97	ICRISAT	60	G61	ICG35	ICRISAT
12	G12	ICG51	ICRISAT	61	G62	ICG86	ICRISAT
13	G13	ICG27	ICRISAT	62	G63	ICG43	ICRISAT
14	G14	ICG99	ICRISAT	63	G64	ICG79	ICRISAT
15	G15	ICG9	ICRISAT	64	G65	ICG88	ICRISAT
16	G17	ICG94	ICRISAT	65	G66	ICG33	ICRISAT
17	G18	ICG24	ICRISAT	66	G67	ICG42	ICRISAT
18	G19	ICG23	ICRISAT	67	G68	ICG38	ICRISAT
19	G20	ICG2	ICRISAT	68	G69	ICG66	ICRISAT
20	G21	ICG17	ICRISAT	69	G70	ICG92	ICRISAT
21	G22	ICG10	ICRISAT	70	G71	ICG39	ICRISAT
22	G23	ICG74	ICRISAT	71	G72	ICG28	ICRISAT
23	G24	ICG45	ICRISAT	72	G73	ICG91	ICRISAT
24	G25	ICG6	ICRISAT	73	G75	ICG32	ICRISAT
25	G26	ICG1	ICRISAT	74	G76	ICG57	ICRISAT
26	G27	ICG100	ICRISAT	75	G77	ICG56	ICRISAT
27	G28	ICG49	ICRISAT	76	G78	ICG13	ICRISAT
28	G29	ICG50	ICRISAT	77	G79	ICG31	ICRISAT
29	G30	ICG72	ICRISAT	78	G80	ICG30	ICRISAT
30	G31	ICG76	ICRISAT	79	G81	ICG83	ICRISAT
31	G32	ICG20	ICRISAT	80	G82	ICG84	ICRISAT
32	G33	ICG71	ICRISAT	81	G83	ICG12	ICRISAT
33	G34	ICG67	ICRISAT	82	G84	ICG14	ICRISAT
34	G35	ICG64	ICRISAT	83	G85	ICG65	ICRISAT
35	G36	ICG96	ICRISAT	84	G86	ICG85	ICRISAT
36	G37	ICG8	ICRISAT	85	G87	ICG19	ICRISAT
37	G38	ICG37	ICRISAT	86	G88	ICG29	ICRISAT
38	G39	ICG41	ICRISAT	87	G89	ICG69	ICRISAT
39	G40	ICG55	ICRISAT	88	G90	ICG93	ICRISAT
40	G41	ICG58	ICRISAT	89	G91	ICG60	ICRISAT
41	G42	ICG53	ICRISAT	90	G92	ICG36	ICRISAT
42	G43	ICG34	ICRISAT	91	G93	ICG78	ICRISAT
43	G44	ICG26	ICRISAT	92	G94	ICG16	ICRISAT
44	G45	ICG48	ICRISAT	93	G95	ICG18	ICRISAT
45	G46	ICG75	ICRISAT	94	Check 1	TMV13	KVK, Tindivanam
46	G47	ICG21	ICRISAT	95	Check 2	TMV8	KVK, Tindivanam
47	G48	ICG81	ICRISAT	96	Check 3	TMV6	KVK, Tindivanam
48	G49	ICG89	ICRISAT	97	Check 4	VRI2	KVK, Tindivanam
49	G50	ICG87	ICRISAT	98	Check 5	TMV7	KVK, Tindivanam

main axis, plant fresh weight, plant dry weight, 100 pod weight, 100 shell weight, kernel color and kernel shape recorded high heritability estimates coupled with high genetic advance over mean. Hence, the aforementioned traits may be under the control of additive gene action. So, selection for these traits would be rewarding, immediately. This implied that additive gene activity primarily governs these traits, enabling improvement by direct selection.

Correlation among yield components

The data illustrated the relationships among yield components. This understanding will contribute towards improving yield traits and overall productivity in breeding programs (Table 3).

Days to 50% flowering exhibited positive correlation with multiple traits, including the number of secondary branches, plant dry weight and 100 shell weight. Plant height is significantly correlated with the number of secondary branches, leaf size, plant dry weight and 100 shell weight.

Number of primary branches had positive correlation with secondary branches but negative one with plant fresh weight, 100 pod weight, plant dry weight and 100 shell weight. Number of secondary branches showed a strong positive correlation with leaf size and plant dry weight, but a negative correlation with kernel colour. Leaf size positively correlated with plant dry weight. The leaf is vital for photosynthesis, respiration and transpiration in plants. Transpiration rates increases with larger leaf areas. This happens because wider leaves typically contain more

Table 2: Estimate of the mean, range and genetic variability for 14 quantitative traits in 98 groundnut genotypes.

Characters	Maximum	Minimum	Mean	PCV	GCV	h ²	GAM
Days to 50% flowering	32.00	25.00	29.10	6.36	5.84	84.16	11.04
Plant height	26.66	11.00	18.52	27.94	23.02	67.88	39.07
No of primary branches	5.00	2.00	3.67	24.55	14.78	36.27	18.34
No of secondary branches	9.00	6.00	7.16	16.77	5.11	9.29	3.21
Leaf size	5.80	2.86	3.99	20.69	14.38	65.59	20.58
Flower on main axils	2.00	1.00	1.34	36.20	22.98	30.37	30.06
Plant fresh weight	121.23	12.33	45.33	74.11	69.05	81.58	132.55
Plant dry weight	34.00	2.63	13.83	73.18	65.27	57.59	119.91
100 pod weight	119.40	44.80	84.11	23.44	22.29	90.48	43.61
100 seed weight	60.20	22.20	37.50	23.13	21.99	90.53	43.12
Kernel colour	9.00	1.00	4.76	44.72	43.55	94.84	87.38
Kernal shape	3.00	1.00	2.05	40.23	37.48	86.80	71.93
100 shell weight	60.00	4.40	24.47	64.79	61.58	90.36	120.59
Shelling percentage	87.93	43.85	58.23	21.52	20.82	93.64	41.52

Table 3: Phenotypic correlation coefficients between 14 groundnut characteristics.

Characters	PH	NPB	NSB	LS	FMA	PFW	HPW	HSW	PDW	KC	KS	HSBW	SP
DFP	0.073	0.09	0.251**	0.05	-0.084	0.174	0.095	0.079	0.204*	-0.101	0.168	0.249**	-0.052
PH		0.132	0.389**	0.364**	-0.057	0.129	0.058	0.089	0.302**	-0.003	-0.114	0.247**	0.04
NPB			0.482**	0.111	0.151	-0.249**	-0.301**	-0.113	-0.219*	-0.041	0	-0.243**	0.249**
NSB				0.290**	-0.147	0.132	-0.028	0.014	0.225*	-0.297**	-0.129	0.153	0.091
LS					0.057	0.074	-0.038	-0.018	0.253**	-0.136	-0.143	0.059	0.067
FMA						-0.283**	-0.155	-0.01	-0.122	0.161	0.029	-0.230*	0.157
PFW							0.468**	0.217*	0.729**	-0.148	0.184*	0.594**	-0.297**
HPW								0.559**	0.487**	0.075	0.147	0.518**	-0.665**
HSW									0.271**	0.211*	0.15	0.377**	0.215*
PDW										-0.239**	0.075	0.671**	-0.271**
KC											0.085	-0.149	0.026
KS												0.197*	-0.072
HSBW													-0.226*

** Correlation is significant at the 0.01 level (2-tailed).

* Correlation is significant at the 0.05 level (2-tailed).

PH- Plant Height, NPB- No. of primary branches, NSB- No. of secondary branches, LS- Leaf size, FMA- Flower on main axils, PFW- Plant fresh weight, HPW- 100 Pod weight, HSW-100 seed weight, PDW- Plant dry weight, KC- Kernel colour, KS- Kernel shape, HSBW- 100 shell weight, SP- Shelling percentage.

stomata. Additionally, breeders use leaf dry weight as a key indicator of a plant's resource use strategy.

The presence of flowers on the main axils exhibited negative correlation with plant fresh weight and 100 shell weight. Plant fresh weight exhibited positive correlation with 100 pod weight, 100 seed weight, plant dry weight, kernel shape and 100 shell weight. Significant correlation was observed between 100 pod weight and both 100 seed weight and plant dry weight. In addition, 100 seed weight was significantly associated with both plant dry weight and kernel color. Plant dry weight exhibited a significant positive correlation with 100 shell weight, while it negatively correlated with kernel colour. The shape of the kernel exhibited positive correlation with the 100 shell weight. Shoba *et al.* (2012), Rao (2016) and Rajarathinam *et al.* (2017) reported analogous findings concerning pod yield.

Shelling percentage positively correlates with the number of primary branches but negatively with plant fresh weight, 100 pod weight, plant dry weight and 100 shell weight. Shukla and Raj (2014), Vijayasekhar (2002), Pavan Kumar *et al.* (2014) and Yenikalayci (2021) found similar results for shelling percentage. Shelling percentage is crucial for seed yield in crops like peanuts, as it shows the ratio of edible seeds in harvested pods. Typically, as pod weight increases, shelling percentage decreases. In simpler terms, larger pods tend to have a lower seed weight compared to their total weight.

CONCLUSION

This study reveals significant genetic variability among the 98 groundnut genotypes for most of the 14 traits examined, offering promising ways for selection. Traits like plant height, pod weight, and shelling percentage exhibit high heritability and genetic advance, suggesting effective improvement through direct selection due to additive gene action. Conversely, traits such as days to 50% flowering and the number of secondary branches show limitations for direct selection due to environmental influence or non-additive gene action. The identified correlations among yield components provide crucial insights for developing targeted breeding strategies to enhance overall productivity in groundnut.

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Conflicts of interest

The authors declare no conflict of interest.

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