ESTIMATION OF GENETIC DIVERSITY IN SOME COTTON (*GOSSYPIUM HIRSUTUM* L) GENOTYPES

BY

MUHAMMAD IYAD ABDULLAHI

DEPARTMENT OF PLANT SCIENCE
FACULTY OF AGRICULTURE
AHMADU BELLO UNIVERSITY, ZARIA
NIGERIA

AUGUST, 2015

ESTIMATION OF GENETIC DIVERSITY IN SOME COTTON (*GOSSYPIUM HIRSUTUM* L) GENOTYPES

BY

Muhammad Iyad ABDULLAHI, B. AGRIC (A.B.U) 2010
MSc/Agric/10525/11-12

A THESIS SUBMITTED TO THE SCHOOL OF POSTGRADUATE STUDIES, AHMADU BELLO UNIVERSITY, ZARIA IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE AWARD OF A MASTER DEGREE OF SCIENCE IN PLANT BREEDING

DEPARTMENT OF PLANT SCIENCE,
FACULTY OF AGRICULTURE
AHMADU BELLO UNIVERSITY, ZARIA
NIGERIA

AUGUST, 2014.

DECLARATION

I hereby declare that this dissertation titled "ESTIMATION OF GENETIC DIVERSITY IN SOME COTTON (*GOSSYPIUM HIRSUTUM* L) GENOTYPES" under the supervision of Prof. C.A. Echekwu, Prof. S.G. Ado and Dr. (Mrs.) M.D. Katung in the Department of Plant Science was written by me and it is a record of my own research work. It has not been presented in any previous application for a higher degree. References made to published and unpublished literature have been duly acknowledged.

Muhammad Iyad ABDULLAHI	_____	_____
Student	Signature	Date

CERTIFICATION

This thesis titled ESTIMATION OF GENETIC DIVERSITY IN SOME COTTON (*GOSSYPIUM HIRSUTUM* L) GENOTYPES by ABDULLAHI, Muhammad Iyad meets the regulations governing the award of the Degree of Master of Science in Plant Breeding of Ahmadu Bello University, Zaria and is approved for its contribution to scientific knowledge and literary presentation.

Prof. C.A. Echekwu Chairman, Supervisory Committee	_____ Signature	_____ Date
Prof. S.G. Ado Member, Supervisory Committee	_____ Signature	_____ Date
Dr. (Mrs.) M.D. Katung Member, Supervisory Committee	_____ Signature	_____ Date
Dr. U.S. Abdullahi Acting Head, Department of Plant Science	_____ Signature	_____ Date
Prof. A. Z. Hassan Dean Postgraduate School	_____ Signature	_____ Date

DEDICATION

This work is dedicated to Almighty ALLAH and to my Late Father, who inspired me to higher ideas of life.

ACKNOWLEDGEMENTS

All praises are due to Allah Almighty, the most Affectionate, the most Beneficent, and the most Merciful, Who granted me the ability to undertake this research work and complete the dissertation. Countless salutation be upon His beloved and last Prophet Muhammad (peace be upon him), who declared it to be an obligatory duty of every Muslim to seek and acquire knowledge. This gives me the privilege to acknowledge few of those people whose sincere help, guidance and prayers enabled me to accomplish my research work in a congenial and serene environment.

First of all, I would like to pay tributes to my worthy supervisor Prof. C.A. Echekwu whose able supervision, guidance, stimulating suggestions and encouragement helped me all through my research and for writing this Dissertation. I ardently extend my warmest and sincerest thanks to my supervisors Prof. S.G. Ado and Dr. (M.D.) Katung for their excellent guidance, invaluable advice, kindness and support in carrying out this research work. I am highly appreciative to Dr. U.S. Abdullahi, Mallam Abdullahi Ibn Yahaya, Dr. Alhassan Usman, Mal. Usman Muhammad and Mal. Muhammad Saba for their timely support, guidance and sharing their knowledge with me. My gratitude goes to all the academic staff of the Department of Plant Science for their guidance, suggestions, and encouragement throughout this research work. Thanks to Mr. Samuel Bot and his staff for performing initial fiber analysis at Fiber Technology Laboratory of Institute for Agricultural Research Samaru. I am thankful to all my field staff for their timely and technical support. I must say thanks to all my family and friends who have been constantly propelling me to complete this important task. It is, by the virtue of their prayers and moral support that I have been able to accomplish this thesis research work.

ABSTRACT

Forty nine cotton genotypes were evaluated at Samaru, Northern Guinea Savanna Zone of Nigeria during 2013 cropping season. The experimental design used was 7×7 lattice design with three replications. Plant data recorded on twelve characters were subjected to analysis of variance, Principal component analysis, Cluster analysis, Rank summation index and Correlation analysis. Analysis of variance revealed highly significant differences ($p<0.01$) for days to 50% flowering, fibre length and fibre fineness, while non-significant differences ($P>0.01$) were observed in the remaining agronomic traits. The phenotypic coefficients of variations were higher than the corresponding genotypic coefficients of variations for the entire traits studied. Seed cotton yield had the highest genotypic coefficient of variation. The first five axes of principal components analysis having eigen value >1 captured 63.60% of the total variability and jointly identified number of sympodia, number of bolls, ginning outturn, seed cotton yield, boll weight, seed index, days to 50% flowering, fiber length, and lint index as characters contributing most to the total variability. Mean performance revealed moderate variability in all the means of the agronomic traits studied. The variability was highest for seed cotton yield, and by plant height. Means of the fiber quality traits showed considerable variability among the genotypes especially for fiber length, and fiber fineness. Correlation analysis revealed that days to 50% flowering, plant height, sympodia per plant, boll weight, seed index, number of bolls and fiber fineness were highly significant and positively correlated with seed cotton yield, while highly significant negative correlations are observed between number of monopodia, ginning outturn, and fiber length with seed cotton yield. From rank summation index genotypes PIMA S4, RSA (79) 4A, ASA (78) 34^{A}, SAMCOT 12 and SAMCOT 13 are the best genotypes for all the

traits studied. Cluster analysis grouped 49 cotton genotypes into five major clusters with each cluster having distinct features. The present investigation provided considerable information useful in genetic improvement of cotton. Genotypes PIMA S4, RSA (79) 4A, ASA (78) 34^{A}, SAMCOT 12 and SAMCOT 13 obtained from the USA, Mexico and Nigeria were the best materials for all the traits studied. These genotypes are therefore considered the best potential parents use in for the hybridization programs for the improvement of cotton in Nigeria. Important morphological and fiber quality traits like greater seed cotton yield potential, plant height, fibre length, fibre fineness, number of sympodia per plant and number of bolls per plant etc. served as selection criterion to produce promising cotton genotypes. The low level of genetic diversity observed among the genotypes studied indicate the need for breeders to search for novel and diverse material in order to explore the unutilized genetic diversity for future cotton breeding program of Nigeria.

TABLE OF CONTENTS

LIST OF TABLE

LIST OF FIGURES

CHAPTER ONE

1.0 INTRODUCTION

Cotton is the leading non-food agricultural and industrial fiber crop grown in more than 80 countries (Dutt *et al*., 2004; Shakeel *et al*., 2011). Man has utilized cotton for his benefits since ancient times (Fryxell, 1992). The word "cotton" is derived from the Arabic word "al qatan" (Chaudhary and Guitchounts, 2003) used to describe fine textile. There are four domesticated species of the cotton, two tetraploid cultivars from Americas, *Gossypium hirsutum* (L.) and *G. barbadense*, and two diploid cultivars from Africa and Asia, namely *G. arboretum* and *G. herbaceum* (Wendel and Cronn, 2003). Of the four species, *G. hirsutum* (upland cotton) has dominated world cotton commerce, being responsible for 95% of the annual cotton, with approximate annual plantation of 35 million ha worldwide and grown in over 50 countries (Wilkins *et al*., 2000). Cotton is the world's most important natural textile fiber and an important source of feed, foodstuff, and oil, with approximate world consumption put at 27 million metric tons per year (Chen *et al*., 2007). The seed has approximately 25,000 cotton fibres', which are specialized single-celled trichomes that occur on the epidermal layer of the ovule (Wendel and Cronn, 2003; Chen *et al*., 2007). Cotton production provides income for approximately 180 million people (Benedict and Altman, 2001), with the fibre industry producing $30 billion worth of raw cotton and its economic impact estimated to be approximately $500 billion/year worldwide (Chen *et al*., 2007). China is the largest producer of cotton followed by the United States, which grows cotton worth $6 billion/year for fiber and approximately $1 billion/year for cottonseed oil and meal, on 12 million acres (Chen *et al*., 2007). Additionally, cotton is a major economic driver for some developing countries like India, Pakistan and Uzbekistan, among others

(Wendel and Cronn, 2003). Hence, it was rational that the genetic improvement of this high-valued multi-purpose crop would not only enhance the nutrition and livelihoods of millions of people in food challenged economies but also that its natural fiber would be competitive with petroleum derived synthetic fibres (Chen *et al*., 2007).The current cotton production in Nigeria as reported by the United State Agency for International Development (USDA) (2012) is 120, 000 tons in the year 2012. According to Raw Material Research Development Council (RMRDC) (2004), consumption of cotton lint by textile industry in Nigeria is about 100, 000 metric tons plus or minus 15%. Textile mills are there for forced to import 15,000 metric tons of cotton in order to cover the shortfall in local supply and for certain specific requirement for finer yarns such as 30-40 inches, which is not grown locally. It is therefore, clear that the local supply is not enough to meet the demand of the product. The report further stressed that against a total demand of about 80, 000 MT of lint per annum (240, 000 MT of seed cotton) textile mills, the total production of lint has been less, thus resulting in a gap between demand and supply. It is expected that this gap will widen further as step taken by the government to revive the textile industry may lead to increase in capacity utilization, thus resulting in higher demand for cotton. The cotton production areas in Nigeria are divided into three ecological zones, namely: The Northern cotton zone which comprises of Kano, Kaduna, Sokoto, Kebbi and Jigawa States. These states contribute 60-65% of the cotton produced. Also the eastern cotton zone comprises of Adamawa, Bauchi, Borno, Gombe, Yobe and Taraba States. These states contribute 30-35% of the cotton production in Nigeria. The third ecological zone also known as Southern cotton zone is made up Kwara, Niger, Kogi, Oyo, Osun, Ondo and Edo states; it contributes 5% of the total cotton production in Nigeria (Anon 1995). Study by

Adeneji (2011) revealed that cotton production in Northern cotton zone is on the increase compared to other zones.

Cotton is harvested as seed cotton, which is then ginned to separate the seed and lint. The long lint fibres are processed by spinning, to produce yarn that is knitted into fabrics. The short fibres (fuzz), covering the seeds is known as 'linters'. The first cut linters have a longer fibre length and are used in the production of belts, mattresses and mops. The second cut linters have a much shorter fibre length and are a major source of cellulose for both the chemical and food industry. These linters are used as a cellulose base in products such as high fibre dietary products as well as a viscosity enhancer (thickener) in ice cream, salad dressings and toothpaste. In the chemical industry, second cut linters are used in combination with other compounds to produce cellulose derivatives such as acetate, nitrocellulose and a wide range of other compounds (Gregory *et al*., 1990; Pillay and Myers, 1999). Delinted cotton seed can be processed to produce oil, meal and hulls. Cottonseed oil has been in common use since the middle of the nineteenth century and achieved GRAS (Generally Recognised As Safe) status under the United States Federal Food Drug and Cosmetics Act because of its common use prior to 1958 (ANZFA, 2002). Cottonseed oil is used in a variety of products including edible vegetable oils and margarine, soap and plastics. Cotton seed cake, meal flour or hulls derived from it is used in food products and for animal feed as carbohydrate roughage, but is limited by the presence of natural toxicants in the seeds (gossypol and cyclopropenoid fatty acids) (Pillay and Myers, 1999).

However, yield and quality of this all-important crop have declined over the last decade due largely to general erosion in genetic diversity of cotton varieties (Meredith, 2000). Worldwide cotton breeders and producers have expressed concern over the narrow genetic basis of cultivated cotton germplasm that has caused a decline in yield and quality. Globally cotton breeding programmes are working with a narrow germplasm pool thus resulting in genetic bottleneck through historic domestication events and selection (Iqbal *et al.,* 1997). Breeders used only a fraction of the available germplasm for cultivar breeding and most of the modern cultivars were developed by reselection rendering a drastic reduction in genetic variability (Bowman *et al*., 1996; Lewis, 2000; Guang and Xiong-Ming, 2006). It has been speculated that decline in yield and fiber properties is a result of a narrow genetic base in elite cotton germplasm (Bowman *et al*., 1996). Another major source of loss of genetic diversity is by changes and or increase in population size, resulting in land use acts promoting deforestation, wars, industrialization, urbanization and other factors. Therefore, the genetic potential of cotton yields has not reached its full potential and current cotton yields are static if not declining.

Genetic variability and heterozygosity within populations existed in both natural and cultivated populations (Jain and Workman 1966). Assessment of the genetic diversity of cotton cultivars is essential to breeding strategies, such as the characterization of individuals, accessions, and for the choice of parental genotypes in breeding programs. For any meaningful plant-breeding programme, accurate determination of genetic diversity is an essential step for an effective utilization of germplasm resources. An accurate estimation of genetic diversity can be invaluable in the selection of diverse parental combinations to generate progenies with maximum genetic variability and heterosis. A systematic

assessment of genetic resources will also help to identify the specific crosses to be made and hence decrease the number of crosses to be designed in a breeding program. 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 (Aremu *et al*., 2007; Nassir and Ariyo, 2005; White and Gonzalez, 1990). This will enable better utilization and management of germplasm resources and also help enlarge the germplasm base hence removing the bottle necks in breeding (Karp, 2002). It is expected that the identified variations would form a pattern of genetic relationship useable in grouping genotypes. The foregoing hence form the basis for employing multivariate statistical tools approaches to estimate genetic variability of some cotton genotypes, especially.

The primary objectives of this study were to;

i. Determine the variation pattern in collection of cotton germplasm.
ii. Identify the characters that differentiate the genotypes into different groups.
iii. Determine the relationship between seed cotton yield and yield components.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 The Cotton Plant

The word “cotton” is derived from the Arabic word “al qatan” (Chaudhry and Guitchounts, 2003) used to describe fine textile. Cotton is a member of order Malvales, family Malvaceae, tribe Gossypieae and genus *Gossypium*. The genus *Gossypium* comprises about 45 diploid and 5 tetraploid species indigenous to arid and semi-arid regions of Africa, Central and South America, Indo Pak subcontinent, Arabia, Australia, the Galapagos, and Hawaii (Fryxell, 1979; 1992) with distribution to various continents except Europe. Based on observations of chromosome pairing, these species are assigned to nine cytological groups or genomes: eight diploid genomes (A, B, C, D, E, F, G and K; 2n = 2x = 26) and one tetraploid genome (AD; 2n = 4x = 52) (Beasley, 1940; Edwards and Mirza, 1979; Fryxell, 1979; Endrizzi *et al*., 1985; Stewart, 1994). All diploid *Gossypium* have the same basic chromosome number (n = 13), their haploid genome sizes vary 1 to 3.5 Gb (Wendel *et al*., 2002; Ulloa *et al*., 2007), variation largely explicable in the best-studied cases (A vs. D) by different amount of dispersed repetitive DNA (Zhao *et al*., 1998). Among diploids only A genome species produce spinnable fiber, whereas species with only a D genome is worthless in terms of fiber production (Applequist *et al.*, 2001). However, there exist genes related for fiber development in both the A-sub genome and the D-sub genome in tetraploid cotton species. There are four cultivated species: two New World tetraploid species, G. *hirsutum* L. [n = 2x = 26, (AD1)] and G. *barbadense* L. [n = 2x = 26, (AD2)], and two Old World diploid species, *G. herbaceum* L. (n = x = 13, A1) and *G. arboreum* L. (n = x = 13, A2) (Brubaker *et al*., 1999).

The most extensively cultivated cotton species are allotetraploid G. *hirsutum* (Upland or American cotton), which accounts for about 90% of fiber production with high yield and wide adaptation, and G. *barbadense* (American Pima cotton or "Egyptian" cotton), which is characterized by its superior quality fiber (extra-long, strong and fine fiber). Two cultivated diploid species are only cultivated in very small acreage in South Asia (China, India, and Pakistan) (Zhang *et al*., 2005). Both these allotetraploids originated in the New World from interspecific hybridization between species closely related to G. *herbaceum* (A1) or G. *arboretum* (A2) and an American diploid, G. *raimondii* L. (D5) or G. *gossypioides* (Ulbrich) Standley (D6) (Beasley, 1940). Generally G. *herbaceum* (A genome) and G. Raimondii (D genome) are regarded as the closest extant relatives of progenitors of At and Dt sub genomes of allotetraploid cotton (Zhao *et al.,* 1998; Liu *et al.,* 2001; Wendel and Cronn, 2003).

2.2 Botany of Cotton

Cotton has a taproot that grows quickly and continues to grow rapidly usually to a depth of 3-4 m under dry conditions. It tapers rapidly and gives rise to numerous laterals, usually arising in four rows opposite the protoxylem elements of the root. Lateral root development is also a function of soil and moisture conditions. (Zhang *et al*., 2005).

2.2.1 The stem

Cotton plant consists of an erect stem and a number of lateral branches. An apical bud grows at the apex of the stem. As long as this bud remains active, the lateral buds remains dormant and the main stem carries branches and leaves but no flowers (Zhang *et al*., 2005).

2.2.2 The leaves

The leaves are spirally arranged on the main stem and upon its vegetative branches, but appear to be alternate on reproductive branches. The leaves are cordate, petiolate, 3-9 lobed and palmately veined as in G. *barbadense*, G. *hirsutum*, G. *ramondii*, dissected to varying degrees depending upon cultivar and species (Zhang *et al*., 2005).

2.2.3 The flowers

Cotton flower is large, solitary, axillary and terminal. The flower opening follows a spiral course in acropetal and centrifugal succession. The inner most bud of the lowest and oldest branch is the first to open while the outer most bud of the highest and youngest branch is the last to do so. The flower is subtended by an epicalyx of three to four, leafy bracts (Zhang *et al*., 2005).

2.2.4 The bolls

G. *hirsutum* has large bolls (5-8g), pale green, smooth skinned, and with few oil glands, as compared to G. *arboreum* which has much lighter (3g) dark green, covered with numerous glands. The big-bolled American types in India takes about 55 days to mature while the Asiatic cottons require only 45 days to mature which may further reduced to 35 days under heavier soil and atmospheric temperatures (Zhang *et al*., 2005).

2.2.5 The Seed

Seed is irregularly pear shaped. Its size varies depending on the variety and conditions of growth. It may be naked or bear short hair called fuzz. All cultivated cottons bear long

fibres named lint and is removed by gins while the fuzz remains attached (Zhang *et al*., 2005)

2.3 Cotton Fibre Quality Traits

Cotton fibre quality is defined by physical properties that relate to its spinability into yarn and contribute to textile performance and quality (Chee *et al*., 2005). The most important of these properties (Table 2.1) are those associated with the length, strength and fineness/ micronaire of the fiber (Poehlman and Sleeper, 1859). Other components of cotton fibre quality include length uniformity index, colour as reflectance (Rd) and yellowness (+b). The naturally wide variations in fiber quality, in combination with differences in end-use requirements, result in significant variability in the value of cotton lint to the processor. Therefore, a system of premiums and discounts has been established to denote a specified base quality. In general, cotton fiber value increases as bulk-averaged fibers increase in whiteness (Rd), length, strength, and micronaire; and discounts are made for both low and high micronaire. Ideal fiber-quality specifications favoured by processors traditionally have been summarized, "as white as snow, as long as wool, as strong as steel and as fine as silk." These specifications are extremely difficult but important to incorporate into a breeding program or to set as goals for cotton producers (Bradow and Davidonis, 2000).

2.3.1 Fiber length

One of the most important aspects of cotton fiber quality is fiber length, including average length of fibers, length uniformity of the bulk fibers and content of short fibers. Fiber or staple length is the normal length of a typical portion of the fibers of a cotton sample. Fiber length is directly related to yarn fineness, strength, and spinning efficiency (Moore, 1996).

Longer fibers can be processed at greater efficiencies, and produce finer and stronger yarns by allowing fibres to twist around each other more times, while shorter fibres require increased twisting during spinning, causing low-strength and poor-quality yarns (Perkins *et al*., 1984; Chee *et al*., 2005). Low fibre length uniformity and high short fibre content are associated with increased manufacturing waste and decreased spinning efficiency during yarn processing. As a result of the demand for improved fibre quality, the cotton marketing system imposes premiums and discounts for fibre length and other related qualities (Jost, 2002). Fibre elongation measures the degree of extensibility or elasticity of the fibres before a break occurs (May, 2002). Increases in elongation are associated with improved yarn strength (May, 2002). Therefore, fibres with good elongation generally cause less costly disruption in the spinning process, and the resulting yarn can endure more vigorous mechanical handling during fabric manufacturing. Span length (distance spanned by a specific percentage of fibres in the test beard) is usually reported as 2.5 and 50%. The uniformity ratio is the ratio between the two span lengths expressed as a percentage of the longer length. Traditionally, staple lengths are reported to the nearest 32^{nd} of an inch or to the nearest millimetre. Short fibre content is the percentage of fibre less than 12.7 mm (half an inch).

2.3.2 Fibre fineness

Cotton fibres of some varieties feel soft and silky, while fibres from other varieties feel coarse and harsh. The difference in the way they feel is determined by the fineness, which is associated with diameter of the fibre and with the thickness of the fibre wall. When the fibres fail to develop an average amount of inner wall they are said to be “immature”. A

mature fibre is a fibre in which two times the cell wall thickness equals or exceeds the diameter of fibre cell lumen, the space enclosed by the fibre cell walls (Ramey, 1982). Fibre fineness is an important component of fibre quality because of its direct impact on processing performance and the quality of end product. Finer mature fibres can be spun into yarns with more fibres per cross-section, resulting in not only stronger and better quality yarns but also less time in the spinning process (Ramey, 1982; Steadman, 1997; Bradow and Davidonis, 2000).

Micronaire (Mic) has been the most widely used method of determining fiber diameter. However, Micronaire reading is a measure of resistance to airflow of a constant weight of fibers and can be confounded by the degree of development of the fibre lumen (Steadman, 1997) that is related to fiber maturity. Therefore, while lower Mic cotton usually indicates the finer fibers that are sought by textile mills, could also result from immature fiber that can cause neps and dye defects because fiber maturity has been associated with dye uptake variability in finished yarn and fabric (Smith, 1991). Although other, more direct methods for measuring fiber diameter are now available, such as fineness measurement through HVI and the relatively new advanced fiber information system (AFIS), micronaire is still widely utilized in combination with other fiber properties in the textile industry to blend sets of cotton bales in order to promote consistency of performance in the yarn-manufacturing process (May, 2002). Another measure of fineness and spinability of cotton fiber is the count of the yarn. The count is the number of hanks of yarn which weighs one pound, while a hank consists of 840 yards of yarn (Poehlman and Borthakur, 1969).

Table 2.1 Standards for cotton fiber quality traits

Fiber Quality Traits	Scales				
Fiber length(mm)	Short	Medium	M. long	Long	E. Long
Value	<21	22-25	26-28	29-34	>34
Fiber fineness (µg/inch)	Very fine	Fine	Average	Coarse	V. Coarse
Value	<3	3-3.9	4-4.9	5-5.9	>5.9

mm: millimeter, M: medium, Mic: micronaire, µg/inch: micro-gram per inch, V: very, E: extra, M: medium,
Source: Bradow and Davidonis, 2000.

2.4 Principal Component Analysis

Several researchers including breeders have employed different data source and type from diverse crops in their methods to study genetic diversity. Such data source include morphological and agronomic, pedigree, proximate or biochemical and molecular data (Aremu, *et al*., 2007 in cowpea; Liu *et al*., 2000 in cotton; Christine *et al.*, 2009 in bent grass). The widely used techniques irrespective of the data source (morphological, biochemical and molecular marker data) are Cluster Analysis, Principal Component Analysis (PCA), Principal Coordinate Analysis (PCOA), Canonical Correlation and Multidimensional Scaling (MDS).

Principal component is used to derive a 2-or-3 dimensional scatter plot of individuals such that the geometrical distances among individual genotypes reflect the genetic distances among them. Wiley (1981), defined principal component as a reduced data form, which clarifies the relationship between breeding materials into interpretable fewer dimensions to form new variables. These new variables are visualized as different non correlating groups. Principal components analysis first determines Eigen values, which explain the amount of total variation displayed on the component axes. It is expected that the first 3 axes will

explain a large sum of the variations captured by the genotypes. Cluster and principal component analyses can be jointly used to explain the variations in breeding materials in genetic diversity studies. 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). The technique of principal component analysis was employed in order to analyze the variability in the genotypes, determine the plant characters which cause the variation to arise and to determine the relative contributions that the various characters make to the total variability in the genotypes. Kaiser (1960) stated that as a criterion, the number of common factors to be retained should be equal to the number of principal components having Eigen values greater than one. The rationale for this consideration is easy to understand. Each of the twelve traits observed contributes one unit of variance to the total variance in the data set. This implies that any component that displays an eigen value greater than 1.00 is accounting for a greater amount of variance than had been contributed by one variable. Thus, such a component is considered accounting for a meaningful amount of variance, and therefore deserves to be retained. On the other hand, a component with an eigen value less than 1.00 is accounting for less variance than had 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 than had been contributed by individual variables. For this reason, components with eigen value less than 1.00 are viewed as trivial and are therefore not retained. Eigen values can be thought of as quantitative assessment of

how much a component represents the data. The higher the eigen values of a component, the more representative it is of the data. Makinde, (2010) worked on 20 cotton 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 20 genotypes. Žáková and Benková (2006) used principal component analysis to identify the main traits that were responsible for the variation or genetic diversity among 106 cotton accessions. They reported that only first six of the 35 principal components had eigen values greater than 1.0 of 7.162, 5.047, 4.258, 3.985, 3.826, and 2.675 respectively, jointly accounted for 70.07% of the total variation among the genotypes. The variation was mainly due to characers as follows: plant height, number of bolls, number of sympodia, and seed cotton yield.

2.5 Cluster Analysis

Cluster analysis presents patterns of relationships between genotypes and hierarchical mutually exclusive grouping such that similar descriptions are mathematically gathered into same cluster (Aremu 2005). Cluster analysis has four methods namely unweighted paired group method using centroids (UPGMA), Single Linkages (SLCA), Complete Linkage (CLCA) and Median Linkage (MLCA). UPGMA and UPAMC provide more accurate grouping information on breeding materials used in accordance with pedigrees and

calculated results found most consistent with known heterotic groups than the other clusters (Aremu *et al*., 2007).

2.6 Correlations

Correlation gives information regarding association among various traits which is an important part for the initiation of any breeding program as it provides an opportunity for the selection of genotypes having desirable traits simultaneously (Ali *et al*., 2009). Knowledge of correlations between traits of economic importance is not only of interest from a theoretical consideration of quantitative inheritance of characters, but of practical value since selection is usually concerned with changing two or more traits simultaneously (Yeye, 2000). Most economically important characters are complex in inheritance and may involve several related characters (Robinson *et al.,* 1959). The degree of phenotypic and genotypic correlations between characters is therefore very important. According to Aghughu (2001), significant positive phenotypic correlation between characters indicates that they can be predicted from each other and that genotypic correlation between them will determine whether this relationship will be passed on to the offspring or not. Hence, this will determine whether or not genetic improvement of one will lead to a corresponding change in the other. The values for the correlation coefficient range from -1 to +1. There are two schools of thoughts in explaining the cause of correlations between yield and yield components. One school of thought is that the relationships between yield and yield components are developmental (Hamid and Grafius, 1978). They argue that the yield components developed in a sequence and yield came at the end of the sequence. The character set earlier had pronounced effects on the subsequent characters.

Alternatively the other school of thought believed that the yield components are related to yield through some genetic system rather than developmental system. Law *et al.* (1978) proposed that relationship between yield and yield components was due to genetical linkage. Miller and Rowling (1967) suggested that intermating population breakage of coupling linkage reduce the correlation, while breakage of repulsion linkage increased the correlation. All these results suggests that the linkages in both coupling and repulsion phases are operative in genetical association in yield and yield components. Seed cotton yield and quality is realized in terms of some component characters, among them are sympodial branches per plant, bolls per plant, boll weight, seed index, lint index and GOT% along with quality components like staple length, fibre fineness and fibre strength. Relationship of this yield components with seed cotton yield have been studied extensively through phenotypic correlations. It has been observed that the yield components are related to seed cotton yield through a complex chain of inter relationships. Manzoor and Faqir (2000) worked out genetic correlation for oil and protein content and various quantitative characters in 56 F_2 families of cotton and their 8 parents and reported that number of bolls as well lint % showed significant positive relationship with seed cotton yield, boll weight, lint index, staple length and fibre fineness. Furthermore, strong association was observed between boll weight with lint %, fibre fineness and seed cotton yield and staple length and fibre fineness with seed cotton yield. Their results concluded that number of bolls and boll weight were the characters with greatest contribution towards final seed cotton yield.

Association of yield with various economic traits in *Gossypium hirsutum* L were tested by Asad *et al*., (2002) in Faisalabad, Pakistan, during 1997 using cotton commercial cultivars,

namely NIAB-78, Karishma, CIM-435, CIM-443, CIM-1100, BH-36 and BH-95. Lint index had maximum genetic association with seed cotton yield/plant. An experiment on correlation for earliness and yield traits in cotton *(G. hirsutum* L.) was carried out by Iqbal *et al.,* 2006. The objective of their study was to get information about a character that is useful for selection in segregating generations for improving seed cotton yield through correlation for earliness and yield components. Their results showed that node of first fruiting branch, monopodial branches/plant, boll number and boll weight were positively and significantly correlated with yield. Their results suggested that for evolving a superior cotton genotype possessing all the three basic characteristics i.e., earliness, high yield and improved fiber quality of international 15 standard, breeder had to use reciprocal recurrent selection method or modified back cross or three- way cross within genetic material under study. An investigation on correlation in hybrid cotton was tested by Soomro *et al.,* (2008), and reported that seed cotton yield/plant exhibited positive and highly significant correlation with plant height, sympodial branches per plant, bolls/plant and boll weight at the phenotypic level. Results further demonstrated that 80.3%, 56.8 and 27.1% of the variation in seed cotton yield was mainly due to the variation in bolls/plant, plant height and boll weight respectively and concluded that selection based on bolls/plant and boll weight could be the most effective tool in breeding high yielding cotton genotypes.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental Materials

The experimental materials for this study comprised of forty nine cotton genotypes selected from the germplasm pool of the Institute for Agricultural Research Samaru. The collections include 19 genotypes each from Nigeria and the USA, 8 from Sudan and 3 from Egypt. List of the genotypes and their origin is presented in Table 3.1.

3.2 Field Trial

Evaluation was carried out in 2013 cropping season at the Institute for Agricultural Research Farm Samaru. The experiment was laid out in a 7 × 7 simple lattice design with three replications. Each replication consisted of seven sub-blocks with seven genotypes in each sub-block. Each genotype was grown in one row of 5m length. A spacing of 75cm between rows and 40cm between plants was maintained. All cultural practices according to IAR recommendations for cotton were adhered to.

Table 3. 1 Genetic materials utilized in the study

Name	Origin	Name	Origin
1. SAMCOT 6	Nigeria	27. Bar 14/25 A	Sudan
2. ASA (78) 17^{f}	Nigeria	28. Pima S-1	Egypt
3. ASA (78) 34^{A}	Nigeria	29. Pima S4	Egypt
4. BJA 592 (79) 2^{B}	Nigeria	30. Giza 69	Egypt
5. RSA (79) 4^{A}	Nigeria	31. TX-CD P37-HH-1-83	USA
6. ACSA (78) 34^{B}	Nigeria	32.TX-L3B2BCH-1-85	USA
7. ACSA (79) 13^{A}	Nigeria	33. TAMCOT CAMD-E	USA
8. BJA 592 (79) 4	Nigeria	34. TAMCOT SP 37H	USA
9. ACSA (79) 19	Nigeria	35. TAMCOT CABCS 1-83	USA
10. ACSA (79) 5	Nigeria	36. TAMCOT SP 37	USA
11. ASA (74) 80	Nigeria	37. TAMCOT SP 21	USA
12. ASA (75) 13	Nigeria	38. G.C.A- NH-1-83	USA
13. SAMCOT 7	Nigeria	39. Y 1422 (79) 19^{B}	USA
14. SAMCOT 8	Nigeria	40. Y 1422 (79) 4^{G}	USA
15. SAMCOT 9	Nigeria	41. TX CABS 1-83	USA
16. SAMCOT 10	Nigeria	42. TAMCOT SP 21^{s}	USA
17. SAMCOT 11	Nigeria	43. TAMCOT $CAMDE^{-E}$	USA
18. SAMCOT 12	Nigeria	44. Y 1422 (79)5	USA
19. SAMCOT 13	Nigeria	45. Y 1422 (79) 30	USA
20. Bar XL7 (79) 8	Sudan	46.TAMCOT SP 374	USA
21. Bar XL7 (79) 35	Sudan	47. TAMCOT SP 37	USA
22. Bar 14/25 (81) 18	Sudan	48. TX CABS 1-83	USA
23. Bar 14/25 (81) 23	Sudan	49. Acala 9151 7C	USA
24. Bar 14/25 (81) 24	Sudan		
25. Bar 14/25 (81) 39	Sudan		
26. Bar 14/25 (81) 43	Sudan		

3.3 Data Collection

Agronomic and fibre quality traits were recorded on 5 randomly selected plants in each entry within each replication for twelve characters as listed below.

1. Plant height (cm) – measured as distance between the base of the plant and apex of the plant at maturity using a metre rule.
2. Number of days to 50% flowering – recorded as numbers of days taken from the date of sowing to when about 50% of the plants flower for each genotype.
3. Number of monopodia per plant - Recorded as the number of branches on main stem which were lateral and axillary in position with vertical growth in acropetal succession at maturity stage, avoiding small sprouts.
4. Number of sympodia per plant - recorded as the number of branches which are extra-axillary in position and normally horizontal with zig-zag pattern of fruiting points at maturity. The numbers of such sympodia on main stem was counted and recorded at maturity.
5. Number of bolls per plant - recorded as the number of bolls that contributed to seed cotton yield at the time of harvest.
6. Boll weight (g) - recorded as fully matured and well dried seed cotton obtained from a random sample of 20 bolls from each plot in grams using electrical sensitive balance.(Type; Citizen electric balance, Model: MP 600)

7. Seed cotton yield (kg/ha) - recorded as the mean seed cotton yield harvested till final picking from the net plot area and expressed in kg/ha. (Type Citizen electric balance, Model: MP 600).
8. Seed index (g) - recorded as the absolute weight of 100 seeds in grams using electrical sensitive balance. (Type: Citizen electric balance, Model: MP 600).
9. Lint index (g) - recorded as the absolute weight of lint obtained from 100 seeds in grams. (Type Citizen electric balance, Model: MP 600).
10. Ginning outturn - recorded as the weight of the lint expressed as percentage of weight of seed cotton. (Type Citizen electric balance, Model: MP 600).
11. Per cent span length (mm) - recorded as the distance spanned by a specified percentage of fibres in the specimen being tested and expressed in millimeters. (Type: Spin lab, Model: Fibre comb 994507 and Fibro sampler 192).
12. Micronaire (µg/inch) - recorded as the average weight of lint per unit length of fibre expressed in micrograms per inch. (Type: Spin lab, Model: Fibre comb 994507 and Fibro sampler 192).

3.4 Statistical Analysis

The data collected was subjected to analysis of variance (ANOVA) (SAS Institute Inc.2004). Mean separation was done by Least Significant Difference (LSD). Coefficient of variation was computed and then used to compare variability of each character studied. The statistical model that was used for the analysis 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 3.1 A Form of analysis of variance with expected mean square for each character

Source of variation	Df	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

r = number of replications

g = number of genotypes

σ_g^2 = genotypic variance

σ_e^2 = error variance

$\sigma_g^2 = M_g - M_e/r$

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

3.5 Estimates of Components of Variances

The contribution of each component of variance to the total phenotypic variation was calculated by equating the appropriate mean squares to the expectation of the mean square from the ANOVA table using the method described by Singh and Chaudhary (1985) as follows:

$$\sigma_e^2 = M_e$$

$$\sigma_g^2 = \frac{M_2 - M_1}{r}$$

Where

σ_e^2 = Error variance

M_1 = Error mean square

σ_g^2 = Genotypic variance

M_2 = Genotypic mean square

r = Number of replications

3.6 Coefficient of Variation

The genotypic and phenotypic coefficienst of variation were estimated using the formula described by Singh and Chaudhary (1985).

GCV= $\frac{\sqrt{\sigma_g^2}}{\bar{x}}$ X 100, PCV= $\frac{\sqrt{\sigma_p^2}}{\bar{x}}$

where;

GCV= genotypic coefficient of variation

PCV= phenotypic coefficient of variation

σ_g^2 =estimate of genetic variance

σ_p^2 =estimate of phenotypic variance

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

3.7 Correlation Analysis

Genotypic and phenotypic correlations analyses were computed to determine the degree of association among the characters according to the formula of Singh and Chaudhary (1985). (SAS Inc.2004) 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 squares of the character X

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

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

3.8 Genetic Divergence

The genetic divergence of the 49 cotton genotypes was estimated based on Ward's method using a squared euclidian distance (Kumar *et al*., 2000). 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:

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

Where,

D^2_{ij} = the squared distance between any two genotypes i and j,

X_i and X_j = 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 Components Analysis (PCA)

Principal component analysis was performed using statistical software SAS version 9.0. The data obtained from the 49 genotypes were analyzed using principal component analysis multivariate technique. With 12 traits and 49 *Gossypium hirsutum* genotypes, a data matrix of 12 × 49 was prepared for the analysis. In principal component analysis, one of the most commonly used criteria for solving the number-of-components problem is the eigenvalue-one criterion, also known as the Kaiser criterion (Kaiser, 1960). With this approach, you retain and interpret any component with an eigen value greater than 1.00. Thus, principal components with eigenvalue > 1 were used for further analyses. Important traits in each principal component were determined from the associated Eigen vectors.

3.10 Rank Summation Index

For the purpose of selection, an index, called Rank Summation Index (RSI) according to Malumba and Mock (1978) was generated from seven most important traits namely plant height, number of sympodia, number of bolls, boll weight, seed cotton yield, fiber length and fiber fineness. Malumba and Mock (1978) described the rank summation index and called it "parameter- free" index. The index was formed by ranking each trait in descending order. Finally, the values assigned to each trait were added, obtaining the sum of the ranks, which indicates the classification of the genotypes (Cruz and Carneiro, 2003). Rank Summation Index as computed by Malumba and Mock (1978) was estimated as follows;

$$RSI = \sum_{i=1}^{n} R_i \, s$$

Where,

RSI = Aggregate performance of a genotypes using the ranking of each of the desired traits

R_i = Rank of the mean of each of the desired traits

.

CHAPTER FOUR

4.0 RESULTS

4.1 Mean Performance of the Genotypes

The performance information for the morphological and fiber quality traits studied is presented in Table 4.1. A wide range of variation was recorded for seed cotton yield per plant 1771.71, while moderate range of variation occurred in the remaining agronomic and fiber quality traits. Plant height ranged from 97.36cm to 116.50cm with a mean of 107.57cm. TAMCOT SP 37 was the tallest among the genotypes with the height of 116.50cm. Days to 50% flowering (dff) ranged from 60.28 to 84.78 with a mean of 75.40. TX-CABS 1 had the lowest dff, while TX-CDP37-HH-1-83-83 had the longest. Number of monopodia ranged from 1.26 to 3.10 with a mean of 1.97. Number of sympodia ranged from 11.78 to 18.47 with a mean of 15.74. TAMCOT SP 21 had the highest number of sympodia while PIMA S4 had the lowest.

Number of bolls ranged from 10.76 to 18.68 with a mean of 13.98. SAMCOT 8 had the lowest number of bolls per plant while TAMCOT SP *21* had the highest number of bolls. Boll weight ranged from 3.43 to 5.16 with a mean of 4.13. ACSA (79)5 had the lowest boll weight while SAMCOT 9 had the highest boll weight. Seed index on the other hand ranged from 7.73 to 11.27 with a mean of 9.75. Lint index ranged from 5.14 to 7.27 with a mean of 6.15. Ginning outturn ranged from 22.60 to 27.77 with a mean of 34.40. Seed cotton yield ranged from 221.31 for GIZA *69* to 2993.02 for BAR 14/25(81)23 with a mean of 989.52.

Table 4.1 Mean performance of 49 cotton genotypes for twelve morphological and fibre quality traits

Genotype	DFF	PH(cm)	NM	NS	NB	BW(g)	SI(g)	LI(g)	GO(%)	SCY(kg)	FL(mm)	FF(ug/inch)
SAMCOT6	81.22	102.96	2.03	17.27	12.40	3.94	9.73	6.23	22.60	1063.73	27.46	3.82
ASA(75)13	81.22	109.86	1.78	15.93	12.72	3.95	9.80	6.45	34.00	1112.53	27.66	3.97
TX-CDP37-HH-1-83	60.28	109.14	1.87	16.03	12.09	3.68	9.37	6.60	34.27	1231.97	27.56	4.53
TAMCOTSP374	92.33	115.32	1.40	16.33	14.17	4.19	9.50	5.39	36.77	1029.08	25.53	4.12
TX-L3B2BCH-1-85	82.17	103.27	1.80	16.17	16.04	3.59	8.87	5.90	32.03	1158.76	27.86	4.09
TAMCOTSP37	72.17	105.83	2.00	15.77	15.16	4.26	8.83	6.23	33.75	1006.68	27.86	4.86
TAMCOTCAMD-E	82.33	104.15	2.13	15.30	13.71	3.75	9.43	5.14	32.45	967.64	25.94	4.42
TXCABS1-83	84.78	106.97	1.93	15.29	11.74	4.44	10.17	5.65	33.55	637.81	28.27	4.43
TAMCOTSP37H	65.50	111.78	1.47	15.32	12.96	3.66	9.97	6.41	33.05	1107.70	28.88	4.12
BarXL7(79)8	79.67	109.36	1.93	16.68	12.93	4.42	9.70	5.97	32.41	1087.59	26.34	4.42
TAMCOTCABCS1-83	81.39	105.94	1.67	15.74	15.70	3.48	9.40	6.08	32.61	1086.90	28.06	4.49
Acala 9151 7C	81.67	106.19	1.73	17.48	12.33	3.70	9.40	5.90	32.90	1269.13	26.75	3.85
TAMCOT SP 37	82.00	116.50	1.68	14.91	12.19	3.74	9.83	5.48	35.82	1250.87	26.65	4.87
Bar XL7(79)35	68.50	105.58	1.42	13.29	14.88	3.55	9.70	5.32	36.61	1247.16	29.08	4.87
TAMCOTSP21	81.83	103.90	1.26	11.78	18.68	3.58	9.87	5.69	37.77	1730.84	28.88	4.64
Bar14/25(81)18	70.94	112.92	1.73	14.96	13.71	3.73	8.90	5.56	35.95	1168.27	29.99	4.65
G.C.A- NH-1-83	74.40	105.75	1.57	15.69	14.92	3.60	8.80	5.65	33.07	1336.67	28.58	4.07
Bar14/25(81)23	81.72	115.33	1.31	16.46	12.18	3.57	9.13	6.39	34.13	1027.47	28.69	4.06
ASA(78)17[f]	61.06	107.75	1.67	14.84	16.24	4.96	9.57	6.21	35.78	1237.10	27.68	4.63
Bar14/25(81)24	91.56	112.83	2.13	15.20	13.38	4.07	9.10	5.95	34.37	1993.02	27.38	4.83
ASA(78)34[A]	81.89	112.83	1.56	18.12	13.00	4.14	9.60	6.33	35.76	1013.08	28.38	5.15
Bar14/25(81)39	92.14	110.92	2.25	13.83	14.91	3.79	10.00	6.83	35.54	677.35	28.79	4.73
BJA592(79)2[B]	79.34	109.92	1.52	15.46	14.37	4.51	11.07	6.70	35.63	763.92	29.39	5.03
Bar14/25(81)43	80.18	111.02	1.59	14.49	10.99	4.00	11.27	6.50	35.20	987.19	29.80	4.22
Y1422(79)19[B]	79.05	114.50	1.93	16.80	12.90	4.51	8.73	7.27	33.23	1331.68	27.38	4.62
Pima S-1	70.58	108.48	2.23	17.31	12.23	4.17	9.30	6.50	33.62	833.66	27.88	4.68

Table 4.1 continued

	DFF	PH(cm)	NM	NS	NB	BW(g)	SI(g)	LI(g)	GO(%)	SCY(g)	FL(mm)	FF(ug/inch)
Y1422(79)4a	79.94	111.96	3.10	17.03	12.83	4.28	9.47	5.93	34.62	940.44	27.58	4.42
PimaS4	79.51	114.32	2.05	18.47	15.00	4.42	10.10	6.30	35.20	1005.44	29.70	3.66
RSA(79)4[A]	82.44	107.28	2.77	16.36	16.17	4.61	10.23	5.80	34.64	969.24	28.79	3.45
Bar14/25A	81.17	107.75	2.19	15.76	15.00	4.16	9.57	6.03	33.56	880.49	29.90	4.62
ACSA(78)34[B]	80.80	97.35	2.52	12.92	14.93	4.10	10.33	6.20	34.85	1170.77	28.38	4.25
Giza69	81.48	105.93	2.28	15.93	11.17	3.86	9.60	6.33	34.29	221.31	28.38	4.22
ACSA(79)13[A]	80.50	106.50	1.69	16.69	12.97	4.73	9.77	6.33	34.48	823.93	27.28	4.96
BarXL7(79)6	81.33	105.94	1.92	15.71	13.20	4.77	7.73	5.43	36.82	875.68	29.19	3.89
TXCABS1-83	81.51	105.03	2.07	16.31	13.57	3.52	9.03	6.77	35.66	525.00	27.58	4.26
SAMCOT8	81.44	101.14	2.34	17.30	10.76	4.68	9.37	6.43	33.14	711.65	27.28	4.04
TAMCOTSP21[s]	79.49	99.92	2.30	14.92	12.94	4.49	9.10	7.23	33.60	619.36	26.37	3.92
SAMCOT9	82.13	108.38	1.81	15.43	16.18	5.16	9.30	6.03	35.46	590.03	26.17	4.94
TAMCOTCAMDE[-E]	76.61	103.21	2.88	12.69	15.04	4.92	9.73	6.63	34.95	893.76	28.58	4.66
SAMCOT10	78.24	100.18	2.97	16.19	12.69	3.89	9.60	5.97	35.12	824.91	27.48	4.27
BJA592(79)4	79.32	106.24	1.88	14.59	13.55	5.06	9.17	6.17	32.96	370.45	27.68	4.56
SAMCOT 11	79.78	102.97	2.45	15.56	14.40	3.65	9.03	5.37	35.15	739.12	29.70	4.32
ACSA(79)19	81.00	100.35	1.82	17.11	17.02	4.73	9.60	6.37	35.31	496.12	27.58	4.31
SAMCOT12	70.67	106.80	1.57	16.42	13.83	3.53	9.30	6.67	36.27	1112.88	28.79	3.88
Y1422(79)5	80.18	109.10	2.50	17.14	12.72	3.99	9.97	5.97	35.20	557.87	24.86	4.13
SAMCOT13	80.71	112.42	1.57	14.71	17.71	4.32	9.93	7.27	37.27	502.02	25.67	4.21
ACSA(79)5	73.33	100.78	1.98	14.97	16.82	3.43	9.17	6.83	36.50	1028.00	26.27	4.65
ASA(74)80	60.62	102.66	2.22	15.47	13.98	4.42	10.30	5.67	35.89	992.50	26.88	4.55
Y 1422 (79) 30	82.40	115.73	2.13	17.98	15.83	4.44	10.47	5.47	31.82	1278.05	26.27	4.94
Mean	75.40	107.57	1.97	15.76	13.98	4.13	9.57	6.15	34.40	989.53	27.81	4.39
Range	31.9	19.4	1.84	6.69	7.92	1.73	3.54	2.13	5.17	1771.71	5.13	1.70
CV (%)	55.46	9.24	42.69	17.15	24.63	21.64	10.09	16.85	11.97	61.11	0.27	0.11
LSD	18.70	16.11	1.36	4.38	5.58	1.45	1.57	1.68	6.68	980.06	0.12	0.01

DFF=Days to 50% flowering, NM=Number of monopodia, NS=Number of sympodia, NB=Number of bolls, BW=Boll weight

SI=Seed Index, LI=Lint Index, SCY=Seed Cotton Yield, PH=Plant height, FL=Fiber length, FF=Fiber fineness, GO=Ginning outturn

Fibre length of all the genotypes fell between medium to long 24.86mm to 29.99 mm with a mean of 27.81 mm. BAR 14/25(81)18 had the longest fibre length while Y 1422(79)5 had shortest fibre length. Similarly, Micronaire values were variable with average micronaire reading of 4.39µg/inch. Micronaire for most of the cotton genotypes ranges from fine 3.45µg/inch to average 4.96 µg/inch except for BJA 592(79)2B and ASA(78)17f which were coarse. RSA (79)4A had the finest Micronaire, while ASA (78)17f had the coarsest Micronaire.

4.2 Analysis of Variance

The results from the analysis of variance are presented in Table 4.2. There were highly significant differences ($P < 0.01$) among the 49 cotton genotypes for days to 50% flowering, fibre length and fineness when analysis of variance was conducted for these traits. Although variation existed among the genotypes for the remaining morphological traits, these differences were not significant Table 4.2. Estimates of components of variances were obtained for all the traits from the analysis of variance Table 4.3, which had higher error variances (σ^2_e) than their corresponding genotypic variances (σ^2_g) except for fiber length and fiber fineness. Estimates of genetic variances ranged from 0.04 for boll weight to 4616.19 for seed cotton yield. The genetic variance was large for seed cotton yield, days to 50% flowering and plant height (Table 4.3). The Phenotypic coefficient of variation was larger than the corresponding genotypic coefficient of variation for all the traits under consideration, except for fiber fineness.

Table 4.2 Mean squares from the analysis of variance for 49 cotton genotypes

Source	df	Mean squares											
		DFF	PH	NM	NS	NB	BW	SI	LI	GO	SCY	FL	FF
Replication	2	42892.75	2.98	2.13	4.25	147.95	0.02	5.17	16.37	30.97	23468.64	2.12	0.11
Genotypes	48	43056.34**	66.57	0.54	5.65	9.47	0.67	1.07	0.89	15.06	50416.41	4.56**	0.45**
Error	96	4307.20	98.74	0.71	7.30	11.85	0.79	0.93	1.08	16.97	3656.85	0.05	0.05

DFF=Days to 50% flowering, NM=Number of monopodia, NS=Number of sympodia, NB=Number of bolls, BW=Boll Weight

SI=Seed Index, LI=Lint Index, SCY=Seed Cotton Yield, PH=Plant Height, FL=Fiber Length, FF=Fiber Fineness, GO=Ginning outturn, 0.05= significant =*and 0.01= highly significant=**

Table 4.3 Estimates of means, error, genotypic, phenotypic variances, genotypic and phenotypic coefficient of variation for morphological and fibre quality traits in cotton genotypes

Traits	σ_e^2	σ_g^2	σ_{ph}^2	GCV	PCV
DFF	4307.20	68.29	4308.49	16.14	48.75
NM	0.71	0.07	0.78	13.43	44.8
NS	7.30	0.55	7.85	4.71	17.78
NB	11.85	0.79	12.64	6.36	25.43
BW	0.79	0.04	0.83	4.84	22.06
SI	0.93	0.05	0.98	2.34	10.34
LI	1.08	0.06	1.86	3.98	22.16
GO	16.97	0.64	17.61	2.33	12.29
SCY	3656.85	4616.19	4118.04	21.7	64.85
PH	98.74	10.72	109.46	3.04	9.73
FL	0.01	1.52	1.53	4.43	4.45
FF	0.00	0.15	0.15	8.82	8.82

DFF=Days to 50% flowering, NM=Number of monopodia, NS=Number of sympodia, NB=Number of bolls, BW=Boll Weight, SI=Sexed Index, LI=Lint Index, GO=Ginning outturn, SCY=Seed Cotton Yield, PH=Plant Height, FL=Fiber Length, FF=Fiber Fineness. σ_e^2 = error variance, σ_g^2 =genotypic variance, σ_{ph}^2 =phenotypic variance, GCV= genotypic coefficient of variation PCV= phenotypic coefficient of variation.

The estimates of phenotypic coefficients of variation (PCV) ranged from 4.45% for fiber length to 64.85 % for seed cotton yield and the corresponding values for genotypic coefficients of variation (GCV) ranged from 2.33 % for ginning outturn and 21.7 % for seed cotton yield, respectively. The highest phenotypic coefficient of variation was obtained for seed cotton yield, followed by days to 50% flowering, number of monopodia, number of bolls, boll weight, lint index, number of sympodia, seed index, plant height, fiber fineness, and the least was that for fiber length.

4. 3 Rank Summation Index

Information on rank summation indices are presented in Table 4.4. PIMA S4 rank first, followed by RSA (79)4^{A}, ASA (78)34^{A}, TAMCOT SP 37^{4}, SAMCOT 12, SAMCOT 13 with rank summation indices of 186, 215, 224, 230, and 234 respectively, while SAMCOT 10 ranked last with rank summation index of 395.

4.4 Estimates of Correlation Coefficients

Table 4.5 shows phenotypic and genotypic correlation coefficients computed for the twelve traits of 49 cotton genotypes. Seed cotton yield showed highly significant and positive phenotypic correlation with plant height, number of sympodia, number of bolls, boll weight, fiber fineness and seed index (r=0.73**, r=0.83**, r=0.71**, r=0.48**, r=0.58** and r=0.02** respectively), but was highly significantly and negatively correlated with number of monopodia, ginning outturn and fiber length (r=-0.77**, r=-0.51** and r=-0.24** respectively).

Table 4.4 Rank summation index for 12 traits in 49 cotton genotypes

GENOTYPE	DFF	PH	NM	NS	NB	BW	SI	LI	GO	SCY	FLT	FF	RNK
Pima S4	41	6	31	1	13	15	8	21	19	25	4	2	186
RSA (79) 4[A]	4	24	46	16	7	9	6	37	25	28	12	1	215
ASA (78) 34[A]	13	8	7	2	30	24	21	18	12	23	17	49	224
TAMCOT SP 374	6	4	3	17	21	21	27	46	4	20	48	13	230
SAMCOT 12	32	26	9	15	23	46	36	8	7	14	13	5	234
SAMCOT 13	31	10	10	42	2	18	12	2	2	46	47	16	238
ASA (78) 17[f]	27	22	13	41	5	3	25	24	11	9	25	34	239
BJA 592 (79) 2[B]	43	15	6	31	20	11	2	7	14	37	6	48	240
TAMCOT SP 21	14	38	1	49	1	43	13	38	1	2	10	35	245
Bar 14/25 (81) 23	15	3	2	14	44	44	39	16	31	22	14	10	254
Bar 14/25 (81) 43	36	13	11	44	48	27	1	11	18	27	3	17	256
Y 1422 (79) 30	5	2	33	3	9	14	3	44	48	5	44	46	256
ASA (75) 13	25	16	18	23	37	29	15	13	32	15	27	8	258
TAMCOT SP 37H	34	12	5	33	32	39	10	15	41	16	9	14	260
ACSA (79) 19	28	46	21	9	3	7	24	17	17	47	30	22	271
Bar 14/25 (81) 39	10	14	39	45	17	33	9	4	15	40	11	40	277
Bar XL7(79) 6	23	30	24	27	29	5	49	45	3	33	7	6	281
Bar XL7 (79) 35	3	35	4	46	18	45	20	48	5	8	8	44	284
Y 1422 (79) 19[B]	45	5	27	11	35	10	48	1	38	4	35	32	291
Bar 14/25 (81) 18	29	7	17	38	25	36	44	42	8	12	1	36	295
Acala 9151 7C	16	29	16	4	41	37	31	36	43	6	39	4	302
TAMCOT SP 37	12	1	14	40	43	35	14	43	10	7	40	43	302
Bar 14/25 A	26	23	36	25	14	23	26	28	36	32	2	33	304
G.C.A- NH-1-83	20	34	8	28	16	41	47	41	40	3	15	11	304
SAMCOT 9	11	21	20	32	6	1	35	29	16	43	45	45	304
ACSA (79) 13[A]	35	27	15	12	31	6	16	20	27	36	36	47	308
TX-L3B2BCH-1-85	8	39	19	20	8	42	45	35	47	13	23	12	311
ACSA (78) 34[B]	30	49	45	47	15	25	4	25	24	11	18	19	312
ACSA (79) 5	1	45	28	37	4	49	38	5	6	21	43	37	314
SAMCOT 6	24	42	30	7	40	30	17	23	49	19	33	3	317
TAMCOT CABCS 1-83	22	31	12	26	10	48	30	27	44	18	21	28	317
TAMCOT SP 37	9	33	29	24	11	20	46	22	33	24	24	42	317
TX CABS 1-83	2	25	25	35	46	13	7	40	37	41	20	27	318
Bar XL7 (79) 8	40	17	26	13	34	17	19	30	46	17	42	25	326

Table 4.4 Continued

GENOTYPE	DFF	PH	NM	NS	NB	BW	SI	LI	GO	SCY	FLT	FF	RNK
ASA (74) 80	33	43	37	30	22	16	5	39	9	26	38	30	328
Bar 14/25 (81) 24	17	9	35	36	28	26	40	33	28	1	34	41	328
TX CABS 1-83	18	36	32	18	26	47	42	6	13	45	29	20	332
TAMCOT CAMDE^{-E}	48	40	47	48	12	4	18	9	23	31	16	38	334
TX-CD P37-HH-1-83	49	18	22	21	45	38	32	10	30	10	31	29	335
Y1422(79)4A	38	11	49	10	36	19	28	34	26	30	28	26	335
SAMCOT 8	21	44	42	6	49	8	33	14	39	39	37	9	341
Y 1422 (79)5	37	19	44	8	38	28	11	32	20	44	49	15	345
Pima S-1	46	20	38	5	42	22	34	12	34	34	22	39	348
Giza 69	19	32	40	22	47	32	22	19	29	49	19	18	348
BJA 592 (79) 4	44	28	23	43	27	2	37	26	42	48	26	31	377
TAMCOT SP 21^{s}	42	48	41	39	33	12	41	3	35	42	41	7	384
SAMCOT 11	39	41	43	29	19	40	43	47	21	38	5	23	388
TAMCOT CAMD-E	7	37	34	34	24	34	29	49	45	29	46	24	392
SAMCOT 10	47	47	48	19	39	31	23	31	22	35	32	21	395

DFF=Days to 50% flowering, NM=Number of monopodia, NS=Number of sympodia, NB=Number of bolls, BW=Boll Weight, SI=Seed Index, LI=Lint Index, SCY=Seed Cotton Yield, PH=Plant Height, =Fiber Length, FF=Fiber Fineness, RNK= rank

Table 4.5 Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients between seed cotton yield and yield components in cotton genotypes

Variables	DFF	NM	NS	NB	BW	SI	LI	GO	PH	FL	FF	SCY
DFF	**1**	0.00	-0.08	0.24*	-0.21*	-0.09	0.18	0.14	-0.21**	-0.18	0.09	0.01
NM	0.22	**1**	0.09	-0.14	0.24*	0.01	0.00	-0.13	-0.34*	-0.09	-0.15	-0.77**
NS	-0.06	0.09	**1**	-0.35**	0.09	-0.12	0.03	-0.36**	0.48**	0.52**	0.72**	0.83**
NB	0.03	-0.14	-0.54**	**1**	0.06	0.02	-0.04	0.29**	-0.02	-0.01	-0.15	0.71**
BW	-0.11	0.23	0.66**	0.06	**1**	0.09	0.12	0.02	-0.01	-0.15	-0.13	0.48**
SI	-0.06	0.01	-0.34**	0.01	0.44**	**1**	0.07	0.02	0.14	0.05	0.09	0.02**
LI	0.16	0.10	0.42**	-0.04	0.38**	0.56**	**1**	0.01	-0.02	-0.04	-0.04	-0.12
GO	0.15	-0.22	-0.12	0.29	0.02	0.02	0.56**	**1**	0.13	-0.51**	0.82**	-0.51**
PH	0.58**	-0.35**	0.44**	0.66**	0.78**	-0.45**	-0.05	-0.03	**1**	0.00	0.19	0.73**
FL	0.23	-0.05	0.15	-0.16	-0.06	0.13	-0.02	0.22	0.01	**1**	-0.74**	-0.24**
FF	-0.18	0.55**	-0.22	-0.44**	-0.15	0.45**	-0.03	0.15	0.08	-0.53**	**1**	0.58**
SCY	0.35**	-0.79**	0.35**	0.66**	0.78**	-0.45**	-0.55**	0.26	0.44**	0.65**	-0.65**	**1**

DFF=Days to 50% flowering, NM=Number of monopodia, NS=Number of sympodia, NB=Number of bolls, BW=Boll Weight, SI=Seed Index, LI=Lint Index, GO=Ginning outturn, SCY=Seed Cotton Yield, PH=Plant Height, FL=Fiber Length, FF=Fiber Fineness, 0.05= significant =*and 0.01= highly significant=**

Highly Positive and significant phenotypic correlations were also obtained between Ginning outturn with number of bolls (r=0.29**), number of sympodia with plant height and fiber length (r = 0.48** r=0.52** respectively) and number of sympodia with fiber fineness (r=0.72**). On the other hand, highly negative and significant phenotypic correlations were also obtained between ginning outturn with number of sympodia and fiber length (r=-0.36** and r=-0.51** respectively), plant height with days to 50% flowering and number of monopodia (r=-0.21** and r=-0.34* respectively), fiber length with fiber fineness (r=-0.74**), and number of bolls with number of sympodia (r=-0.35**) respectively. All other associations either positive or negative were not significant.

SCY showed highly significant and positive genotypic correlations with DFF, NS, NB, BW, PH and FL (r= 0.55**, r= 0.35**, r= 0.66**, r= 0.78**, r= 0.44**, and r= 0.65** respectively), but showed highly significant and negative genotypic correlation with NM, FF, SI and LI (r= -0.79**, r=-0.65**, r=-0.45** and r=-0.55** respectively). Highly significant and positive genotypic correlations were also obtained between DFF with PH (r= 0.58**), NS with BW, LI, and PH (r=0.66**, r=0.42**, and r= 0.44** respectively), BW with SI and LI (r= 0.44** and r= 0.38** respectively), SI with LI and FF (r= 0.56**, and r=0.45** respectively), LI with GO (r=0.56**) and NM with FF (r= 0.55**). On the other hand, highly significant and negative genotypic correlations were obtained between NM with PH (r= -0.35**), NS with NB and SI (r=-0.54** and r=-0.34** respectively), FL with FF (r=-0.53**), NB with FF (r=-0.44).

4.5 Principal Components Analysis

Results from the principal component analysis for morphological and fiber quality traits are presented in Table 4.6. Eigen values and variances associated with each principal axis were extracted by principal component analysis. Five out of the twelve principal components (PC) extracted had eigen values greater than one and altogether explained 63.60% of the total variation among the 49 cotton genotypes and were thus considered for further analyses. Eigen vectors of Principal Components for 12 Characters in 49 cotton genotypes are presented in Table 4.7. Principal component 1, contributed 17.25%, to the total variability. The variation on principal component 1 was mainly attributed to number of sympodia, followed by number of bolls, and ginning outturn. The PC2 contributed 14.34% to the total variability and was depicted mainly in, plant height, followed by seed cotton yield, days to 50% flowering and number of monopodia. The PC3 contributed 12.02% to the total variability and was mainly attributed to boll weight and seed index. Principal component 4 contributed 10.66% to the total variability and was mainly attributed to days to 50% flowering and fibre length. The PC5 described additional contribution of 9.32% to the total variability, illustrated primarily the divergence in lint index, fiber length and boll weight.

Table 4.6 Eigen values of the Correlation Matrix and the Proportion and Total Variance Explained by the principal Components

Principal components	Eigen values	Contribution (%)	Cumulative (%)
PC1	2.07	17.25	17.25
PC2	1.72	14.34	31.58
PC3	1.44	12.02	43.61
PC4	1.28	10.67	54.27
PC5	1.11	9.32	63.60

Table 4.7 Eigen vectors of Principal Components for 12 Characters in 49 cotton genotypes

Traits	PC1	PC2	PC3	PC4	PC5
DDF	-0.190	-0.335	-0.289	-0.505	0.147
NM	0.324	-0.355	-0.006	0.208	-0.300
NS	0.476	0.251	0.025	-0.332	-0.002
NB	-0.416	-0.287	0.001	-0.055	-0.186
BW	0.177	-0.223	0.565	0.031	-0.330
SI	-0.051	0.009	0.434	0.197	0.222
LI	0.092	-0.257	0.193	-0.280	0.624
GO	-0.422	-0.144	0.227	0.007	0.103
SCY	-0.284	0.391	-0.255	-0.064	-0.276
PH	-0.069	0.556	0.351	-0.248	0.110
FL	-0.169	0.128	-0.074	0.603	0.368
FF	-0.354	0.039	0.353	-0.202	-0.269

DFF=Days to 50% flowering, NM=Number of monopodia, NS=Number of sympodia, NB=Number of bolls, BW=Boll Weight, SI=Seed Index, LI=Lint Index, GO=Ginning outturn, SCY=Seed Cotton Yield, PHT=Plant Height, FLT=Fiber Length, FF=Fiber Fineness.

The principal component scores of the 49 nine cotton genotypes based on the first five principal components are presented in Table 4.8. On principal component 1, the highest score (-4.83) was recorded by RSA (79)4^{A}, followed by SAMCOT 6, Y 1422(79)4^{G}, BAR 14/25(81)24, and SAMCOT 11. On principal component 2, SAMCOT 11 has the highest score PIMA S-1, BAR 14/25(81)39, TX-CABS-1-83 and BAR XL 7(79)8. SAMCOT 11, Y 1422(79)5 and ACSA (79)13^{A} had the highest score on principal components 3. On principal components 4, SAMCOT 11 had the highest score, followed by BAR-XL 7(79)8, Giza 69, ASA (74)80, and TAMCOT SP 37. For principal components 5, ACSA (79)5, SAMCOT 13, TAMCOT SP 27, SAMCOT 8, and G.C.A-NH-1-83 contributed highest to the total variability.

4.5.1 Estimation of genetic distance and clustering of genotypes

The D^2 statistic values which is based on the pooled mean of genotypes resulted in classifying the 49 genotypes into five distinct clusters (Table 4.9). The 49 genotypes were classified into five clusters with cutting point at 0.5 unit cluster. Each cluster has a distinct feature from other genotypes in the characteristics under consideration (Table 4.10). Cluster I had one genotype (2%) which was outstanding type by its performance in some of the traits. It had the highest plant height, highest number of days to 50% flowering, highest fiber length, high micronaire, high ginning outturn, moderate seed index. Cluster II had one genotype (2%). This cluster is characterized by high plant height, highest seed cotton yield, moderate number of sympodia, highest number of bolls, highest boll weight, highest micronaire, and low number of monopodia.

Table 4.8 Principal component scores for 12 traits in 49 cotton genotypes

S/N	Genotypes	PC1	PC2	PC3	PC4	PC5	S/N	Genotypes	PC1	PC2	PC3	PC4	PC5
1	SAMCOT 6	3.75	0.78	-2.11	0.11	-0.04	26	Y 1422 (79) 30	1.26	0.25	0.40	-0.54	0.17
2	TX-CD P37-HH-1-83	0.57	0.75	-0.21	-0.12	1.02	27	ASA (75) 13	1.57	-0.01	0.50	0.09	-1.07
3	TX-L3B2BCH-1-85	0.17	0.92	-0.36	-0.63	0.72	28	TAMCOT SP 374	1.05	1.00	0.68	0.49	1.25
4	TAMCOT CAMD-E	-0.39	1.50	0.48	-1.36	-0.86	29	TAMCOT SP 37	1.10	-0.98	0.06	1.69	-0.37
5	TAMCOT SP 37H	0.03	0.08	-2.16	0.07	-0.41	30	TX CABS 1-83	-0.32	-0.05	0.11	1.13	0.05
6	TAMCOT CABCS 1-83	-0.39	-0.38	-0.09	-0.37	-0.84	31	Bar XL7 (79) 8	-0.85	-2.12	-0.47	2.11	-0.22
7	TAMCOT SP 37	0.41	0.06	-1.21	-0.01	-1.87	32	Acala 9151 7C	1.58	-0.57	-0.04	0.74	1.25
8	TAMCOT SP 21	0.66	0.16	0.76	1.01	-0.07	33	Bar XL7 (79) 35	0.29	-0.04	1.59	-0.74	-0.31
9	G.C.A- NH-1-83	-0.22	1.45	-0.34	0.34	1.71	34	Bar 14/25 (81) 18	0.35	-0.14	-1.15	0.97	-1.01
10	ASA (78) 17^{f}	1.10	0.67	0.42	-0.83	-0.85	35	Bar 14/25 (81) 23	0.60	-0.76	-0.72	-0.39	1.27
11	ASA (78) 34^{A}	-0.70	0.42	-1.18	-0.05	0.13	36	Bar 14/25 (81) 24	2.82	-0.91	-0.05	0.10	-0.01
12	BJA 592 (79) 2^{B}	1.40	1.20	-1.53	-0.58	0.02	37	Bar 14/25 (81) 39	1.76	-2.35	-0.25	-0.26	0.67
13	Y 1422 (79) 19^{B}	-1.23	2.11	0.66	-0.72	-0.65	38	Bar 14/25 (81) 43	-0.54	-1.16	2.07	-1.03	-1.66
14	Y 1422(79)4^{G}	-3.03	0.65	-0.64	1.29	-0.36	39	Pima S-1	-0.55	-2.62	1.23	1.57	-0.66
15	RSA (79) 4^{A}	-4.83	-0.16	-0.87	1.34	-0.36	40	Pima S4	1.38	-1.43	-0.77	0.92	-0.70
16	ACSA (78) 34^{B}	-1.61	1.59	-0.61	0.87	0.03	41	Bar 14/25 A	0.63	-1.14	1.17	0.26	-0.54
17	ACSA (79) 13^{A}	-0.53	0.96	-2.18	0.43	-0.24	42	Giza 69	-0.14	-0.50	-1.52	1.82	-0.53
18	TX CABS 1-83	0.16	2.21	-0.67	-0.49	1.80	43	Bar XL7(79) 6	0.32	-1.90	0.71	-0.11	-0.20
19	TAMCOT SP 21^{s}	-1.38	-0.48	1.29	-0.14	-0.87	44	SAMCOT 8	-0.22	0.52	-1.14	0.08	1.87
20	TAMCOT CAMDE^{-E}	-1.73	2.59	-0.91	-0.78	-2.14	45	SAMCOT 9	1.87	-0.39	0.52	-1.07	-0.59
21	BJA 592 (79) 4	-0.32	1.59	1.38	-1.16	0.41	46	SAMCOT 10	-1.10	-1.39	1.88	-1.60	1.29
22	ACSA (79) 19	-1.19	-0.71	0.99	0.57	1.31	47	SAMCOT 11	-2.72	-4.00	-2.89	-4.48	1.15
23	Y 1422 (79)5	-1.31	0.09	2.74	0.49	1.51	48	SAMCOT 12	-0.15	-0.86	0.73	0.51	-1.17
24	ACSA (79) 5	-0.45	1.09	1.31	1.54	2.55	49	SAMCOT 13	0.29	1.54	1.62	-1.30	-2.03
25	ASA (74) 80	0.77	0.90	0.76	-1.79	0.47							

Table 4.9 Mean values of 12 traits of the 5 clusters for cotton genotypes

TRAITS	CLUSTER 1	CLUSTER2	CLUSTER 3	CLUSTER 4	CLUSTER 5
PH	100.20	50.60	35.70	40.80	56.00
DFF	68.00	60.20	67.02	70.50	75.10
NM	4.60	2.30	1.00	3.10	5.20
NS	20.00	10.20	15.60	13.60	17.30
NB	10.00	18.50	14.00	16.50	15.00
BW	3.00	6.60	2.00	4.13	5.20
SI	6.00	10.80	11.00	5.00	4.00
LI	6.60	4.50	3.50	8.10	5.30
GO	20.60	15.00	30.20	15.00	22.00
SCY	800.62	1000.25	100.00	250.50	600.02
FL	29.00	25.00	22.00	27.00	22.50
FF	5.20	7.20	3.60	5.00	4.50

DFF=Days to 50% flowering, NM=Number of monopodia, NS=Number of sympodia, NB=Number of bolls, BW=Boll Weight, SI=Seed Index, LI=Lint Index, GO=Ginning outturn, SCY=Seed Cotton Yield, PHT=Plant Height, FLT=Fiber Length, FF=Fiber Fineness.

Table 4.10 The 49 cotton genotypes grouped into clusters

Cluster	Genotype
1.	BAR14/25(81)24
2.	TAMCOT SP 21
3.	GIZA 69 AND BJA 592(79)4
4. A	TXCABS1-83, ACSA (79)19, SAMCOT 13, TXCABS-1-83, TAMCOT SP 21S SAMCOT 9, Y 1422 (79)5.
4. B	BJA 592(79)28, SAMCOT 11, BAR 1425(81)39, SAMCOT 8, PIMA S-1, ACSA (79)13A, SAMCOT 10, TAMCOT CAMD-E, BAR 14/25A, BAR XL 7(79)6.
5. A	GCA-NH-1-83, Y 1422(79)198, ACALA 91517C, Y 1422(79)80, TX-CDP37-HH-1-83, TAMCOT SP 37, BAR XL7(79)35, ASA(78)17F
5. B	Y1422(79)4A, TAMCOT CAMD-E, RSA(79)4A, TAMCOT CAMD-E, RSA(79)A, ACSA(79)5, TAMCOT SP 374, BAR 14/25(81)23, BAR 14/25(81)43, ACSA(79)5, BAR 14/25(81)18, TX-L382BCH-1-85, ACSA(78)34A, PIMAS4, SAMCOT 8, BAR XL7(79)8, TAMCOT CABCS1-83, TAMCOT SP 37H, ASA(75)13, SAMCOT 12.

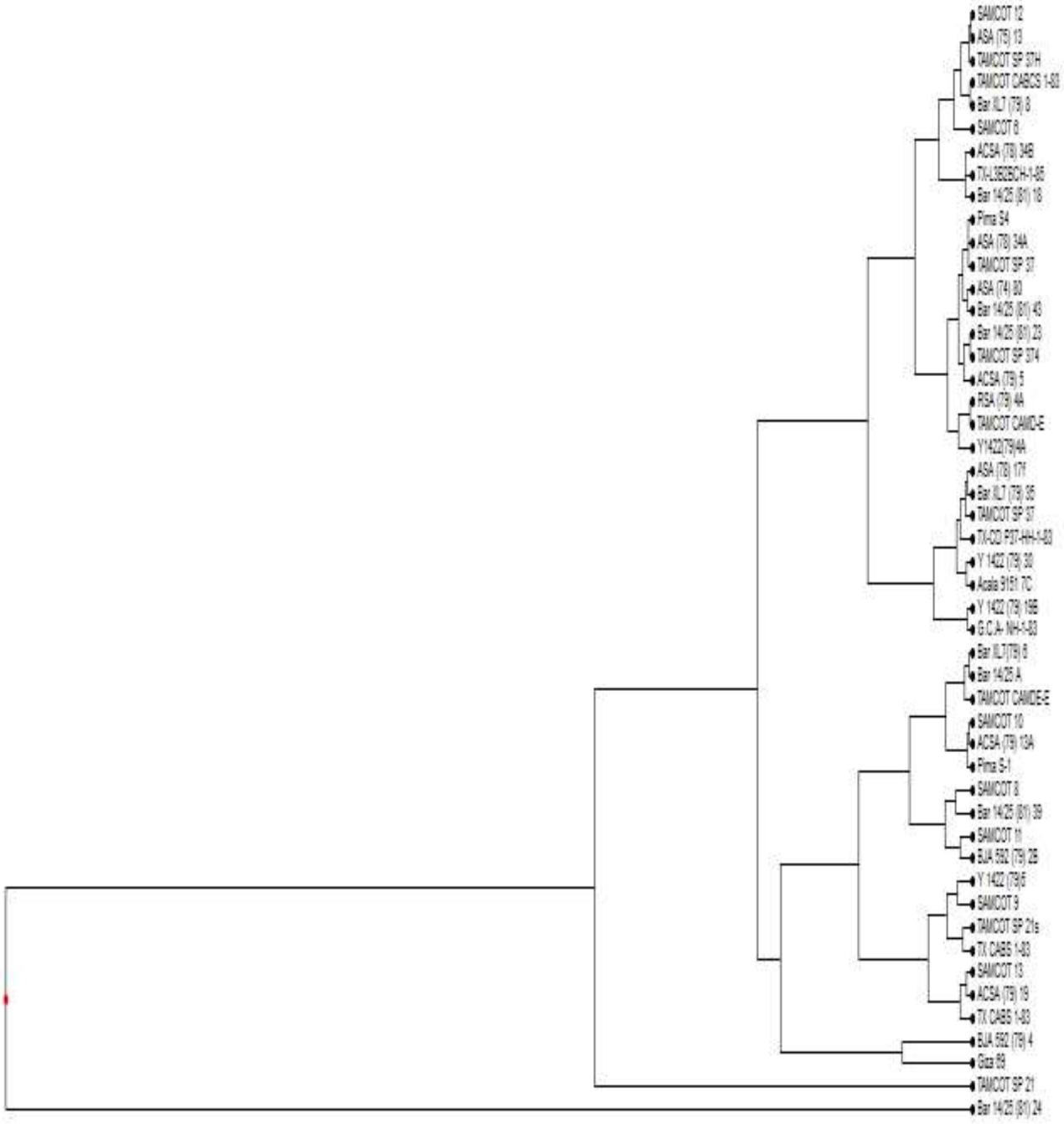

Figure 4.1 Dendrogram of genotype clusters based on twelve morphological and fibre quality traits of 49 cotton genotypes

Cluster III consisted of two genotypes (4%) having the characteristics as follows; high days to 50% flowering, lowest seed cotton yield, high number of sympodia, highest seed index, highest ginning outturn, lowest plant height, moderate number of bolls, low fiber fineness, and low number of monopodia. Cluster IV consisted of seventeen genotypes (34%) characterized by the following features: high days to 50% flowering, highest lint index, high fiber length, moderate number of sympodia, high number of bolls, low seed cotton yield and plant height. Cluster V consisted of twenty eight genotypes (57%) with characteristics features as follows: moderate seed cotton yield, low fiber length, high days to 50% flowering, moderate plant height, high number of monopodia, high ginning outturn, lowest seed index, and high number of sympodia. Figure 4.1 presents dendrogram of genotype clusters of 49 cotton genotypes. It classified the 49 genotypes into 5 clusters. Cluster 1 consists of 1 genotype, cluster 2 had 1 genotype, cluster 3 had 2 genotypes, cluster 4 had 17 genotypes and cluster 5 comprised of 28 genotypes.

CHAPTER FIVE

5.0 DISCUSSION

5.1 Analysis of Variance

The existence of significant and highly significant differences in the parameters studied for these traits suggests the presence of considerable genetic variability among the genotypes for these traits depicting the possibility of improvement in the yield by recombination and selection in segregating generations. On the other hand, the existence of insignificant differences for some of the morphological traits suggests lack of ample genetic variability among the genotypes. This is most likely, because cotton already has narrow genetic base, coupled with the fact that most of the materials used for breeding cotton in Nigeria originated from USA, which could have possibly resulted in narrowing the genetic variability. This is in line with an earlier study which observed that most cotton varieties had been developed from a few genetic sources that resulted in lowering the level of genetic diversity in modern cultivars (Guang and Xiong-Ming, 2006). It is also in agreement with the report of Iqbal *et al*. (2001), who stated that lack of significant diversity in cultivated Upland cotton is due to extensive use of few genetic sources during the recent breeding efforts to improve it and that most of the Upland cotton cultivars growing in the modern world have been originated from USA in the 19th and early 20th century.

The extent of variability as measured by PCV and GCV also gives information regarding the relative amount of variation. The highest coefficients of both phenotypic 64.85 and

genotypic 21.70 coefficients of variation showed by Seed cotton yield, to days to 50% flowering 48.75 and 16.14 and number of monopodia 44.8 and 13.43 indicate the extent of genetic diversity among the materials studied and their potential use for improvement through hybridization and selection. These results are in agreement with the findings of Sumathi and Nadarajan (1996), Jagtap and Mehetre (1998), and Rao and Reddy (2001). The equal magnitudes of PCV and GCV for fiber length and fiber fineness depict ample scope for improvement through selection. The high differences between PCV and GCV indicate influence of environment on the expression of the traits thereby restricting the scope for their improvement through selection. Low values of GCV and PCV for plant height, seed index, ginning percentage, fiber length and micronaire indicate narrow range of variability for these traits thereby restricting the scope for selection. These results are in agreement with the findings of Sumathi and Nadarajan (1996), Jagtap and Mehetre (1998), Kumar *et al.* (2000), Rao and Reddy (2001) and Girase and Mehetre (2002).

Generally, the range observed in all the means of all the morphological and fibre quality traits also indicates presence of moderate variability among the genotypes. Best genotypes could be selected for each trait and as no single genotype possesses all the desirable traits, hybridization can give a desirable improved variety. Thus, as a strategy for obtaining superior *Gossypium hirsutum* genotypes possessing traits of interest, selection on the basis of the desirable traits followed by hybridization will be very effective. The results from the rank summation index indicated that genotypes PIMA S4 followed by RSA (79)4^{A}, ASA (78)34^{A}, TAMCOT SP 37^{4}, SAMCOT 12, and SAMCOT 13 which were obtained from USA, Mexico and Nigeria belonging to cluster 5 and 4 are the best genotypes for all the

traits studied. These genotypes are therefore considered the best potential parents that could be used in hybridization programs for the improvement of seed cotton yield in Nigeria.

5.2 Correlations Coefficients

Before launching any breeding program information regarding association among various traits is a pre-requisite as it provides the opportunity for the selection of genotypes having desirable traits simultaneously (Ali *et al*., 2009). This result indicates that phenotypic selection of plants with good number of sympodia per plant, plant height, boll weight, fibre length, number of bolls and days to 50% flowering will indirectly results in high cotton seed yield obtainable from a plant. Genotypic coefficient of correlation suggested that selection of plants with good number of sympodia per plant, plant height, boll weight, fibre length, number of bolls and days to 50% flowering will indirectly results in high cotton seed yield obtainable from a plant. The positive correlation among these yield contributing traits suggested that these characters are important for direct selection of high yielding genotypes. This result is in line with the finding of Farooq *et al.,* (2013) who reported positive correlation of yield with yield contributing traits in cotton.

5.3 Principal components analysis

Results from PCA presented in revealed that only first five principal components of the twelve principal components contributed more than one eigen values and jointly accounted for (63.60%) to the total variance among the genotypes, indicating that the total variation was fairly distributed across all of the studied traits and the level of variability exhibited by this population is low, substantiating the results from the analysis of variance, that revealed

non-significant differences for most of the studied traits. To avoid a status quo whereby all the germplasms look alike, breeders must search for novel and diverse material in order to explore the unutilized genetic diversity for future generations. This result corroborates the findings of Makinde *et al*. (2010) and Aremu *et al.* (2007). In this experiment, PC1 laid more weight on the number of sympodia (0.476), number of bolls (0.416) and ginning outturn (0.422). PC2 showed high loading for, plant height, seed cotton yield, with eigen vectors of (0.556 and 0.391). PC3 described largely by boll weight, and seed index with eigen vectors of 0.565 and 0.434 respectively. PC4 and PC5 had more weight on, days to 50% flowering, fibre length, and lint index with eigen vectors 0.505, 0.603 and 0.624 respectively.

5.4 Cluster Analysis

When dissimilarity between a pair of variety is defined on a multivariate criterion, it is useful to determine the plant characters responsible for the dissimilarity and the relative contributions that the various characters make to the total variability in the germplasm (Albert, 2014). The range of dissimilarity obtained between the 49 genotypes was 1.376 (for genotypes in cluster 1) to 1.778 (for genotypes in cluster 5). In the present study, cluster 5 was more divergent than the others since it recorded high for seed cotton yield and other traits that contributed indirectly to improve yield. Therefore, hybridization between genotypes belonging to clusters 5 and especially cluster 1 is expected to produce genotypes with high heterotic values. 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 genotypes of

cluster 5, with any other cluster are suggested to exhibit high heterosis and could result in segregates with higher cotton seed yield.

CHAPTER SIX

6.0 SUMMARY, CONCLUSION AND RECOMMENDATION

6.1 Summary

Forty nine cotton (*Gossypium hirsutum* L.) genotypes obtained from different sources were evaluated in 2013 cropping season, in a 7 × 7 complete lattice design with three replications. Data were recorded on agronomic and fiber quality traits and were subjected to analysis of variance, principal components analysis, cluster analysis and correlation analysis. Results from the analysis of variance revealed highly significant differences for fiber fineness, days to 50% flowering and fiber length while non-significant differences were observed for the other agronomic traits.

Mean performance showed considerable differences for both morphological and fiber quality traits, each character exhibited considerable range of its expression. Coefficient of variation observed generally from low, moderate to high. The phenotypic variances were consistently higher than genotypic variances for virtually all the traits. Similarly, phenotypic coefficients of variation are greater than the corresponding genotypic coefficients of variation for all the traits except for fiber fineness. The highest phenotypic coefficient of variance was observed for seed cotton yield (64.85%) and days to 50% flowering (48.75%). The magnitudes of phenotypic variances are suggestive that improvement is feasible through hybridization and selection in these traits. From rank summation index genotypes PIMA S4, RSA (79) 4A, ASA (78) 34^{A}, SAMCOT 12 and SAMCOT 13 obtained from the USA, Mexico and Nigeria were the best materials for all

the traits studied. These genotypes are therefore considered the best potential parents use in for the hybridization programs for the improvement of cotton in Nigeria.

Based on the D^2 statistics, the genotypes were grouped into five clusters with cluster V having the maximum number of genotypes (28). However, clusters showed some character distinctions that could be employed for hybridization purposes. Phenotypic and genotypic correlations were positive and significant for some yield components with seed cotton yield, indicating that selection of plants with good NS, NB, NS, PH, FF and days to 50% flowering can effectively be utilized to improve yield.

Principal component analysis also revealed that only the first five components having eigen value greater than 1 contributed 63.60% to the total variability and was mainly due to traits such as number of sympodia, number of bolls, ginning outturn, plant height, seed cotton yield, boll weight, seed index, days to 50% flowering, fibre length, and lint index, indicating that these characters contributed maximum to the total genetic diversity in the population.

6.2 Conclusion

Information on the genetics of economic values controlling traits of economic values in species is very important for breeding purposes. Based on the results of the current work, parental materials have been identified and classified in cotton germplasm. Important morphological and fiber quality traits like greater seed cotton yield potential, plant height,

fibre length, fibre fineness, number of sympodia per plant and number of bolls per plant etc. served as selection criterion to produce promising cotton genotypes. The present investigation provided considerable information useful in genetic improvement of cotton Genotypes belonging to cluster 5 showed maximum inter cluster diversity. From cluster mean values, genotypes in cluster 1, 2, 4, and 5 deserve consideration for their direct use as parents in hybridization programs to develop high yielding cotton varieties. The genotypes in cluster 5 may be used for improvement and other desirable characters other than seed cotton yield. Presence of low genetic variability among tested genotypes emphasized the need for breeders to search for novel and diverse materials and explore the unutilized genetic diversity for future generations.

6.3 Recommendations

For the improvement of cultivated cotton, it is pertinent that breeders must search for novel and diverse materials and unravel the unutilized genetic diversity for use in future cotton breeding programs in Nigeria. Although these studies provide information about the levels of genetic diversity in small subsets of Institute for Agricultural Research cotton genotypes, a comprehensive study is still needed to fully characterize the genetic structure and relationships among cotton germplasm of the Institute. Furthermore, plant breeders who are interested in improving many traits in cotton simultaneously must take care of the relationship existing between them. Information obtained through principal component analysis may assist plant breeders to identify the number of highly differentiated populations for use in crossing and selection programs.

REFERENCES

Adeniji, O.B. (2011). Adoption of improved Technologies for Cotton Production in Katsina State, Nigeria. *Ph.D Thesis*, Unpublished. Ahmadu Bello University, Zaria.

Aghughu, O. (2001). Provenance variation in acacia Senegal (l) wild. (*Gum Arabica*) in Nigeria. An unpublished *Ph.D. thesis* Department of plant science, Ahmadu Bello University, Zaria.

Albert, A. (2014). Genetic diversity studies on groundnut genotypes. *M.Sc. Thesis* Department of plant science, Ahmadu Bello University, Zaria, Nigeria.

Ali, M.A., N.N. Nawab, A. Abbas, and M. Sajjad (2009). Evaluation of selection criteria in *Cicer arietinum* L. using correlation coefficients and path analysis. Australian *journal of crop Science* 3: 65-70.

Altaf, M., H.A. Sadaquat, M.A. Khan and M. Zubair, (1996). Genetic variability and correlation studies in some promising cotton strains under cotton leaf curl virus epidemic. *The pak Cottons*, 40(3-4): 80-90.

Anonymous (1992). *Cotton: review of the world situation*. ICAC, Nov-Dec 60 (2):17.

Anonymous (1995). *Cropping Scheme Meeting Report on Fiber Programme*. Institute for Agricultural Research (IAR), Samaru Ahmadu Bello University Zaria, Nigeria.

Ansari, A.H., S.M. Qayyum, M.I. Sohu, M.M. Baig and M.K.K. Rajput, (1991). The influence of seeding dates on the yield, its components and their interrelation in cotton (*Gossypium hirsutum* L). *Sarhad Journal of Agriculture* 7(2): 11-19.

ANZFA, (2002). Draft assessment report: oil and linters derived from insect protected cotton containing event 15985. Full assessment S15, Application A436. Australia new Zealand food authority.

Applequist, W.L., Cronn, R. and Wendel, J.F. (2001). Comparative development of fiber in wild and cultivated cotton. *Evolution and development*, 33-17.

Aremu, C.O. (2005). Diversity selection and genotypes environment interaction in cowpea unpublished *Ph.D thesis*. University of Agriculture, Abeokuta, Nigeria. P. 210.

Aremu, C.O., Ariyo, O.J., and Adewole, B.D. (2007). Environment interraction in cowpea (*Vigna unguiculata* (L) Walp). *African Research*, 2(8): 253-355.

Asad, M.A.; F.M. Azhar and Zafar Iqbal. (2002). Association of yield with various economic traits in *Gossypium hirsutum L. International Journal Agricultural Biology* 4(1): 105-106.

Baloch, M.J., G.H. Tunio and A.R. Lakho, (2001). Expression of heterosis in F_1 and its deterioration in intra-hirsutum f2 hybrids. *Pakphyton* 3: 95-106.

Beasley, J. O. (1940). The origin of American tetraploid Gossypium species.*Am. Nat*. 74:285-286.

Bowman, D.T., May O.L., and Calhoun, D.S., (1996). Genetic base of Upland cotton cultivars released between 1970 and 1990 *crop science*, 36: 577 581.

Bradow, J. M. and G. H.Davidonis.(2000). Quantitation of fiber quality and the cotton production-processing interface: *A physiologist perspective*. *Journal Cotton Sci*nce 4:34-64.

Brubaker, C.L. and Wendel, J.F. (1994) Re-evaluating the origin of domesticated cotton (*Gossypium hirsutum*; Malvacaea) using nuclear restriction fragment length polymorphisms (RFLPs). *American Journal of Botany*, 81: 1309-1326.

Brubaker, C.L., Paterson, A.H. and Wendel, J,F. (1999). Comparative genetic mapping of allotetraploid cotton and its diploid progenetors. *Genome*, 42:184- 203.

Chahal, G. S., and Gasal, S.S. (2002). Principles and Procedures of Plant Breeding: Biotechnology and Conventional Approaches. Narosa Publishing House, New Delhi. Pp 108.

Chaudhary, M.R. and Guitchounts A. (2003). Cotton facts. Technical paper no. 25 of the common fund for commodities. ICAC, USA.

Chee, P., Draye, X., Jiang, C.X., Decainini, L., Delmonte, T., Bredhauer, R., Smith, C. W. and Paterson, A. H. (2005). Molecular dissection of interspecific variation between *Gossypium hirsutum* and *Gossypium barbadense* (cotton) by a backcross-self approach: I. Fiber elongation. *Theoritical Application of Genetics*, 111:757: 763.

Chen, Z.J, Scheffler B.E, Dennis, E., Triplett, B.A., Zhang, T., Guo, W., Chen, X., Stelly, D.M., Rabinowicz, P.D., Town, C.D., Arioli, T., Brubaker, C., Cantrell, R.G., Lacape, J.M., Ulloa, M., Chee, P., Gingle, A.R., Haigler C.H., Percy, R., Saha S., Wilkinns, T., Wright, R.J., Van, D.A., Zhu, Y., Yu, J.Z., Kohel, R.J., Wendel, J.F., Paterson, A.H. (2007). Toward Sequencing Cotton (*Gossypium*) *genomes*. *Plant Physiology*, 145:1303-1310.

Christine, B., Joshua, H., William, A., Stacy, A. (2009), Genetic diversity of creeping bent grass cultivars using SSR markers. *International turf grass society Research Journal*, 123:11-15.

Cruz, C. D. and Carneiro, A. J. (2003). Biometric models applied to genetics. In: Dekker J. and Hospital F. (2002). The use of molecular genetics in the improvement of Agricultural populations. *Natural Review Genetics* 3:22-32

Dutt, Y., Wang, X.D., Zhu, Y.G., and Li, Y.Y. (2004). Breeding for high yield and fiber quality in coloured cotton. *Plant Breeding*. 123: 145-151.

Edwards, G.A. and M.A. Mirza. (1979). Genomes of the Australian wild species of cotton. 11. The designation of a new G Genome for *Gossypium bickii*. *Canada journal of Genetics Crytol*, 21:367-372.

Endrizzi, J.E., Turcotte, E.L. and Kohel, R.J. (1985). Genetics, cytology and evolution of *Gossypium*. *Advances in Genetics*, 23: 271-375.

Farooq, A., Farooq, J., Mahmood, A., Batool, A., Rehman, A., Shakeel, A., Riaz, M., Shahid, M.T.H. and Mehboob, S. (2013). An over view of cotton leaf curl virus disease (CLCuD) a serious threat to cotton productivity. *Australian Journal of Crop Sci*ence, 5 (12):1823-1831.

Fryxell, P.A. (1979). The natural history of cotton tribe. Texas A and M University Press, College Station, Texas. Pp 153-162.

Fryxell, P.A. (1992). A revised taxonomic interpretation of *Gossypium hirsutum* L. (Malvacea). *Rheedea*, 2: 108-165.

Girase, V.S. and Mehetre, S.S. (2002). Variability, heritability and genetic advance studies on cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*, 16(1): 81-82.

Gregory, S.R., Hernandez, E. and Savoy, B.R. (1990). Cotton seed processing technics 123-135.

Guang, C. and Xiong- Ming, D. (2006). Genetics diversity of source germplasm of upland cotton in China as determined by SSR marker analysis. *Acta. Genetic Sinca*, 33: 733-745.

Hamid, A.Z. and Grafius.J.E. (1978). Developmental allometry and its implication to grain yield in Barley. *Crop Science*, 18: 83-86.

Iqbal, M., K. Hayat, R.S.A. Khan, A. Sadiq and N. Islam. (2006). Correlation and path coefficient analysis for earliness and yield traits in cotton (*G. hirsutum* L). *Asian Journal Plant Science*, 5(2): 341-344.

Iqbal, M.J., Aziz, N., Saeed, N.A., Zafa, Y., and Malik, K.A. (2001). Genetic diversityevaluation of some elite cotton varieties by RAPD analysis. *Theoritical Application Genetics*, 94: 139 -144.

Jagtap, D.R. and Mehetre, S.S. (1998), Genetic variability inter-varietal crosses of upland cotton (*Gossypiumhirsutum* L.). *Annals of Agricultural Research*, 19(2): 130-132.

Jain, S.K and Workman P.L. (1966). The genetics of inbreeding species. *Advanced genetics*, 14:55-13.

Jost, P. (2002). Planning for fiber qulity.In :Jose, P.(ed) UGA Georgia Cotton Newsletter.http://www.griffin.peachnet.edu/caes/cotton/cn1041902.htm

Kaiser, H.F. (1960). The application of electronic computers to factor analysis. *Educational and Psychological Measurement,* 20,141-151.

Kaps, M., and Lamberson, W.R. (2004). *Biostatistic for animal Scince*. CABI Publishing, CAB International, Walling ford, Oxfordshir.

Karp, A. (2002). *The new genetic era*: Will it help us in managing genetic diversity? 105:13-18.

Kumar, P.R., Raveendran, T.S. and Venkata Krishnanan, (2000). Genetic diversity and association studies for fibre characters in cotton (*G. hirsutum* L.). *Journal of the Indian Society for Cotton Improvement*, 25(3): 111-118.

Law, C.N., Sanpe,J.W. and Worland,A.J. (1978).The genetical relationship between height and yield in wheat. *Heridity,* 40: 133-151.

Lewis, C.F. (2000). *Cotton yield and quality yesterday, today and tomorrow*. In: Chewning, C.H. (edition), Proc. 13th Annual Engineered Fiber Selection System Conference Cotton Incorporated. Raleigh, North Carolina, USA.

Liu, B., Brubaker, G., Cronn, R.C. and Wendel, J.F. (2001). Polyploid formation in cotton is not accompanied by rapid genomics changes. *Genome,* 44:321-330.

Liu, S., Cantrell, R.G., McCarty, J.C.J. and Stewart, J.M. (2000). Simple sequence repeats based assessment of genetic diversity in cotton race stock accessions. *Crop Sci*.,40:1459-1469.

Mahalanobis, P.C. (1936). On the generalized distant on statistics. *Journal of genetics*, 41: 154-193.

Makinde S. C. (2010). Genetic Characterization of Okra (*Abelmoschus esculentus* L.) Moench.) Cultivars. *Unpublished M.Sc. Thesis*, Facultyof Science, University of Ilorin, Ilorin, Nigeria.

Malumba, N. N. and Mock J. J. (1978). Improvement of yield potentials of the Eto Blanco maize (*Zea mays* L.) population by breeding for plant traits. *Egyptian journal of Genetics and Cytology,* 7:40-51.

Manzoor, A. and M.A. Faqir. (2000). Genetic correlation and path coefficient analysis of oil and protein content and other quantitative characters in F2 generation of *Gossypium hirsutum* L. Pak. *Journal Biological Science,* 3(6): 1049-1051.

May, O.L. (2002). Quality Improvement of upland Cotton (*Gossypium hirsutm* L.). In: Basra, A.S. and I.S. Randhawa (edition) quality improvement in field crops. The Haworth Press Inc. Pp. 371-1051.

Meredith, W.R.J. (1990). Continued Progress for Breeding for Yield in the USA In Kechagia U, Ed., proceeding of world Cotton Research Conference II. Athens, Greece, pp. 97-101.

Miller, P.A. and Rowling, J.O. (1976). Breaking up linkage blocks through intermating in cotton population. *Crop Science,* 7:637-640.

Moore, J.F. (1996). Cotton classification and quality. In: Glade, E. H. Jr., L. A. Meyer and H. Stults (eds). The cotton industry in the United States. USDAAERS Agricultural Economics Rep. 739. U.S. Government Printing Office, Washington, DC. Pp. 51-57.

Nassir, A.L. and Ariyo, O.J. (2005).Genotype x Environment stability analysis of grain yield of rice (*Oriza sativa* L.). Tropical Agriculture, (*Trinidad*). 2005:1-8.

Olukosi, J.O., Isotor, S.U. and Ode, M.O. (2007). Agricultural Marketing and Prices: Principles and Application. Living Bookshop Series Gu Publications, Abuja, FCT pp 78-85.

United State Agency for International Development (2012). Global Cotton Production Trend. From http//www.Usaid (Retrieved January 2013).

Perkins, H.H., Ethridge, D.E. and Bragg. C.K. (1984). Fiber. In: Kohel, R.J. and C.F. Lewis (eds) Cotton. *American Society of Agronomy Madison*, Pp. 438-508.

Pillay, M. and Myers, G.O. (1999). Genetic diversity in cotton assessed by variation in ribosomal RNA genes and AFLP markers. *Crop science*, 39: 1881-1886.

Poehlman, J.M. and D. Borthakur. (1969). *Breeding Asian Field Crops*. Oxford and IBH Publication Company New Delhi.

Poehlman, J.M. and Sleeper. D.A. (1995). *Breeding field crops*. Iowa State University Press, USA.

Ramey, H. H. (1982). *The meaning and assessement of cotton fiber fineness*. International Institute for Cotton Manchester, UK. Pp 83.

Rao, G.N. and Reddy, M.S.S. (2001). Studies on heritability and variability for yield and its components in *hirsutum* cotton. *Journal of Cotton Research and Development*, 51(1): 84-86.

Raw Material and Research Development Council (2004). Report on Survey of Agricultural Raw Materials in Nigeria Federal Ministry of Agriculture Abuja FCT Nigeria.

Robinson, H.F., Comstock, R.E. and Harvey, R.H. (1959). Genotypic and Phenotypic correlations in Corn and their implications in selection. *Agronomy Journal*, 43:282 287.

Shakeel, A., Farooq, J., Ali, M.A., Riaz, M., Farooq, A., Saeed, A., and Saleem, M.F. (2011). Inheritance pattern of earliness in cotton (*Gossypium hirsutum* L.) *Australian Journal of crop Science*, 5(10):1224-1231.

SAS Institute Inc (2004). SAS/STAT 9.1 User's Guide. Version 6, fourth edition, volume 1.

Singh, R.K., and Chaudhary, B.D. (1985). Biometric Method in Quantitative Genetics Analysis, New Delhi.

Singh, S. K., Singh, R. S., Maurya, D. M., and Verma, O. P. (1987). Genetic divergence among lowland rice cultivars: Indian Agricultural Research Institute (IARI), New Delhi, India.

Smith, B. (1991). A review of the relationship of cotton maturity and dye ability. *Textile Research Journal,* 61:137-145.

Soomro, Z.A., A.S. Larik, M.B. Kumbhar, M. Khan and N.A. Panhwar. (2008). Correlation and Path analysis in hybrid cotton. SABRAO, *Journal of Genetics and Breeding,* 40(2): 39-46.

Steadman, R .G. (1997). Cotton Testing. *Textile progress* 27:1-66.

Stewart, J. McD. (1994). Potential for Crop improvement with exotic germplasm and genetic engineering in: Constable, G.A and N.W Forrester (eds) *Challenging the future*: Proceedings of the World Cotton Research Conference 1, Brisbane Australia, February 14-17 CSIRO, Melbourne. PP.13-327.

Sumathi, P. and Nadarajan, N. (1996), Genetic variability in cotton. *Journal of the Indian Society for Cotton Improvement*, 21(1): 33-36.

Tatinen, V., Cantell, R.G. and Davis, D. (1996). Genetic diversity in elite cotton germplasms determined by morphological characteristics and RAPDs. *Crop Science,* 36:186-192.

Ulloa, M.C., Brubaker and P. Chee. (2007). Cotton.in: kole, C. (ed) *Genome mapping and Molecular breeding in plant*, Volume 6. Springer verlag Berlin Heidelberg.

Wendel, J.F, and Cronn, R.C. (2003). Polyploidy and the evolutionary history of cotton *Advance Agronomy,* 78: 139- 186.

Wendel, J. F., Cronn, R.C., Johnson, J. S. and Price, H. J. (2002). Feast and famine in plant genomes. *Genetica,* 115:139- 47.

White, J. W., and Gonzalez, A. (1990) Characterization of negative association between seed yield and size among genotypes of common bean. *Field crop Research,* 23:159-175.

Wiley, E.O. (1981). *Phylogenetics*: The theory and practice of phylogenetics and systemic. John Wiley, New York. 10: 200-250.

Wilkins, T. A, Rajasekaren, K, and Anderson, M. (2000). Cotton biotechnology. *Critical Review Plant Science,* 19:511-550.

Yeye, M.Y. (2000). Variability analysis of three synthetic populations of Nigerian pearl millet (*Pennisetum americanum* L.) and implication in crop improvement published Thesis. Ahmadu Bello University, Nigeria.

Žáková, M., and Benková, M. (2006). Characterization of cotton accessions based on multivariate analysis. CommunBiom. *Crop Science*, 1: 124-134.

Zhang, J., Lu, Y., Cantrell, R.G. and Hughs, E. (2005). Molecular marker diversity and field performance in commercial cotton cultivars evaluated in south west USA. *Crop Science*, 45:1483-1490.

Zhao, X.P., Ji, Y.F., Ding, X.L., Stelly, D.M. and Paterson, A.H. (1998). Macromolecular organization and genetic mapping of a rapidly evolving chromosome specific tandem repeat family (B77) in cotton (*Gossypium*). *Plant Molecular Biology*, 38(6):1031 1042.