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Full Length Research Paper

Multivariate analysis of genetic divergence in twenty two genotypes of groundnut (*Arachis hypogaea* L.)

Makinde S.C.O[1]* and Omolayo Johnson Ariyo[2]

[1]Department of Botany, Faculty of Science, Lagos State University, Ojo Campus, P.O Box 001, LASU Post Office Ojo, Lagos State, Nigeria.

[2]Department of Plant Breeding and Seed Technology, College of Plant Science, University of Agriculture Abeokuta, P. M. B. 2240 Abeokuta, Ogun State, Nigeria.

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Twenty- two groundnut genotypes collected from different germplasm centers were cultivated in botanical nursery of the Lagos State University Ojo-Campus during the raining season of 2009. The data collected on 33 characters were subjected to multivariate analysis to study the variability within the genotypes and to determine the efficiency of the methods in classifying genotypes. The first three axes each of factor analysis and principal component analyses (PCA) captured 42 and 55% respectively of the total variance and jointly identified final plant height, leaflet length, stem pigmentation, nodes on the main stem and number of leaves per plant at flowering as characters contributing most to variation. The first three axes of the canonical and discriminant analyses accounted for 85 and 90% of the total variation respectively and identified in addition to the above characters, pod beak, hairiness of mature leaflet, pod constriction, lateral branch pattern and peg colour as important. Genotype clustering using single linkage clustering technique did not follow a particular pattern, as genotypes from different sources were grouped together, while some from same source were also separated into eight different groups. The effect of genetic divergence on the choice of parental stock in improvement breeding programme was discussed.

Key words: Groundnut, factor analysis, principal component analysis, canonical discriminant analysis, single linkage cluster analysis.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.), a member of the family *Fabaceae* is a major source of vegetable oil and plant protein in Africa. It is the World's thirteenth most important food crop, the fourth most important source of edible oil and the third most important source of vegetable protein (Encyclopedia of Agricultural Science, 1994). Multivariate statistical methods and numerical taxonomy has been used extensively in summarizing and describing variation pattern in a population of crop genotypes (Ram and Panwar, 1970; Bartual et al., 1985; Rezai and Frey, 1990; Ariyo, 1990b; Ariyo and Odulaja, 1991; Ariyo, 1993; Flores *et al*., 1997; Cardi, 1998). The Mahalanobis D^2 statistic has been used to quantify the degree of divergence in different crops (Ram and Panwar, 1970; Das and DasGupa, 1984; Ariyo, 1987a; Nair et al., 1998; Pintu et al., 2007). The technique gave insight into the most genetically divergent parents that could be used for hybridization purpose. Das and DasGupa (1984) and Ariyo (1987a) noted earlier that, geographical diversity was not always related to genetic diversity and therefore not an adequate index of genetic diversity. Genotypes within clusters often showed great geographical diversity.

Successful establishment of germplasm collections and plant introduction for crop improvement as well as for germplasm conservation require studies in genetic variability within plant populations. Jain and Workman (1966) stated that such genetic variability and heterozygosity within populations existed in both natural and cultivated populations. Wright and Debzhonsky (1970) emphasized that the maintenance of this variability depended on complex interactions among a number of genetic and

*Corresponding author. E-mail: scmakinde@yahoo.com, bunmi.makinde@lasunigeria.org. Tel: +234(0)8033277358, +234(0)8088494428.

Table 1. Code names and source/ origin of groundnut genotypes.

Number	Genotype	Source/ Origin
1	ICG – 4998	ICRISAT India
2	ICG – 862	ICRISAT India
3	ICG – 6402	ICRISAT India
4	ICG – 8490	ICRISAT India
5	ICG – 4412	ICRISAT India
6	ICG – 156	ICRISAT India
7	ICG – 14466	ICRISAT India
8	ICG – 12370	ICRISAT India
9	ICG – 2106	ICRISAT India
10	ICG – 4343	ICRISAT India
11	ICG – 12189	ICRISAT India
12	ICG – 442	ICRISAT India
13	ICG – 4598	ICRISAT India
14	ICG – 7000	ICRISAT India
15	ICG – 1399	ICRISAT India
16	ICGY-6M- 5236	Zaria, Nigeria
17	ICG-IS- 11687	Zaria, Nigeria
18	ICGY-5M- 4746	Zaria, Nigeria
19	ICG-IS- 6646	UNILORIN, Nigeria
20	ICG- IS- 3584	UNILORIN, Nigeria
21	ICG49- 85A	UNAAB, Nigeria
22	UGA-7- M	UNAAB, Nigeria

and environmental factors. Ariyo (1987a and b) buttressed this fact further by stating that progress in breeding for economic characters often depends on the availability of a large germplasm representing a diverse genetic variation. He added that for a long term improvement programme, a large and diverse germplasm collection is an invaluable source of parental strains for hybridization and subsequent development of improved varieties. According to White and Gonzalez (1990), Nassir and Ariyo (2005), Aremu et al. (2007) accurate cultivar evaluations and ability to differentiate between cultivars in respect of genetic parameters associated with adaptedness in cultivated plants and their wild progenitors are critical to any plant breeding programme.

The objectives of this study therefore, are to evaluate and determine the variation pattern in collection of groundnut, identify the characters that sort the genotypes into different groups, suggest potential parents that could be used in improvement programme and appraise the suitability of the various multivariate techniques for classification of variation in groundnut.

MATERIALS AND METHODS

The twenty two genotypes of groundnut used in this study comprised of 15 accessions collected from International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India. The remaining 7 genotypes were collected from different research centers within Nigeria, Table 1 presents the genotype coding with their collection centre. Planting was done during the raining season of 2009 (April) in the Department of Botany Nursery, Lagos State University-Ojo Campus, Lagos (6° 36'N, 3° 34'E) Lagos State, Nigeria. Following land preparation, they were grown in double-row plots, replicated 3 times in a randomized complete block design.

Each row was 4 m long with 1 m between rows and plants were spaced 40 cm apart within the row to give ten plants in a row. Each stand was thinned to one plant at two weeks after planting. Manual weeding was done at two weeks after planting and subsequently at three weeks intervals to ensure minimal crop-weeds competition. There was no application of inorganic fertilizers and chemicals (herbicides and pesticides).The rainfall, relative humidity and temperature data of the study sites are presented in Table 2.

Data collection

Agronomic and yield data were collected on each genotype. Five internal plants were sampled in each row (that is ten plants in each plot). At maturity, pods were harvested on plant basis to obtain some characteristics. Altogether, data were collected on 33 characters. Table 3 presented the 33 characters and their methods of scoring. Mean values of the characters were computed for the ten sampled plants in each plot. The means of the characters were subjected to analysis of variance and covariance (SAS 2000) . The Principal Component Analysis (PCA) and Canonical Analysis were also done. The PCA analysis reduces the dimensions of a multivariate data to a few principal axes, generates an Eigen vector for each axis and produces component scores for the characters (Sneath and Sokal, 1973; Ariyo and Odulaja, 1991). Canonical analysis also measures the axis along which variation between

Table 2. Mean monthly temperature, T (°C), relative humidity, RH (%) and rainfall R (mm) for the study months.

Months	Environmental variable		
	T (°C)	RH (%)	R (mm)
April	29.0	74	157.4
May	28.5	78	320.7
June	26.9	83	69.5
July	26.3	83	18.5
August	26.0	84	85.2

Table 3. Characters used in the analysis and their methods of measurement/ scoring.

S/No	Character	Measurement/ Scoring (s)
1	Days to 50% flowering	Estimated using calendar
2	Height at flowering	Measured (cm)
3	Number of leaves/ plant at flowering	Counted
4	Final height/ plant	Measured (cm)
5	Days to maturity	Estimated using calendar
6	Number of branches/ plant at maturity	Counted
7	Nodes on the main stem/ plant at maturity	Counted
8	Stem girth/ plant at maturity	Measured (cm)
9	Leaflet length	Measured (cm)
10	Leaflet width	Measured (cm)
11	Leaflet length/ width ratio	Estimated
12	Pod width	Measured (cm)
13	Pod length	Measured (cm)
14	Seed length	Measured (mm)
15	Seed width	Measured (mm)
16	Shelling %age	Estimated (%)
17	Number of pods/ plant	Counted
18	Sample seed weight (100 seeds)	Measured(g)
19	Yield/ plant	Measured(g)
20	Growth habit	1 (procumbent); 2 (procumbent 2); 3 (decumbent 1); 4 (decumbent 2); 5 (decumbent 3); 6 (erect); 7 (others)
21	Stem branching pattern	1 (alternate); 2 (sequential); 3 (irregular with flowers on the main stem); 4 (irregular without flowers on the main stem); 5 (others)
22	Stem pigmentation	1 (absent); 2 (present)
23	Stem hairiness	3 (scarce); 7(abundant)
24	Lateral branch habit	1 (non-distichous); 2(distichous)
25	Peg colour	1 (absent); 2 (present)
26	Leaflet shape	1 (cuneate); 2 (obcuneate); 3 (elliptic); 4 (lanceolate); 5 (others)
27	Hairiness of young leaflets	1 (almost glabrous); 2 (sparse and short); 3 (sparse and long); 4 (profuse and short); 5 (profuse and long); 6 (others)
28	Hairiness of mature leaflets	1 (almost glabrous); 2 (sparse and short); 3 (sparse and long); 4 (profuse and short); 5 (profuse and long); 6 (others)
29	Pod beak	1 (absent); 3 (slight); 5 (moderate); 7 (prominent); 9 (others)
30	Pod constriction	0 (none); 3 (slight); 5(moderate); 7 (deep); 9 (very deep)
31	Pod reticulation	0 (smooth); 3 (slight); 5 (moderate); 7 (prominent); 9 (others)
32	Seed colour	1 (one colour); 2 (variegated)
33	Number of seeds/ pod	1 (2-1); 2 (2-1-3); 3 (2-3-1); 4 (2-3-4-1); 5 (2-4-3-1) 6 (3-2-4-1); 7 (3-4-2-1); 8 (others)

Source: IBPGR/ ICRISAT groundnut Descriptors (1981).

Table 4. Eigen values, % and cumulative variance, factor scores and communality of the ten most important characters from factor analysis

Eigen value	Proportion of variation accounted for (%)	Cumulative percentage
7.162	28.170	28.170
5.047	14.262	42.432
4.258	12.690	55.122
3.826	10.951	66.073
3.234	9.423	75.496

Table 5. Eigen values, percent and cumulative variance, factor scores and communality of the ten most important characters from factor analysis.

Character	Factor I	Factor II	Factor III	Factor IV	Communality
Yield per plant	0.281	0.196	-0.655	0.125	0.963
Seed colour	0.033	0.736	-0.325	0.075	0.935
Number of pods per plant	-0.195	-0.210	-0.412	0.438	0.924
Matures leaflet length	-0.701	0.531	-0.108	0.037	0.918
Sample seed (100 seeds) weight	0.352	0.370	0.299	-0.456	0.913
Pod width	0.697	0.538	-0.223	0.208	0.909
Height per plant at flowering	0.144	-0.315	-0.502	-0.499	0.905
Final height per plant	-0.744	0.213	0.165	0.356	0.899
Pod length	0.341	0.803	0.195	-0.144	0.897
Pod beak	0.424	0.105	-0.364	0.375	0.887
Eigen values	6.062	4,047	3.859	3,318	
Percent Variance	18.37	12.26	11.69	4.232	
Cumulative variance	18.37	30.63	42.32	52.58	

entries were maximum (Rezai and Frey, 1990; Ariyo, 1993). Factors and discriminant canonical analysis were also performed using the SPSS (Version 10.0) package. Factor analysis used the covariance matrix of characters (Harman, 1967; Ariyo, 1992) to generate factor loadings and communalities using the method of principal component extraction.

The discriminant canonical analysis summarizes the multivariate data in the same way as the canonical correlation. The analysis uses the Wilks' lambda as the statistics for entering or removing new variables and thereby identifies the variables that provide the best discrimination among the entries. Single Linkage Clusters Analysis (SLCA) was performed to obtain dendrogram and sort genotypes into clusters using the FASTCLUS technique of SAS.

RESULTS

Factor analysis

The results obtained from the factor analysis of the characters are presented in Table 4. The analysis identified 33 factors out of which only four were extracted which together explained 53% of the variance among the entries. The first factor with Eigen value of 6.062 accounted for only 18.37% of the variance and is primarily related to final plant height, pod width, leaflet length, stem pigmentation, number of nodes on the main stem at maturity and number of leaves at flowering. The factor that accounted for 12.26 % of the total variance is mainly loaded by pod length. The third factor that accounted for 11.69 % of the total variance is mainly described by days to maturity and hairiness of young leaflet. The fourth factor is loaded by pod constriction, plant height at flowering, weight of 100 seeds, stem hairiness and it accounted for just 4.23 % of the total variance. The communality values ranged from 0.963 for yield/ plant to 0.680 for stem branching pattern.

Principal component analysis (PCA)

Results from the PCA presented in Table 5, revealed that only five of the thirty three principal components had Eigen values greater than 3.0 while, the first four axes with Eigen values of 7.162, 5.047, 4.258 and 3.826 respectively, jointly accounted for 66.07% of the total variation among the genotypes. The first five principal axes together explained above 70% of the total variation among the 33 characters that described the 22 genotypes. The major characters described by the first four principal axes are presented in Table 6. The first principal component axis was mainly loaded by vegetative characters.

Table 6. Eigen vectors for major traits of the first four principal components used in the ordination.

Axis 1		Axis 2		Axis 3		Axis 4	
Trait	**Score**	**Trait**	**Score**	**Trait**	**Score**	**Trait**	**Score**
Final plant height	-0.302	Pod length	0.399	Days to maturity	0.413	Leaflet shape	-0.318
Leaflet length	-0.285	Seed colour	0.366	Hairiness of young leaflet	0.336	Pod constriction	0.274
Stem pigmentation	-0.268	Pod width	0.268	Yield/ plant	-0.333	Plant height at flowering	-0.273
Number of nodes on the main stem at maturity	-0.259	Leaflet length	0.264	Days to 50% flowering	0.304	Stem hairiness	0.271
Number of leaves at flowering	0.251	Seed length	0.263	Plant height at flowering	-0.255	Weight of 100 seeds	-0.250
Leaflet width	-0.251	Leaflet length/ leaflet width ratio	0.253	Stem branching pattern	-0.219	Seed width	-0.244
Number of seeds/ pod	0.241	Seed width	0.234	Number of pods/ plant	-0.209	Growth habit	-0.243
Peg colour	-0.231	Hairiness of mature leaflet	-0.228	Pod beak	-0.185	Number of pods/ plant	0.241
Seed length	0.219	Weight of 100 seeds	0.184	Seed colour	-0.166	Number of seed/ pod	0.225
Pod beak	0.172	Pod reticulation	0.180	Leaflet shape	-0.162	Hairiness of young leaflet	0.220

These were final plant height leaflet length, stem pigmentation, nodes on the main stem at maturity, number of leaves at flowering, leaflet width, seeds per pod, peg colour, seed length and pod beak in that order. Axes two and three were described largely by pod and seed characteristics like pod length, pod width, pod reticulation, pod beak, seed colour, seed length, weight of 100 seeds and number of pods per plant. The fourth axis is loaded by leaflet shape, pod reticulation, plant height at flowering, stem hairiness, weight of 100 seeds, seed width, number of pods per plant, seeds per pod and hairiness of young leaflet.

The configuration of the twenty two groundnut genotypes, along the first three principal component axes are shown in Figures 1, 2 and 3. The ordination of the genotypes on axes 1 and 2 (Figure 1) revealed that ICG 6402 (genotype 3), ICG 12370 (genotype 8), ICG 1399 (genotype 15) and ICG-IS-6646 (genotype 19) were the most distinct genotypes. ICGY-5M-4746 (genotype 18), ICG49-85A (genotype 21) and UGA-7-M (genotype 22) from local sources were most distinct from others in Figures 2 and 3. The remaining genotypes from ICRISAT-India and local sources (Nigeria) did not show any specific pattern in their distribution

Single linkage cluster analysis (SLCA)

The dendrogram from the Single Linkage Cluster Analysis is presented in Figure 4. All genotypes were distinct at 100% level of similarity while at 25% they could no longer be discriminated. ICGY-5M-4746 (G18) and ICG-IS-11687 (G17), both collected locally (from Zaria), were most similar to each other and different from others above 85% level of similarity. ICGY-6M-5236 (genotype 16)

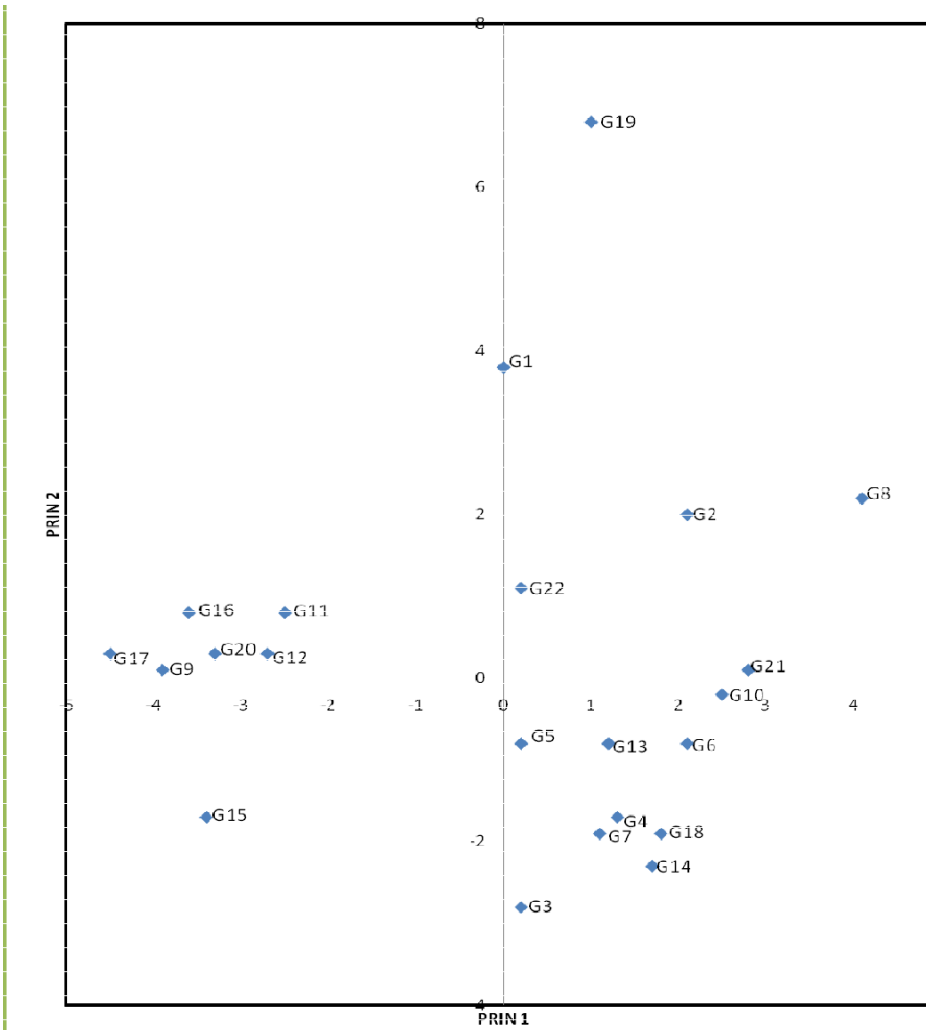

Figure 1. Configuration of the 22 groundnut genotypes under principal component axes 1 and 2.

formed cluster with others from Zaria collection at 65% level of similarity. At 64% genotype ICG49-85A (G20) and UGA-7-M (G22) formed a cluster, while ICG- 4998 (G1) and ICG - 862 (G2) from ICRISAT (India) formed cluster at 63% level of similarity and they where the most similar genotypes with the local collections. The last two sub-clusters cannot be distinguished from each other at 50% level of similarity. ICG- IS- 6646 (G19) and ICG-IS-3584 (G20) joined the cluster at 49 and 48% levels of similarity respectively. Above 45% ICG-4412 (G5) and ICG-156 (G6) cannot be distinguished from each other, ICG-12189 (G11) and ICG-8490 (G4) had joined them to form a cluster at 49 and 35% levels of similarity respectively. Above 33% all the entries had formed eight sub-clusters and by 29% the last three entries ICG- 12370 (G8), ICG-2106 (G9) and ICG-4343 (G10) had formed a single cluster with the others.

Table 7 presents the eight clusters, obtained with the FASTCLUS procedure of SAS, showing the pattern of association with characters. Clusters I and VII contained 8 and 2 genotypes respectively. Four genotypes each were grouped into clusters II and III, while the other clusters contained one entry each. Genotype in cluster V was the tallest at flowering and had the largest days to maturity, number of branches at maturity and weight of 100 seeds. Entries 8 and 10 in cluster VII are late flowering with highest yield, while entry 9 that made up cluster VIII had the tallest plants at maturity, highest number of nodes on the main stem at maturity with thickest stems and produced the highest number of pods per plant.

Canonical analysis (CA)

The Eigen values, total variances and correlations between original variables and canonical variables that described the variation in the characters measured are

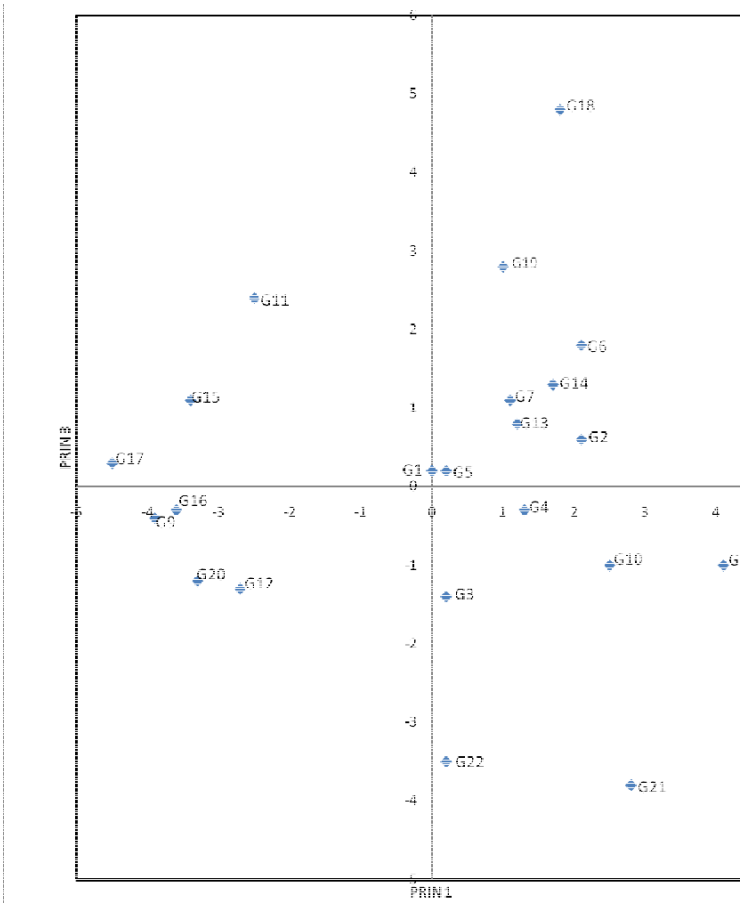

Figure 2. Configuration of the 22 groundnut genotypes under principal component axes 1 and 3.

presented in Table 8**.** The first five canonical variables had Eigen values greater than 2.0 and accounted for 46.14, 27.72, 11.67, 7.54 and 6.92% of the total variance, respectively. The first four canonical variables however, recorded 93.07% of the variation. Number of leaves at flowering and lateral branch habit, were among the important characters in the first canonical variable while the second canonical variable comprised of number of pods per plant, yield per plant and stem pigmentation. The third canonical variable comprised of number of pods per plant, yield per plant, pod constriction and peg colour while number of leaves per plant, leaflet length and leaflet width were important for the fourth variable.

Discriminant analysis

Table 9 presents the Eigen values, variance and pooled within group correlation between discriminant variable and the canonical discriminant functions. The first four functions had Eigen values that are above 2 and jointly accounted for 99.34% of the total variance. The first two functions accounted for about 84% of the total variance within the genotypes whereas the third and the fourth functions explained 14.77 and 1.08% of the total variance respectively. The first discriminant function, which accounted for 60.82% of the variance, was highly negatively correlated with number of leaves per plant at flowering (-0.799) but positively correlated with leaflet length (0.392). Number of pods per plant (-0.872) and yield per plant (-0.641) had high negative correlations with the second function while number of seeds per pod had the highest positive correlation (0.368) with the second function. Leaflet shape had the highest positive correlation (0.319) with the third function while hairiness of mature leaflet had the least correlation (0.111) with the third function. The fourth discriminant function correlated negatively with lateral branch habit (-0.495) while number of pods per plant had the least correlation (-0.230). The step-wise order of inclusion of the ten most important variables in the discriminant analysis is shown in Table 10**.** The order in which the variables were included in the discriminant analysis indicates their relative importance in classifying entries. Number of pods per plant was ranked first in the order of relative importance for discriminating the genotypes. It was followed by number of leaves per

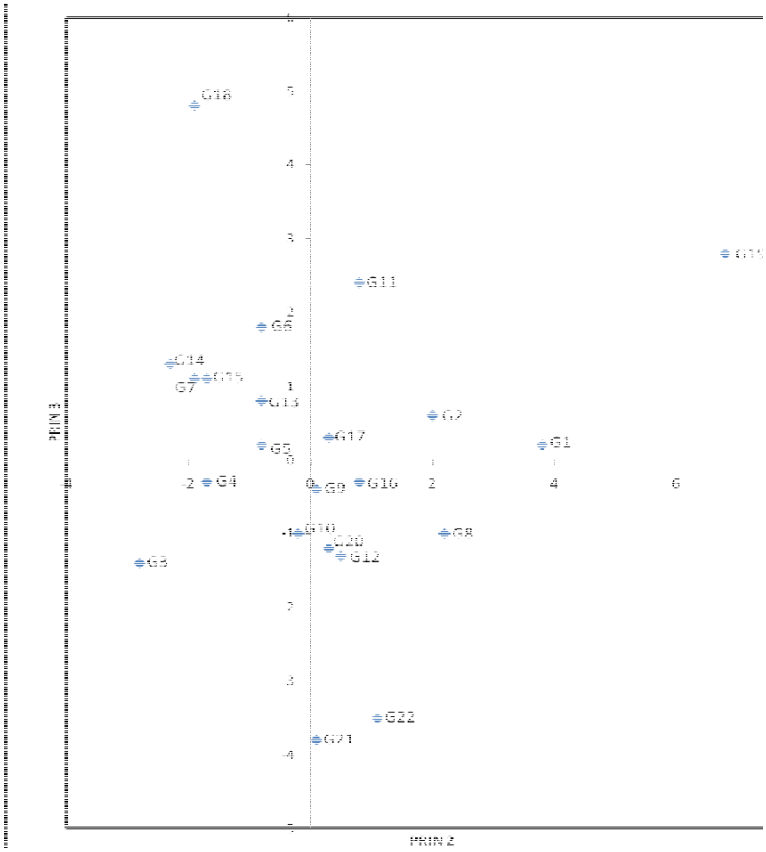

Figure 3. Configuration of the 22 groundnut genotypes under principal component axes 2 and 3.

plant at flowering and hairiness of young leaflet respectively, while the least ranked variable among the top ten was pod reticulation.

DISCUSSION

When dissimilarity between a pair of variety is defined on a multivariate criterion, it is useful to be able to determine the plant characters which cause the dissimilarity to arise and the relative contributions that the various characters make to the total variability in the germplasm (Ariyo, 1993). Factor analysis and principal component analysis identified some similar characters as the most important for classifying the variation among groundnut genotypes. These included; final plant height, leaflet parameters, pod parameters, stem pigmentation, number of nodes on the main stem at maturity and number of leaves at flowering. The similarity between the two techniques had been reported earlier in okra by Ariyo (1993) and rice by Nassir and Ariyo (2007). Although, the two techniques produced similar results, their underlying principles are substantially different from each other. While PCA does not rely on any statistical model and assumptions, factors analysis does. It is also imperative to note that factor analysis suffers from other drawbacks, such as absence of 'error' structure and the dependence upon scale used to measure the variables (Bartual et al., 1985).

The canonical analysis gave a different picture of the relative importance of the various characters within the entries when compared to the principal component and factor analyses. The analysis considered number of leaves per plant at flowering as the character that best discriminated the groundnut genotypes. Other important variables included, lateral branch habit, pod beak, hairiness of mature leaflet and peg colour. The discriminant analysis also identified number of leaves at flowering as the most important discriminatory trait among the entries. Pod beak, leaflet length, leaflet width, pod constriction and stem branching pattern were other important characters identified by discriminant analysis. Factor analysis captured more of the variation within the entries in higher number of axes compared to other techniques used in this study. However, the techniques showed considerable differences in the characters considered most important for describing the variation among the entries. Differences in results of multivariate techniques, with respect to characters which best summarized the within population variance, had earlier been reported by Ariyo (1993) and Nair et al. (1998).

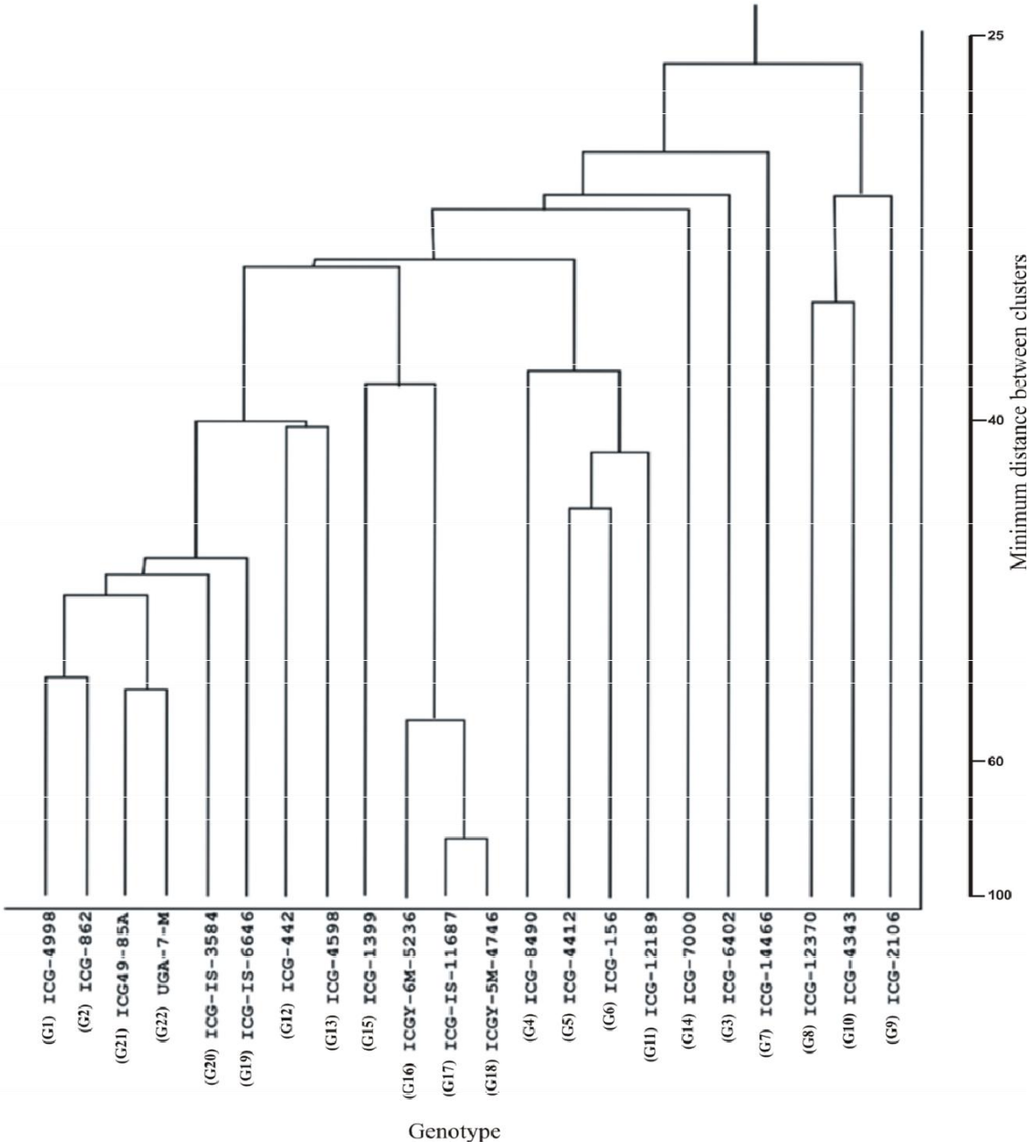

Figure 4. Dendrogram representing relationships of 22 genotypes of groundnut derived from nearest neighbour sorting using Single Linkage Cluster Analysis (SLCA)**.**

Compared to PCA analysis (55%), the canonical correlation analysis accounted for 85.53% of the within entries variance in the same number of axes while the discriminant analysis explained a high figure of 90.16%. The three techniques were, however, better than the factor analysis, which accounted for just 40% of the total variance within entries in the same number of axes. The factor analysis identified final plant height, pod length, days to maturity and pod width as important characters while the discriminant analysis identified number of leaves per plant at flowering, number of pods per plant, leaflet shape and pod beak as the most discriminatory characters. Thus, a combination of factor analysis and any of the PCA, canonical correlation or discriminant analyses would be appropriate for describing the variation in groundnut germplasm.

The grouping of the genotypes by clustering technique did not follow a particular pattern. Some genotypes from the same source were grouped together while others from different sources were clustered together. This

Table 7. Major characteristic pattern of eight clusters (using single linkage cluster method) of groundnut genotypes with their mean values and the standard deviation in parenthesis.

Character	Genotype clusters								Grand mean
	I 1,2,12,13,19,20,21,22,	II 15,16,17,18	III 4,5,6,11	IV 14	V 3	VI 7	VII 8,10	VIII 9	
Days to 50% flowering	29.42 (5.51)	25.92 (0.66)	27.65 (2.63)	28.93	24.13	26.73	32.99 (0.84)	25.80	27.70 (2.75)
Plant height at flowering	20.62 (3.36)	19.71 (4.15)	20.44 (1.00)	22.47	25.02	20.27	22.26 (1.27)	21.65	21.56 (1.71)
Number of leaves at flowering	46.41 (13.99)	40.71 (24.19)	44.32 (15.98)	33.72	36.39	57.84	75.88 (4.14)	33.08	46.04 (14.51)
Days to maturity	126.93 (18.23)	118.05 (6.54)	123.73 (10.83)	126.27	134.93	118.00	133.33 (0.66)	116.40	124.71 (7.03)
Final plant height	47.71 (6.66)	54.58 (15.30)	47.53 (11.96)	49.76	55.21	49.36	47.66 (11.52)	70.11	52.74 (7.65)
Number of branches at maturity	5.07 (0.33)	5.05 (0.24)	4.73 (0.24)	4.61	5.62	4.95	4.92 (0.04)	4.96	4.99 (0.30)
Number of nodes on the main stem at maturity	32.13 (4.28)	31.24 (1.58)	28.85 (3.55)	28.77	32.32	30.13	28.28 (3.29)	35.19	30.86 (2.34)
Stem girth at maturity	2.01 (0.13)	1.82 (0.14)	1.94 (0.24)	2.12	2.17	1.90	2.00 (0.27)	2.20	2.02 (0.13)
Number of pods/ plant	116.90 (38.29)	105.9 (36.41)	134.43 (73.89)	113.49	115.12	130.95	138.63 (49.96)	139.60	124.38 (12.99)
Weight of 100 seeds	42.15 (13.02)	35.31 (3.61)	46.86 (10.94)	50.00	52.64	37.82	39.44 (12.51	34.04	42.28 (6.89)
Yield/ plant	20.11 (6.14)	20.83 (6.83)	24.06 (7.57)	21.22	17.29	22.95	24.42 (6.26)	19.59	21.31 (2.41)

Table 8. Eigen values, total variance, cumulative variance and correlation between original and canonical variables that describe the variation in 33 traits measured on 22 groundnut genotypes

Canonical variable	Eigen value	Proportion of variance accounted for (%)	Percentage cumulative	Correlation of canonical variable with					
1	14.925	46.14	46.14	Number of leaves/ plant at flowering (-0.318)	Lateral branch habit (0.311)	Pod beak (-0.215)	Hairiness of mature leaflet (0.202)	Pod constriction (-0.184)	Peg colour (-0.178)
2	8.969	27.72	73.86	Number of pods/ plant (-0.671)	Yield/ plant (-0.501)	Stem pigmentation (-0.475)	Lateral branch habit (0.398)	Number of leaves at flowering (0.372)	Number of seeds/ pod (0.309)
3	3.775	11.67	85.53	Number of pods/ plant (-0.588)	Yield/ plant (-0.429)	Pod constriction (-0.324)	Peg colour (0.279)	Leaflet shape (0.258)	Number of seeds/ pod (0.236)
4	2.440	7.54	93.07	Number of leaves at flowering (0.728)	Leaflet length (-0.487)	Leaflet width (-0.452)	Final plant height (-0.385)	Stem branching pattern (-0.362)	Hairiness of young leaflet (0.341)
5	2.240	6.92	100.00	Leaflet shape (0.319)	Stem hairiness (-0.235)	Peg colour (0.194)	Pod constriction (0.187)	Pod beak (0.113)	Hairiness of mature leaflet (0.105)

implies that geographical diversity is not a measure of genotypic diversity in groundnut as reported in okra by Ariyo (1987a). Mean values of characters were more or less continuous across clusters, hence, no sharp distinction between clusters was observed. This was an indication that the characters were under polygenic control. Therefore, improvement programme in groundnut through varietal selection will require painstaking and continuous hybridization and selection efforts for appreciable success (Nassir, 2002). However, clusters showed some character distinctions that could be employed for hybridization purpose. Cluster III for instance, recorded highest yield per plant but fewer number of pods per plant when compared with cluster VIII, hence genotypes in cluster III may give even higher yield if the number of fruits and the number of nodes on the main stem are increased through a careful hybridization with any genotypes in cluster VIII. A high yielding progeny which will have a better combination of height, number of pods per plant and seed weight could be selected from a cross between suitable entries in clusters V and VII. The large amount of genetic variability observed among the genotypes supported the earlier observation by Rao (1985), Siddiquey et al. (2006) and Pintu et al. (2007) that abundant genetic divergence existed in groundnut germplasm. In addition, the pattern of genetic variation would be of great importance to germplasm collectors and plant breeders. The categorization of the diversity among the genotypes into groups with similar characteristics can be used to design a collection strategy (Ariyo, 1993; El- Nasir et al., 2006). Furthermore, the high level of variability exhibited by this population

Table 9. Eigen values, total variance, cumulative variance and pooled within group correlation between discriminant variables and the canonical discriminant functions.

Discriminant Canonical variable	Eigen value	Proportion of variance accounted for (%)	Percentage cumulative	Pooled within group correlation * with					
1	13.698	60.815	60.815	Number of leaves/ plant at flowering (-0.799)	Pod beak (-0.393)	Leaflet length (0.392)	Leaflet width (0.379)	Pod constriction (-0.304)	Stem branching pattern (0.280)
2	3.566	15.829	76.644	Pods/ plant (-0.872)	Yield/ plant (-0.641)	Stem pigmentation (-0.499)	Number of seeds/ pod (0.368)	Leaflet shape (0.314)	Pod reticulation (-0.256)
3	3.045	13.517	90.159	Leaflet shape (0.319)	Stem hairiness (-0.217)	Pod constriction (0.216)	Peg colour (0.173)	Pod beak (0.145)	Hairiness of mature leaflet (0.111)
4	2.217	9.841	100.000	Lateral branch habit (-0.495)	Peg colour (0.413)	Number of leaves at flowering (-0.347)	Pod constriction (-0.302)	Hairiness of mature leaflet (-0.288)	Pods/ plant (-0.230)

* Largest absolute correlation between each variable and any discriminant function.

Table 10. Stepwise order of inclusion of the ten most important variables from discriminant analysis.

Variable	Wilks' Lambda	F- value
Number of pods per plant	0.247	95.779
Number of leaves at flowering	0.075	82.068
Hairiness of young leaflet	0.054	67.044
Seed length (cm)	0.041	58.879
Peg colour	0.033	53.040
Seed width (cm)	0.024	52.893
Stem girth at maturity (cm)	0.019	50.424
Stem hairiness	0.015	49.719
Pod length (cm)	0.012	49.181
Pod reticulation	0.009	48.206

*= All F- values are significant at P 0.01.

indicates that heterosis could be utilized to produce superior hybrid which can be used to enhance crop production. Development of such genotype, however involves the understanding of the variance components in the population (Lukhele, 1981; Makinde, 1988).

Conclusion

Factor analysis captured more of the variation within the entries in higher number of axes compared to other techniques used in this study. However, the techniques showed considerable differences in the characters considered most important for describing the variation among the entries. Thus, a combination of factor analysis and any of the PCA, canonical correlation or discriminant analyses would be appropriate for describing the variation in groundnut germplasm. Genotypes ICG-2106, ICG49-85A and UGA-7-M could serve as a source of genes for earliness. ICG-4998, ICG -12370, ICG-4598, ICG-12189 and ICG-IS-6646 could be exploited for increase in pod yield.

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