Genetic Variability, Heritability, and Genetic Advance Estimates in Selected Groundnut Genotypes (*Arachis hypogaea* L.) for Agro-Morphological and Yield Traits.

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Abstract

Groundnuts (Arachis hypogaea L.), is a crucial food and oil crop in the tropics, require genetic variability assessment for efficient breeding programs using appropriate parameters like genetic coefficient of variation, heritability estimates, association among yield related traits and genetic advance. This study aims to identify genotypes with desirable traits to improve yield and adaptability, contributing to better crop improvement strategies. The study used a randomized complete block design with three replications, consisting of fourteen selected genotypes. Quantitative traits were used to estimate genetic variability parameters, heritability, and genetic advance. The analysis of variance revealed significant differences (p < 0.005) for all studied traits, indicating greater variability in genotypes. Characters exhibited different levels of variability, heritability, and genetic advance among the genotypes. The estimate of the broad-sense heritability ranged from 13.33% to 33.33% for canopy spread and days to maturity respectively. Low to high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded. The study found that traits such as number of branches, pods per plant, fresh and dry plant weight, kernel yield, pod yield, and shelling percentage showed high genotypic coefficient of variation, moderate broad sense heritability, and high genetic advance. These traits can be beneficial for groundnut improvement through effective phenotypic selection, resulting in high expected genetic gain. The study found that pod yield is significantly correlated with kernel yield, grain length, grain width, 100-seed weight, fresh and dry 100-pod weight, and number of pods per plant. Kernel yield is positively correlated with the number of branches per plant, pod per plant, fresh and dry 100-pod weight, 100-seed weight, grain length, and grain width. In addition, the first four principal components accounted for 90.37% of total variation in all morphological traits.

Keywords: *Arachis hypogea*, Correlation, Genetic advance, Genetic variability, Heritability

INTRODUCTION

In the semiarid tropics, groundnuts are a significant food and oil crop that supports household food consumption and monetary earnings. Yields in Asia and Africa are poor due to a variety of production restrictions (Desmae *et al.*, 2019). Groundnut (*Arachis hypogaea* L.), as a source of nutritional proteins in underdeveloped nations, makes a substantial contribution to global food production (Banla *et al.*, 2020). Groundnut is a self-pollinating autotetraploid with the chromosomal number 2n=4x=40. It belongs to the largest and most important of the three leguminosae divisions, the papilionaceae subfamily (Khandebharad *et al.*, 2022). Groundnut, a vital crop in many nations, especially in SSA, is a smallholder crop farmed in semi-arid tropical regions. It provides vitamins, cooking oil, and protein. In addition, it provides farmers with an extra source of revenue and is fed to cattle during the dry season. Nigeria is the major producer of groundnuts in West Africa, accounting for 51% of total output (Ajeigbe *et al.*, 2015). Groundnut is and has long been a significant crop in Nigeria, where it is primarily cultivated under smallholder and rain-fed systems (Echekwu, 2010). In the 1970s, Nigeria, Africa's leading groundnut exporter, experienced a disease-induced decline. Improved, biotic-resistant high-yielding varieties have been produced by International Crops Research Institute for Semi-Arid Tropics (ICRISAT), Institute for Agricultural Research (IAR), and collaborators (Ajeigbe *et al.*, 2015). Although Sub-Saharan Africa accounts for approximately 31.6% of global production, many African states are unable to meet their peanut demand, with Sub-Saharan Africa having low groundnut productivity levels. Importing groundnuts to compensate for a production shortfall has raised financial issues (Daudi *et al.*, 2021).

The primary necessity for any plant breeding operation to generate a superior cultivar is genetic variability (Tesfaye, 2021). A barrier to groundnut improvement is the polyploidy and limited genetic diversity of important features (Janila *et al.*, 2013). Genetic variability can be assessed using parameters such as genotypic coefficient of variation, phenotypic coefficient of variation, and heritability estimates. Combining them with genetic advances as a percentage of the mean improves prediction and identifies features for transformation (Vinithashri *et al.*, 2019). For groundnut genotypes to be developed with high yields, it is essential to comprehend the link between yield-related characteristics and yield (Abady *et al.*, 2019). The yield of groundnut pods per plant had a positive link with the following parameters: harvest index, shelling %, kernel number, pod number, and kernel weight. With this information, breeding groundnuts could create more effective selection criteria (Abady *et al.*, 2019).

Heritability describes the degree to which traits are passed down to offspring, whereas genetic advance describes the degree of progression achieved in a specific variety by a given pressure of selection. In breeding programs, information on the components of variation and the character connection of various component qualities with yield is also critical. Morphological descriptors are critical for identifying and distinguishing genotype accessions, allowing crop modification for increased grain and oil yield. These descriptors have a high heritability, implying that they are manifested in various situations. Since the inception of modern breeding programs, they have played an important role in crop development by allowing for easy identification and discrimination of accessions (Adu-Gyamfi *et al.*, 2019). Understanding heritability aids in selecting breeding techniques that could be useful for improving plants (Sawadogo *et al.*, 2023). Therefore, the main objective of the study was to ascertain the heritability and correlation between the traits as well as the genetic variability among a selection of chosen cultivated groundnut genotypes based on agronomic and yield traits.

MATERIALS AND METHODS

Study Area. The experiment was conducted at the Bayero University research farm in Kano, Nigeria. The research location is 475 meters above sea level at 11.9813375^0N latitude and 8.4203656^0E longitude. The Sudan Savannah agroecology of the research area receives 300–600 mm of rainfall annually. The soil used in the experiment was a sandy loam with a pH (H_20) of 6.23, Electrical conductivity of 0.00717ds/m with a proportion of sand 74.64%, silt 17.28%, and clay 8.08%.

Plant Materials. Table 1 shows fourteen groundnut genotypes decided on as experimental materials (9 from the Centre for Dry Land Agriculture, Bayero University Kano, Nigeria, and 5 from farmers in various locations in Katsina and Bauchi states), based on the availability, and acceptability by farmers in the respective areas.

Field Management. The field was prepared and divided into three halves. Each block was 5x27 square meters, with 14 plots of 2x3 square meters and containing one of the 14 genotypes. The seeds were fungicide-treated (Carbendazim 12+ Mencozeb 63 WP @ 3gm/kg seed) and planted with 0.25m intra- and 0.75m inter-row spacing. The two seeds were planted at a depth of 4-5cm and trimmed to one seedling two weeks after emergence (WAE). After each manual weeding, NPK 15:15:15 fertilizer was applied at a rate of 200kgha^{-1} at 2 and 5 weeks after seedling emergence. Insecticide (Acephate 750 SP sprayed at 80gm in 16L water; Lancer, UPL Company Gujarat, India) and fungicide (SAAF, Carbendazim 12 Mencozeb 63 WP sprayed at 65gm in 16L water; UPL Company Gujarat, India),(Ajeigbe *et al*., 2015).

Data Collection and Analysis. Morphological traits were assessed at various growth stages using groundnut descriptors produced by the International Plant Genetic Resources Institute (IBPGR and ICRISAT 1992). There were seventeen (17) quantitative characteristics examined in all. The number of days to 50% flowering was calculated as the number of days from sowing to the point at which 50% of the plot stand had reached flowering, as well as plant height, number of branches per plant, canopy spread during the active stage of plant development, and plant yield and kernel yield from a sample of three representative plants. When the plant was ready for harvest, the days to maturity period was recorded. The fresh and dry weight of the plant, the number of pods per plant, the fresh and dry weight, the number of branches, the 100-seed weight, the shelling percentage, the seed yield per plant, the pod yield per plant, and the harvest index were all recorded. Using a Vernier caliper, the seed length (SDL) and seed width (SDW) in a micrometer were measured.

The mean of the parameters for each treatment was determined, and using the general linear model method in SPSS Version 23 and GenStat computer software, 17th edition, an analysis of variance (ANOVA) was performed. The mean value separation test was carried out by an LSD test (Least Significant Difference) with a probability level of 5% (Khan *et al*., 2020). To demonstrate variability among genotypes, means were used to calculate genetic parameters such as genotypic variance (σ^2g), phenotypic variance (σ^2p) environmental variance (σ^2p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV), genotypic variance, phenotypic variance, environmental variances, heritability, genetic advance, and genetic advance as a percentage of mean. To illustrate the highest discriminating trait and level of association among the traits, principal component, and hierarchical cluster analyses were performed (Ene *et al*., 2016; Tesfaye, 2021).

Table 1: Description of the Groundnut Genotypes included in the study and their Sources of collection

Genotype	Accession Number	Source
Gn1	Samnut21	CDA
Gn2	Samnut22	CDA
Gn3	Samnut23	CDA
Gn4	Samnut24	CDA
Gn5	Samnut25	CDA
Gn6	Samnut26	CDA
Gn7	Samnut27	CDA
Gn8	Samnut28	CDA
Gn9	Samnut29	CDA
Gn10	Mai Bargo	Kaura Yamma, Katsina
Gn11	Bahausa	Bakiyawa gari,Katsian
Gn12	Yarjingila	Kaware , Katsina
Gn13	Ex Dakar	Bakiyawa gari,Katsina
Gn14	Mai Zabuwa	Soro Ganjuwa, Bauchi

Gn: Genotype, CDA : Centre for Dryland Agriculture

RESULTS
Analysis of Variance for Quantitative Traits
The analysis of variance (ANOVA) for the seventeen quantitative morphological traits among the genotypes were all statistically significant at ($p \leq 0.05$) in the experiment is presented in Table 2.

Table 2. Mean square values for different quantitative traits among groundnut genotypes evaluated during the study

Source of Variation	Df	D50%F	CNS	NBR	BRH	DMT	NPOD	FW100P	DW100P	FWPL	DWPL
Replication	2	8.74	135.43	1.54	2.3	0.02	4.308	1.70	9.94	44	9.4
Genotypes	13	48.59**	313.8**	131.77**	306.99**	693.37**	217.64**	5940.50**	982.14**	48962.84**	5182.64**
Error		1.62	134.5	1.48	2.02	0.02	1.793	5.76	11.41	6.62	48.94

Table 2. cont..

Source of Variation	Df	100SW	SHLG%	GRNL	GRNW	KYLD	PYLD	HI
Replication	2	1.707	0.487	1.03	0.07	6.92	2.57	9.85
Genotypes	13	163.27**	102.74**	10.87**	1.47**	365.48**	530.41**	1589.98**
Error		2.38	2.811	0.3359	0.22	2.76	2.74	10.81

**Significant at 5% level of probability,D50%F= days to 50% flowering, CNS= canopy spread, NBR= number of branches, BRH=branch height, DTM = days to maturity, NPOD=number of pods/plant,FW100P=fresh weight of 100 pods, DW100P=dry weight of 100 pods, FWPL=fresh plant weight, DWPL=dry plant weight, 100SW= 100 seed weight, SHLG%= shelling percentage, GRNL=grain length, GRNW=grain width, KYLD=kernel yield/plant, PYLD=pod yield/plant, HI=harvest index.

Mean performance of the genotypes for seventeen quantitative traits evaluated during this study

Results for the mean performance of the genotypes for seventeen agronomical traits evaluated under this study are presented in Table 3. The traits showed a significant difference (p ≤0.05) among all the genotypes. All the triats demonstrated wide range of variability except days to 50% flowering and number of branches per plant in some genotypes. Pod yield/plant (g) and seed yield/ plant (g) which are the key interest in most breeding program, showed a wide range of variation (22.59-72.16) in Samnut27 and Samnut 23 for pod yield respectively and (21.53-56.91) in Samnut28 and Samnut23 respectively for seed yield.

Genetic parameters for 17 agronomical traits of 14 groundnut genotypes evaluated

Estimates of phenotypic(σ^2p), genotypic (σ^2g), and environmental variance (σ^2e), phenotypic, genotypic, and environmental coefficients of variation , broad sense heritability (H_b), genetic advance, and genetic advance as a percentage of the mean calculated from all the characters shown in Table 4. The phenotypic variances were high in all characters studied due to environmental effects. For all attributes, the results revealed a larger difference between the PCV and GCV. The broad sense heritability ranged from13.33% to 32.99%, and most the parameters showed moderate heritability within the range of 30–60%, with the exception of canopy spread and grain width (13.33% and 24.65%, respectively), which fall within the range of 0–30% as low heritability. In this study, high GA was observed in the number of branches (56.65) and the lowest was observed in canopy spread (6.81). Genetic advance as a percentage of the mean was high for the number of branches (414.14%), harvest index (214.33), and grain length (119.62%). While a low percentage was recorded for canopy spread and shelling percentage (7.79% and 10.13%) respectively.

Table 3: Mean performance of the genotypes evaluated for all quantitative traits during the study

Genotypes	D50%F	CNS	NBR	BRH	DMT	NPOD	FW100P	DW100P	FWPLNT
Samnut21	35.30d	83.56bc	14.3d	48.67a	124.00m	41.33e	213.8g	118.0g	443.9k
Samnut22	35.00d	87.78bc	15.0d	46.57a	123.0l	43.03ef	260.2j	134.6h	514.3m
Samnut23	26.33b	76.28ab	13.6d	47.80a	93.00f	60.50h	229.9h	119.9g	135.5a
Samnut24	24.33a	58.00a	10.6a	57.67c	84.00a	37.05d	120.6a	81.90a	226.9b
Samnut25	26.00ab	96.56	13.0b	70.27f	92.00e	33.50c	154.0c	107.0f	281.3h
Samnut26	26.00ab	89.78bc	13.6b	67.10e	94.00g	36.78d	153.5c	85.10ab	267.1e
Samnut27	27.00b	98.78c	13.8b	68.17ef	90.00c	34.12c	198.4f	132.6h	243.0c
Samnut28	26.67b	94.22bc	9.90a	75.23g	105.00h	25.58a	181.7d	88.30bc	247.5d
Samnut29	26.67b	84.11bc	12.5ab	62.27d	105.00h	44.95fg	186.1e	96.90de	358.2i
Maibargo	32.33c	89.66bc	15.7bc	74.00g	122.00k	42.17e	246.7i	123.0g	497.5l
Bahausa	35.00d	88.34bc	15.0b	46.57a	120.00j	37.50d	197.7f	107.3f	556.7n
Yargingila	26.00ab	87.45bc	14.2b	55.67bc	87.00b	45.50g	121.2a	84.50ab	274.0f
Exdakar	26.67b	85.01bc	14.1b	68.67ef	91.00d	32.07bc	133.3b	92.20cd	277.6g
Maizbuwa	35.00c	76.26ab	13.7b	54.00	119.70i	30.06b	200.6f	99.00e	436.3j
MEAN	28.98	85.41	13.7	60.18	103.60	38.86	185.6	105.04	339.99
CV%	4.40	13.60	6.80	6.70	0.100	4.35	1.30	3.20	0.80
LSD$_{0.05}$	2.13	19.40	2.81	9.83	0.26	2.24	4.02	5.65	4.31
LED	1.03	9.47	1.02	2.12	0.13	1.90	1.96	2.76	2.10

Figures followed by the same letters along the columns are not statistically different according to Fishers protected LSD at 5% level; D50%F: Days to 50% flowering; CNS: canopy spread; NBR: number of branches; BRH: branch height; DTM: Days to maturity; NPOD: Number of pods/plant; FW100P: Fresh weight of 100 pod; DW100P: dry weight of100 pod; FWPL: fresh plant weight; DWP: dry plant weight; 100SW: 100 seed weight; SHLG%: shelling%; GRNL: grain length; GRNW: grain width; KYLD: kernel yield/plant; PYLD: pod yield/plant; HI: harvest index

Table 3 cont..

Genetic Variability, Heritability, and Genetic Advance Estimates in Selected Groundnut Genotypes (*Arachis hypogaea* L.) for Agro-Morphological and Yield Traits.

Genotypes	DWPLNT	100SWT	SHL%	GRNL	GRW	KYLD	PYLD	HI
Samnut21	151.2fg	56.93 fg	75.53b	15.01ij	9.22def	47.26h	48.77g	31.25bcde
Samnut22	185.1h	59.47g	88.62g	17.98k	8.98def	51.26i	57.74i	27.70bc
Samnut23	50.7a	47.13e	78.89cd	13.77fgh	9.50ef	56.91j	72.16j	51.43g
Samnut24	77.8b	36.53a	89.20g	12.14bcd	8.57bcd	27.02cd	30.28b	35.92ef
Samnut25	85.1bc	42.47d	79.73d	12.63cde	8.71cde	28.46d	35.82c	33.46de
Samnut26	104.3de	43.07d	74.54b	11.57ab	7.96abc	31.07e	31.22b	30.26bcd
Samnut27	79.9b	46.80e	70.49a	12.05bcd	9.31def	32.29ef	22.50f	40.43f
Samnut28	77.4b	41.53cd	87.17efg	12.94def	8.16abc	21.53a	22.59a	27.82bc
Samnut29	113.6e	41.53cd	76.00bc	13.84gh	8.16abc	37.58g	43.02ef	33.11cde
Maibargo	159.6g	56.13f	84.33e	15.84j	9.63f	47.02h	51.95h	29.46bcd
Bahausa	173.6h	42.80d	79.82d	14.38hi	8.09abc	32.07ef	40.38de	18.49a
Yargingila	101.3d	37.80ab	87.49fg	10.79a	7.55a	34.21f	38.37cd	34.42de
Exdakar	93.4cd	38.87ab	84.71ef	12.03bc	7.76a	25.06bc	29.54b	26.82b
Maizbuwa	146.3f	39.80bc	80.44d	13.17efg	7.78ab	23.81ab	29.62b	16.27a
MEAN	114.22	45.10	81.2	13.44	8.53	35.43	41.20	35.56
CV%	6.10	3.40	2.10	4.30	5.50	4.70	4.00	9.20
LSD$_{0.05}$	11.70	2.82	2.80	0.09	0.78	2.78	2.79	5.50
LED	5.71	1.26	1.37	0.47	0.38	1.36	1.35	2.69

Figures followed by the same letters along the columns are not statistically different according to Fishers protected LSD at 5% level D50%F: Days to 50% flowering; CNS: canopy spread; NBR: number of branches; BRH: branch height; DTM: Days to maturity; NPOD: Number of pods/plant; FW100P: Fresh weight of 100 pod; DW100P: dry weight of100 pod; FWPL: fresh plant weight; DWP: dry plant weight; 100SW: 100 seed weight; SHLG%: shelling%; GRNL: grain length; GRNW: grain width; KYLD: kernel yield/plant; PYLD: pod yield/plant; HI: harvest index.

Table 4: Estimation of genetic parameters for 17 quantitative traits in 14 groundnut genotypes in the field during the experiment

Traits	Mean	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$	PCV%	GCV%	ECV%	H$^2_{bs}$%	GA	GAM%
D50%F	28.98	50.21	15.66	1.62	24.45	13.65	4.39	31.18	15.71	54.20
CNS	85.41	448.30	59.77	134.50	24.79	9.05	13.58	13.33	6.81	7.97
NBR	13.68	133.25	43.43	1.48	84.38	48.17	8.89	32.59	56.65	231.94
BRH	60.18	309.01	101.66	2.02	29.21	16.75	2.36	32.90	19.80	32.89
DMT	103.55	693.39	231.12	0.02	25.43	14.68	0.14	33.33	17.46	16.86
NPOD	38.86	219.43	71.95	1.79	38.12	21.83	3.45	32.79	25.75	66.26
FW100P	185.55	5946.26	1978.25	5.76	41.56	23.97	1.29	33.27	28.48	15.35
DW100P	105.04	993.55	323.58	11.41	30.01	17.13	3.22	32.57	20.13	19.17
FWPLNT	339.99	48969.46	16318.74	6.62	65.09	37.57	0.76	33.32	44.68	13.14
DWPLNT	114.22	5231.58	1711.23	48.94	63.32	36.22	6.12	32.71	42.67	37.36
100SW	45.10	165.65	53.63	2.38	28.54	16.24	3.42	32.38	19.03	42.20
SHLG%	81.21	105.55	33.31	2.81	12.65	7.11	2.06	31.56	8.22	10.13
GRNL	13.44	11.21	3.51	0.34	24.91	13.94	4.31	31.33	16.08	119.62
GRNW	8.53	1.69	0.42	0.22	15.24	7.57	5.50	24.65	7.74	90.74
KYLD	35.43	368.24	120.91	2.76	54.16	31.04	4.69	32.83	36.63	103.40
PYLD	41.20	533.15	175.89	2.74	56.04	32.19	4.02	32.99	38.09	92.45
HI	35.56	1600.79	526.39	10.81	112.51	64.52	9.25	32.88	76.22	214.33

D50%F=Days to 50% flowering, CNS= canopy spread, NBR= number of branches, BRH=branch height, DTM = days to maturity, NPOD=number of pods/plant, FW100P=fresh weight of 100 pods, DW100P=dry weight of 100 pods, FWPL=fresh plant weight, DWPL=dry plant weight, 10 0SW= 100 seed weight, SHLG%= shelling percentage, GRNL=grain length, GRNW=grain width, KYLD=kernel yield/plant, PYLD=pod yield/plant, HI=harvest index. $\sigma^2 p$= phenotypic variance, $\sigma^2 g$=genotypic variance, $\sigma^2 e$ = environmental variance, PCV = phenotypic coefficients variance, GCV =genotypic coefficient of variance, ECV=environmental coefficient of variance, CV = coefficient of variance, H$^2_{bs}$= heritability in broad sense, GA= genetic advance, GAM= genetic advance as percentage of mean.

Association among the traits

The phenotypic correlation (r) matrix among the quantitative traits of groundnut genotypes is presented in Table 5. A highly significant correlation was observed between days to 50% flowering with the number of branches, days to maturity, fresh pod weight, fresh plant weight, dry plant weight, 100 kernel weight and grain length (r = 0.777, p<0.01). The traits that revealed significant correlation with Pod yield were number pods per plant (0.542, p<0.05), fresh 100pods weight (r= 0.704, p<0.01), dry 100pods weight (0.759, p<0.01), 100 kernel weight (r = 0.567, p<0.05), Grain length (r=0.558, p<0.01), grain width (r=0.639, p<0.05), seed yield (r= 0.934, p<0.01) and harvest index (r = 0.687, p<0.01). Seed yield per plant is positively correlated with number of branches number pods per plant, fresh 100pods weight, dry 100pods weight,100seed weight, Grain length and grain width (r= 0.592, p<0.05). Principal component for seventeen agronomical traits measured among the genotypes.

The first four main components accounted for 90.37% of the overall variation in the experiment (Table 6). PC1's eigenvalue was 9.51, and it explained 55.92% of the variation in total. The features like grain length, plant dry weight, days to 50% flowerings, plant fresh weight, weight of 100 fresh pods, number of branches, days to maturity, pod yield, kernel yield, branch height, and weight of 100 seeds were major characters associated with PC1, according to the Eigenvectors' contribution to variation. While PC2 was associated with the harvest index, canopy spread, grain width, and dry plant weight, which account for 17.78% of the total variation, the number of pods per plant, shelling percentage, branch height, canopy spread, and harvest index dominated the PC3 and explained 10.87% of the overall variation. However, the shelling percentage is the most important contributing factor in PC4, accounting for 5.80% of the overall Variation.

Table 5: Pearson's correlation showing the association of phenotypic traits of 14 groundnut genotypes evaluated

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Traits	D50%F	CNS	NBR	BRH	DTM	NPO	FWP	DWP	FWPL	DWPL	SWT	SHLG%	GRL	GRNW	SYLD	PYLD	HI
D50%F	1.00																
CNS	-0.166	1.00															
NBR	0.845**	-0.171	1.00														
BRH	-0.510	0.609*	-0.402	1.00													
DTM	0.933**	-0.188	0.825**	-0.332	1.00												
NPO	-0.185	-0.488	-0.026	-0.478	-0.252	1.00											
FWP	0.699**	-0.118	0.689**	-0.295	0.752**	0.026	1.00										
DWP	0.528	0.191	0.579*	-0.225	0.429	0.075	0.815**	1.00									
FWPL	0.902**	-0.042	0.862**	-0.323	0.887**	-0.248	0.526	0.342	1.00								
DWPL	0.908**	0.096	0.844**	-0.390	0.872**	-0.200	0.529	0.339	0.981**	1.00							
SWT	0.649*	0.137	0.586*	-0.118	0.668**	-0.021	0.839**	0.784**	0.464	0.492	1.00						
SHLG%	0-.019	-0.136	-0.137	-0.031	-0.001	0.174	-0.166	-0.293	0.075	0.101	-0.096	1.00					
GRL	0.777**	-0.138	0.777**	-0.376	0.811**	0.106	0.863**	0.690**	0.705**	0.714**	0.806**	0.151	1.00				
GRNW	0.120	0.057	0.110	-0.291	0.027	0.381	0.498	0.729**	-0.173	-0.166	0.541*	-0.346	0.376	1.00			
SYLD	0.390	-0.291	0.541*	-0.478	0.345	0.573*	0.704**	0.698**	0.198	0.260	0.702**	-0.102	0.657*	0.592*	1.00		
PYLD	0.296	-0.289	0.468	-0.462	0.204	0.542*	0.663**	0.759**	0.081	0.121	0.567*	-0.160	0.558*	0.639*	0.934**	1.00	
HI	-0.333	-0.330	-0.201	-0.231	-0.353	0.623*	0.209	0.275	-0.589*	-0.566*	0.087	-0.168	0-.029	0.587*	0.577*	0.687**	1.00

**.Significant at the 0.01 level. * Significant at the 0.05 level.D50%F= days to 50% flowering, CNS= canopy spread, NBR= number of branches ,BRH=branch height ,DTM = days to maturity, NPOD=number of pods/plant,FW100P=fresh weight of 100 pods, DW100P=dry weight of 100 pods, FWPL=fresh plant weight, DWPL=dry plant weight, 10 0SW= 100 seed weight, SHLG%= shelling percentage, GRNL=grain length, GRNW=grain width, KYLD=kernel yield/plant, PYLD=pod yield/plant, HI=harvest index

Table 6: Principal Component Analysis for agro morphological traits of groundnut genotypes evaluated

Traits	Component			
	PC1	PC2	PC3	PC4
D50F%	0.938	-0.222	-0.135	-0.075
CNS	-0.172	0.770	-0.359	0.238
NBR	0.906	-0.125	-0.064	-0.167
BRH	-0.608	0.353	-0.419	0.321
DTM	0.899	-0.274	-0.244	0.025
NPO	0.113	0.072	0.943	-0.086
FWP	0.918	0.142	-0.239	0.111
DWP	0.802	0.521	-0.127	-0.006
FWPL	0.925	-0.311	-0.070	-0.035
DWPL	0.941	-0.297	0.018	-0.019
SWT	0.839	0.378	-0.131	0.196
SHLG	0.112	-0.310	0.455	0.802
GRL	0.943	0.047	0.052	0.234
GRNW	0.464	0.706	0.081	-0.173
KYLD	0.855	0.297	0.296	0.012
PYLD	0.835	0.355	0.223	-0.034
HI	-0.329	0.853	0.351	-0.065
Eigenvalue	9.506	3.022	1.848	0.987
% of Variance	55.916	17.776	10.869	5.808
Cumulative %	55.916	73.692	84.562	90.370

D50%F: Days to 50% flowering; CNS: canopy spread; NBR: number of branches; BRH: branch height; DTM: Days to maturity; NPOD: Number of pods/plant; FW100P: Fresh weight of 100 pod; DW100P: dry weight of100 pod; FWPL: fresh plant weight; DWP: dry plant weight; 100SW: 100 seed weight; SHLG%: shelling%; GRNL: grain length; GRNW: grain width; KYLD: kernel yield/plant; PYLD: pod yield/plant; HI: harvest index.

DISCUSSION

The results of the analysis of variance showed that for every morphological parameter under investigation, the mean squares resulting from genotypes were extremely significant. The seventeen characters from the analysis of variance revealed highly significant differences among all fourteen genotypes. Suggesting the existence of genetic differences in groundnut genotype-related features. The genotypes could be utilized in a breeding program to improve yield and its components (Tesfaye 2021).

Groundnut (*Arachis hypogaea*) mean performance reveals significant morphological variability within and between genotypes. Early flowering indicates the early stages of reaching maturity (Khan *et al*., 2020). Our research suggests that the early flowering genotypes Yargingila, Samnut24, Samnut25, Samnut26, and Exdakar could be chosen for early (less than 100 days) maturity following (Yol *et al*., 2018). The days to maturity for each genotype varied considerably (p≤0.05) and ranged from 84 to 124 days, roughly matching the range described by Yol *et al*. (2018) and Gangadhara *et al*. (2023). In our investigation, plant height varied greatly as well (from 46.57 cm to 75.23 cm), and all other morphological characteristics varied significantly as well. A strong significant difference (p ≤ 0.05) was found between yield and yield contributing traits such as plant/biomass fresh and dry weight, number pods per plant, 100-fresh and dry pod weight, grain size, and hundred seed weight showed high genetic variation among these traits. A comparable variation in yield-contributing features has been stated by Gangadhara *et al*. (2023), and it was proposed that these variations were due to the genotype by environment (G×E) effect on groundnut yield (Yol *et al*., 2018). All fourteen genotypes chosen produced the highest field output. These genotypes could be utilized in breeding to improve these traits (Kumar *et al*., 2019). According to (Yol *et al*., 2018), shelling

percentage is an index of the percentage of grains or seeds and is one of the main selection criteria in groundnut breeding, and Samnut23 had a significantly higher value in this study. The phenotypic coefficient of variance (PCV) showed a wider and higher value than the genotypic coefficient of variance (GCV) for all of the traits, indicating that the traits under study were strongly influenced by the environment. Similar results on groundnut were also reported earlier by Gangadhara *et al*. (2023) where the PCV showed a slightly higher value than the GCV for the majority of traits. According to Chaudhari et al. (2017), PCV and GCV values less than 10% were classified as low, 10-20% as moderate, and greater than 20% as high. Based on these settings, the results of this study showed that both GCV and PCV were moderate to high, except for shelling% and grain width displaying a low feature during this experiment. This low PCV and GCV in shelling percentage and kernel width agree with the earlier findings of Gangadhara *et al*., (2023). The low PCV and GCV achieved in this experiment demonstrated the low prevalence of additive gene actions in the expression of these traits as well as the difficulties in improving them through simple selection (Robsa Shuro, 2021). High variability is present in the number of branches, number of pods per plant, fresh 100-pod weight, fresh and dry plant weight, kernel yield, pod yield, and harvest index, as indicated by the highest GCV and PVC values (Gangadhara *et al*., 2023). High GCV and PCV were also recorded by Balaraju and Kenchanagoudar, (2016) for the number of secondary branches per plant, pod yield per plant, pods per plant, pod yield per plant, and harvest index. The results of high GCV and PCV found in the current experiment revealed variability for the majority of the traits assessed.

Heritability estimates are helpful when breeding quantitative traits, given that they offer insight into the degree to which a specific trait can be inherited by succeeding generations (Fobi *et al*., 2010). Heritability values have been categorized as low (0-30%), moderate (30-60%), or high (>60%) (Robinson *et al*., 1949; Fobi *et al*., 2010). In the present investigation, estimates of broad sense heritability (H_b) ranged from 13.33% to 33.33% for canopy spread and days to maturity respectively. Moderate heritability was observed for all the traits except canopy spread and kernel width. These results are in agreement with the findings of previously published reports by Gangadhara *et al*. (2023) for days to maturity; Robsa , (2021) for the number of days to 50% flowering, Plant height, number of pod per plant, number of branches and Shelling percentage. John *et al*. (2023) reported similar for 100 pod weight, 100 kernel weight, shelling percentage, dry haulms yield per plant, kernel yield per plant, and pod yield per plant. It shows a strong environmental influence on these characteristics' inheritance.

Heritability only doesn't indicate genetic improvement from genotype selection, and selection effectiveness relies on genetic advancement (GA) rather than heritability alone (Rathva, 2018). Thus, understanding genetic advance alongside heretabitilty is more beneficial. Furthermore, GA plays a significant role in forecasting the anticipated genetic gain from the selection cycle (Tesfaye, 2020). GA and GAM were categorized as low (0-10%), moderate (10.1-20%), and high (> 20%) (Gangadhara *et al*., 2023). In the present study, genetic advance as a percentage of the mean (GA) ranged from 6.81% to 76.22% for canopy spread and harvest index respectively. The characteristics, grain width, and canopy spread with low GA. Genetic advance as a percentage of the mean (GAM) is a reliable measure for assessing the success of selection in enhancing traits since it takes into consideration heredity, phenotypic standard deviation, and selection intensity. From these results, high genetic advance as a percent of mean and moderate heritability was recorded for Days to 50% flowering, number of branches, branch height, number of pods/plant, dry plant weight, 100-seed weight, grain length, pod yield per/plant, kernel yield and harvest index. Suggesting that phenotypic selection and the

pedigree breeding approach can be used to improve these traits (John *et al.*, 2023). Similar findings were reported by Robsa (2021), for the number of branches and number of pods per plant. Moderate heritability coupled with high genetic advance as a percent of the mean was also reported by Vasanthi *et al.* (2015), Kumar *et al.* (2019) and John *et al.* (2023) for pod yield per plant and Nagaveni and Hasan (2019) for kernel yield per plant. Waidkar *et al.* (2019) reported similar kind of results for moderate heritability together with high genetic advance as a percent of the mean for plant height. Moderate heritability and low genetic advance were identified for days to days to maturity, fresh and dry 100-pods weight, fresh plant weight, and shelling %, and these outcomes coincide with the findings of Gangadhara *et al.* (2023) for days to maturity.

The association or correlation is an important tool for researchers to assess what attributes are best suited for inclusion in the genotype selection procedure (Khan *et al.*, 2020). Correlation analysis evaluates the link between yield and its components (Tesfaye, 2020). Pod yield is a complicated trait that is influenced by numerous factors, either directly or indirectly. Because of this, considering the crucial factors that influence the yield throughout the selection process can greatly boost success (Killi and Beycioglu, 2022). According to the correlation analysis results of this study, pod yield was negatively non-significantly correlated with branch height and canopy spread, but it had a significant and very positive correlation with kernel yield, grain length, grain width, 100-seed weight, fresh and dry 100-pod weight, and number of pods per plant. It suggests that pod production might be improved by selecting the above strongly positive linked features, whilst plants with short branch height and less canopy cover could be simultaneously chosen for high yield. These findings are consistent with those of Hampannavar *et al.*, (2018) for pods per plant and kernel yield (Kumar *et al.*, 2019; Killi and Beycioglu, 2022) for pods per plant, 100 pods weight, kernel yield and Patil *et al.* (2020), Killi & Beycioglu, (2022) for 100- seed weight. These characteristics can be directly selected to increase pod yield regularly (Khan *et al.*,2021). Kernel yield was positively correlated and highly significantly associated with the number of branches per plant, the number of pods per plant, the fresh and dry 100-pod weight, the 100-seed weight, and the length and width of the grain. Patil *et al.* (2020) reported similar findings regarding kernel size. In contrast, hundred seed weight and seed qualities have an advantageous impact on yield. As a result, they are ideal candidates for yield improvement programs. Seed features contribute more to the yield than pods. (Olanrewaju *et al.*, 2021).

Various studies employ various approaches to evaluate variability and genetic diversity, including multidimensional scaling, grouping, and PCA (Olanrewaju *et al.*, 2021). In this study, the first four primary components accounted for 90.370% of the total variation. According to the current Principal Component Analysis study, the vector loading for each agronomic character with Eigen values greater than one and the first four Principal Components (PC) described variation percentage. The first four PCs represented 90.37% of the variation in the specified genotypes under study. Younis *et al.* (2020) reported that the first four components explained 83.27% of the overall variation among the 20 groundnut genotypes. Furthermore, PC1 is the most effective criterion for selection for yield improvement (Olanrewaju *et al.*, 2021). A large portion of the variation among genotypes in this study was explained by PC1, which accounted for 52.18% of the total variation. The traits that dominated this variation were plant fresh weight, grain length, fresh and dry 100-pod weight, plant fresh and dry weight, number of branches, days to maturity, days to 50% flowerings, 100-seed weight, kernel yield, and pod yield. Indicating that these traits accounted for much of the variation among genotypes and could be used for selection. The first principle component is more relevant because it accounts for more than half of the total variance

produced by the first four PCs (Upadhyaya, 2003). According to Amarasinghe *et al*. (2016), the first PC leads to greater variation. Makinde and Ariyo (2010) as well as Kumar (2010) observed 76% of the overall variation among genotypes from the first five PCs, whereas Upadhyaya *et al*. (2009) found that the first nine PCs accounted for 79% of the entire variation. Similarly, Patil *et al*., 2020 reported 78.23% variation for the first seven components. Groundnut accessions with higher performance in these traits could be chosen for improvement (Daudi *et al*., 2021). Similarly, (Denwar *et al*., 2019) reported that trait contribution to distinct PCs varied according to the level of variance for the given trait amongst experimental genotypes.

CONCLUSION

This study reveals significant variability in agronomic traits among groundnut genotypes, including yield attributes and seed yield, suggesting potentials for further genetic improvement. The genotype, SAMNUT24 were discovered to have least number of days to maturity and a highest number of pods. Similarly, BAHAUSA, and SAMNUT22, were found to have good vegetative traits with high plant dry weight. The genotypes SAMNUT23, were associated to needed grain and pod yield traits. The study found that traits such as the number of branches, pods per plant, kernel yield, pod yield, and shelling percentage showed a high genotypic coefficient of variation and moderate broad-sense heritability. These characteristics are beneficial for developing groundnuts by effective phenotypic selection, with a high predicted genetic gain. The study revealed that pod yield has a significant correlation with kernel yield, grain length, grain breadth, 100-seed weight, fresh and dry 100-pod weight, and pod count per plant. Kernel production is positively associated with the number of branches per plant, pods per plant, fresh and dry 100-pod weight, 100-seed weight, grain length, and grain width. Plants with short branch heights and low canopy cover can also produce significant yields. The first four main components accounted for approximately 90.37% of total variation across all morphological features.

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