ANALYSIS OF GENETIC DIVERSITY OF SOME GROUNDNUT (*Arachis hypogaea* L.) GENOTYPES USING PRINCIPAL COMPONENT ANALYSIS

By

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DECLARATION

I declare that the work in the thesis entitled **ANALYSIS OF GENETIC DIVERSITY OF SOME GROUNDNUT (*Arachis hypogaea* L.) GENOTYPES USING PRINCIPAL COMPONENT ANALYSIS** have been carried out by me in the Department of Plant Science under the supervision of Prof. C. A. Echekwu, Dr. Y. Mansir and Dr. M. D. Katung. The information derived from literature has been duly acknowledged in the text and a list of references provided. No part of this thesis was previously presented for another Degree or Di*p*loma at any other institution.

Albert Anthony ---------- ----------

Signature Date

CERTIFICATION

The thesis entitled **ANALYSIS OF GENETIC DIVERSITY OF SOME GROUNDNUT (*Arachis hypogaea* L.) GENOTYPES USING PRINCIPAL COMPONENT ANALYSIS** by **Albert Anthony** meets the regulation governing the award of the Degree of Master of Science (M. Sc.) of the Ahmadu Bello University, Zaria and is approved for its contribution to scientific knowledge and literary presentation.

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DEDICATION

This research is dedicated to my late parents Anthony and Victoria, and my brother Sylvanus; all of blessed memory - for teaching me that life is all about struggle.

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ABSTRACT

An investigation was carried out with Fifty (*Arachis hypogaea* L.) genotypes to assess the genetic diversity for yield and yield related traits. i.e. plant height, canopy spread, number of branches, number of pods per plant, pod yield shelling percentage etc. The experiment was conducted at the Institute for Agricultural Research (IAR) research Farm Samaru Zaria in a Randomized Complete Block Design with three replications. The Ward's Method using Squared Euclidian distance technique was used for the analysis. The genotypes were evaluated for nine traits which include (plant height, canopy spread, number of branches, number of pods per plant, pod yield etc.) and showed wide variability for the components studied. Positive correlation was observed between plant height, canopy spread and yield. The cluster analysis grouped the fifty Groundnut genotypes into eight different clusters. This indicates the presence of wide diversity among the tested genotypes. The cluster analysis grouped the fifty Groundnut genotypes into eight different clusters. This indicates the presence of wide diversity among the tested genotypes. From cluster mean values, genotypes in cluster 1, 2, 3 and 4 deserve consideration for their direct use as parents in hybridization programs to develop high yielding Groundnut varieties. The genotypes in cluster 5 may be used for improvement and other desirable characters other than grain yield. The result of the principal components analysis revealed that four principal components (PC1 to PC4) accounted nearly 76.92 % of the total variation. It was also noted that differentiation of genotypes into different clusters was because of the small contribution of few character rather than the cumulative effect of a number of characters.

The information obtained from this study can be used to plan crosses and maximize the use of genetic diversity and expression of heterosis.

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CHAPTER ONE

INTRODUCTION

Groundnut (*Arachis hypogaea* L.), also known as peanut is a self pollinated crop an allotetrapoloid (2n=4x=40), which originated through the hybridization of two diploid species with distinct genomes (*A. duranensis* the AA genomes donor and *A. ipaensis* the BB donor) giving rise to a sterile hybrid. A spontaneous duplication of the chromosomes restored fertility which formed the tetraploid species *A. monticola* and gave rise to the cultivated peanut but left the plant reproductively isolated from its wild relations (ICRISAT, 2006; Krapovickas and Gregory, 1994; Upadhyaya, 2003). Groundnut is one of the protein rich vegetable oil seed crops of the world belonging to the family *Fabacaea***,** which ranks thirteenth among the world food crops, fourth as most important source of edible oil, and third as most important source of vegetable protein (FAOSTAT 2010). In Africa, the crop is mainly grown for human consumption and it is rich source of oil (40-50%), protein (20-50%) and carbohydrate (10-20%), in addition to minerals and vitamins, (Belamka *et al*., 2011). Groundnut is native to South America (Brazil) but it is now being grown throughout the tropical and warm temperate region of the world (Ferguson *et al*, 2004). The crop is cultivated in more than 100 countries on an expanse of land covering about 23.95 million hectre with a total annual production of about 36.45 metric tons and an average yield of 1520 kg/ha in 2009 worldwide, of which China (41%), India (21%), and Nigeria (8%), and the United States (7%) are the largest producers (FAOSTAT, 2010). In Africa, groundnut seems to have been introduced by the Portuguese into Senegal and Gambia from where it spread to the different parts of Africa (FAOSTAT 2010). Nigeria

has more area under groundnut cultivation in Africa followed by Sudan. Groundnut crop is widely grown in Nigeria covering over two million hectares of land with major concentration in the northern region of the country encompassing the Sahel (12^{o}-14^{o}N), Sudan (10^{o}- 13^{o}N) and Northern half of the Northern Guinea Savannah (8^{o}- 11^{o}N) where the rainy seasons last from a period of about 75-150 days with annual precipitation ranging between 500mm-1400mm and pod yield of about 1000kg/ha (Olorunju *et al*., 1999; Udom *et al.,* 2009). Groundnut is and has always been an important crop in Nigeria where it is grown largely under smallholder system and rain-fed conditions. It constitutes a major source of protein and dietary oil as well as cash income for both subsistence farmers and urban dwellers (Echekwu, 2010).

Until 1974, Nigeria was the leading exporter of peanut and accounted for about 70% of total export earnings, making it, as of then, the country's single export crop before the unprecedented epidemic of rosette in 1975 and the prevalence of rust and leaf spot diseases which resulted in the considerable decline of its production, (Upadhyaya *et al.*,2001).

Knowledge of the nature and extent of this variation could be useful for genetic improvement of groundnut. Until a collection has been properly evaluated and its attributes become known to breeders, it has little practical use. After collection of germplasm, there is a need for a systematic evaluation of data collected on various morphological, physiological and developmental characters including some special features such as stress tolerance, pest and disease resistance (Maji and Shaibu, 2012). One way to make meaning to this data is to reduce its dimensionality. Principal component analysis (PCA) is among the techniques that reduce the data into two dimensions (Rao, 1964; Raychaudhuri *et al.*,

2000; Smith, 2002). Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production. One of the important approaches to groundnut breeding is hybridization and subsequent selection. Parent choice is the first step in plant breeding program through hybridization. In order to benefit from transgressive segregation, genetic distance between parents is necessary (Joshi *et al.,* 2004). The higher the genetic distance between parents, the higher the heterosis in progeny can be observed (Joshi and Dhawan, 1996; Anand and Murrty, 1968). Estimation of genetic distance is one of the appropriate tools for parental selection in hybridization programs. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase (Islam, 2004).

1.1 Justification

In spite of its importance and wide utilization, yields from Africa and Nigeria in particular remain low. According to FAOSTAT (2010) the average yield of peanut is 1.55metric tons lower than world average yield of 34.4 metric tons in 2010. This large difference has been attributed to several factors including non availability of improved varieties, drought, pest and disease, inappropriate crop management practices, and less attention given to agricultural sector, limited knowledge on the inheritance of importance traits and lack of proper understanding of genetic diversity at the level of inter and intra-species and population structure among the lines within and between genus. Analysis of genetic diversity in germplasm collections can facilitate reliable identification and classification of accessions with possible utility for specific breeding purpose. This study attempts to

conduct classificatory analysis on the groundnut genotypes obtained from ICRISAT groundnut gene bank in Patancheru, India by means of Principal Component Analysis, which would enable us to classify the available germplasm into distinct groups on the basis of their genetic diversity. If genetic diversity is narrow, genetic improvement may be slow but if genetic diversity is broad genetic improvement may be rapid.

1.2 Objectives

The objectives of this study were to:

a. Determine the genetic diversity among fifty groundnuts genotypes obtained from ICRISAT groundnut gene bank in Patancheru, India using principal component analysis.
b. Identify the genotypes that best combined agronomic characters for future use in groundnut breeding.
c. Determine the magnitude of correlation between the yield and yield components

CHAPTER TWO

LITERATURE REVIEW

2.1. Centers of Origin and Diversity

The cultivated groundnut (*A. hypogaea*) most probably originated in the region of southern Bolivia and Northern Argentina, since *A. monticola*, the only wild tetraploid species that crosses with *A. hypogaea*, is found in this area. Hence, this region was presumed as center of origin and primary center of diversity for *A. hypogaea*. Krapovickas (1969) and Gregory and Gregory (1976) recognized six gene centers for cultivated groundnut in South America where the greatest amount of genetic diversity is found. Whereas, Brazil was presumed as center of origin for (*A. hyprogaea fastigiata* variety, *fastigiata*; North-West Mato Grosso as the center of variation for the *Arachis hypogaea*). The center of origin of the genus *Arachis* was most probably, South America (Gregory *et al.*, 1980).

2.2 Genetic Diversity in Groundnut

Genetic diversity is the sum of genetic characteristics within any species or genus. It is different from genetic variability, which describes the variation within these genetic characteristics (Rao and Hodgkin 2002). Analysis of genetic relationships in crop species is an important component of crop improvement programmes, as it serves to provide information about genetic diversity and is a platform for stratified sampling of breeding populations (Smith, 1984; Cox *et a*l., 1986). Hallauer and Mirander, (1988) added that, genetic diversity analysis would facilitate classification of accessions and identification of subsets of core accessions with possible utility for specific breeding purposes. Upadhyaya

(2003) examined a core collection of 1704 of peanut accessions for genetic divergence using principal component analysis. This analysis revealed that 15 agronomical traits were important in explaining multivariate polymorphism. However, seed width and protein content did not significantly account for variation in the first five principal components of *fastigiata* and *hypogaea* types as well as for the core collection. Evaluating the core collection for response to drought, Upadhyaya (2005) reported, five *vulgaris* and 13 *hypogaea* accessions selected on the basis of specific leaf area, specific chlorophyll meter reading values compared with the control cultivars. These accessions and four control cultivars were grouped in different clusters by scores of the first 15 principal components (PCs). The selected 11 entries and control cultivar M 13 grouped in cluster 2 with ICG 6766 and ICG 14523 forming two separate clusters, indicating that they were diverse from the control cultivars. The groundnut core collection of 1704 accessions was subjected to Shannon-Weaver diversity index (Upadhyaya, 2003). Among the morphological descriptors primary seed colour in *fastigiata* group and pod beak in *hypogaea* group showed highest.

Among the agronomic traits in *fastigiata* group, 100 seed weight in rainy season and plot yield in post rainy season, and in *hypogaea* group pod width in rainy season and seed length in post rainy season had the highest H'. The average H' values across traits were similar between rainy and post rainy seasons in both groups as well as in entire core collection. The Shannon-Weaver diversity index (H') was calculated to compare phenotypic characters in the core and a mini core subset. The average H' for the 13 morphological descriptors and agronomic traits in the mini core subset was similar to the core sub set indicating that the diversity of the core was represented in the mini core

subset. (Upadhyaya *et al.*, 2002). Mallikarjuna Swamy *et al.*, (2003) took Asia core collection of 504 accessions to understand the nature of genetic divergence using principal component analysis. This showed that 20 agronomical traits were important in explaining multivariate polymorphism but pod yield per plant did not significantly account for variation in the first five principal components of *fastigiata* and *hypogaea* types as well as for the entire regional collection. Evaluation of Asian core collection for Shannon diversity index, showed that in *fastigiata* group leaf let length in rainy, pod width in post rainy, seed length in rainy and plant height in post-rainy Seed length in rainy, number of total pods in post rainy number of primary branches in rainy and plant height in post rainy had the highest H'. The average H' value across seasons and locations was highest for leaflet length in the *fastigiata* group and for seed length in the *hypogaea* group. The average H' across traits was similar between rainy post rainy seasons in both locations and groups.

2.3 Germplasm Resource

Germplasm resource is a very wide term that covers all the allelic resources spread in types ranging from most primitive wild progenitors to the highly bred cultivated varieties and strains (Isleib *et al,* 2001). Genetic variability is the gift of nature and its fruitful utilization in any crop species requires systematic collection, evaluation, description and grouping based on economic descriptors. The world collection and assembly of groundnut genetic resource was enhanced through specific collection expeditions in various groundnut-growing regions of the world and in centers of diversity in South America. In these expeditions various international agencies such as International Bereau for Plant Genetic Resource (IBPGR) and national programmes, such as those of countries of exploration and the United States Department of Agriculture (USDA) have collaborated very closely

(Simpson 1982, 1984). The largest collection of domesticated peanut is at International Crop Research Institute for Semi-Arid Tropics (ICRISAT), where there are 14,310 accessions from 92 countries and 413 accessions of *Arachis* species (Upadhyaya *et al*. 2001). These collections provide basic genetic stock to the international scientific community for further improvement of groundnut. Williams (2001) discussed the use of the geographic information system (GIS) for more effective study, locate and conserve *Arachis* genetic resources based on existing germplasm collections and geographical distribution of genetic diversity within primary and secondary centers of diversity or origin

2.4 Collections of Germplasm

Very large collections of germplasm from around the world are being assembled in efforts to conserve the genetic variation of numerous species for further evaluation and utilization. The concept of core collection was given by Brown (1989) to represent genetic diversity of a species with minimum repetitiveness and it represents a subset of collection which includes all useful characters so that identification of useful entry becomes easy and accessible for special attention. Brown and Frankel (1984) and Brown (1988 and 1989), described methods to select a core collection using information on the origin and characteristics of the accessions. This core collection could serve as a working collection that could be extensively examined and the accessions excluded from the core collection would be retained as the reserved collection.

The development of a core collection in peanut would provide a working collection, which could be extensively evaluated to generate the information that would allow estimation of genetic variation for economically important traits, and these data would also provide an indication of clusters in the collection that should be extensively examined for particular

traits. Holbrook *et al* (1993) developed a peanut core collection of 831 accessions on the basis of six morphological variables (plant type, pod type, seed size, testa color, seed per pod and seed weight) of 7432 US peanut accession and data that regards to six phenotypic traits indicated that the genetic variation expressed for each trait in the entire collection has been preserved in this core collection.

2.5 Preservation of Germplasms

In *Arachis hypogaea,* collection is generally straightforward and regeneration decisions are based on the total number and age of seeds available in storage, and the number of requests made by the user community. Both the USDA peanut curator and plant breeders from private industry, state-funded universities, and the USDA have taken a vested interest in the germplasm collection and have cooperated to assure adequate seed reproduction. Sanders *et al.* (1982) indicated that the sum of temperature (F) plus relative humidity should be less than 100 to have optimal seed storage. Under ideal storage conditions, peanuts remain viable for 15 or more years. Norden (1990) stored seeds for 20 years with good germination percentages when seeds were stored at 10^0C and 45 percent relative humidity.

2.6 Coefficient of Correlation

The correlation coefficient measures the relationship among traits. Correlation provides only limited information because they disregard complex interrelationships among traits. Accordingly, they must be used with caution in making decision regarding indirect selection criteria (Board *et al*, 1997). Chiteka *et al*, (1988) demonstrated that partitioning correlation coefficient into direct and indirect effects provide more useful information. Yield, being a complex quantitative trait, is influenced by various component traits. For

effective improvement, simultaneous selection of the most important yield components is necessary. For this reason, knowledge of the magnitude and nature of the association between yield and the related characters is important. Ali *et al*, (1986) reported that when phenotypic and genotypic correlation coefficients are very close in magnitude, then the environmental variance and covariance had been reduced to zero. Bos and Qi (1997) also reported that within clones, purelines and single cross hybrid the phenotypic correlation between two traits is equal to the environmental correlation. Variation between plants due to the quality of growing conditions, cause plants environmental deviation for another trait to be correlated. Singh and Singh (1987) reported significant association between plant height and yield. Ogunbodede (1988) noted that there have been reports of positive association between seedling vigor and yield in several crops, he concluded that specialize seedling vigor trait might be useful selection criteria for yield in most crops. The information on nature and magnitude of correlation coefficient help breeders to determine the selection criteria for simultaneous improvement of various characters along with seed yield (Thanki and Sawargaonkar, 2010). The association can be positive when the two characters tend to rise or fall together or negative when rise or fall in one of the characters leads to a change in the other character in the opposite direction. The importance of correlation studies in selection programmes is appreciable when highly heritable characters are associated with the important character like yield (Manggoel, 2012).

2.8 Multivariate Statistical Tools

Numerical taxonomic techniques have been successively used by many workers to classify variation patterns at both inter and intra-specific levels (Sneath and Sokal, 1973; Cheda

and Fatokun, 1982; Ariyo, 1990). Multivariate are aimed at finding proximities between entities characterized by multiple traits by summarizing and describing the inherent variation in the population of crop genotypes. Multivariate Statistical tools identify plant traits that characterize the distinctness among selected genotypes. Multivariate statistical techniques which simultaneously analyze multiple measurements on each individual under investigation are widely used in analysis of genetic diversity irrespective of whether it is morphological, biological or molecular based and subsequently, classification of germplasm collections.

They are often extended into classification of a population into groups of distinct orders based on symbols in one or more characters and thus guide in the choice of parents for hybridization (Ariyo, 1987; Nair et al 1998; Mohammad, 2011). Multivariate analysis has been useful for genetic diversity in many crops such as barley (*Hordeum vulgare* L.*) (*Cross., 1992), sorghum (*Sorghum bicolor L.), (*Ayana and Bekele, 1999), wheat (*Triticum spp.) (*Hailu *et al.*, 2006), peanut (*Arachis hypogeae* L.) (Upadhyaya *et al.*,2009) and rice (*Oriza sativa* L.) (Bharadwaj *et al.*, 2001). Among the multivariate techniques, PCA, cluster analysis, principal co-ordinate analysis (PCoA), multi-Dimensional Scaling (MDS) are at present, and Cluster Analysis (CA) is most commonly employed and appears particularly useful (Mohammadi and Prasanna, 2003).

2.9 Principal Component Analysis (PCA)

Principal component analysis (PCA) extracts principal components and provides information on the importance of traits for defining groups. The principal components are extracted so that they keep most of the variability (Martines-Calvo et al., 2008). The

Eigenvalues determine how many principal components are retained. The rationale for this consideration is easy to understand. Each of the traits observed contributes one unit of variance to the total variance in the data set. This implies that any component that displays an eigenvalue greater than 1.00 is accounting for a greater amount of variance that has been contributed by one variable. Thus, such a component is considered accounting for a meaningful amount of variance, and therefore deserves to be retained (Idehen, 2007). . On the other hand, a component with an eigenvalue less than 1.00 is accounting for less variance that has been contributed by one variable. The purpose of principal component analysis is to reduce the number of observed variables into a relatively smaller number of components; this cannot be effectively achieved if you retain components that account for less variance that have been contributed by individual variables. For this reason, components with eigenvalue less than 1.00 are viewed as not important and are therefore not retained. Sum of Eigenvalues equals the number of variables. One way to make meaning to multivariate data is to reduce its dimensionality. Principal component analysis PCA is among the techniques that reduce the data into two dimensions (Smith, 2002; Rao, 1964; Raychaudhuri *et al*., 2000). According to (Adams, 1995; Amy and Pritts, 1991). PCA is a technique that reduces data dimensionality by performing a covariance analysis between factors. It can be done by Eigenvalue decomposition of a data covariance matrix or singular value decomposition of a data matrix. The Eigenvalue represents the relative participation of each principal component in presenting the general variability of sampled materials. Eigenvalues are scaled from -1 to+1, the higher the value, the more closely a given trait is connected with a component thereby accounting for the meaningful amount of variation in a population. In such case, principal component analysis (PCA) may be

used to reveal pattern and eliminate redundancy in data sets as morphological and physiological variations routinely occur in crop species. Makinde *et al*., 2010 worked on 20 groundnut genotypes and used principal component analysis to ascertain the contribution of characters towards diversity of the genotypes. The result showed that only five of the 33 principal components had Eigenvalues greater than 3.0 while, the first four axes with Eigenvalues 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 thirty three (33) characters that described the twenty two (22) genotypes.

2.10 Cluster Analysis

Clustering is a straightforward method to show association among data. The cluster analysis is an appropriate method for determining family relationships (Mellingers, 1972). The analysis can be performed using either presence - absence or quantitative data. The aim of using a cluster technique in the analysis of data from plant breeding trials is to group the varieties into several homogenous groups. This is in such a way that those varieties within a group have similar response pattern across the locations since it is assumed that all the varieties in the trial will not behave independent of one another. If the entire data array containing information on a number of varieties can be reduced to the information on a number of groups of varieties this will simplify the interpretation of data by the breeder. Cluster Analysis has been widely used in different crops like Apple (Pereira, 2003); Deciduous Forest trees (Nath *et al.,* 2006), Wheat (Mostafa *et al*., 2011). Results of using PCA showed that this method is limited when the pattern of variation is not based on a 0 and 1 scores. Therefore, combined PCA and other techniques can be

appropriately used for grouping (Mohammadi and Prasanna, 2003). The main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only (Mohammadi, 2002). Similar to the findings by Ali *et al*., (2008) who reported that cluster analysis can be useful for finding high yielding wheat genotypes and Singh and Dwivedi (2002). Mohammed *et al.*, (2011) also worked on wheat, the results of their study showed the presence of a high genetic divergence among wheat genotypes using cluster analysis. However, results showed that cluster analysis based on PCA is a more precise indicator of differences among wheat genotypes than cluster analysis not based on PCA.

CHAPTER THREE

MATERIALS AND METHODS

3.1 Experimental Materials

The experimental materials for this study comprised of fifty groundnut genotypes of Prof. Echekwus' reference collection from International Crop Research Institute for Semi-Arid Tropics (ICRISAT), Patencheru, India as listed in Table 3.1.

3.2 Experimental Design and Field Trial

Evaluation was carried out in 2012 cropping season at the Institute for Agricultural Research (IAR) Farm Samaru (Northern Guinea Savanna 11^0 11' N: 7^0 38' E, 686m). The experiment was conducted in a Randomized Complete Block Design (RCBD), replicated three times. The plot size was two ridges by five meters (2 ridges x 5m) while inter-plant and intra-plant spacing was 0.75m and 25cm respectively and a meter strip separating each block.

3.3 Cultural Practices

Management practices recommended for production of groundnut was based on IAR recommendations. Single Super Phosphate (SSP) was top dressed 3 weeks after sowing (WAS), to boost growth, weeding was done to keep the field relatively clean and reduce competition. All recommended cultivation practices for peanut were adhered to.

Table 3.1: Reference collection list of groundnut genotypes.

1.	ICGV 8670	26.	ICGV 86590
2.	ICG 434	27.	ICG 405
3.	ICG 3102	28.	ICG 1834
4.	ICG 13858	29.	ICG 2031
5.	ICG 442	30.	ICG 1790
6.	ICG 5475	31.	ICG 3673
7.	ICG 5891	32.	ICG 13099
8.	ICG 12665	33.	ICG 3140
9.	ICG 111	34.	ICGV 93470
10.	ICG 1415	35.	ICG 6703
11.	ICG 1144	36.	ICG 4798
12.	ICG 02038	37.	ICG 12189
13.	ICG 1711	38.	ICG 94361
14.	ICG 12921	39.	ICG 15287
15.	ICG 4890	40.	ICG 1699
16.	ICG 13603	41.	ICG 544
17.	ICG 115	42.	ICG 4729
18.	ICG 8517	43.	ICG 95377
19.	ICG 15419	44.	ICG 9987
20.	ICG 12991	45.	ICG 3681
21.	ICG 4911	46.	ICG 10890
22.	ICG 3584	47.	ICG 3053
23.	ICG 334	48.	ICG 9507
24.	ICG 6888	49.	ICG 92234
25.	ICGV 02290	50.	ICG 9632

3.4 Data Collection and Observations

Agronomic and yield data of each genotype were observed and recorded on five randomly selected stands.

Plant height (PH): The length of the main stem was measured using a meter rule and expressed in centimeter.

Canopy spread (CS): Using a tape, the horizontal spread of the branches from the top was measured to determine the canopy spread and expressed in centimeter**.**

Number of branches (NB): Branches that emerged directly from the main stem were counted and recorded as number of primary branches.

Number of pods per plants (NPP): The pods obtained from each plot were counted and divided by the number of plants in the plot.

Pod length (PL): Using a Vanier caliper, the length of the pod were measured and recorded in centimeter**.**

Pod yield per plant (PY): This was calculated by dividing total pod yield per plot by number of plants in the plot expressed as grams/plant.

Number of seeds per plant (NS): Numbers of seeds per plant were counted. This represents the amount of seeds shelled from pods per plant.

100-seed weight (HSW): The well-dried and cleaned pods from each genotype were shelled and 100-seed at random were counted, weighed and recorded in grams**.**

Shelling percentage (SH%) = This was calculated by dividing weight of dry seed by weight of dry pod expressed in grams x 100.

3.5 Statistical Analysis

The data collected were subjected to analysis of variance (ANOVA) and means were compared using Duncan multiple range test (DMRT) whenever F is significant at $P < 0.05$. The statistical model used for the analysis of variance and determination of expected mean square was based on the linear model for randomized complete block design according to Kaps and Lamberson, (2004).

$$Y_{ij} = \mu + \tau_i + \beta_j + \varepsilon_{ij}$$

$i = 1... a; j = 1... b$

Y_{ij} = an observation in treatment i and block j

μ = the overall mean

τ_i = the effect of treatment i

β_j = the fixed effect of block j

ε_{ij} = random error with mean 0 and variance σ^2

a = the number of treatment; b = the number of blocks

Table 3.2 A form of analysis of variance (ANOVA) with expected mean square (EMS) for each Trait

Source of variation	d.f	MS	EMS
Replications	(r-1)		
Genotypes	(g-1)	M_g	$\sigma_e^2 + r\sigma_g^2$
Error	(r-1)(g-1)	M_e	σ_e^2

Where;

r = number of replications

g = number of genotypes

σ_e^2 = error variance

σ_g^2 = $\frac{ms_g - ms_e}{r}$

$M_{\text{subscript}}$ = Observed mean squares of the subscripted effect

3.6 Coefficient of variation (CV)

3.6.1 Genotypic coefficient of variation

The genotypic coefficients of variation was estimated using the formula described by Singh and Chaudhary, (1985)

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \text{ X } 100$$

where;

GCV= genotypic coefficient of variation

σ_g^2 =estimate of genetic variance

$\overline{X}$ = grand mean of the respective character.

3.6.2 Phenotypic coefficient of variation

$$PCV = \frac{\sqrt{\sigma_P^2}}{\bar{x}} \text{ X } 100$$

where;

PCV= Phenotypic coefficient of variation

σ_p^2 =estimate of genetic variance

$\overline{X}$ = grand mean of the respective character.

3.7 Correlation Analysis

Genotypic and phenotypic correlation analysis was computed to determine the degree of association among the characters according to the formula of Singh and Chaudhary (1985). SAS statistical software version 9.0 (2002) was used in executing the analysis.

3.7.1 Genotypic correlation;

Genotypic correlation coefficient was computed using mean squares and mean cross products as follows:

$$r_{gxy} = \frac{\sigma^2_{gxgy}}{\sqrt{\sigma^2_{gx} \bullet \sigma^2_{gy}}}$$

Where;

r_{gxy} = correlation coefficient of character X and Y.

σ^2_{gxgy} = genotypic covariance of character X and Y

σ^2_{gx} = genotypic variance of character X

σ^2_{gy} = genotypic variance of character Y

3.7.2 Phenotypic correlation

Phenotypic correlation coefficient was computed using mean squares and mean cross products as follows:

$$r_{ph} = \frac{M_{gxgy}}{\sqrt{M_{gx} \bullet M_{gy}}}$$

Where;

r_{ph} = phenotypic correlation coefficient of character x and y

M_{gx} = entry mean square of the character X

M_{gy} = entry mean square of the character Y

M_{gxgy} = entry mean product of the character X and Y

3.8 Genetic Divergence

The genetic divergence of the 50 genotypes was estimated based on ward's method using a squared Euclidian distance (kumar *et al*., 2009). Divergence analysis is a technique used to categorize genotypes that are similar into one group and others into different groups. D-square statistics (D^2) developed by Mahalanobis (1936), has been used to classify the divergent genotypes into different groups. Squared distance (D^2) for each pair of genotype combinations was computed using the following formula:

$D^2 = (y_{it} - y_{jt})\ S^{-1}\ (X_{it} - X_{jt})$

Where,

D^2ij = the square distance between any two genotypes i and j,

Xi and Xj = the vectors for the values for genotype i^{th} and j^{th} genotypes, and

S^{-1} = the inverse of pooled variance covariance matrix.

3.9 Principal Component Analysis (PCA)

Principal Component Analysis was performed using statistical software SAS., (2004). version 9.0. The values of the first four components which are greater than 1.00 were selected and analyzed; the related clusters were plotted based on the main components.

CHAPTER FOUR

RESULTS

4.1. Mean Performance of Fifty Groundnut *Arachis hypogaea* Genotypes

The mean performance for the studied traits as shown in the table below indicated that Plant height ranged from 6.57cm to 24.87cm (ICG 02271) and a pooled mean of 14.12cm. Where, genotype (ICG 02271) had 24.87cm and emerged as the tallest among all the genotypes while genotype (ICG 6065) had 6.57cm in height emerging as the shortest. ICGV 02148 had the highest number of branches (15) while ICG2271 had the lowest number of branches (4). The overall mean was 6.64 for number of branches. An overall mean of (31.16cm) was recorded for canopy spread and ranged from 17.9 cm to 44.33 cm in which genotype (ICG 8285) had 44.33 while (ICG 12000) had 17.9 cm. Values obtained for 100 seed weight ranged from 7.17g to 52.00g with an overall mean of 33.96 which genotype (ICG 6643) had 7.17g while (ICGV3681) had 52.00g . Number of seeds per pod ranged from 2 to 4 and a pooled mean of 2.22. Genotype (ICG 5663) had 2 while (ICG 9249) had 4. An overall mean of 19.24 pods was obtained for number of pods per plant which ranged 6.67 to 31.00. Genotype (ICG 4998) had 6.67 while (ICG 8285) had 31.00. Length of pod ranged from 1.63cm to 3.67cm with a pooled mean of 2.58.genotye (ICG 5663) had 1.63cm while genotype (ICG 9249) was having 3.67cm. Pod yield per plant had a weight ranging from 9.63g to 160.87g. Genotype (ICG 6375) had 9.63g while (ICG 12276) had 160.87g and an overall mean of 83.70g.

Table 4.1. Mean performance of nine traits for 50 groundnuts (*Arachis hypogaea* L.) genotypes.

GENOTYPE	PHT	NB	CS	NPP	PL	NS	HS	SH%	PY
ICG 02271	24.87^{a}	6.00^{g}	31.23^{ghijk}	24.67^{abcdefg}	2.83^{cdefgh}	3.00^{b}	34.80^{l}	70.82^{efghijk}	102.63^{ghi}
ICG 11386	12.10^{b}	6.00^{g}	36.10^{cdef}	28.33^{abcde}	3.17^{bc}	3.00^{b}	29.97^{pq}	94.58^{bcd}	98.43^{hij}
ICG 1142	9.43^{b}	6.00^{g}	31.97^{efghijk}	15.00^{klmnop}	2.13^{mnopq}	2.00^{c}	22.87^{w}	65.46^{fghijklm}	40.63^{rs}
ICG 11426	9.20^{b}	9.00^{d}	35.43^{defgh}	11.33^{mnopqr}	1.90^{pqr}	2.00^{c}	24.13^{v}	46.97^{lmnopqr}	27.3st
ICG 11515	14.53^{b}	5.00^{i}	19.63^{pq}	22.33^{defghij}	2.17^{lmnopq}	2.00^{c}	29.93^{pq}	74.94^{defghi}	101.07^{ghi}
ICG 11542	13.67^{b}	5.00^{i}	31.53^{efghijk}	22.67^{cdefghij}	2.87^{cdefgh}	2.00^{c}	27.77st	81.57^{cdefgh}	71.63^{lmn}
ICG 11687	10.33^{b}	7.00^{f}	22.23^{opq}	30.00^{ab}	2.23^{klmnopq}	2.00^{c}	33.03^{m}	90.76^{cde}	139.77^{bc}
ICG 118	14.23^{b}	6.00^{g}	31.77^{efghijk}	28.33^{abcde}	2.87^{cdefgh}	2.00^{c}	43.07^{d}	65.84^{ghijklm}	73.7^{lmn}
ICG 12000	12.40^{b}	4.00^{j}	17.90^{q}	16.67^{ijklmn}	2.67^{defghijk}	3.00	39.93^{g}	41.74^{nopqrst}	112.03^{efgh}
ICG 12276	14.20^{b}	5.00^{i}	21.90^{opq}	12.00^{mnopqr}	1.83^{qr}	2.00^{c}	26.67^{u}	45.15^{mnopqrs}	58.1^{nopq}
ICG 12370	11.90^{b}	10.0^{c}	32.90^{efghi}	27.67^{abcde}	2.23^{klmnopq}	2.00^{c}	32.6^{mn}	84.81^{cdefg}	100.03^{ghi}
ICG 12672	6.67^{b}	7.00^{f}	26.77^{lmn}	8.67^{pqr}	2.70^{defghij}	2.00^{c}	41.03^{f}	21.26^{tu}	37.9^{rst}
ICG 12697	10.63^{b}	6.00^{g}	33.43^{efghi}	10.67^{nopqr}	3.03^{bcde}	2.00^{c}	30.77^{op}	34.74^{opqrstu}	58.67^{nopq}
ICG 13982	14.30^{b}	10.0^{c}	39.57^{bcd}	20.33^{fghijk}	2.90^{bcdefg}	2.00^{c}	41.80^{ef}	48.64^{lmnopqr}	84.6^{jkl}
ICG 14118	6.57^{b}	7.00^{f}	30.37^{ijkl}	9.00^{opqr}	2.60^{efghijkl}	2.00^{c}	28.07^{s}	32.14^{pqrstu}	49^{qr}
ICG 1415	12.43^{b}	15.0^{a}	26.67^{lmn}	12.00^{mnopqr}	2.27^{jklmnop}	2.00^{c}	35.10^{kl}	34.22^{opqrstu}	50.77^{pqr}
ICG 14523	14.67^{b}	6.00^{g}	36.23^{cde}	16.00^{ijklmno}	3.30^{b}	2.00^{c}	33.23^{m}	48.27^{lmnopqr}	95.17^{ijk}
ICG 15236	17.57^{b}	7.00^{f}	34.23^{efghi}	19.67^{fghijkl}	2.73^{defgh}	2.00^{c}	30.63^{op}	64.15^{ghijklm}	160.03^{a}
ICG 1563	16.13^{b}	6.00^{g}	34.23^{efghi}	22.33^{fghijk}	2.83^{defgh}	3.00^{b}	32.63^{op}	68.66^{efghijklm}	122.53^{def}
ICG 1668	15.87^{b}	6.00^{g}	35.57^{defg}	9.33^{opqr}	2.47^{ghijklm}	2.00^{c}	32.6^{mn}	28.61^{qrstu}	65.33^{nop}
ICG 188	11.10^{b}	5.00^{i}	33.00^{efghi}	15.67^{jklmnop}	3.03^{bcde}	3.00^{b}	27.7^{stu}	56.60^{ijklmno}	67.7^{no}
ICG 2019	8.23^{b}	6.00^{g}	33.23^{efghi}	21.33^{efghijk}	2.67^{defghijk}	2.00^{c}	38.83^{h}	54.90^{ijklmno}	97.9^{hij}
ICG 2273	10.47^{b}	6.00^{g}	35.90^{cdefg}	26.00^{abcdef}	2.03^{nopqr}	2.00^{c}	34.80^{l}	74.74^{defghij}	101.73^{ghi}
ICG 2925	10.67^{b}	5.00^{i}	22.10^{opq}	18.00^{ghijklm}	2.63^{efghijk}	2.00^{c}	29.70^{pq}	60.54^{hijklm}	68.93^{mn}
ICG 3681	16.80^{b}	5.00^{i}	33.30^{efghi}	30.33^{a}	2.57^{ghijklm}	2.00^{c}	52.00^{a}	58.30^{hijklmn}	143.29^{b}
ICG 3746	14.70^{b}	6.00^{g}	27.77^{jklm}	11.33^{mnopqr}	2.67^{defghijk}	2.00^{c}	40.77^{fg}	27.85^{rstu}	72.4^{lmn}
ICG 397	11.67^{b}	5.00^{i}	25.77^{mno}	22.00^{efghijk}	2.43^{ijklmn}	2.00^{c}	42.77^{de}	51.42^{jklmnopq}	72.6^{lmn}

GENOTYPE	PHT	NB	CS	NPP	PL	NS	HS	SH%	PY
ICG 4389	17.90^{b}	6.00^{g}	35.90^{cdefg}	12.7^{lmnopqr}	2.67^{defghijk}	2.00^{c}	46.93^{c}	26.98^{rstu}	60.97^{nopq}
ICG 4998	11.57^{b}	12.0^{b}	35.23^{defgh}	6.67^{r}	2.70^{defghij}	2.00^{c}	36.10^{jk}	18.47^{u}	24.87^{t}
ICG 5016	16.40^{b}	12.0^{b}	34.70^{efghi}	17.00^{hijklmn}	2.97^{bcdefg}	3.00^{b}	34.70^{l}	48.94^{klmnopqr}	49.2^{qr}
ICG 5327	13.03^{b}	5.00^{i}	33.70^{efghi}	28.67^{abcd}	2.23^{klmnopq}	2.00^{c}	32.2^{mn}	89.08^{cde}	99.67^{ghi}
ICG 5663	10.33^{b}	6.00^{g}	27.43^{klm}	18.33^{ghijklm}	1.63^{r}	2.00^{c}	35.80^{jkl}	51.32^{jklmnop}	52.77^{pqr}
ICG 5779	13.70^{b}	6.00^{g}	30.43^{ijkl}	30.67^{a}	2.33^{ijklmno}	2.00^{c}	26.90^{u}	113.94^{ab}	119.63^{def}
ICG 6057	19.00^{b}	10.0^{c}	35.23^{defgh}	19.33^{fghijk}	2.70^{defghij}	2.00^{c}	42.57^{de}	45.54^{mnopqrs}	139.47^{bc}
ICG 6375	12.90^{b}	5.00^{i}	30.77^{hijkl}	28.67^{abcd}	2.23^{lmnopq}	2.00^{c}	35.40^{jkl}	81.09^{cdefgh}	130.73^{bcd}
ICG 6643	9.27^{b}	8.00^{e}	20.77^{pq}	7.33^{r}	2.23^{lmnopq}	2.00^{c}	7.17^{x}	101.27^{bc}	9.63^{u}
ICG 6766	12.33^{b}	5.33^{h}	40.43^{ab}	24.0^{abcdefgh}	2.70^{defghij}	4.00^{a}	28.57^{rs}	83.93^{cdefg}	104.07^{ghi}
ICG 6888	11.87^{b}	5.33^{h}	21.23^{pq}	8.33^{qr}	2.83^{cdefgh}	2.00^{c}	36.17^{jk}	23.07^{stu}	34.27st
ICG 7181	10.90^{b}	6.00^{g}	33.23^{efghi}	28.67^{abcd}	2.50^{ghijklm}	2.00^{c}	23.2^{vw}	123.26^{a}	101.9^{ghi}
ICG 7867	11.47^{b}	6.00^{g}	34.80^{efghi}	29.67^{abc}	1.97^{opqr}	2.00^{c}	22.33^{w}	133.05^{a}	110.43^{fghi}
ICG 8106	12.43^{b}	8.00^{e}	33.67^{efghi}	27.67^{abcde}	1.97^{opqr}	2.00^{c}	31.60^{no}	87.55^{cdef}	114.9^{efg}
ICG 8285	14.13^{b}	5.33^{h}	44.33^{a}	31.00^{a}	3.17^{bc}	2.00^{c}	43.37^{d}	71.50^{efghijk}	160.87^{a}
ICG 8517	13.90^{b}	8.00^{e}	31.43^{fghijk}	15.67^{jklmnop}	3.23^{bc}	2.00^{c}	48.03^{b}	32.55^{pqrstu}	83.13^{klm}
ICG 862	12.33^{b}	6.00^{g}	32.57^{efghi}	10.67^{nopqr}	2.47^{ghijklm}	2.00^{c}	37.77^{i}	28.22^{qrstu}	67.4^{no}
ICG 875	14.33^{b}	5.00^{i}	41.73^{ab}	22.00^{defghijk}	2.53^{ghijklm}	2.00^{c}	42.53^{de}	51.69^{ijklmnopq}	100.3^{ghi}
ICG 9249	15.57^{b}	5.00^{i}	25.70^{mno}	21.33^{efghijk}	3.67^{a}	4.00^{a}	30.17^{pq}	70.69^{efghijk}	108.23^{fghi}
ICG 9315	12.87^{b}	5.00^{i}	40.10^{bc}	18.33^{ghijklm}	2.50^{ghijklm}	2.00^{c}	29.43^{qr}	62.28^{hijklmnop}	51.63^{pqr}
ICG 97183	13.00^{b}	8.00^{e}	23.63^{mnop}	10.67^{nopqr}	2.70^{defghij}	2.00^{c}	41.20^{f}	26.16^{s}	49.77^{qr}
ICV 02038	12.57^{b}	7.00^{f}	22.87^{nop}	10.33^{nopqr}	2.37^{ijklmno}	2.0^{c}	36.33^{j}	28.37^{qrstu}	31.03st
ICV 02148	18.80^{b}	5.00^{h}	27.77^{jklm}	23.00^{bcdefgh}	3.10^{bcd}	3.00^{b}	32.7^{mn}	70.4^{efghijkl}	126.63^{cde}
Means	14.12	6.64	31.17	19.25	2.58	2.22	33.97	59.94	84.11
Range	6.6-19	4-15	17.9-44.3	6.67-31	1.63-3.67	2-4	7.17-52	18.47-133.05	9.63-160.03
C.V	26.4	2.1	7.5	19.1	9.7	8.5	0	1.8	19.8

Means followed by the same letters are not significantly different according to DMRT. PHT=Plant height; NB=Number of branches; CS= Canopy spread; NPP = Number of pod/plant; PY=Pod yield; HSW=100 seed weight; SH%= shelling percentage. DMRT=Duncan multiple range test; CV=Coefficient of variation.

4.2 Analysis of Variance

The analysis of variance of the study as presented in table 4.2, revealed highly significant difference among the genotypes used as treatments for this study in all nine characters considered, namely; plant height, canopy spread, number of branches, 100 seed weight, number of seeds per plant, number of pods per plant, pod length and the dependent trait, pod yield per plant. A wide range for the traits indicated existence of variation among the genotypes.

Table 4.2 Mean square from analysis of variance for the studied traits in groundnut (*Arachis hypogaea* L.) genotypes.

Source	DF	PHT	NB	CB	NPP	PY	PL	NS	HSW	SH %
genotype	49	25.25**	14.01**	110.08**	167.3**	3961.2**	0.5**	0.8**	180.8**	2212.5**
Replication	2	5.87	0.02	9.2	41.08	45.5	0.07		5.3	340.5
Error	98	199.05	0.02	5.5	13.4	66.6	0.05	0.0	0.4	140.4
CV (%)		26.4	2.1	7.5	19.05	9.7	8.5	0	1.8	19.8

PHT=Plant height; NB=Number of branches; CS= Canopy spread; NPP = Number of pods per plant at maturity; PY=Pod yield; PL=Pod length; NS=Number of seeds per pod; HSW=100 seed weight; SH%= shelling percentage; 0.05= significant =*and 0.01= highly significant=**

4.3 Components of Variation

Estimates of components of variance were calculated as presented in (Table 4.3) and all the traits had higher error variances (σ^2_e) greater than their genotypic variances (σ^2_g) except for plant height. Estimates of genetic variance ranged from 0.16 to 1298. Pod yield had the highest value (1298.17). Shelling percentage had 690.67, hundred seed weight had (60.13), Number of pods per plant had (51.31), Canopy spread also had (34.88), number of branches (4.66), Plant height (4.49) and number of seed per pod (0.27), pod length had the least value (0.16) respectively. (Table 4.3). The range of phenotypic variance was from 0.28 to 1364.86. Pod yield had (1364.86), number of seed per pod, Plant height, number of branches, canopy spread, number of pods per plant, number of seed per pod and pod yield was, (0.28, 16.29, 4.86, 40.36, 64.79, 0.65, , 60.50, and 831.12) respectively. From the result, phenotypic coefficient of variations was greater for all the traits under consideration (Table 4.3). The phenotypic coefficient of variation (PCV) ranged from 20.38 for canopy spread to 48.84 for shelling percentage followed by pod yield with PCV 43.92 (Table 4.2). The highest phenotypic coefficient of variation was noticed in the SH%, PY, NPP, NB, PL, PH, NS, HSW and the least was CS (48.84, 43.92, 41.81, 33.20, 31.12, 28.54, 22.97, 22.90 and 20.38 respectively (Table 4.3). When compared to the genotypic coefficient of variation, indicating that these characters were more affected by the environment. The genotypic coefficient of variation (GCV) ranged from 15.01 for plant height to 43.84 for shelling percentage (Table 4.2). Overall, genotypic coefficient of variation as percent of

mean obtained was highest in the shelling percentage, followed by pod yield with GCV 42.84, number of pod per plant 37.21, number of branches 32.51, number of seed per pod 23.41, 100 seed weight 22.82, canopy spread 18.95, pod length 15.44 and the least was plant height respectively.

Table 4.3 Estimates of genetic (GCV) and phenotypic coefficient of variation (PCV) for the studied traits of groundnut genotypes.

Trait	Mean	σ_g^2	σ_e^2	σ_p^2	GCV (%)	PCV (%)
PHT	14.12	4.49	11.80	16.29	15.01	28.54
NB	6.64	4.66	0.20	4.86	32.51	33.58
CS	31.17	34.88	5.48	40.36	18.95	20.38
NPP	19.25	51.31	13.48	64.79	37.21	41.81
PL	2.59	0.16	0.49	0.65	15.44	31.12
NS	2.22	0.27	0.01	0.28	23.41	23.83
HSW	33.97	60.13	0.37	60.50	22.82	22.90
SH%	59.94	690.67	140.45	831.12	43.84	48.09
PY	84.11	1298.17	66.69	1364.86	42.84	43.92

PHT=Plant height; NB=Number of branches; CS= Canopy spread; NPP= Number of pods per plant; PY=Pod yield; PL=Pod length; NS=Number of seeds per pod; HSW=100 seed weight; SH%= shelling percentage. Mean, Range, Phenotypic (σ^2_{ph}), genotypic (σ^2_g), and environmental (σ^2_e) components of variance for morphological characters in *Arachis hypogaea* genotypes. GCV = Genotypic Coefficient of Variation. PCV = Phenotypic Coefficient of Variation.

4.4 Coefficient of Correlation.

The phenotypic and genotypic correlation computed for the nine traits as presented in Table 4.4**,** the result indicated that, there was highly significant and positive correlation between canopy spread with pod yield at (r = 0.826), number of pod per plant with pod yield at (r = 0.825) and number of pod per plant with shelling percentage at (r = 0.761). Significant and positive correlation was recorded between plant height with pod yield at (r = 0.621), plant height with pod length at (r = 0.521), number of seed per pod with hundred seed weight at (r = 0.605) and hundred seed weight with shelling percentage at (r = 0.552) respectively. Moderate and positive correlation was recorded between pod length with shelling percentage (r = 0.499), number of branches with number of seed (r = 0.478), canopy spread with number of seed (r = 0.454).

On the other hand, significant and positive genotypic correlation was observed between with number of branches with number of seed at (r = 0.696) and number of seed with hundred seed weight at (r = 600). Moderate and positive correlation was recorded between pod length with number of seed(r = 0.431) and plant height with number of seed (r = 0.366) respectively.

Table 4.4 Phenotypic and genotypic correlation between nine traits of groundnut (*Arachis hypogaea* L.) genotypes.

	PHT	NB	CS	NPP	PY	PL	NS	HSW	SH%
PHT	1	0.037	0.212	0.250	0.621*	0.521*	0.212	0.478	0.098
NB	0.115	1	0.098	-0.295	-0.286	-0.076	0.478	-0.321	0.206
CS	0.245	-0.047	1	0.318	0.826**	0.198	0.454	0.158	0.131
NPP	0.019	-0.049	0.243	1	0.825**	-0.566*	-0.052	0.068	0.761**
PY	-0.044	-0.030	0.008	-0.417	1	0.184	0.252	0.241	0.499
PL	0.162	-0.114	0.157	0.139	-0.205	1	0.293	0.312	-0.242
NS	0.366	0.696*	-0.124	-0.188	0.180	0.431	1	0.605*	-0.095
HSW	0.169	-0.047	0.121	-0.059	-0.079	-0.204	0.600*	1	0.554*
SH%	0.242	-0.278	0.046	-0.082	-0.096	-0.010	-0.230	-0.078	1

PHT=Plant height; NB=Number of branches; CS= Canopy spread; NPP= Number of pods per plant; PY=Pod yield; PL=Pod length; NS=Number of seeds per pod; HSW=100 seed weight; SH%= shelling percentage. The upper diagonal (phenotypic) and lower (genotypic). **, * significant at P=0.01 and P=<0.05 respectively.

4.5 Principal Component Analysis (PCA)

The variation among 50 genotypes was assessed through principal component analysis based on the morphological traits. Four of the nine principal components extracted, had Eigenvalue greater than 1 and accounted for 76.92% of the total variation among 50 genotypes (Table 4.5). The first principal component accounted for (31.01% of the total variation. The variation in principal component 1 was mainly attributed to number of pods per plant followed by pod yield, shelling percentage, number of seeds per pod, canopy spread, plant height, pod length. The principal component 2 contributed 19.94% of the total divergence and depicted the pattern of variation mainly in pod length, 100 seed weight, plant height, number of seed per pod, canopy spread, pod yield and number of branches per plant. The principal component 3 constituted 14.82% of the total variation and was mainly attributed to 100 seed weight, canopy spread, number of primary branches per plant, number of pods per plant, pod yield, number of seed per pod, pod length , plant height and shelling percentage (Table 4.6).

Principal component 4 described an additional 11.13% of the total variation and was dominated by number of primary branches per plant, canopy spread, number of seeds per pod, plant height and pod length.

The principal component scores of the fifty groundnut genotypes based on the first four principal components are presented in Table 4.7. On principal component 1, the highest score was recorded by ICG 188, followed by ICG 3746, ICG 6766, ICG 13982, and ICG 12672. On principal component 2, ICG 11542 has the highest score ICG 13982, ICG 1668

and ICG 2273. ICG 12276, ICG 11542 and ICG 13982 had the highest score on principal component 3

Table 4.5 Eigen values, percent and cumulative variance of the nine most important characters from principal component analysis

	Eigen value	Difference	Proportion of variation (%)	Cumulative (%)
1	2.79118662	0.9966607	31.01	31.01
2	1.79452591	0.46044335	19.94	50.95
3	1.33408257	0.33259873	14.82	65.78
4	1.00148384	0.11670344	11.13	76.9

Table 4.6 Principal components, eigenvalues, percent and cumulative variance, for nine characters from principal component analysis.

Characters	PC 1	PC 2	PC 3	PC 4
Plant height	0.185296	0.293083	-0.19092	0.119044
No. Of primary branches	-0.25873	0.011294	0.263145	0.68043
Canopy spread	0.204284	0.2078	0.402855	0.540101
No. of pods per plant	0.547761	-0.11692	0.221918	-0.0332
Pod Yield	0.508887	0.097112	0.221673	-0.15705
Pod Length	0.080435	0.598519	-0.24827	0.052338
No. of Seed per pod	0.23817	0.261807	-0.59383	0.246701
Hundred Seed Weight	-0.01098	0.526087	0.45829	-0.34319
Shelling Percentage	0.484426	-0.37968	-0.09654	0.154872
Eigen value	2.791186	1.794525	1.334082	1.001483
Variability	31.01%	19.94%	14.82%	11.13%
Cumulative	31.01%	50.95%	65.78%	76.92%

Table 4.7. Principal component scores for nine traits in fifty groundnut (*Arachis hypogaea)* genotypes

S/no	Genotype	PC 1	PC 2	PC 3	PC 4	S/no	Genotype	PC 1	PC 2	PC 3	PC 4
1	ICG 02271	-0.93	-1.90	-0.42	0.39	26	ICG 3746	-2.88	-0.53	1.08	2.02
2	ICG 11386	-0.28	1.29	1.62	1.36	27	ICG 397	1.07	-1.10	1.18	-0.01
3	ICG 1142	-1.55	-0.10	0.41	0.07	28	ICG 4389	1.33	0.39	0.52	0.20
4	ICG 11426	-2.60	-0.53	-0.27	-0.82	29	ICG 4998	1.42	-1.52	1.15	0.62
5	ICG 11515	-1.48	1.27	0.00	-0.96	30	ICG 5016	0.26	1.55	1.55	0.69
6	ICG 11542	-2.02	-3.72	-2.39	1.06	31	ICG 5327	1.68	-1.57	0.71	-0.24
7	ICG 11687	-0.89	1.18	-0.40	2.53	32	ICG 5663	1.57	-2.09	0.48	0.46
8	ICG 118	-2.56	1.05	-0.02	-0.73	33	ICG 5779	-1.59	0.00	0.66	-0.50
9	ICG 12000	0.72	0.62	0.76	-0.52	34	ICG 6057	-0.01	0.07	-0.04	0.60
10	ICG 12276	1.86	1.87	-3.41	0.22	35	ICG 6375	1.83	-1.26	0.90	-0.83
11	ICG 12370	0.87	-1.46	1.31	1.15	36	ICG 6643	0.23	0.55	0.70	-0.48
12	ICG 12672	2.54	0.75	-1.97	1.46	37	ICG 6766	2.78	1.12	2.04	-0.11
13	ICG 12697	-2.06	-1.39	0.07	1.50	38	ICG 6888	0.80	1.35	1.35	-0.12
14	ICG 13982	2.68	2.53	-2.15	0.94	39	ICG 7181	0.81	-0.60	-0.48	-0.03
15	ICG 14118	1.62	0.76	-0.80	0.45	40	ICG 7867	2.26	-0.10	-0.85	0.97
16	ICG 1415	-0.33	-0.46	0.63	-1.57	41	ICG 8106	0.15	0.38	-1.64	0.38
17	ICG 14523	1.75	0.62	-1.34	-0.38	42	ICG 8285	-2.51	0.62	-1.12	-1.58
18	ICG 15236	1.47	-0.96	-0.15	0.37	43	ICG 8517	-1.02	-0.94	0.21	-0.79
19	ICG 1563	-2.05	0.12	-0.56	0.14	44	ICG 862	-0.45	-0.48	-1.04	-1.17
20	ICG 1668	2.01	-2.09	0.40	-0.11	45	ICG 875	-1.41	0.49	-0.28	-0.02
21	ICG 188	-3.17	1.22	0.60	1.88	46	ICG 9249	-1.47	-1.40	-0.98	-1.14
22	ICG 2019	-0.08	0.66	0.27	0.13	47	ICG 9315	-2.24	1.06	-0.11	-0.64
23	ICG 2273	-1.18	2.01	0.82	-0.44	48	ICG 97183	1.64	-1.95	0.53	-0.94
24	ICG 2925	-1.02	1.70	1.07	-0.42	49	IGV 02038	0.12	1.05	-1.72	-2.10
25	ICG 3681	1.85	1.63	1.68	-1.46	50	IGV 02148	0.45	-1.78	-0.53	-1.46

4.6 Estimation of Squared Distance (D^2) and Clustering of Genotypes

Significant differences among varieties for all or majority of the characters would justify further calculation of D^2 (Sharma, 1998). Analysis of variance (ANOVA) revealed the presence of highly significance difference among the tested genotypes for all the characters studied (table 3.2) justifying the need to estimate squared distance values for the genotypes. The D^2 values based on the pooled mean of genotypes resulted in classifying the 50 genotypes in to eight distinct clusters (Table 4.8). This indicated the presence of wide diversity or variability among the genotypes. The genotypes were classified into eight with cutting point at 0.5 unit cluster, each clusters has a distinct feature and characteristics from other genotypes in the characteristics under considerations (figure 1). The mean value of the nine quantitative characters in each cluster was presented in Table 4.9.

Cluster 1 had one (2%) genotype which was outstanding type by its performance in most of the traits or agronomic characters, the cluster was characterized by the following essential features, highest plant height (25cm) and highest canopy spread (31cm), the highest in number of pod per plant (25), highest in pod length (3cm), highest in number of seed per pod (3) high in pod yield next to cluster 2. The genetic distance value of these varieties was 1.477.

Cluster 2 had four (8%) genotypes. This cluster could be characterized by high plant height(15.7cm), high number of branches (8), high canopy spread (36.7cm), high number of pod per plant (25),highest pod yield (143.75g/plot), high pod length (3cm), relatively high 100 seed weight (37.3g) and highest number of seed per pod (3) and high shelling percentage next to cluster 4. The genetic distance value of these genotypes was 1.637.

Cluster 3 consisted of 15 (30%) genotypes having the characteristic of high number of pod per/plant (22.2), less 100 seed weight (29.3) relatively high shelling percentage (71.67), relatively high pod yield per plant (102.3), next to cluster 2 and 1. The genetic distance value of these genotypes was 1.149. Cluster 4 consisted of 6 (12%) genotypes characterized by the following features: high canopy spread (34.5), relatively long pod (2.8cm) and number of branches (7). Cluster 7 consisted 5 (12%) genotypes with a characteristic feature of relatively high plant height (13cm) low number of pod per plant (16), low pod yield (50.6). The genetic distance value of these varieties was 1.978. One genotype (2%) had cluster 5 with a characteristic feature of shortest height (cm), highest number of branches (8), lowest pod yield, canopy spread, pod length, 100 seed weight, (7g, 21cm, 7, 2cm respectively. The genetic distance value of these varieties was 1.376. Cluster 6 consisted of 12 (24%) genotypes. This cluster could be characterized by high 100 seed weight (38.67g/plot), it had the less number of pod/plant (12.3). The genetic distance value of these varieties was 1.376. Cluster 7 consisted 5 (12%) genotypes with a characteristic feature of relatively high plant height (13cm) low number of pod per plant (16), low pod yield (50.6). The genetic distance value of these varieties was 1.477. Six genotypes made up of Cluster 8 (12%). This cluster had features of late flowering (57.40), short time for capsule filling period (33.90 days), short time for capsule filling period (33.90), short canopy spread (29cm), less number of branches (5) and relatively high shelling percentage (63.4) The genetic distance value of these varieties was 1.477.

Table 4.8 Distribution of genotypes into nine clusters for fifty (*Arachis hypogaea* L.) genotypes.

Cluster	No. of genotypes	Pedigree name
Cluster 1	1	ICG 9249
Cluster2	4	ICG 6766, ICG 4998, ICG 5016, and ICG 4389.
Cluster3	15	ICG 97183, ICV 02148, ICG 8517, ICG 5663, ICG 5327, ICG 4998, ICG 397, ICG 3681, ICG 1668, ICG 15236, ICG 14523, ICG 14118, ICG 12672, ICG 12370 and ICG 12276.
Cluster4	6	ICG 11386, ICG 2019, ICG 2925, ICG 6375, ICG 6643 and ICG 6888.
Cluster5	1	ICG 13982
Cluster6	12	ICG 1142 , ICG 118, ICG 15236, ICG 188, ICG 11426, ICG 11515, ICG 2273, ICG 4389, ICG 5779, ICG 8285, ICG 9315, and ICGV 02038.
Cluster7	5	ICG 12000, ICG 15236, ICG 7181, ICG 8106 and ICG 862.
Cluster 8	6	ICG 97183, ICG 8285, ICG 6057, ICG 14118, ICG 11687 and ICG 02271.

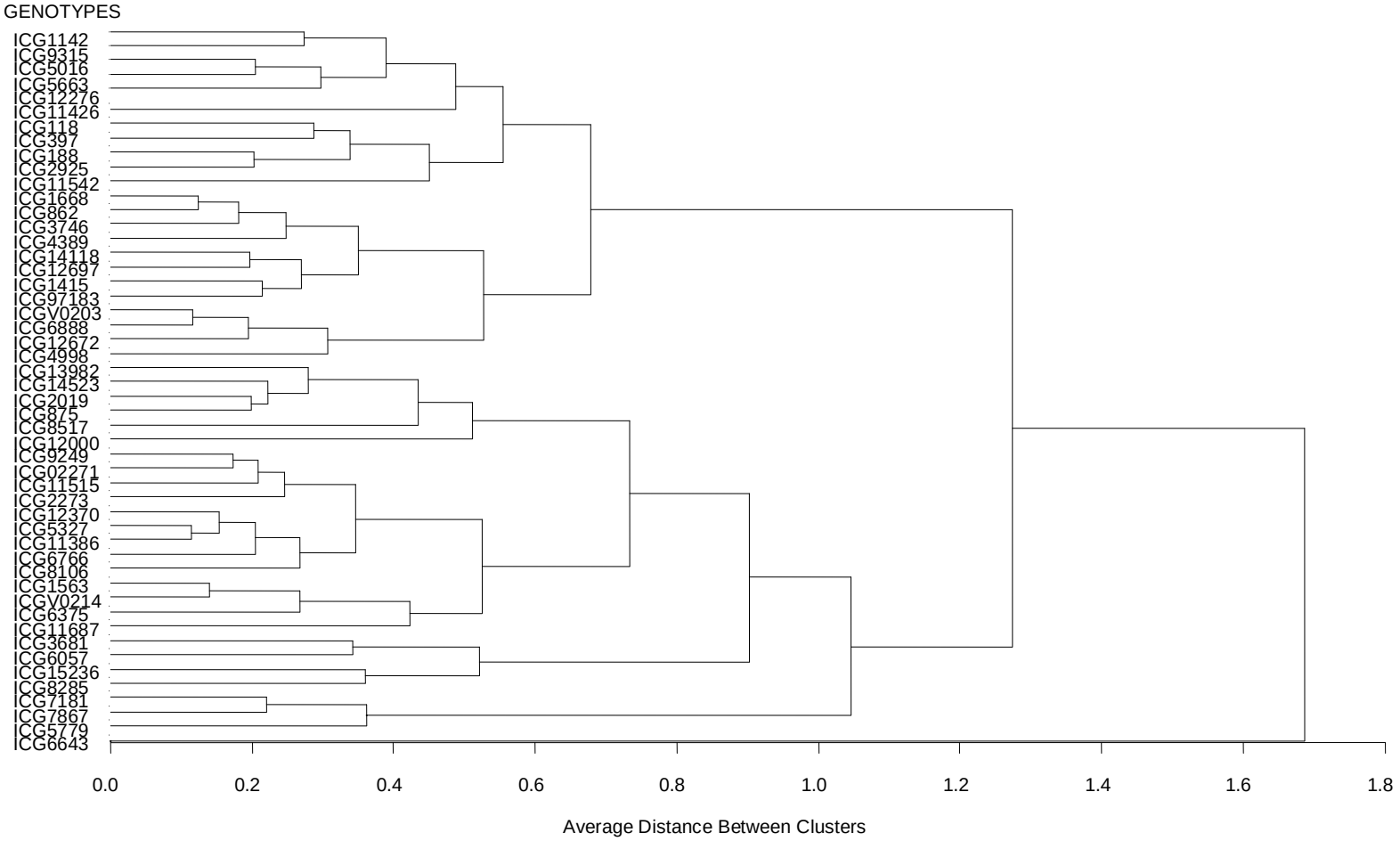


Fig. 1 Dendrogram showing genetic relationship based on Euclidean distance among ICRISATgroundnut refrence collection.

Table 4.9 Mean value of nine traits of the eight clusters for groundnut genotypes

Trait	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Plant height.	25	15.7	12.2	13	9	12.3	12.4	12.8
No. branches.	6	7.5	5.53	6.67	8	6.58	5.2	6.7
Canopy spread.	31	36.7	28.4	34.5	21	28.4	29	29.7
No. of pod/plant.	25	24.5	22.2	21.67	7	12.3	21.3	15.6
Pod yield/plant.	103	143.75	102.3	98.6	10	65.67	71.2	50.6
Pod length.	3	2.7	2.4	2.8	2	2.7	3	2.3
No. of seed/pod.	3	2	2.3	2.1	2	2.1	2.2	2.1
100 seed weight.	35	37.3	29.3	38.5	7	38.67	34.4	30.3
Shelling percentage.	71	67.5	71.67	56.5	89	32.25	63.4	52.3

CHAPTER FIVE

DISCUSSION

5.1 Mean Performance Mean performance

Mean performance in this study for the most of the characters have similar trend. However, the mean performance for plant height was higher than the rest. Environmental factors were most likely to be responsible for these variations. Unfortunately, these are variables which the breeder has very little control. The choice of genotypes and breeding procedure to be adopted in an improvement programme will depend upon the mean performance and on the magnitude and quality of genetic variability present (Eckebili et al 1977) for most of the traits considered, the range of the values were wide and the mean difference observed was significant. This agrees with the findings of (Knauft and Wynne, 1995) who reported that, variation exist among peanut genotypes for different attributes. This highly significant variation in plant attribute within a population suggests s that selection is possible for each character. The overall picture suggests that high genetic variability or diversity exists among the genotypes studied. In other words, they are diverse in their genetic base. This may be because the the genotypes were derived from collection and crosses form different countries and countries and climate, which could warrant adaptive variability. Since variability in a population suggests a possibility of improvement through selection, it means that greater amount of improvement can be obtained in plant height which has the highest genetic variations; presence of genetic variation in genotypes is an essential requirement for achieving success in selection programme (Singh and Singh 1979).

Analysis of variance for the different traits revealed that generally, there was highly significant difference among the 50 genotypes of (*Arachis hypogaea* L.) for all the morphological traits studied. The existence of these differences indicates the presence of sufficient genetic variability among the genotypes for these traits. This is most likely because these genotypes were obtained from different natural environments which might have been affected by natural selection. This indicates that significant improvement could be achieved through selection for the traits of interest. The present findings are in agreement with the findings of Kadam *et al*. (2007), Khote *et al*. (2009) and Ladole *et al*. (2009). In this study, the values of GCV and PCV for number of primary branches per plant revealed that the magnitudes of GCV and PCV were high for this trait. The high estimates of genotypic and phenotypic coefficients for number of primary branches per plant have been reported by John *et al*. (2008). Plant height, pod length and canopy spread recorded moderate value of GCV. This result is in agreement with result obtained by Meta (2007) who also reported moderate magnitude of GCV for plant height. Whereas; only high GCV recorded by Kadam *et al*. (2007) and Ladole *et al*. (2009). The genotypic coefficient of variation and phenotypic coefficient of variation were found high for number of pods per plant, suggesting wide spectrum of genotypic variation for this trait. The result also agrees with the findings of Meta (2007) who also reported high magnitude of both GCV and PCV for number of pods per plant in groundnut. The values of genotypic coefficient of variation and phenotypic coefficient of variation were high for pod yield per plant, shelling percentage, number of pod per plant. These findings are confirmed by Khote *et al*. (2009). The genotypic coefficient of variation and phenotypic coefficient of variation

were moderate for plant height, canopy spread and pod length. The present findings are in accordance with the findings of Meta (2007) and John *et al*. (2008).

In general, the estimates of genotypic and phenotypic coefficient of variation were high for pod yield per plant, number of pods per plant, number of branches per plant, number of seed per pod, 100 seed weight and shelling percentage. The higher estimates of GCV and PCV have been earlier reported by John *et al*. (2006), Meta (2007) and Ladole *et al*. (2009). Moderate magnitudes of GCV and PCV were observed plant height, canopy spread and pod length. Whereas, no low estimates of GCV and PCV were observed.

5.2 Coefficient of Correlation

Correlation studies between characters have been of great value in determination of the most effective procedures for selection of superior genotypes (Adebisi *et al.,* 2004). The results indicates clearly the different patterns of association between the characters measured (Tables 4.4). The result indicated that, there was highly significant and positive correlation between canopy spread with pod yield at (r = 0.826), number of pod per plant with pod yield at (r = 0.825) and number of pod per plant with shelling percentage at (r = 0.761). Significant and positive correlation was recorded between plant height with pod yield at (r = 0.621), plant height with pod length at (r = 0.521), number of seed per pod with hundred seed weight at (r = 0.605) and hundred seed weight with shelling percentage at (r = 0.552) respectively; indicating that pod yield may be improved through the selection of any of these characters. This agrees wiyh the findings of (Jonah *et al.,* 2010). Number of pod per plant indicated a significant phenotypic correlation coefficient with seed yield per

plant, indicating that Number of pod per per plant is a strong contributor to pod yield per plant this agrees with findings of Ahamed, (1995) in groundnut.

5.3 Principal Component Analysis (PCA)

The morphological and agronomical diversity among the groundnut populations is further classified by principal component analysis, which indicated that the total variation was fairly distributed across all of the studied traits. Furthermore, the high level of variability exhibited by this population 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). Assessment of genetic variability between populations is of interest not only for their protection and registration but also for conservation of germplasm and breeding purposes (sunseri et al 2010). PCA of the agro-morphological traits revealed 76.92% of total variation can be explained by 4 principal components, comprising (31.01, 19.94, 14.82 and 11.13%, respectively) in table 8 and 9. PCA performed on the studied characters analyzed showed that the first component (PC1) positively related to number of pod per plant, pod yield, shelling percentage, pod length, plant height, canopy spread and number of seed per pod whereas number of primary branches and 100 seed weight showed negative association. The second component (PC2) showed higher loadings for pod length, 100 seed weight and plant height. The third component (PC3) positive related to100 seed weight, canopy spread, pod yield and number of pod per plant. While, shelling percentage, number of seed per pod, pod length and plant height were negatively related. The forth component (PC4) was positively related to the

number of primary branches, canopy spread, number of seed per pod, pod length, plant height and shelling percentage. Thus, the nine studied characters were able to discriminate the 50 investigated genotypes, with a clear separation between them.

5.4 Cluster Mean Analysis

The mean value of the characters in each cluster is presented in Table 4. The characteristic feature of each cluster is discussed here below. Cluster 1 consisted of 1 genotype (ICG 9249). This cluster was found to have a characteristic feature of high biomass production, high number of seeds per pod and having more number of pod per plant. The genetic distance value of these varieties was 1.477. Four genotypes which include (ICG 6766, ICG 4998, ICG 5016, and ICG 4389) constitute cluster 2. This cluster can be characterized by having high biomass and yield. The genetic distance value of these genotypes was 1.637. Cluster 3 had 15 genotypes with a characteristic feature of high pod yield, biomass production. These cluster exhibited the greatest genetic distance from all other genotypes included in this study. According to Ghaderi *et al.*, (1984), increasing parental distance implies a great number of contrasting alleles at the desired loci, and to the extent that these loci recombine in the F2 and F3 generation following a cross of distantly related parents, the greater will be the opportunities for the effective selection for yield factors. Thus, crossing of genotypes from these clusters with other clusters may produce higher amount of hetrotic expression in the first filial generations (F1's) and wide range of variability in subsequent segregating (F2) populations. The genetic distance value of these genotypes was 1.149.

Cluster 4 had Six genotypes with a characteristics feature of, relatively moderate yielding, number of seeds per pod and plant height. The genetic distance value of these varieties was 1.978. Cluster 5 had one genotype and this cluster could be characterized by having low pod yield, shorter in height and canopy spread. The genetic distance value of these varieties was 1.376. Cluster 6 had twelve genotypes and this cluster could be characterized by having moderate to high grain and biomass yield but with low shelling percentage. The genetic distance value of these varieties was 1.376. Cluster 7 had five genotypes having a characteristics feature of relatively good pod length and pod yield. The genetic distance value of these varieties was 1.477. Cluster 8 had six genotypes. This cluster is mainly characterized by having moderate to high performance for all the traits. The genetic distance value of these genotypes was 1.477. The range of dissimilarity obtained was 1.149 (for genotypes in cluster 3) to 1.978 (for genotypes in cluster 4). Crosses involving parents belonging to more divergent clusters would be expected to manifest maximum hetrosis and wide variability in genetic architecture (Singh *et al*., 1987). In the present study, cluster 3 was more divergent than the others. However, the chance of getting segregates with high yield level is quite limited when one of the characters has a very low yield level. Cluster 3 had the lowest mean performance in seed yield and other important characters. This indicates that the chance of getting segregates with high yield is limited between crosses of cluster 3 with the other clusters. The selection of parents should also consider the special advantage of each cluster and each genotype within a cluster depending on specific objective of hybridization (Chahal and Gasal, 2002). Thus, crosses involving cluster 3, with any other cluster are suggested to exhibit high hetrosis and could result in segregates

with higher seed yield. At a cutoff 5.00 the dendrogram revealed 8 distinct clusters which are stemmed from two main clusters.

CHAPTER SIX

6.1 Summary

Fifty genotypes of groundnut (*Arachis hypogaea* L.) obtained from International Crop Research Institute for Semi-Arid Tropics (ICRISAT) India were evaluated in 2012 cropping season, in a complete randomized block design with three replications. Data were taken on agronomic traits and subjected to analysis of variance.

Mean performance showed highly significant difference, each character exhibited considerable range of its expression. Coefficient of variation observed generally moderate, the highest phenotypic coefficient of variance was observed for shelling percentage 48.09% followed by pod yield 43.92%. The phenotypic variance was consistently higher than genotypic variances for virtually all the traits. The magnitude of genotypic variance and of variation is suggestive that improvement feasible through selection in these traits.

Based on the D^2 statistics, the genotypes were grouped in eight clusters with cluster III having the maximum number of genotypes (15). However, clusters showed some character distinctions that could be employed for hybridization purpose. Phenotypic and genotypic correlations were positive and significant for some yield components with pod yield, indicating that selection based on phenotype can be effectively improve yield.

Principal component analysis also revealed that, plant height, number of pod per plant, pod yield, number of primary branches and shelling percentage were positive indicating that these characters contribute to maximum genetic diversity in the population.

Conclusion

Knowledge of the genetics concerning interesting traits of species is very important for breeding improvement. Based on the results of current work parental materials have been identified and classified in groundnut germplasm. Important morphological traits like greater yield potential, seeds per pod and pods per plant etc. served as a criterion to select promising groundnut genotypes.

The present investigation provided considerable information useful in genetic improvement of Groundnut (*Arachis hypogaea* L). Genotypes grouped into cluster 3 showed maximum inter cluster diversity. From cluster mean values, genotypes in cluster 1, 2, 3 and 4 deserve consideration for their direct use as parents in hybridization programs to develop high yielding wheat varieties. The genotypes in cluster 5 may be used for improvement and other desirable characters other than grain yield. There is significant genetic variability among tested genotypes that indicates the presence of excellent opportunity to bring about improvement through wide hybridization by crossing genotypes in different clusters.

Recommendation

For the improvement of cultivated groundnut, it is pertinent to use diverse collections with more variability for the purpose of variety development and for use in future breeding programs of Nigeria. So plant breeders who are interested in improving many traits simultaneously must take care of the relationship existing between them. Information obtained throughout principal component analysis may assist plant breeders to identify the number of highly differentiated population for use in crossing and selection programs.

Based on the present results, it was recommended to make crosses among genotypes in different clusters. The categorization of the diversity among the genotypes into groups with similar characteristics can be used to design a collection strategy.

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