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GENOTYPIC VARIANCE AND SELECTION CRITERIA IN GROUNDNUT (*ARACHISHYPOGAEA*L.) BASED ON OIL QUALITY AND AGRONOMIC TRAITS

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ABSTRACT
Variability gives room for recombination which is important for any crop improvement program. Based on this contextual, this work was conducted to evaluate genetic variability among groundnut germplasm and establish relationships between oil quality and agronomic traits using multivariate analysis. To achieve this objective, fifteen groundnut genotypes were evaluated in a randomized complete block design with three replications. Data were collected on oil and yield quality traits. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for number of pods and number of seeds per plant, carbohydrate and protein. Broad sense heritability estimates for agronomic and oil content traits ranged from 49.57% - 99.06% while the genetic advance expressed as percentage of mean estimates ranged from 17.73% -114.38%. The evaluated genotypes were clustered into four main groups based on oil and yield quality traits using UPGMA dendrogram. Hence, hybridization of group II with either group I, III or IV could be used to achieve higher vigor or heterosis among the genotypes. The number of pods per plant showed a significant correlation with pod weight per plant (r =0.79) and the number of seeds (0.99). However, most of the oil content traits recorded a non-significant negative correlation. It was concluded that number of pods, seeds per plant, and fat content might be the major agronomic and oil quality traits as selection criteria for improving groundnut genotypes. Also, this assessment could be used in development of reliable selection criteria for important agronomic traits in groundnut.

Keywords: Genetic Advance, Genotype, Heritability, Traits association, Phenotype

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is a valuable leguminous cash crop grown for both food and oil (FAOSTAT 2010). Although the crop originated in South America, it is now produced in over 100 nations. It is grown on a total of 23 million hectares, with a production estimate of 36.45 million tonnes and an average productivity of 1520 kg/ha. Around 90% of overall production is concentrated in semi-arid tropics emerging countries, with India and China accounting for nearly half of world output. Nigeria, Senegal, and Sudan are important producers in Africa. After common beans (*Phaseolus vulgaris* L.), the crop is Uganda's second most significant legume (FAOSTAT 2019). It is primarily produced in Uganda's semi-arid, dry eastern and northern areas (Ronner and Giller, 2012). It is a non-animal protein source that's also a cash and food crop. Furthermore, smallholder farmers grow groundnut with little or no inputs (Mugisha *et al*., 2011; Mugisha *et al*., 2014).

Research on improvement of groundnut has mainly focused on improving agronomic traits. Very few efforts have been made to improve groundnut's nutritional quality, as biochemical estimation of quality is laborious through traditional breeding.Only a few attempts have been made to evaluate various germplasm for nutritional traits in combination with agronomic performance (Sarvamangala et al., 2011). Kernels with a high oil content and a low Oleic acid/ Linoleic acid ratio (O/L ratio) are preferred for edible oil, however the quality requirements for confectionery groundnut are more severe because it is not an oilseed crop. They will necessitate further work to develop confectionery-grade types with large pod and seed sizes, high protein and sugar content, high oil content, low aflatoxin risk, and a high O/L ratio. However, the limited genetic variability in groundnut oil content limits the potential for significant increases or decreases in oil content through conventional breeding Pasupuleti *et al*., (2013). However, by attempting crosses that are properly planned, especially in light of the parents' diversity, a lot of variation can be created. The goals of this study were to determine the degree of association between agronomic and oil quality traits, as well as to estimate genetic variability, heritability, and expected genetic advance; identify genotype(s) with high levels of oil content and better performance; and estimate genetic variability, heritability, and expected genetic advance.

MATERIALS AND METHODS

Planting Materials

Genetic material comprised of 15 groundnut genotypes details in Table 1.

Table 1: List of groundnut genotypes studied.

No	Genotypes	Collection Source	Distinct character
1	SAMNUT 10	I.A.R	1036 (Rosette resistant) x Mani Pinter (Rosette susceptible)
2	SAMNUT 11	I.A.R	48-37 (Rosette resistant) x Mani Pintar (Rosette Susceptible)
3	SAMNUT 14	I.A.R	Short season drought tolerant Spanish Bunch type.
4	SAMNUT 21	I.A.R	Pedigree; RMP 12 x ICGS (E) 52. Rosette resistant and leaf spot tolerance.
5	SAMNUT 22	I.A.R	Pedigree; RMP 91 x (4750.70x 3520.71). Rosette resistant.
6	SAMNUT 23	I.A.R	Pedigree; ICGV-SM 85048 x RG 1. Rosette resistant and leaf spot tolerant.
7	SAMNUT 24	I.A.R	Pedigree; ICGM 751/754 x ICGV 87922. Rosette resistant and leaf spot tolerant.
8	GH 119_20	I.A.R	Advance breeding line from ICRISAT. Seeds are large seeded with low oil quality.
9	ICGV 94222	I.A.R	Advance breeding line from ICRISAT. Seeds are large seeded with low oil quality.
10	ICGV 88434	I.A.R	Advance breeding line from ICRISAT. Seeds are large seeded with low oil quality.
11	ICGV 94204	I.A.R	Advance breeding line from ICRISAT. Seeds are large seeded with low oil quality.
12	ICGV 93194	I.A.R	Advance breeding line from ICRISAT. Seeds are large seeded with low oil quality.
13	ICGV 93030	I.A.R	Advance breeding line from ICRISAT. Seeds are large seeded with low oil quality.
14	ICGX_XM 00020/5/P15	I.A.R	Advance breeding line from ICRISAT. Seeds are large seeded with low oil quality.
15	NC 7	I.A.R	Advance breeding line from ICRISAT. Seeds are large seeded with low oil quality.

Experimental Design

During the 2014 rainy season, fifteen groundnut genotypes were arranged in a randomized full block design with three replications. On March 31, 2014, three seeds were sowed in each experimental pots, two pots were allocated for each genotype in all replications. The research was conducted in the screen house of Ahmadu Bello University's Department of Plant Science in Zaria (Longitude 08° 027'E, Latitude 11° 39'N, and 500 m above sea level) in Nigeria's Northern Guinea savannah ecological zone (Olanuga, 1979). Irrigation was applied once daily until physiological maturity, and all agronomic techniques were followed according to the Institute of Agricultural Research's (I.A.R.) recommendations.

Data Collection

Plant height (cm), number of pods per plant, pod weight per plant (g), seed weight per plant (g), 100-seed weight (g), and shelling percentage (%) were among the agronomic traits measured. Proximate analysis, such as moisture content, ash content, fibre, lipids (fat), protein, and carbohydrate, were also taken, and these were gathered using established procedures (AOAC 2012).

Statistical Analysis

Results were analyzed using SASsoftware (version 9.1) for all traits to carry out the analysis where the variance component could be obtained.and means were compared/ separated using Fischer's LeastSignificance Difference (LSD) at 5% level.

The model for analysis of RCBD is

$$y_{ijk} = \mu + r_i + g_j + \varepsilon_{ijk}$$

Where: y_{ijk} = Observed effect for i^{th} replication j^{th} genotype and k^{th} block, μ = grand mean of the experiment, r_i = effect due to i^{th} replication, g_j = effect due to j^{th} genotype, ε_{ijk} = effects due to the residual or random error of the experiment.

Estimate of Genetic Parameters

The extent of genetic progress expected by character selection was computed as follows (Johnson et al., 1955):

In this work, genetic characteristics such as genotypic and environmental variance, broad-sense heritability, and genetic advance (GA) of Arachishypogaea variants were calculated. Variation information is only available through genotypic and phenotypic variations, but heritability assessment determines

the heritable part of this variation. A sufficient genetic variety of these qualities, as well as their heritability values, are required for efficient selection of traits under improvement. In a broad sense, heritability was calculated as the ratio of homozygous parents' genetic variance to their phenotypic variance.

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2} \quad \sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where,

σ_p^2 = This is the phenotypic (inter-varietal) variance obtained from the fifteen varieties.

σ_e^2 = This is the environmental (intra-varietal) variance estimated by the average of the phenotypic variance and the environmental variance.

The heritability was assessed on a mean basis by averaging the total genetic variation and on a varietal basis by calculating the genetic variance for each of the 15 genotypes. According to Singh and Chaudhary (1985), the mean values were utilized for genetic analysis to determine phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) using:

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100 \text{ and } PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

Where,

σ_g^2 = genotypic variance, σ_p^2 = phenotypic variance, $\bar{X}$ = sample mean.

Expected genetic advance (GA) of the genotypes as percent of mean was calculated using Singh and Chaudhary's method (1985).

$$\Delta G\left(\%_{\bar{X}}\right) = i \frac{\sqrt{\sigma_p^2}}{\bar{X}} h_b^2 \times 100$$

Where,

i = the selection intensity in the selection at 5 % was 2.06 and at 10% it was 2.755 (Allard, 1960)

$\sqrt{\sigma_p^2}$ = phenotypic standard deviation, h_b^2 = the heritability value and

$\bar{X}$ = mean of the population.

The degree of relationship between different factors was determined using the correlation coefficient (r). The Pearson's formula was used to calculate the correlation coefficient between pairs of characters at phenotypic levels.

Cluster Analysis

Cluster analysis (CA) was utilized to evaluate the genetic diversity of oil quality and agronomic parameters in this study. To differentiate the varieties, the agromorphological data were computed using multivariate analysis. Individuals were grouped together using cluster analysis based on their features. As a result, individuals with comparable traits were correctly clustered together based on relatedness, similarity, and distance of variations. To begin, the data were standardized to eliminate the effects of parameter variances using the STAND option, then the distance coefficient was calculated using the DICE similarity index. In the numerical taxonomy system NTSYS pc 2.02 software, the standardized data and information were represented in a dendrogram using the Shan clustering program and the unweighted pair group method with arithmetic average (UPGMA). To support the cluster analysis, the DECENTRE, EIGEN, and GRAPHICS tools of NTSYS pc were used to calculate principal component analysis (PCA).

RESULTS

Mean square for agronomic and oil content traits

The results of analysis of variance showed highly significant difference (P≤0.01) among the genotypes for both agronomic oil content traits. The mean squares for plant height, days to 50% flowering, number of pods, pod weight, number of seeds, seed weight, 100 seed weight, shelling percentage, moisture content, fat, ash, carbohydrate and protein is presented in Table 2.

Mean Performance for agronomic traits

The mean for the agronomic traits for the 15 groundnut genotypes is presented in (Table 3). Wide range of variation was recorded for all the traits. The overall mean performance for plant height is 50.58 cm and it ranged from 39.87 cm for SAMNUT 21 to 63.07 cm for GH119-20. Three genotypes SAMNUT 21 (39.87cm), ICGV 94222 (43.43cm) and SAMNUT 14 (44.10 cm)

Table 2: Mean squares from ANOVA for agronomic and oil quality traits of groundnut genotypes grown at Samaru 2014

SOV	DF	PHT	DFF	NPP	PWT	NSP	SWT	HSWT	SHP
Replication	2	37.97	13.09	27.22	124.02	108.60	126.48	79.94	242.49
Genotype	14	110.43**	84.80**	650.46**	420.20**	2245.77**	275.89**	168.64**	141.76**
Error	28	34.92	8.16	98.39	101.44	278.17	48.75	85.05	41.08
SOV	DF	moisture	Fat	Ash	Carbohydrate	protein			
Genotype	14	22.05**	22.51**	14.44**	62.03**	53.20**			
Error	28	0.43	0.86	0.06	0.58	0.60			

**= highly significant at P≤0.01, SOV=Source of variation, DF= degree of freedom, PHT= plant height, DFF= days to 50% flowering, NPP= number of pods per plant, PWT= pod weight, NSP= number of seeds per plant, SWT= seed weight, HSWT= hundred seed weight and SHP= shelling percentage

have plant height less than 45 cm while 10 genotypes recorded plant height more than 50 cm with SAMNUT 22, ICGV 88434 and GH119-20 being genotypes with highest plant height (57.77cm, 58.20 cm and 63.07 cm), respectively.

The performance of genotypes in terms of days to 50% flowering has an overall mean of 34 days. SAMNUT 10 flowered earliest (28 days) while SAMNUT 21 flowered late (43 days). Four genotypes have days to 50% flowering of 29 days (SAMNUT 11, SAMNUT 24,ICGV-XM/00020/5/P15 and ICGV 88434) while 2 groundnut genotypes GH119-20 and SAMNUT 21 recorded more than 40 days to 50% flowering.

Number of pods per plant has an overall mean of 33 and it range from 12 pods for ICGV 93030 to 65 pods for SAMNUT 10, 5 genotypes (ICGV 93030, GH119-20, SAMNUT 21, ICGV 93194 and ICGV 94204) have less than 30 pods per plant while 3 genotypes (SAMNUT 24, SAMNUT 11 and SAMNUT 10) have the highest number of pods per plant (45 pods, 59 pods and 65 pods), respectively.

Overall mean of pod weight was 32.88 and it ranged from 11.57g for ICGV 93030 to 49.93g for SAMNUT 10. Five groundnut genotypes (ICGV 93030. GH119-20, ICGV 93194, NC7 and SAMNUT 21) weighed less than 30 g (11.57 g, 15.1 g, 18.77 g, 23.6 g AND 27.67 g), respectively. Four groundnut genotypes (SAMNUT 11, ICGV-XM00020/5/P15, SAMNUT 14 and SAMNUT 10) recorded pod weight greater than 40 g (40.6 g, 46.6 g, 49.00 g and 49.93 g), respectively.

Table 3: Mean performance for agronomic and oil quality traits of groundnut genotypes grown in Samaru, 2014

Genotypes	PHT	DFF	NPP	PWT	NSD	SWT	HSWT	SHP	Moisture	Fat	Ash	Carbohydrate	Protein
SAMNUT 10	51.13	28	65	49.93	118	38.67	32.67	77.03	3.40	50.04	1.93	16.74	27.65
SAMNUT 11	51.60	29	59	40.60	108	31.67	29.33	77.90	4.26	51.12	2.16	20.35	22.11
SAMNUT 14	44.10	31	34	49.00	62	35.67	55.73	71.17	3.68	51.26	3.05	24.21	17.8
SAMNUT 21	39.87	43	19	27.67	31	14.67	46.40	51.30	3.20	48.12	2.53	22.14	24.02
SAMNUT 22	57.77	30	31	36.00	57	25.00	45.57	68.97	4.08	49.55	1.67	25.75	18.95
SAMNUT 23	50.93	38	32	32.33	54	20.00	37.40	62.00	3.34	54.19	2.34	27.74	12.39
SAMNUT 24	45.87	29	45	38.83	77	28.33	38.77	72.77	3.93	54.74	2.48	16.10	22.74
NC7	53.20	40	34	23.60	53	15.33	29.87	65.63	3.53	47.33	2.24	31.07	15.83
ICG 88434	58.20	29	35	34.80	59	24.67	42.70	71.20	3.83	50.31	2.75	18.31	24.80
ICGV 94222	43.43	39	30	37.47	46	23.00	51.70	61.30	3.20	55.18	2.00	18.01	21.62
ICGV 93194	49.87	38	20	18.77	34	12.67	37.97	67.80	3.90	44.53	2.36	24.29	24.91
ICGV 93030	48.47	36	12	11.57	18	7.33	41.80	63.03	3.64	51.31	2.37	28.65	14.03
ICGV 94204	48.83	30	28	30.43	49	17.67	37.07	60.47	4.02	50.63	2.68	20.15	22.53
GH119-20	63.07	41	16	15.10	31	8.57	37.23	64.96	4.59	47.05	1.88	25.63	20.85
ICGX-XM00020/5/P15	52.40	29	40	46.60	68	30.33	45.20	65.63	3.42	49.97	1.92	29.69	14.99
Mean	50.58	34	33	32.88	58	22.24	40.63	66.74	3.73	48.02	2.29	23.26	20.35
LSD	9.88	4.78	16.59	16.85	27.9	11.68	15.42	10.72	0.37	1.55	0.42	1.27	1.29
Min	39.87	28	12.33	11.57	18.33	7.33	29.33	51.30	3.2	44.53	1.67	16.1	12.39
Max	63.07	42.67	65.33	49.93	118	38.67	55.73	77.03	4.59	54.74	31.07	31.07	27.65
CV	11.68	8.44	29.86	30.63	28.89	31.40	22.70	9.60	5.98	1.84	10.86	3.27	3.8

PHT= plant height, DFF= days to 50% flowering, NPP= number of pods per plant, PWT= pod weight, NSP= number of seeds per plant, SWT= seed weight, HSWT= hundred seed weight and SHP= shelling percentage, LSD= Least Significant Difference, CV= Coefficient of Variation

The overall mean performance for number of seeds per plant was 57.73 and ranged from 18 seeds per plant for ICGV 93030 to 118 seeds per plant for SAMNUT 10. Six genotypes ICGV 93030, GH119-20, SAMNUT 21, ICGV 93194, ICGV 94222 and ICGV 94204 recorded less than 50 seeds per plant 18 seeds per plant, 31 seeds per plant, 31 seeds per plant, 34 seeds per plant and 46 seeds per plant, respectively. Nine genotypes recorded more than 50seeds per plant with SAMNUT 11 and SAMNUT 10 recording the highest number of seeds per plant (108 seeds per plant and 118 seeds per plant), respectively.

The performance of the 15 groundnut genotypes for seed weight has an overall mean of 22.24, ranging from 7.33 g for ICGV 93030 to 38.67 g for SAMNUT 10. Six genotypes ICGV 93030, GH119-20, ICGV 93194, SAMNUT 21, NC7 and ICGV 94204 recorded low seed weight (<20 g) which are 7.33 g, 8.57 g, 12.60 g, 14.67 g, 15.33 g and 17.67 g, respectively while 4 genotypes ICGV-XM00020/5/P15, SAMNUT 11, SAMNUT 14 and SAMNUT 10 recorded highest seed weight (>30 g) which are 30.33 g, 31.67 g, 35.67 g, respectively.

Hundred seed weight has a mean of 40.63 g and ranged from 29.33 g for SAMNUT 11 to 55.73 g for SAMNUT 14. Two genotypes, SAMNUT 11 (29.33 g) and NC 7 (29.87 g) weighed less than 30 g indicating low 100 seed weight while 13 genotypes weighed more than 30 g with ICGV 94222 and SAMNUT 14 recorded highest 100 seed weight (51.7 g and 55.73 g), respectively.

The performance of the groundnut genotypes in terms of shelling percentage has an overall mean of 66.74 and ranged from 51.3 % for SAMNUT 21 to 77.90 % for SAMNUT 11. SAMNUT 21 recorded the lowest shelling percentage 51.30 % while 2 genotypes SAMNUT 10 and SAMNUT 11 recorded highest shelling percentage of more than 75 % (77.03 % and 77.90 %), respectively.

Mean performance for the 15 groundnut genotypes for moisture content has an overall mean of 3.73 and ranged from 3.2 % for ICGV 94222 and SAMNUT 21 to 4.59 % for GH119-20. Low moisture content <3.5 % was recorded in 5 genotypes, ICGV 94222, SAMNUT 21, SAMNUT 23, SAMNUT 10 and ICGV-XM00020/5/P15 visa viz 3.20 %, 3.20 %, 3.34 %, 3.40 % and 3.42 %, respectively while 10 genotypes recorded moisture content >3.5 % with GH119-20 having the highest moisture content 4.5% in Table 3.

Fat content has an average of 48.02 % and ranged from 44.53 % in ICGV 93194 to 55.18 % in ICGV 94222. Five genotypes, ICGV 93194, GH119-20, NC7, SAMNUT 21, SAMNUT 22 and ICGV-XM00020/5/P15 recorded fat content less than 50% while 9 genotypes recorded fat content >50 % with SAMNUT 23, SAMNUT 24 and ICGV 94222 are genotypes with highest fat content (54.19 %, 54.74 % and 55.18 %), respectively.

Ash content had an overall mean of 2.29 % and ranged from 1.67 % in SAMNUT 22 to 3.05% in SAMNUT 14. Four groundnut genotypes SAMNUT 22, GH119-20, ICGV-XM00020/5/P15 and SAMNUT 10 recorded ash content <2 %; 1.67 %, 1.88 %, 1.92 % and 1.93 %, respectively while 11 genotypes recorded ash content from and above 2 % with SAMNUT 14 having the highest ash content 3.05 %.

Carbohydrate has an overall average of 23.26 % and it ranged from 16.10 % in SAMNUT 24 to 31.07% in NC 7. Four genotypes SAMNUT 24, SAMNUT 10, ICGV 94222 and ICGV 88434 recorded carbohydrate content <20 %. Eleven genotypes recorded carbohydrate content >20 % with NC 7 having the highest carbohydrate 31.07 %.

Protein content has a mean of 20.35 % and ranged from 12.39 % in SAMNUT 23 to 27.65 % for SAMNUT 10. Less than 20 % protein content were recorded in 6 genotypes; SAMNUT 23 (12.39 %), ICGV 93030 (14.03 %), ICGV-XM00020/5/P15 (14.99 %), NC 7 (15.83 %), SAMNUT 14 (17.80 %) and SAMNUT 22 (18.95 %). Nine genotypes had protein content >20 % with ICGV 93194 having the highest protein content 24.91 %.

Variance components estimated of agronomic and oil content traits

The extent of variability in respect of phenotypic and genotypic variances, phenotypic and genotypic coefficients of variance (PCV) and (GCV) respectively, broad-sense heritability $\left(H^2\right)$ and genetic advance expressed as percentage of mean ΔG(%) for agronomic traits for the 15 groundnut genotypes are presented in (Table 4). For all agronomic traits, a large proportion of the phenotypic variance were gained by genetic component, that contributes to (>70%) of the phenotypic variance.GCV estimates for number of seeds (76.83 percent), number of pods per plant (70.72 percent), seed weight (67.77 percent), and pod weight (67.77 percent) were all high (53.30 percent). The remaining attributes had GCVs that ranged from moderate to low. Number of seeds (82.08 percent), number of pods per plant (76.77 percent), seed weight (74.69 percent), and pod weight (62.34 percent) all had high PCV estimates, whereas the remaining features had moderate to low PCV. For all characteristics, PCV values were higher than GCV values, indicating that the environment has an impact on trait expression.

Table 4: Estimate of variance components, GCV, PCV and % genetic advance for agronomic and Oil Quality traits of 15 groundnut genotypes grown in Samaru 2014

Traits	Variance components			GCV (%)	PCV (%)	$H^2(\%)$	$\Delta G(\%)$
	σ_g^2	σ_e^2	σ_p^2				
Plant height (cm)	75.51	34.92	110.43	17.18	20.78	68.38	19.80
Days to 50% flowering	76.64	8.16	84.80	25.87	27.21	90.04	22.84
Number of pods per plant	552.07	98.39	650.46	70.72	76.77	84.87	59.63
Pod weight (g)	318.76	101.44	420.20	54.30	62.34	75.86	42.84
Number of seeds per plant	1967.6	278.17	2245.77	76.83	82.08	87.61	14.38

Seed weight (g)	227.14	48.75	275.89	67.77	74.69	82.33	37.67
Hundred seed weight (g)	83.59	85.05	168.64	22.50	31.96	49.57	17.73
Shelling percentage (%)	100.68	41.08	141.76	15.03	17.84	71.02	23.30
Moisture	0.38	0.05	0.43	16.53	17.58	88.37	28.07
Fat	21.65	0.86	22.51	9.69	9.88	96.18	14.21
Ash	0.38	0.06	0.44	26.92	28.97	86.36	45.71
Carbohydrate	61.45	0.58	62.03	33.70	33.86	99.06	72.80
Protein	52.60	0.60	53.20	35.64	35.84	98.87	71.09

σ_e^2 = the environmental (intra-varietal) variance, σ_p^2 = phenotypic variance, σ_g^2 = genotypic variance, GCV= Genotypic Coefficient of Variation, PCV= Phenotypic Coefficient of Variation, h^2 = the heritability value in broad-sense, $\Delta G(\%)$ = Genetic advance expressed as a % of mean.

Broad sense heritability for agronomic traits indicated high heritability for all the traits (>50%).For each character, the predicted genetic advance values are reported as a percentage of the genotype mean (Table 4). High heritability and genetic progress are essential elements in anticipating the subsequent effect and picking the finest people. Number of pods per plant exhibited a high heritability (84.87%) and a high genetic advance (59.63%), whereas other variables had a high heritability but a low genetic advance.

For all oil quality traits(Table 4), the genetic component accounted for a considerable amount of the phenotypic variance, with genetic variance contributing >90% to phenotypic variance. GCV estimates were high for ash (26.92 percent), carbohydrate (33.07 %), and protein (35.64 %), but moderate to low for moisture and fat. PCV estimations for protein (35.84 percent), carbohydrate (33.86 percent), and ash were also high (28.97%). PCV estimations for moisture and fat were moderate to low. For all of the oil quality traits, PCV values were higher than GCV values, indicating that the environment had an impact on trait expression.

All of the oil quality traits reported had high heritability values, according to the results of heritability calculations. For glucose and protein, the genetic advance expressed as a percentage of mean was significant, but for all other variables, the GA was moderate to low.

Cluster Analysis based on oil quality and yield traits

The homogeneous agro-morphological traits were employed to calculate the Euclidean distances among the 15 groundnut accessions. TheUPGMAdendrogram was constructed using these values presented in Table 3 for cluster analysis and PCA. In thedendrogram shown in figure 1 and 2, the 15 groundnut accessions were grouped into 4main clusters. Among the four clusters, group II had the largest number of genotypes (7), groupI and IV had 3 genotypes each while group III had only 2 genotypes.

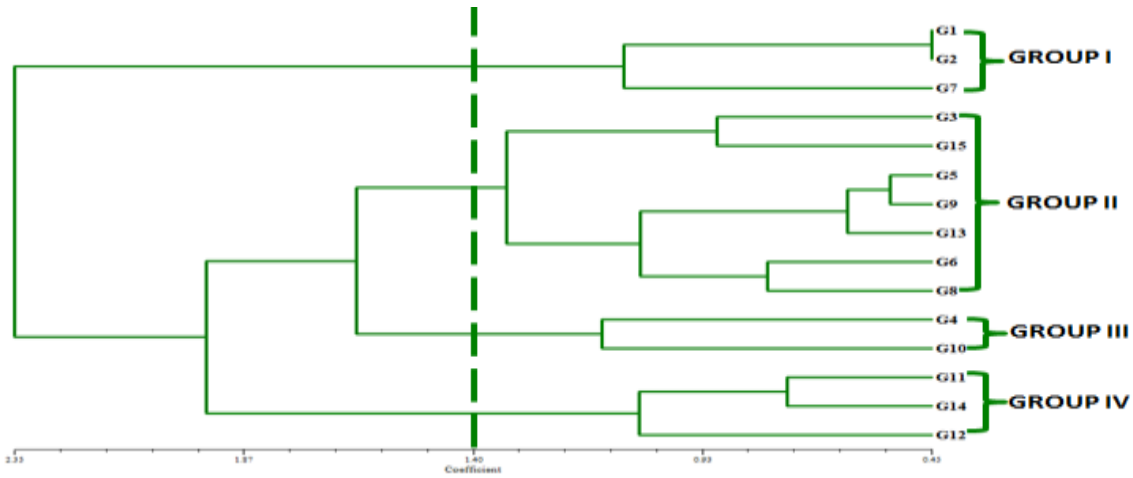

Figure 1. Description of clustering pattern which divides the 15 groundnut accessions into four groups at dissimilarity coefficient of 1.40

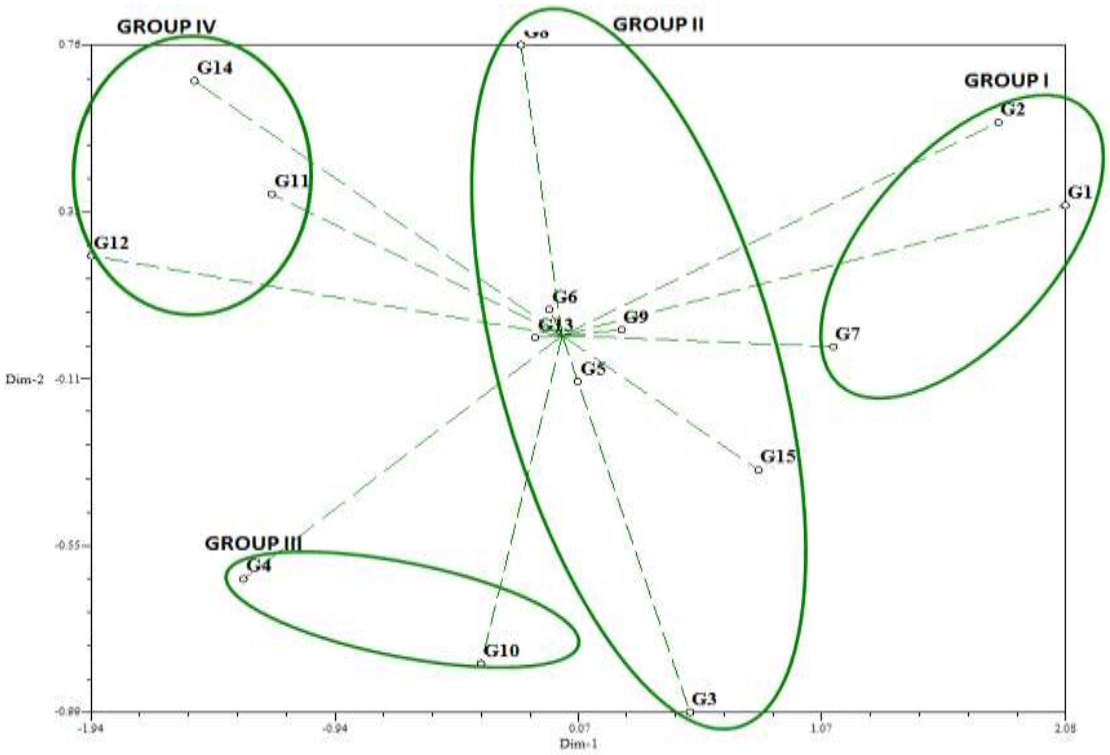

Figure 2. Two-dimensional graph of PCA indicating pattern of relationships among the 15 groundnut accessions supporting the cluster analysis

Correlation between agronomic and oil content traits

A highly significant positive correlation was recorded between number of pods per plant and all agronomic traits except 100 seed weight ($P \leq 0.01$) while it was negatively correlated with ash and carbohydrate with non-significant different ($P > 0.05$). Significant ($P \leq 0.05$) positive correlation was recorded between moisture and carbohydrate. Protein had a strong negative and highly significance with carbohydrate (Table 5).

Table 5: Correlation between agronomic and oil quality traits of 15 groundnut genotypes grown at Samaru 2014

	PHT	DFF	NPP	PWT	NSP	SWT	HSWT	SHP	MOI	FAT	ASH	CAR	PRO
PHT	1.00	-0.17	0.01	-0.21	0.05	-0.14	-0.40	0.35	0.54*	-0.35	-0.65**	0.52*	-0.33
DFF		1.00	-0.68**	-0.67**	-0.71**	-0.74**	0.07	-0.72**	-0.19	-0.32	0.04	0.17	0.04
NPP			1.00	0.79**	0.99**	0.86**	-0.36	0.74**	-0.10	0.36	-0.24	-0.23	0.04
PWT				1.00	0.78**	0.97**	0.24	0.48	-0.30	0.52	-0.04	-0.13	-0.18
NSP					1.00	0.87**	-0.37	0.77**	-0.02	0.31	-0.25	-0.17	-0.09
SWT						1.00	0.13	0.66**	-0.20	0.46	-0.06	-0.01	-0.16
HSWT							1.00	-0.33	-0.32	0.28	0.28	-0.13	0.07
SHP								1.00	0.32	0.08	-0.26	-0.06	0.18
MOI									1.00	-0.30	-0.11	-0.06	0.18
FAT										1.00	-0.11	-0.37	-0.23
ASH											1.00	-0.18	0.06
CAR												1.00	-0.81**
PRO													1.00

**= highly significant at P≤0.01, DF= degree of freedom, PHT= plant height, DFF= days to 50% flowering, NPP= number of pods per plant, PWT= pod weight, NSP= number of seeds per plant, SWT= seed weight, HSWT= hundred seed weight and SHP= shelling percentage, MOI=Moisture content, CAR= Carbohydrate, PRO= Protein

DISCUSSION

The wide range of variation, highly significant difference (P≤0.01) observed in the mean square of all the agronomic traits suggest that a reasonable amount of variability was present in the experimental materials for all the traits. Similar trends of variability for different agronomic traits were reported by Wolf *et al*. (2000) and Vasic*et al*. (2001). This variation could be attributed to genetic and environmental effects as well as their interactions. The measurement, evaluation and existence of variability provide the opportunity for improvement through selection (Marwede*et al*., 2004, Subramanian *et al*., 2010).

The mean performances of carbohydrate obtained suggest that groundnut could be used to manage protein malnutrition since a great amount of protein and fat is also found present. Mean values of carbohydrate obtained for the 15 groundnut genotypes are not significantly different from each other. ICGV 93194 had the highest crude protein of 24.91% and SAMNUT 23 had the lowest crude protein content of 12.39%. All 15 groundnut genotypes were non-significant in their crude fat contents. The crude fat values obtained were higher than Asibou*et al.*, (2008) crude fat values of 33.60-54.96 percent. Dietary fat is significant because it aids in the absorption of fat-soluble vitamins. It is a high-energy nutrient that does not make up a significant portion of the diet (Atasie*et al*., 2009). The high crude fat values found could indicate that groundnut genotypes could be employed to improve the palatability of meals that contain them. These groundnut cultivars have high crude fat contents, indicating that they are good sources of oil and may be appropriate for commercial oil production. SAMNUT 10 has a high protein level, however the largest fat content was found in SAMNUT 23 and SAMNUT 24. SAMNUT 23 and SAMNUT 24 had the highest fat content, high to moderate protein, and ash content mean performances, which was consistent with the findings of Aurand*et al.* (1987) for the same genotypes.

Coefficient of Variation

The calculation of genotypic coefficient of variation (GCV) in connection to their respective phenotypic coefficient of variation could better explain the comparison of traits in terms of the level of genetic variation (PCV). In both crosses and generations, relatively minimal differences between GCV and PCV were identified for agronomic and oil quality parameters such as seed number per pod (Table 6). It implies that the observed characteristic changes were primarily attributable to genetic factors. The environment, on the other hand, had only a minor impact on the expression of thesetraits.

The genotypic coefficient of variation (GCV) compares the variability present in different traits and evaluates the degree of diversity in crops. The phenotypic coefficient of variation (PCV) estimate was larger than the genotypic coefficient of variation (GCV) estimate for all traits evaluated among the 15 groundnut genotypes in this study. This revealed that the environment has a significant impact on the manifestation of these features. Similar observations in pearl millet were discovered by (Abuali Al, 2006, Subramanian *et al*., 2010, Bezaweletawet*et al*., 2006, Sumathi*et al*., 2010, Ghazy*et al*., 2012). The GCV and heritability estimates give accurate estimates of how much genetic progress can be predicted through phenotypic selection (Burton, 1952). For the parameters pod number per plant, 100-seed weight, and seed yield per plant, however, there was a significant difference between GCV and PCV. This revealed the importance of the environment in shaping this character's personality (Table 6). High GCV was seen in this experiment in features such as seed yield per plant. The significant GCV for this variable suggested that genotype improvement may be achieved by further selection.

The magnitude of inheritance of traits is determined by heritability. The information on heredity alone may not be sufficient to make an informed decision. As a result, heritability estimations combined with expected genetic advancements will be more accurate. According to Johnson *et al*. (2011), the effectiveness of selection is determined not just by heredity but also by genetic progress. In the number of pods, number of seeds per plant, and oil quality parameters, strong heritability was associated by high genetic progress as a percentage of the mean. This suggests that certain characteristics are inherited. The heritability is most likely due to additive gene effects, and selection for these traits may be successful in early generations. Similar findings have been observed by other researchers (Ali *et al*., 2008). However, the substantial heritability of pod weight, seed weight, plant height, and shelling %, along with the poor genetic advance, suggests non-additive gene action.

The unweighted pair group method with arithmetic mean (UPGMA) dendrogram approximately clustered the groundnut accessions into four main groups at dissimilarity coefficients 1.40. This indicates a high level of agro-morphological diversity among the evaluated genotypes. This study showed the efficacy of morphological or quantitative traits in grouping groundnut accessions. It was reported that analysis of genetic variance among groundnut accessions based on morphological traits can be used to differentiate and classify genotypes in a population (Swamy*et al*., 1988). This genetic diversity plays a significant role in selection of diverse cultivar for improvement of groundnut through selective breeding (Asibou*et al*., 2008). The evaluated genotypes were clustered into four main groups based on oil and yield quality traits using UPGMAdendrogram. Hence, to achieve higher vigour orheterosis among the genotypes, hybridization of group II with either group I, III or IV.

Regarding the associations among the agronomic traits, it was observed that number of pods per plants had a highly significant positive association with seed weight, number of seeds and shelling percentage. Another important yield viz. The number of seeds positively associated shelling percentage and seed weight (SwamyRao*et al*., 1988). Therefore, any direct selection for increased number of pods is likely to be associated with improvement of these traits. A weak association of shelling percentage 100 seed weight noticed indicate that large seeded types have poor shelling and negative relationship needs to be broken. However, seed weight and protein content observed to be negatively correlated which was also reported by (Mishra *et al*., 1992) as they do not go hand in hand but efforts to enhance protein content in the large seed kernels would be of prime interest in future breeding programs but must observe a high significant positive correlation with shelling percentage. The present study revealed a higher magnitude of variability for most agronomic and oil quality traits, accompanied by high heritability and genetic advance. Therefore, direct selection may yield desired combination of traits wherever favourable

traits are associated, if not, negative relationships have to be broken by adopting appropriate breeding techniques to develop suitable confectionery groundnut varieties.

Study of association among the oil quality traits is important. As the association of pod yield with oil content is positive, it is difficult to combine high yield with low oil in a single genotype, which is essential for confectionery genotype. However, notice of negative and significant association of pod yield with protein content is again undesirable. Further, seed weight was observed to be negatively correlated with protein content, carbohydrate, moisture and ash (Mishra *et al*., 1992) as they do not go hand in hand but efforts to enhance protein content in the large seed kernels would be of prime interest in future breeding programs.

CONCLUSION

The present study revealed considerable amount of genetic variability for most of the agronomic and oil quality traits, which was also accompanied by high heritability and genetic advance. Therefore, direct selection for yield and oil quality may be desired in combination with other traits wherever they are favourably associated. The genetic parameters discussed here are functions of environmental variability, so estimates may differ in other environment.

Based on the high heritability and genetic progress of several variables, such as the number of pods per plant, the number of seeds per plant, protein, and fat, it may be argued that the genetic influences of phenotypic expression of these traits are primarily additive. As a result, after numerous selection cycles, a high response should be possible. It is concluded that SAMNUT 10, SAMNUT 11, SAMNUT 23 and SAMNUT 24 have been identified as the best performing genotypes in terms of yield (number of pods per plant) and high oil (fat) content.

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