

**GENETIC DIVERSITY OF TANZANIAN AND KENYAN ADAPTED
LANDRACES OF COWPEA, SORGHUM AND PIGEONPEA**

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**A DISSERTATION SUBMITTED IN PARTIAL FULFILMENT OF THE
REQUIREMENT FOR THE DEGREE OF MASTER OF SCIENCE IN CROP
SCIENCE OF SOKOINE UNIVERSITY OF AGRICULTURE. MOROGORO,**



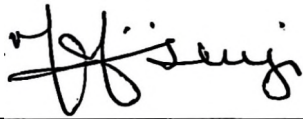
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ABSTRACT

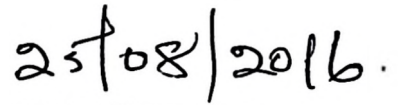
Improvement of cowpea, pigeonpea and sorghum can be enhanced by knowledge of genetic diversity available between and within accessions. This variability is the foundation of all three crop improvement programs. A total of 85 accessions as 22 cowpea, 32 pigeonpea and 31 sorghum from Tanzania and Kenya gene banks were used for this study. Quantitative and qualitative traits such as, grain color, grain coverage, seed shape, days to 50% flowering, plant height, days to 50% maturity and grain yield were among the few traits used to assess the collected accessions. The main objective of the study was to determine existing diversity of three food security crop accessions in Tanzania. Different agro- morphological traits collected were analyzed using GENSTAT 15 and XLSTAT 2014 statistical packages to determine Phylogenetic relationship of the three selected crops based on agro-morphological traits. Accessions were classified based on their agro-morphological relationships using principal component analysis and un-weighted pair-group average cluster analysis. Results showed a relatively high level of genetic diversity between and within both accessions; levels of similarity differed for qualitative and quantitative data for all three crops. Some quantitative agro-morphological traits such as days to 50% flowering, days to maturity, seed width, pods per plant in cowpea, grain weight per panicle, grain number per panicle, grain yield, number of nodal tillers per plot in sorghum; days to maturity, plant height and raceme number per plant in pigeonpea. For qualitative traits, raceme position for cowpea; grain color and bird attack for sorghum; seed color pattern for pigeonpea were distinguished more efficiently between and within the accessions to get superior materials for future use in breeding programs. A few of the best materials selected were GBK 013187 (cowpea), TZA 2496 (pigeonpea) and TZA 3991 (sorghum). In a number of groups the accessions were different from other accessions in some important traits. Implications of the variability in pigeonpea, cowpea and sorghum improvement are discussed.

DECLARATION

I, Zabron Mkumbo Msengi, do hereby declare to the Senate of the Sokoine University of Agriculture that the work presented here is my own original work and has not been submitted or concurrently being submitted for a higher degree award in any other institution.



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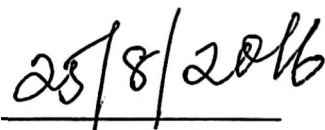


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DEDICATION

I would like to dedicate this work to my parents Lazaro Mkumbo, Juliana Kagila, my sister Upendo Msengi for caring, educating me and all members of my family for their moral support during my study.

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LIST OF ABBREVIATIONS AND SYMBOLS

100SW	100 seed weight
ANOVA	Analysis of variance
ARP	Average raceme number per plant
B.att	Bird attack
BRS	Biotic reaction stress
Btil	Basal tillers
BTP	Basal tillers per plot
CV	Coefficient of variation
DDF	Days to duration of flowering.
df	Degree of freedom
DF	Days to 50% flowering.
DM	Days to maturity
FP	Flowering pattern
GH	Growth habit
GLC	Glume color
GNP	Grain number per panicle
GP	Growth pattern
GrC	Grain color
GrCov	Grain coverage
GYLD	Grain yield
H	Diversity index
HP	Heads per plot
ICS	Inflorescence compactness and shape
IE	Inflorescence exertions

IL	Inflorescence length
IPP	Immature pod pigmentation
IW	Inflorescence width
JF	Juice flavor
LC	Leaf color
LMC	Leaf midrib color
LODG	Lodging
LSH	Leaf shape
n	Correlation matrix Pearson
NB	Number of branches
NFS	Number of flowering stem per plant
NNTP	Number of Nodal tillers per plot
Ntil	Nodal tillers
P/PL	Pods per plant
PAP	Pod attachment to peduncle
PBL	pod bearing length
PC	Pod color
PCA	Principal Component analysis
PCurv	Pod curvature
PF	Pattern of flowering
PHT	Plant height
PL	pod length
PLC	Plant color
PP	Plant pigmentation
PW	Pod width
r	Correlation coefficient

RBSD	Reaction to biotic stress (diseases)
RCBD	Randomized complete block design
RP	Raceme position
SCP	Seed color pattern
SE	Standard error
Senc	Senescence
SEP	Seed eye pattern
SEW	Seed eye width
SL	Seed length
SPD	Seeds per pod
SS(H)	Seed shape
STH	Stem thickness
SUA	Sokoine University of Agriculture
SW	Seed width
TLL	Terminal leaf length
TLS	Terminal leaf shape
TLW	Terminal leaf width
TT	Twinning tendency
Ttex	Testa texture
UPGMA	Un-weighted pair group arithmetic average method
WB	Waxy bloom
YLD	Yield

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background

Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production (Khodadadi *et al.*, 2011). Sorghum (*Sorghum bicolor* L. Moench) is the fifth most important cereal grain crop originated from West Africa and staple food for millions of poor in semi-arid tropics of Africa and Asia (Hausmann *et al.*, 2002). It has gained importance as both fodder (green/dry) and food crop. Besides being an important food, feed and forage crop, it provides raw materials for the production of starch, fiber, dextrose syrup, biofuels, alcohol and other products (Prakash *et al.*, 2006).

Sorghum yield is limited by inadequate and/or erratic rainfall, poor soil fertility, insect pests, disease invasion and high temperatures (FAO, 2005). Pigeonpea [*Cajanus cajan* (L.) Millsp] belongs to the genus *Cajanus*, subtribe *Cajaninae*, tribe Phaseoleae, and family Fabaceae. It is one of the major pulse crops of the tropics and sub-tropics, grown in approximately 50 countries in Asia, Africa and America. Pigeonpea is predominantly a crop of tropical areas mainly cultivated in semi-arid regions of India, Kenya and Tanzania, mostly as an intercrop with cereals.

In Tanzania it is a third crop among pulses after beans and cowpeas (Lyimo and Myaka, 2001). The origin of the crop is India. Pigeonpea grows as an annual crop, reaching 3–12 ft (1–4 meters) in height. The length of growing season is from 120 to 180 days (Sing and Oswalt, 1992). In Tanzania it is mainly grown in Arusha, Manyara, Dodoma, Mtwara, Lindi and Kilimanjaro. Pigeonpea is a crop of prime importance in human diet since it is

rich in protein (21%) and controls soil erosion, also can provide fuel wood, soil improvement, and animal feed like fodder. It is cash exported to middle East.

Cowpea (*Vigna unguiculata* (L.)Walp.) this belongs to the family Fabaceae is one of the most important pulse crop native to central Africa. Cowpea is a major source of cheap protein in human diets; its grain contains about 23 % to 25 % protein (Bressani, 1985). Estimated protein content of cowpea leafy parts consumed annually in Africa and Asia is equivalent to five million tons which 30% of total food legume production in lowland tropics (Singh *et al.*, 2003). Cowpea is called vegetable meat due to high amount of protein in grain with better biological value on a dry weight basis (Gupta, 1988). Apart from this, cowpea forms excellent forage and it checks soil erosion because it covers the soil. Cowpea fixes about 70 – 240 kg per ha of nitrogen per year (Withanage, 2005). The crop varies in growth habit from erect and semi-erect to trailing types with less than 100 days to more than 120 days growth durations respectively (The web: www.daff.gov.za). In Tanzania, cowpea is grown in almost all the areas below 1500 m above sea level (Price *et al.*, 1982). It is usually found intercropped with cereals or other crops, although it is also sometimes grown as a monocrop. Despite the importance of cowpea, its production like other grains is limited because of with constraints such as drought, flooding, salt stress and extreme temperatures, all of which are expected to worsen with climate change. Drastic changes in rainfall patterns and rise in temperatures introduce unfavorable growing conditions which reduce crop yield in averages of 0.10t/ha to 1.55t/ha (Ajetomobi and Abiodun, 2010).

It is important therefore to increase sorghum, cowpea and pigeonpea yields to meet the growing demand due to expanding population. In Tanzania sorghum contributed 6% in food crop composition (MAFC report, 2008). Legumes including pigeonpeas and

cowpeas contributed 5% in food crops composition (MAFC report, 2008). In plant breeding programs, assessment of genetic relationship is useful for determining the uniqueness and distinctness of a phenotype, genetic constitution of genotypes and selection of parents for hybridization (Bretting and Widrelechner, 1996). There is a growing demand from neighboring countries such as Kenya on pigeonpeas for white grained and local markets on cowpeas and sorghum where they purchase 700-1000Tshs per kg, 600-800 Tshs per kg and 1200-2000 Tshs/kg respectively. Also the crops are food security commodities, in that they can produce under marginal conditions of rainfall and fertility in the face of climate change scenarios.

1.2 Problem Statement and Justification

General Circulation Models (GCM) used to develop scenarios predicts that in Tanzania; mean daily temperatures have increased by 3.5°C (Hubert *et al.*, 2006). This increase will have differing effects over seasons and in different regions. Rainfall is predicted to decrease in some regions by 5 – 15% (Hubert *et al.*, 2006). The resulting climate and ecological zone shifts will have drastic effects on crop production. Genetic diversity is a fundamental tool in breeding and conservation of crop species. Tanzania is a country with considerable diversity in plant genetic resources including many local crop species (Tanzania report on genetic resource, 2009). The number of germplasm accessions, mainly landraces or traditional cultivars, conserved in Tanzania is over 5000. The management of plant germplasm falls under control of the National Plant Genetic Resources Centre (NPGRC) which is only responsible for surveys and inventorizing of the resources. This means there is little information on genetic diversity from gene bank accessions which are most useful to the breeders to select for the superior germplasm according to the breeders interest. Threats to crop genetic diversity in Tanzania including sorghum, cowpea and pigeonpea are caused by climate changes, drought and temperature

(heat) (Tanzania report on genetic resource, 2009). Entrance and establishment of staple food crop businesses which are desirable on the market interest, influences farmers to reject the local varieties which are more diverse and certain specific attributes of quality and agronomic importance. For example Mali and Tumia varieties of pigeonpeas are sourced from ICRISAT and used as commercial or cash crops in Babati and Karatu. These have a great demand in India.

Tanzania's grain legumes export is estimated at nearly 135 000 MT, valued at US\$ 54 million each year (Website: <http://www.icrisat-tropicallegumes.org>). Pigeonpea and cowpea account for approximately 56% and 16% of the total volume of exports respectively (Website: <http://www.icrisat-tropicallegumes.org>). MTAMA 1 and MACIA varieties of sorghum originated from Kenya and are used in making beverages (Eagle in Tanzania and Senator beer in Kenya).

Richard Lankau, reported that "If any one type is removed from the system, the cycle can break down, and the community becomes dominated by a single species." Therefore diversity within important staple crops in Tanzania is reportedly threatened and a number of crop species are under threat of extinction with some of these having important uses (Tanzania report on genetic resource, 2009). Species with greater genetic diversity are more likely to be able to evolve in response to a changing environment than those with low diversity while species that lack genetic diversity may experience high mortality due to among other factors, climate change, drought, temperature, even in the environments that are not changing (Hunter, 1996). Several research results (Bekele, 1983; Demissie and Bjornstrand, 1996; Staub *et al.*, 1997; Keneni *et al.*, 2007) have reported significant impact of genetic diversity on crop productivity, resulting from increased breeding flexibility and long term selection gains.

Although genetic diversity and morphological characterization for various crop species have been done worldwide, little information is available about the genetic diversity characterization using morphological approach in cowpea, sorghum and pigeon pea in Tanzania, where also research activity for these particular crops is low. This work aims at assessing genetic diversity and characterization of locally adapted sorghum, cowpea and pigeon pea landraces in Tanzania using morphological approach and materials obtained from the study will assist in breeding programmes for these crops.

1.3 Objectives

1.3.1 Overall objective

- i. To determine diversity of three food security crop accessions in Tanzania.

1.3.2 Specific objectives

- i. To assess genotype performance in agronomic traits of three selected crops.
- ii. To determine phylogenetic relationships of the three selected crops based on agro-morphological traits.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Cowpea, Pigeonpea and Sorghum Production Constraints

The production of most of the crops like, cowpea, pigeonpea, sorghum in tropical Africa are constrained by a number of stress factors, including a complex of insect, disease organisms and abiotic stresses like drought, high temperatures and low soil fertility (Ngugi *et al.*, 2002). Many crops are susceptible to a wide variety of pests and pathogens that attack the crop at all stages of growth (Allen, 1983). This significantly reduces the quantity and quality of production (Chauhan *et al.*, 1987). Different disease complexes affect crop production in semi arid countries in East Africa including Tanzania, often reduce production and cause up to 90-100% yield loss under severe epidemics depending on environmental conditions and nature of the crop (Abebe, 2008 and IITA, 2000).

However, the threat of climate change and global warming leading to variable and drier climate, still no clear policy and government commitment for the development of these crops which can prove to be of use in this era of changing climate. These crops have a lot of undeveloped genetic potential and that's partly what this study aims to address. Agro-morphological studies need to be carried out so as to unlock this genetic potential and therefore used to address the issue of food security and to mitigate and adapt to the global warming and climate change.

2.1.1 Abiotic stress in cowpea, pigeonpea and sorghum

In abiotic (drought) stress of these three crops was considered in study of genetic diversity and collected as qualitative data (abiotic reaction stress or senescence) in order to know how they can vary when affected by drought using different accessions collected.

Even though cowpea, pigeonpea and sorghum for a while can tolerate drought, but still there is a need of doing more research in order to get many materials to combat the problem. Agricultural drought occurs when there is not enough moisture available at the right time for the growth and development of crops. As a result, yields and/or absolute production decline (Glantz, 1987). Diagram below shows the dimension of drought.

DROUGHT → Failure of crops → Food shortage → Greater demands in the international markets → Reduction of stocks → Price increases → Difficulties in buying → Famine

The dimensions of drought (Garcia, 1981).

Drought tolerance has been shown to be highly complex trait, influenced by many different genes and should not be regarded as a unique heritable trait, but as a complex of often fully unrelated plant properties (Visser, 1994). Working on drought stress of cowpea found that the flowering stage is the most susceptible to severe imposed stress (-14 to -28 bars leaf water potential) (Hiler *et al.* (1972). The unpredictable and variable forms in which drought stress will manifest itself, makes selection of promising individual plants and breeding for drought tolerance extremely difficult. Drought can hardly be separated from other important abiotic stresses such as temperature and salinity. Due to these interrelations, no single mechanism exists by which multiple stresses are alleviated.

Moisture stress contributes to poor crop performance and low yield. Insufficient, unevenly distributed, and unpredictable rainfall are usually experienced in drier parts of Tanzania. Typically, rain may be abundant and perhaps wasted through runoff or in some years much rain may fall completely outside the growing season. In other years, the amount of rain may be low and occur after the crops have germinated. Overall, soil moisture may be

severely useless under such conditions. Consequently, in almost all lowland areas, crops are prone to periodic moisture stress in one way or another because of such adverse effects (EARO, 2001). The effect of moisture stress on crop yield is dependent on the stage of plant development. Anthesis and grain filling stages appear to be most vulnerable. Occurrence of drought at these stages may result in reduced yield and/or complete crop failure (Khanna-Chopra and Sinha, 1988). However, drought stress at the beginning of the growing season (seedling stage) will severely affect plant establishment, sorghum has the capacity to recover soon after the onset of rain. Most of the crops including cowpea, pigeonpea and sorghum have growing periods ranging from 60 to 120 days (FAO, 1987). According to FAO classification of climates, fewer than 120 days of growing period are described as dry land crops (FAO, 1987).

Crop productivity is the function of the genetic potential of the crops and of the total environment in which the crops are growing. However, in the dry land areas, the environment is more yield limiting and hinders crops from expressing their full genetic potential (Ceccarelli *et al.*, 2004). Evaluation of accessions in an area of adaption of a particular collection is vital to develop high yielding stable varieties (Frankel, 1970). Therefore assessing the performance of cowpea, pigeonpea and sorghum landraces by using quantitative characters like days to flowering, days to maturity, yield and qualitative traits like senescence of the crop etc are very important since this will enable a breeder to identify the best performing genotypes.

In Tanzania, the incidence of drought has increased from year to year. In the past, when the rainfall situation was relatively better, farmers used to grow different late maturing crop landraces. In times of delayed onset of rainfall, and shortened rainy seasons, farmers could switch to growing early maturing crops including cowpea, pigeonpea and sorghum.

Nevertheless, due to the prevalent shift in the rainfall patterns, farmers are increasingly growing less productive early maturing varieties, leading to loss of highly productive late maturing landraces. This suggests an urgent need to conserve traditional varieties. Hence, knowledge of the diversity of landraces and better understanding of qualitative and quantitative characters present in the accessions in order to be used by breeder to combat the drought stress effects of crop growth and development processes. For example quantitative characteristics like days to maturity if is early or late maturing, to drought would help breeders to improve drought tolerance /escaper of crop plants more effectively. Also landraces shows waxy bloom as qualitative characteristic helps plant to tolerate drought (Ceccarelli *et al.*, 2004) (Figure 1).



Figure 1: Sorghum landraces shows waxy bloom characteristic which helps plant to tolerate drought

2.1.2 Biotic stresses

In biotic includes effects of diseases and insect pests of the crops. This character was collected as qualitative data (biotic reaction stress) in order to know how these accessions in a particular crop can vary when affected by diseases or insect pests by using different accessions collected as shown in figure 2.



Figure 2: Sorghum affected by disease

2.1.3 Cowpea

Cowpea (*Vigna unguiculata* (L.)Walp.) which belongs to the family Fabaceae is one of the most important pulse crops native to central Africa. Cowpea (*Vigna unguiculata*) is one of the most ancient human food sources and has probably been used as a crop plant since Neolithic times (Summerfield *et al.*, 1974). A lack of archaeological evidence has resulted in contradicting views supporting Africa, Asia, and South America as origin (Summerfield *et al.*, 1974; Tindall, 1983; Coetzee, 1995). One view is that cowpea was introduced from Africa to the Indian sub-continent approximately 2000 to 3500 years ago

(Allen, 1983). Before 300 BC, cowpeas had reached Europe and possibly North Africa from Asia. In the 17th century AD the Spanish took the crop to West India. The slave trade from West Africa resulted in the crop reaching the southern USA early in the 18th century. Another view was that the Transvaal region of the Republic of South Africa was the centre of speciation of *V. unguiculata*, due to the presence of most primitive wild varieties (Padulosi and Ng, 1997). Presently cowpea is grown throughout the tropic and subtropic areas around the whole world.

2.1.3.1 Diseases

Cowpea is susceptible to a wide variety of pests and pathogens that attack the crop at all stages of growth (Allen, 1983), for instance cowpea wilt caused by *Fusarium oscysporium*, cowpea root rust caused by a nematode (*Meloidogynes sp*) cowpea bacterial blight caused by *Xanthomonas vignicola* and powdery mildew caused by *microsphaera diffusa* (Figure 3). Losses due to diseases infection can be as high as 90% (IITA, 2000).



Figure 3: Cowpea affected by disease

2.1.3.2 Insects

Some of the major insect enemies of cowpea are cowpea weevil (*Callosobruchus maculatus*), cowpea cuculus (*Chalcodermus sermus*) and the southern cowpea weevil (*Mylabris quadrimaculatus*). Yield losses which can be caused by cowpea insect pest attacks reaches up to 90% (IITA, 2000).

2.1.4 Pigeonpea

Pigeonpea [*Cajanus cajan* (L.) Millsp] belongs to the genus *Cajanus*, subtribe *Cajaninae*, tribe Phaseoleae and family Fabaceae. The origin of the crop is India.

2.1.4.1 Diseases

Major and most destructive diseases of Pigeonpea are fusarium wilt caused by fungal pathogen (*Fusarium udum* Butler). The plant mortality up to 50% has been observed with severe infection of wilt (<http://www.krishisewa.com/articles/disease>). Stem rot (*Phytophthora dreschleri* var. *cajani*, sterility mosaic virus. The virus is spread under field conditions through *Eriophyid* mite. If plants get infected in early vegetative stage, it results in complete sterility of the plants. Infection at an early stage (45-day-old plants) depend on the level of infection (i.e., number of affected branches per plant) and range from 26 to 97% (Kannaiyan *et al.*, 1984).

2.1.4.2 Insects

Insects are the most important among biotic constraints to pigeonpea production worldwide, causing losses of more than \$ 1000 million every year (Lateef, 1991). More than 200 species of insects feed on pigeonpea, of which *Helicoverpa armigera*, *Maruca vitrata*, *Melanagromyza obtusa*, *Clavgralla* spp., *Nezara viridula* and *Callosobruchus*

spp. are the most important (Lateef, 1991). Of these, legume pod borer, *Helicoverpa armigera*, is the most destructive and notorious pest of the field crops (Lateef, 1991) sources of resistance to pod borer, pod wasp and Phytophthora (Sharma *et al.*, 2000). The use of deferent accessions in pigeonpea improvement for various qualitative traits has been reported long back but to a very limited extent (Lateef, 1991). The attention paid towards pigeonpea improvement, with the use of the landraces, yet, remarkable improvements in this area have been very few. Plant breeding history shows that diverse gene pools are the foundations for effective crop improvement programmes. Exotic gemplasm from weedy species has been used nearly exclusively as a source of genes for improving qualitatively inherited characters, such as disease resistance. The assessment of diversity has focused mainly on cultivated types in the primary gene pool and little is known of the extent of variation or the nature of traits available in local species belonging to other gene pools. Further, the taxonomic confusions and lack of evaluation information on traits of interest, particularly with reference to resistance to serious pests and diseases seem to have excluded their intensive study and utilization.

2.1.5 Sorghum

Sorghum (*Sorghum bicolor* L. Moench) is the fifth most important cereal grain crop originated from West Africa and staple food for millions of poor in semi-arid tropics of Africa and Asia (Hausmann *et al.*, 1999).

2.1.5.1 Diseases

Many types of fungus, some bacteria and viruses cause diseases in sorghum seedlings, roots, leaves, stalks and grain (examples are anthracnose (*Colletotrichum graminicola*), charcoal rot (*Macrophomina phaseolina*), gray leaf spot (*Cercospora sorghi*), smut (*Sporisorium spp*) (Frederikson *et al.*, 2000).

2.1.5.2 Insects

Cutworms (*Agrotis* and *Euxoa spp.*), Yellow sugarcane aphid (*Sipha flava*), Corn leaf aphid (*Rhopalosiphum maidis*). These are some species can damage stems and leaves in the sorghum (Greg *et al.*, 2007).

2.1.5.3 Adaptation to drought stress

Higher plants like cowpea, pigeonpea and sorghum when exposed to water stress, show a variety of morphological and physiological changes at the whole plant level believed to be an adaptation response to stress (Hsiao, 1973). For instance in figure 4, pigeonpea plants illustrates respond to yellowish due to drought.

These crops may cope with water stress by avoiding or escaping the periods of drought, in particular during the most sensitive periods of its development. One breeding strategy is to shorten the life cycle of a crop to enable it to mature safely during a rainfall period. For example, in the Sahel, very short season cowpeas developed by researchers at the International Institute of Tropical Agriculture (IITA) avoid drought by early maturing days before any substantial stress develops (Singh, 1987), whereby in this study days to maturity for all three crops will be among the quantitative traits to be considered in data collection.

These crops can endure or withstand a dry period by maintaining a favorable water balance under drought conditions by having a thicker layer of waxy material at the plant surface e.g. sorghum have this character (waxy bloom) and a more extensive and deeper rooting (Cowpea and pigeonpea) (Kramer, 1980).



Figure 4: Yellowish of pigeonpea, plants respond to yellowish due to drought

2.2 Genetic Diversity

Genetic diversity or the level of biodiversity refers to the total number of genetic characteristics in the genetic makeup of a species (NBII, 2011). It is distinguished from genetic variability, which describes the tendency of genetic characteristics to vary. Genetic diversity serves as a way for populations to adapt to changing environments (NBII, 2011). With more variation, it is more likely that some individuals in a population will possess variations of alleles that are suited for the environment. Those individuals are more likely to survive to produce offspring bearing that allele. The population will continue for more generations because of the success of these individuals (NBII, 2011).

2.2.1 Importance of Genetic Diversity for crop improvement

Genetic diversity is of fundamental importance in the continuity of a species as it provides the necessary adaptation to the prevailing biotic and abiotic environmental

conditions, and enables change in the genetic composition to cope with changes in the environment (Muhmut, 2012). Plant genetic resources have been defined as the “genetic material of plants, which is of value as a resource for the present and future generations of people” (IPGRI, 1993). A wide range of genetic variation is needed within species to help them adapt to changing environmental conditions and new insect pests and diseases (Schoen and Brown, 1993). The plants we use as crops either directly as food or as fodder for animals are dependent in terms of resilience and adaptability, on the broad genetic base of variation that exists both in the crops developed over millennia of farmer experimentation and from their landraces (Maxted, 2003). Almost all modern varieties of crops have been improved using genetic diversity derived directly from a wild relative.

Crop genetic resources are the product of the interaction between human and natural selection of the environment, yielding a set of domesticated crops and varieties used in agricultural production (Romina *et al.*, 2006). The uses of crop diversity go beyond the production of food. In many cases crop diversity is at the root of sustainable agriculture and provides environmental benefits (Romina *et al.*, 2006). Genetic diversity provides an extensive range of material fundamental for food, fiber, medicine, and industry (Teshome *et al.*, 1999). It is not only a necessary condition to improve yield and yield stability (Falco and Perrings, 2003; Tilman *et al.*, 2005), but also the raw material used by breeders to develop improved varieties (Buanec, 2005). It is also the basic condition for evolutionary success to species survival and adaptation (Rao and Hodgkin, 2002). Genetic diversity in specific crops includes landraces, primitive forms, cultivars, introductions, weedy and wild relatives of crop species (Harlan, 1992). In past reports indicated that, some sorghum landraces are resistant to shoot fly (Maiti *et al.*, 1984), disease resistance (Tegegne *et al.*, 1994), have high grain quality (Singh and Axtell, 1973), high sugar content (Subramanian *et al.*, 1987), cold tolerance (Singh, 1985) and drought tolerance

(Subudhi *et al.*, 2000). The large variation that has been observed in many local varieties is attributable to the diversity of environmental conditions in which it grows such as rainfall, temperature, altitude, growing period and edaphic factors. In Tanzania, the largest genetic diversity in, cowpea, pigeonpea and sorghum is reported in the central, lake and northern zone parts of the country (Lyimo and Myaka, (2001). In addition, the advantages with landraces, however, are that they perform well under moisture stress because they are best adapted to the local conditions.

Further landraces possess farmers' preferred attributes, in spite of their low productivity. The importance of landraces is also well recognized, particularly in the lowland areas where rainfall is unreliable and crop failures are common due to recurrent drought (Kebede and Menkir, 1987). Additionally, in the event of good seasons the local landraces yield better than the improved varieties; the improved varieties are likely to be attacked due to their extreme earliness (Adugna and Tesso, 2006), whereby in this study was seen for MTAMA 1 in sorghum and KOMBOA is improved and early mature was attacked by insect pest.

In sorghum growing of belts of Ethiopia, red and brown grain color, tallness, high biomass yield, early maturity, drought resistance qualities are the most important farmers' preferred traits for selecting sorghum varieties (Wortmann *et al.*, 2006). Although, Tanzania has wide genetic diversity available for cowpea, pigeonpea and sorghum still the improvement efforts are mainly focused on selection of genotypes from exotic sources (Adugna, 2007). As a result, the potential of the local landraces as sources of breeding material is not yet well known and exploited enough. Hence, knowledge of the diversity of landraces as a source of breeding material would be highly important. The proposed study, therefore, seeks to collect indigenous landraces. Knowledge about cowpea,

pigeopea and sorghum landraces, characterize them for their response of quantitative and qualitative traits including abiotic and biotic stresses to assess their potential as a source of novel genes for breeding programmes in Tanzania.

2.3 Genetic Variability

Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Variability is different from genetic diversity, which is the amount of variation seen in a particular population (Yale University, 1995). The variability of a trait describes how much that trait tends to vary in response to environmental and genetic influences (Yale University, 1995).

2.3.1 Importance of genetic variability in crop improvement

Genetic variability in a population is important for biodiversity (Sousa *et al.*, 2011) because without variability, it becomes difficult for a population to adapt to environmental changes and therefore makes it more prone to extinction. The possibility of achieving improvement in any crop depends on the magnitude of genetic variability. The efforts taken by Johanssen (1909) and East (1916) have led to the partitioning of total variability into genetic and environmental components and both heritable and non-heritable factors contributed to phenotypic variation in segregating populations and that variation in pure line is entirely due to environment (Johnson *et al.*, 1955).

Adaptability of genotypes varies due to their genetic differences. The environmental conditions have a significant effect on the expression of yield and other quantitative characters. In order to manage and use large genetic resource collections effectively, it is essential to determine the genetic and morphological characteristics of the material preserved (IBPGR and ICRISAT, 1993).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental Site of Study

Three experiments were conducted at Sokoine University of Agriculture (SUA) farm crop museum. SUA lies at the base of the Uluguru Mountains three kilometers from Morogoro town. The experimental area was located between 37° 39' 17.6" E/ 6° 50' 49.4" S at altitude of 539 meters above sea level. The station is distinguished by two main rain seasons; long rains season which starts early in March and ends in late May. Short rain season starts at the end of October and ends in late December.

3.2 Plant Materials

The study accessions were collected from Tanzania and Kenya gene banks. A total of 85 plant materials consisting of 32 pigeonpea, where 22 were from Tanzania and 10 from Kenya, 31 sorghum, 24 from Tanzania and 7 from Kenya and 22 cowpea, 19 from Tanzania and 7 from Kenya. Two checks of each crop were used in this particular study as shown in Tables 1, 2 and 3. The experiments were set out in March, 2014.

Table 1: Pigeopea accessions used in the study

Accession no.	Origin	Accession no.	Origin
TZA 5596	Tanzania	GBK 045980	Kenya
TZA 2509	Tanzania	GBK 045983	Kenya
TZA 5541	Tanzania	GBK 045990	Kenya
TZA 2464	Tanzania	GBK 045991	Kenya
TZA 2514	Tanzania	GBK 045993	Kenya
TZA 197	Tanzania	GBK 045995	Kenya
TZA 2439	Tanzania	GBK 046005	Kenya
TZA 2496	Tanzania	GBK 041787	Kenya
TZA 5555	Tanzania	GBK 045976	Kenya
TZA 2672	Tanzania	GBK 041802	Kenya
TZA 2466	Tanzania	TZA 2807	Tanzania
TZA 5582	Tanzania	TZA 5557	Tanzania
TZA 5463	Tanzania	TZA 2456	Tanzania
TZA 250	Tanzania	TZA 2785	Tanzania
TZA 5464	Tanzania	MALI (check)	Tanzania
TZA 253	Tanzania	KOMBOA (check)	Tanzania

Table 2: Sorghum accessions used in the study

Accession no.	Origin	Accession no.	Origin
TZA 3965	Tanzania	GBK 000365	Kenya
TZA 394	Tanzania	GBK 044667	Kenya
TZA 3991	Tanzania	GBK 000387	Kenya
TZA4222	Tanzania	GBK 028460	Kenya
TZA 4369	Tanzania	GBK 034278	Kenya
TZA 3147	Tanzania	GBK 033984	Kenya
TZA 471	Tanzania	GBK 000108	Kenya
TZA 4226	Tanzania	TZA 3228	Tanzania
TZA 4171	Tanzania	TZA 242	Tanzania
TZA 4004	Tanzania	TZA 4001	Tanzania
TZA 4189	Tanzania	TZA 2702	Tanzania
TZA 4027	Tanzania	TZA 195	Tanzania
TZA 4021	Tanzania	TZA 244	Tanzania
TZA 393	Tanzania	MACIA (check)	Tanzania
TZA 3205	Tanzania	KARI-MTAMA1 (check)	Tanzania
TZA 179	Tanzania		

Table 3: Cowpea accessions used in the study

Accession no.	Origin	Accession no.	Origin
TZA 130	Tanzania	GBK 047042	Kenya
TZA 2324	Tanzania	GBK013187	Kenya
TZA 2314	Tanzania	GBK 047036	Kenya
TZA 3847	Tanzania	TZA 263	Tanzania
TZA 3085	Tanzania	TZA 264	Tanzania
TZA 75	Tanzania	TZA 256	Tanzania
TZA 2694	Tanzania	TZA 3979	Tanzania
TZA 3625	Tanzania	TZA 3998	Tanzania
TZA 4108	Tanzania	TZA 2736	Tanzania
TZA 2970	Tanzania	VULI 2 (check)	Tanzania
TZA 3681	Tanzania	TUMAIN (check)	Tanzania

3.3 Experimental Design and Layout

The experiment was laid out in Randomised Complete Block Design (RCBD) with three replications of each crop. Experimental units consisted of two rows of each accession of five meters long with inter- and intra-row spacing of 50cm x 20cm cowpea, 120cm x 30cm pigeonpea and 75cm x 30cm sorghum. The trials were weeded manually with no fertilizer application and chemical to control insect pest and diseases. Two weeks after emergence, thinning was done to leave one seedling per hill for each crop.

3.4 Data Collection

The assessment of agro-morphological characteristic variations of the three selected crops were appropriately measured based on quantitative (e.g. plant height) and qualitative (e.g. pod or grain color) traits using the method of standardized crop descriptors

according to (IBPGR and ICRISAT, 1993) for sorghum and pigeonpea, also (IBPGR, 1983) for cowpea. Most of the data collected started at flowering stage.

3.5 Data Analysis

The data on 85 accessions with quantitative and qualitative traits of 31 sorghum, 22 cowpeas and 32 pigeonpea accessions were analyzed separately for each crop. Analysis of variance (ANOVA) was done using GenStat 15th version statistical package. Where ANOVA revealed significant differences means were separated using Duncan Multiple Range Test (DMRT) according to Steel and Torrie (1980) at 0.05 probability level.

The following statistical model was used for single crop analysis:

$$Y_{ijk} = \mu + \beta_i + r_j + \varepsilon_{ijk} \dots\dots\dots (1)$$

Where:

Y_{ijk} = measurement for i^{th} accession of j^{th} replicate in k^{th} plot

μ = overall mean

β_i = i^{th} treatment effect

r_j = j^{th} block effect (replication) and

ε_{ijk} = random experimental error

3.6 Estimates of Variance Components and Method of Determination

The form of ANOVA and expected composition of pertinent mean squares are presented in Table 4. Variance component estimates were obtained by equating the mean square for a source of variation to its expectations and solving for unknown, hence separated the effect of accessions, replications and their interaction. A fixed statistical model was used for analyzing variance. The data which were significant were then subjected to cluster

CHAPTER FOUR

4.0 RESULTS

4.1 Analyses of Variance among 85 Accession Populations of Cowpea (22), Sorghum (31) and Pigeonpea (32)

4.1.1 Analysis of variance for selected cowpea accessions

The analysis of variance revealed that most of the traits showed highly significant ($p < 0.001$) differences among the accessions of cowpea (Table 5). The trait of days to flowering, days to maturity, pods per plant, seeds per pod, pod length, pod width, seed width, terminal leaf length, terminal leaf width and yield showed greatest variation at $p < 0.001$, while seed length indicated higher variation with significant level of $p < 0.01$ and 100 seed weight showed significant difference among accessions at ($p < 0.05$). Seeds per pod did not show any significant variation among accessions.

Table 5: ANOVA summary for the studied variables mean squares given in cowpea

Source of variation	df	100swt (g)	DF	DM	P/PL	PL (cm)	PW (cm)	SW (mm)	TLL (cm)	TLW (cm)	YLD/Plot(m ²)	SL (mm)	S/PD	Mean squares (MS)	
														13.5	1.2
Treatments	21	14.7*	63.4***	34.3***	39.0***	4.1***	0.01***	0.7***	2.8***	1.8***	51419***	1.01**	1.1ns		
Error	42	7.8	12.9	5.4	5.7	0.9	0.004	0.2	0.5	0.3	7186	0.3	0.9		
Total	65														

Where: *** = 0.001, ** = 0.01, * = 0.05 significance levels and ns= no significant. df=degrees of freedom, 100sw=100 seed weight, DF=days to flowering, DM=days to maturity, P/PL=pods per plant, PL=pod length, PW=pod width, SW=seed width, TLL=terminal leaf length, TLW=terminal leaf width, SL= seed length and YLD = yield per plot(g) and S/PD=seeds per pod.

4.1.2 Mean performance of variables studied for selected cowpea accessions

The 100 seed weight ranged from 9.9g to 17.3g with a general mean of 13.5 g among cowpea accessions. The accessions TZA 130 and TZA 3625 had the highest 100 seed weight of 17.3g and 17.0g respectively, while TZA 2694 had the lowest seed weight of only 9.9g (Table 6). The coefficient of variation among the accessions in 100 seed weight was 20.6% with a standard error of the mean (SE) of 1.68. For days to 50% flowering, the accessions varied between 42 and 60 days. More than 73% of these accessions recorded less than 50 days to flowering.

However, six genotypes out of 22 had days to 50% flowering greater than 50 days, these can be considered to be late maturing populations. TZA 3625 had the most days to maturity (71) and TZA 3998 was the lowest with 59 days. Pod length ranged from the value of 13.5 for TZA3847 to 17.6 for TZA 2314. In terms of pod width 86% of the accessions ranged from 0.8 to 0.9 cm while three genotypes (TZA 3998, TZA 3085 and 3979) had 1cm width. GBK 047036 had the greatest number of pods per plant (15), while TZA 3998 had the smallest number of pods (1). For seed length, accession TZA 2324 was the longest (7.3mm) while TZA 3847 was the shortest in width (4.7mm). The widest seed width of 6.3mm was for TZA3625 and TZA 3847 was the lowest (4.6cm).

In seeds per pod there was no much variation since most of the accessions ranged between 16 to 17 seeds per pod, whereby only TZA 3998 and TUMAIN had 15 and 18 seeds per pod respectively. Accession TZA 3085 had the longest terminal leaf (14cm) and GBK 047036 had the shortest of terminal leaf (10cm). Terminal leaf width was measured the widest (9.8cm) with TZA 3998 genotype, while GBK 047036 recorded narrowest (6.9cm) terminal leaf width.

Table 6: Mean performances for the studied variables in 22 cowpea grown at SUA during the 2014 growing season

Acc. no	100swt	DF	DM	PL (cm)	PW (cm)	P/PL	SL (mm)	SW (mm)	S/SD	TLL (cm)	TLW (cm)	YLD/(m ² (g)
TZA 2314	12.5abc	43.3ab	65.7c-f	17.6h	0.9cde	6.3bcd	7.0ef	5.6b-e	17.6bc	11.7b-f	8.2b-e	219abc
VULI 2	16.3bc	42.7a	60.7ab	17.0e	0.9cde	13.3ef	6.1b-e	5.0ab	17.8bc	11.6b-e	8.6c-f	510e
TZA 75	14.2 abc	45.7a-g	66.3def	16.0c-h	0.9cde	6.3bcd	6.0b-e	5.3abc	16.5abc	10.9abc	7.4ab	120a
GBK 047042	15.0 abc	44.3a-d	59.7a	13.8ab	0.8a-d	9.7de	5.6abc	4.8ab	16.9abc	10.7ab	7.3ab	322bcd
TZA 3998	16.2 bc	50.3b-h	59.0a	17.4gh	1.0e	1.3a	6.9def	6.2de	15.5a	13.5gh	9.8h	136a
TUMAIN	10.5a	45.3a-e	65.3c-f	17.2fgh	0.9cde	5.0abc	6.4b-f	5.0ab	18.3c	11.5b-e	8.1b-e	442de
TZA 2970	13.3abc	45.3a-f	65.7c-f	15.2a-e	0.9cde	3.3abc	6.2b-e	5.3abc	16.1ab	11.5b-e	7.7a-d	192abc
TZA 4108	12.8abc	48.0a-g	68.0efg	15.7c-g	0.9cde	2.0ab	6.5b-f	6.0cde	16.9abc	11.6b-e	7.7a-d	111a
TZA 264	14.8abc	44.0a-d	61.3abc	16.4d-h	0.9cde	6.0a-d	5.8bcd	5.2abc	16.6abc	11.9b-f	7.9b-e	345cd
GBK 047036	13.1abc	50.7c-h	66.3def	14.2abc	0.8a-d	14.7f	5.5ab	4.8ab	17.0abc	10.0a	6.9a	338cd
TZA 3085	12.8abc	56.7hi	69.3fg	16.4d-h	1.0e	2.0ab	6.6c-f	6.3e	17.3abc	14.0h	9.7gh	94a
TZA 2324	10.6a	46.3a-g	68.0efg	15.4a-f	0.8a-d	3.3abc	7.3f	5.6b-e	17.4bc	11.0ab	7.8a-e	171ab
TZA 2694	9.9a	43.7abc	63.0a-d	15.6b-g	0.9cde	5.7a-d	5.9bcd	5.2abc	17.3abc	12.5d-g	8.8efg	411de
TZA 130	17.3c	45.7a-g	65.0c-f	15.7c-g	0.9cde	4.3abc	6.6c-f	5.4bcd	17.3abc	12.6efg	8.1b-c	184abc
TZA 3847	10.2a	46.0a-g	65.0c-f	13.5a	0.8a-d	6.0a-d	4.7a	4.6a	17.5bc	11.3a-e	7.6abc	236abc
TZA 3625	17.0bc	60.3i	71.0g	17.4gh	0.9cde	3.0abc	6.6c-f	6.3e	17.3abc	13.1fgh	9.5fgh	169ab
TZA 256	13.5abc	44.7a-d	62.3a-d	15.0a-d	0.8a-d	7.3cd	5.9bcd	5.0ab	17.8bc	12.0b-f	7.8a-e	342cd
TZA 263	14.0abc	47.3a-g	66.7def	15.8c-h	0.9cde	6.0a-d	6.1b-e	5.4bcd	16.4abc	12.1 b-f	8.6c-f	151a
TZA 2736	12.2abc	51.0d-h	64.3b-e	14.7a-d	0.9cde	4.0abc	5.8bcd	5.1ab	17.3abc	12.5d-g	8.8efg	248abc
GBK 013187	16.2bc	42.0a	59.0a	14.8a-d	0.8a-d	12.3ef	5.8bcd	4.8ab	17.3abc	11.2a-d	8.0b-e	547e
TZA 3979	13.1abc	52.3egh	69.0fg	16.1d-h	1.0e	4.7abc	6.6c-f	5.6d-e	17.6bc	12.3c-g	8.0b-e	189abc
TZA 3681	11.7ab	45.0a-d	65.7c-f	14.8a-d	0.8a-d	4.7abc	5.7abc	5.0ab	17.5bc	13.0fgh	8.5cde	330bcd
Mean	13.5	47.3	64.8	15.7	0.9	6.0	6.1	5.3	17.1	11.9	8.2	263.8
C.V %	20.6	7.6	3.6	6.1	6.8	39.9	9.1	8.0	5.6	5.9	6.4	32.1
SE	1.68	2.069	1.342	0.558	0.035	1.375	0.323	0.246	0.351	0.410	0.306	48.9

Among the studied accessions, GBK013187 showed the highest yield (547g/3.75m²) superscript it followed by the improved Vuli (510 g/3.75m²) and TUMAIN (442 g/3.75m²). The other landrace that yielded high was TZA2694 (411g/3.75m²). The lowest yielding accessions were TZA 3085 (94 g/3.75m²) and TZA 4108 (111g/3.75m²).

4.1.3 ANOVA for selected pigeonpea accessions

In pigeonpea the analysis of variance for the measured traits showed that most of the accessions were highly significant differently ($p < 0.001$) (Table 7). The traits days to flowering, days to maturity, plant height, seeds per pod, leaf length, leaf width demonstrated highest variation at $p < 0.001$. Days for duration of flowering, pod width, pod bearing length, branches per plant demonstrated variation at $p < 0.01$. Average racemes per plant and yield were found to be significantly different at ($p < 0.05$), while pod length and 100 seed weight were not significant at probability level of 0.05 which means there was no variation among those traits.

Table 7: ANOVA summary for the studied variables (Mean squares given) in pigeonpea

Source of Variation	df	100SW	DF	DM	DDF	PHT (cm)	PL (cm)	PW (cm)	S/PD (cm)	LL (cm)	LW (cm)	ARP (cm)	PBL (cm)	NB	YLD/M ² (g)	Mean square (MS)	
																MS	DF
Reps	2	10.4	328.3	465.1.	1302.9	1048.7	415.1	0.01	0.1	0.3	0.1	7889.2	311.5	48.2	126458.		
Treatments	31	6.1 ns	470.0 ***	281.6 ***	146.9 **	1490.0 ***	146.1 ns	0.03 **	0.8 ***	1.0 ***	0.4 ***	791.7 *	290.2 **	11.2 **	100219*		
Error	62	3.9	95.4	44.8	64.7	274.3	143.9	0.01	0.2	0.3	0.1	444.8	146.9	4.8	52212.		
Total	95																

Where: *** = 0.001, ** = 0.01, * = 0.05 significant of levels and ns = no significant, df = degree of freedom, 100SW = 100 seed weight, DF = days to flowering, DM = days to maturity, DDF = days of duration to flowering, PHT = plant height, PL = pod length, PW = pod width, S/PD = seeds per pod, LL = leaf length, LW = leaf width, ARP = average raceme number per plant, PBL = pod bearing length, NB = number of branches per plant and YLD = yield per plot (g)

4.1.4 Mean performance of pigeonpea accessions studied

In the pigeonpea landraces, 100 seed weight ranged from 12.1g to 18.4g with a common mean of 13.9 g among accessions. The accession TZA 2456 had the heaviest 100 seed weight of 18.4g, while TZA 5541 was the lightest at 12.1g (Table 8). The coefficient of variation among accessions in 100 seed weight was 14.2% with a standard error of 1.139. For days to 50% flowering, the accessions varied between 86 to 157 days. GBK 045991 had the longest days to flowering (157) and KOMBOA was the shortest with 86 days. Pod length ranged from the value of 6.0 to 10.8cm. The highest accession in plant height was MALI at 234.1 cm followed by GBK 045990 (224.5cm) and TZA 5582 (163cm) while KOMBOA was the lowest at 107.0cm. MALI and KOMBOA were used as checks and are improved varieties. In terms of pod length and width, the longest and widest landraces were TZA 2466 and TZA 2509, GBK045990 at 10.8cm and 1.3mm respectively.

In the case of seeds per pod 91% of the accessions ranged from 6 to 7 seeds with exception of only three genotypes (KOMBOA and TZA 2456, GBK045976) that had 5 and 5.3 respectively, so that the accessions do not have much variation. The longest and widest leaves at 10.7cm length, 4.7cm width was GBK 045991 and KOMBOA had the shortest and narrowest leaves at (8.0cm, 3.0cm) respectively. Accession GBK041787 had the greatest raceme number per plant (94) and TZA 2672 had the smallest at 34. The highest pod bearing length per plant was recorded (91.3cm) with GBK 045995 genotype, while KOMBOA recorded lowest (51.9cm) length. The accession, GBK 041787 showed the greatest number of branches per plant (17) compared to lowest TZA 5463 with (7) branches. TZA 2496 yielded the highest (946g/plot) among all accessions compared to the improved varieties like KOMBOA the lowest at (191g/plot) and Mali (777g/plot), followed by TZA 2785 with 900g/plot.

Table 8: Mean performances for the studied variables in 32 pigeonpea accessions grown at SUA during the 2014 growing season

Acc.no:	100 swt	DF	DM	DDM	PHT	PL	PW	SPD	LL	LW	ARP	PBL	NB	VLD/ M ² (e)
GBK 045993	13.7ab	137.3c-h	173.0 bcd	163.7a-d	211.5e-i	8.0a	1.0abc	6.0bcd	10.2efg	4.1e-i	80.3b-e	83.9de	13.0cde	749 bcd
GBK 041787	15.8abc	138.3d-h	177.0 bcd	169.0 a-d	212.2f-i	8.2a	1.2de	6.0bcd	9.8 c-g	4.2f-j	93.7e	83.2 de	16.7e	761 bcd
TZA 2807	12.7ab	118.0bc	168.3b	157.7ab	188.5b-g	9.7a	1.2de	6.0bcd	9.1b-e	3.6b-h	63.7 a-e	75.4a-e	11.0a-d	804cd
TZA 2456	18.4c	129.7 b-g	183.3def	172.7b-e	196.5 c-h	10.1a	1.2de	5.3ab	9.8 c-g	3.5a-d	57.7 a-e	70.4a-e	13.7de	570 a-d
TZA 5464	12.6ab	121.7 b-f	167.0b	156.0a	167.9bc	9.6a	1.1bcd	7.0e	9.0bcd	3.4abc	65.0 a-e	68.8a-e	10.3a-d	563 a-d
GBK 041802	14.2ab	125.3 b-f	171.7bcd	165.7 a-d	168.7bc	6.0a	1.0abc	6.3cde	8.3ab	3.3ab	53.7 a-e	81.2cde	10.7a-d	361 abc
TZA 2785	12.6ab	125.3 b-f	172.7 bcd	157.3ab	193.1b-h	10.3a	1.1bcd	6.3cde	10.0d-g	3.9c-h	86.0de	79.3cde	8.0ab	900 d
TZA 2466	15.5abc	134.0c-h	175.0 bcd	166.3 a-d	206.0d-i	10.8a	1.0abc	6.3cde	10.4fg	3.8b-g	71.3 a-e	85.8 de	8.7abc	788cd
TZA 5541	12.1a	122.3 b-f	167.7b	163.3abc	179.8b-f	7.7a	1.0abc	7.0e	9.8 c-g	3.7b-f	73.0 a-e	78.0 b-e	11.7bcd	724 bcd
GBK 045983	14.5ab	126.0 b-f	169.0bc	163.7abc	196.4c-h	8.2a	0.9ab	6.0bcd	9.6c-f	3.5a-d	84.7cde	88.6 de	9.3a-d	793 cd
TZA 197	12.5 ab	132.3b-g	182.7de	175.0cde	191.1 b-g	9.5a	1.0abc	5.7abc	9.7 c-g	3.5a-d	73.0 a-e	69.8a-e	11.0a-d	594 a-d
TZA 5557	13.2 ab	119.3bcd	168.3b	156.0a	176.8bcd	9.6a	1.2de	6.7de	9.7 c-g	3.6b-e	35.7a	71.68a-e	9.0abc	726 bcd
TZA 253	12.4 ab	132.7b-g	176.7 bcd	174.0cde	198.3 c-h	8.3a	1.1bcd	6.7 de	10.5fg	4.0d-h	44.7a-d	76.8 b-e	9.0abc	562 a-d
GBK 045980	13.4 ab	139.3e-i	182.0cde	171.7 a-d	190.9 b-g	7.8a	1.1bcd	6.0bcd	9.9 c-g	3.8b-g	43.0abc	68.9a-e	11.0a-d	383abc
TZA 2672	12.8 ab	137.0c-h	175.7 bcd	171.3 a-d	167.1bc	10.2a	0.8a	6.3cde	9.6c-f	3.5a-d	34.3a	58.8abc	8.7abc	367 abc
GBK 045995	13.2 ab	114.3b	166.0b	163.0abc	192.4b-h	9.0a	1.1bcd	5.7abc	9.6c-f	3.5a-d	50.7a-d	91.3e	9.3a-d	413 abc
TZA 5555	13.7 ab	119.3bcd	173.3 bcd	165.0 a-d	183.7 b-g	9.5a	1.1bcd	7.0e	9.7c-g	3.6b-e	44.3a-d	73.5a-e	9.0abc	732 bcd
TZA 5463	13.9 ab	124.7 b-f	174.3 bcd	167.3 a-d	175.5bcd	9.7a	1.0abc	6.7 de	9.7 c-g	3.6b-e	48.0a-d	77.4 b-e	7.0a	598 a-d
KOMBOA	12.7 ab	86.3a	141.7a	161.7a-d	107.0a	7.8a	1.1bcd	5.0a	8.0 a	3.0a	40.7ab	51.9a	10.7a-d	191a
TZA 2514	14.4 ab	121.0b-f	171.3 bcd	164.7 a-d	178.6b-e	8.4a	1.2de	6.7 de	10.2efg	4.0d-h	38.3ab	85.9 de	9.0abc	693bcd
TZA 2509	15.2abc	121.0b-f	178.7b-e	169.7 a-d	179.5b-f	10.2a	1.3e	6.0bcd	10.3fg	3.8b-g	56.7 a-e	67.7a-e	8.0abc	496 a-d
TZA 2439	13.6 ab	128.0d-g	173.0 bcd	174.7cde	183.3 b-g	9.4a	1.1bcd	6.3cde	10.3fg	4.0d-h	48.0a-d	79.0b-e	8.3ab	526 a-d
TZA 5596	13.1 ab	128.3 b-g	173.0 bcd	170.0 a-d	185.6 b-g	9.7a	1.2de	7.0e	9.8 c-g	3.7b-f	43.3abc	74.5a-e	7.7ab	578 a-d
GBK 045991	12.5 ab	156.7i	194.7fg	187.7e	214.6ghi	7.2a	1.1bcd	6.3cde	10.7g	4.7i	42.7abc	54.9ab	11.0a-d	363 abc
GBK 045990	14.3 ab	151.7hi	191.0efg	179.3de	224.5hi	8.2a	1.3c	6.0bcd	10.4fg	4.4hi	59.7 a-e	76.5b-e	8.7abc	578 a-d
TZA 2464	14.8abc	120.0b-e	171.0 bcd	166.3 a-d	194.0b-h	7.9a	1.1bcd	6.7 de	10.4fg	3.6b-e	57.3 a-e	78.0 b-e	9.3a-d	631 a-d
MALI	16.2bc	140.3f-i	179.3b-e	175.7cde	234.1i	8.4a	1.1bcd	6.0bcd	10.2efg	4.3g-k	75.3 a-e	83.5de	11.7bcd	777 bcd
TZA 2496	15.8abc	120.7b-e	170.0 bcd	164.7 a-d	199.0 c-h	6.3a	1.0abc	6.0bcd	10.2efg	4.1e-i	53.7 a-e	90.9e	10.0a-d	946 d
TZA 250	14.0 ab	129.7b-g	176.0 bcd	171.7 a-d	188.5b-g	7.2a	1.1bcd	6.7 de	10.4fg	4.0d-h	61.0 a-e	90.7e	8.3ab	542 a-d
GBK 046005	15.3abc	145.7ghi	198.0g	174.3cde	197.3 c-h	6.6a	1.2de	6.0bcd	9.8 c-g	4.3g-k	33.7a	69.9a-e	9.7a-d	322ab
TZA 5582	12.3 ab	131.7 b-g	176.0 bcd	168.7 a-d	163.0b	9.8a	1.2de	7.0e	8.9abc	3.4abc	42.3abc	65.1a-d	10.3a-d	601 a-d
GBK 045976	14.0 ab	133.3b-h	174.0 bcd	162.3abc	205.0d-i	7.7a	1.2de	5.3ab	9.6c-f	3.8b-g	62.7 a-e	74.8a-e	10.0a-d	362 abc
Mean	13.9	128.5	174.7	167.8	189.1	9.1	1.1	6.3	9.8	3.8	56.8	75.8	10.0	594
C.V %	14.2	7.6	3.8	4.8	8.8	11.5	10.4	7.2	5.4	7.4	37.1	16.0	22.0	38.5
SE	1.139	5.538	3.865	4.642	9.560	6.93	0.066	0.259	0.303	0.163	12.18	7.00	1.27	131.9

4.1.5 ANOVA for selected sorghum accessions

Most agronomic traits in sorghum accessions analysis of variance revealed highly significant ($p < 0.001$) difference (Table 9). 100 seed weight, days to flowering, plant height, inflorescence length, inflorescence width, grain number per panicle and yield illustrated the highest significance at 0.001. Nodal tillers per plot, number of flowering stems per plot and grain weight per panicle were found to be significant at P-value 0.01, while basal tillers per plot were not significant at the probability level of 0.05.

Table 9: ANOVA summary for the studied variables mean squares (MS) given in sorghum

Source of variation	df	100SW	DF	BTP	NTP	HP	PHT	NFS	IL	IW	GNP	GWP	YLD/M ² (g)	Mean Squares (MS)		
														(cm)	(cm)	(cm)
Reps	2	0.04	29.1	4.2	0.5	0.2	1473.2	2.3	2.3	1.2	49806	39.9	42141			
Treatments	30	0.45 ***	153.1 ***	0.8 ns	0.4 **	0.2 *	8107.4 ***	8.9 **	143.1 ***	6.9 ***	1256105 ***	384.6 **	104413 ***			
Error	60	0.08	29.7	0.9	0.2	0.1	497.3	4.1	3.1	2.2	449692	174.5	33033			
Total	92															

Where: *** = 0.001, ** = 0.01, * = 0.05 significant of levels and ns = no significant df=degree of freedom, 100SW=100 seed weight, DF=days to flowering, BTP=basal tillers per plot, NTP=nodal tillers per plot, HP=head per plot, PHT=plant height, NFS=number of flowering stem per plant, IL=inflorrescence length, IW=inflorrescence width, GNP=grain number per panicle and YLD=yield per plot(g)

4.1.6 Mean performance of variables studied in sorghum accessions

The 100 seed weight variable ranged from 1.3g to 2.6g with an overall mean of 1.8g among accessions of sorghum (Table 10). The accessions TZA3228 and GBK 000108 had the highest 100 seed weight of 2.6g while TZA 4001 was lowest, with only 1.3g. The coefficient of variation among the accessions in terms of 100 seed weight was 15% with a standard error of mean (of 0.161). Days to 50% flowering of these accessions varied between 67 and 94 days. Over 60% of these accessions recorded >80 days to flowering. However, twelve genotypes out of 31 had days to 50% flowering less than 80 days, these can be considered to be early maturing populations. Plant height ranged from the value of 145.8 for MACIA to 384.7 for TZA 2702. TZA 2702 had also longest inflorescence (39.4 cm) while TZA 4222 had the shortest (11.1cm) inflorescence. In terms of IW, genotype TZA 3991 had the widest inflorescence at 11.6cm and TZA 471 was the narrowest (4.8cm). TZA 4189 had the greatest number of grains per panicle (3134) and TZA 2702 had the lowest grain number (246). Grain weight per panicle measured the heaviest (67.4g) with TZA 3991 genotype, while TZA 2702 recorded the lightest (5.8 g). Yield per plot measured the highest with accessions of TZA 3991 (777g) followed by GBK 000387 (766g) and GBK 044667 (726g); whereas TZA 2702 had the lowest (61g).

Table 10: Mean performances for the studied variables in 31 sorghum grown at SUA during the 2014 growing season

Acc.no:	100SW (g)	DF	BTP	NTP	HP	PHT (cm)	NFS	IL (cm)	IW (cm)	GNP	GWP (g)	YLD ¹ m ² (g)
TZA 3205	1.4ab	73abc	0.0a	10.0de	1.7abc	252.7d-g	4.7	18.7e-i	7.1 a-d	1796 b-h	36.6b-e	303a-e
GBK 000108	2.6h	85d-k	1.0ab		2.0bc	286.9f-i	2.3a-d	20.1g-k	8.2 b-e	2188 b-h	53.3def	706f
GBK 000387	2.3d-f	73abc	0.0a	0.3ab	1.0a	196.7bc	0.3a	19.1f-i	11.3 fg	2292 b-h	58.1ef	766f
TZA 4189	1.4ab	87f-k	0.0a	3.0 a-d	1.0a	307.4j-o	0.7ab	20.9g-k	7.9 bcd	3134 h	49.8c-f	526c-f
GBK 028460	2.0b-g	75a-d	0.0a	1.7 abc	1.0a	244.8def	1.0abc	16.2 b-f	9.8 d-g	2056 b-h	45.8 b-f	650def
TZA 3991	1.8a-f	78b-f	0.0a	3.0 a-d	1.3ab	236.0 de	1.0 abc	19.3f-i	11.6 g	2878 fgh	67.4f	777f
TZA 3147	1.4ab	90h-k	0.7ab	8.3cde	1.3ab	246.7 def	3.0 a-d	15.3b-e	10.8 efg	2618d-h	46.5 b-f	544c-f
TZA 179	1.5abc	91ijk	0.0a	0.0a	1.3ab	299.3h-m	2.0 abc	19.8g-j	6.7 abc	1328 a-c	23.2abc	196abc
TZA 4001	1.3a	89g-k	1.0ab	5.3a-e	1.0a	227.4cd	1.7 abc	13.4ab	7.8bcd	2674 e-h	37.2 b-e	328a-e
TZA 4004	1.4ab	86e-k	0.0a	2.0 abc	1.0a	260.2d-h	2.7 a-d	16.0 b-f	8.7b-f	2304 b-h	41.7b-f	471b-f
MACIA	2.3d-f	77a-f	0.0a	0.0a	1.0a	145.8a	2.0 abc	21.6h-k	6.5abc	2052 b-h	43.4 b-f	186abc
TZA 4171	1.5abc	70ab	0.0a	0.0a	1.7abc	254.8d-g	3.7a-e	19.1f-i	7.5a-d	1386a-e	33.8 b-e	482 b-f
TZA 4021	1.5abc	85d-k	0.7a	5.3a-e	1.0a	294.3g-l	7.3e	18.6d-i	9.7d-g	1842 b-h	38.1 b-e	545e-f
TZA 242	1.8 a-f	93jk	0.0a	0.3ab	1.0a	357.7pq	5.0cde	39.8n	7.3a-d	1251abc	28.7a-d	160ab
TZA 4369	2.0 b-g	83c-j	0.0a	2.7a-d	1.0a	323.6l-p	1.0 abc	23.0jk	8.9b-g	1908 b-h	44.7 b-f	542e-f
TZA 394	1.7a-e	84c-k	1.3ab	1.0 abc	1.0a	264.1d-i	2.3 a-d	15.0bcd	7.7 bcd	2517c-h	43.9 b-f	659ef
GBK 00441	1.8 a-f	76a-e	0.0a	2.7 a-d	1.0a	237.1 de	0.3a	21.1g-k	7.8 bcd	2070 b-h	39.5 b-e	448 b-f
TZA 471	1.7a-e	94k	0.0a	0.0a	1.0a	341.8mop	0.7ab	30.4i	4.8a	1010 ab	22.2ab	287a-d
TZA 3965	1.7a-e	84c-k	0.0a	2.7 a-d	1.3ab	299.5h-n	1.0 abc	14.3bc	7.9 bcd	2123 b-h	36.5 b-e	478 b-f
TZA 195	2.3d-g	87f-k	0.0a	0.7abc	1.0a	303.3i-o	1.3 abc	18.1d-h	6.4abc	1318a-d	30.6bcd	153ab
TZA 2702	2.0 b-c	90h-k	2.0b	1.0 abc	1.0a	384.7q	6.0de	39.4n	8.3 b-e	246a	5.8a	61a
TZA 4222	1.6a-d	79b-g	1.0ab	4.7a-e	1.0a	240.2de	2.7 a-d	11.1a	6.2ab	3021gh	41.1 b-e	472 b-f
TZA 3228	2.6h	85d-k	0.0a	0.0a	1.0a	339.7m-p	2.7 a-d	34.5m	8.3 b-c	1726b-g	45.5 b-f	413 b-f
TZA 4226	1.4ab	77a-f	1.0ab	11.3e	1.7abc	241.3 de	3.3 a-d	14.4bc	7.3a-d	2904fgh	44.8 b-f	453 b-f
TZA 393	1.5abc	85d-k	0.3ab	2.3 abc	1.0a	266.5d-h	2.7 a-d	15.9b-f	8.3 b-e	2572c-h	48.3 b-f	602def
MTAMA 1	2.2c-f	67a	0.0a	0.0a	1.0a	176.6ab	0.7ab	23.4k	7.8 bcd	1251abc	39.6 b-e	449 b-f
TZA 4027	1.7a-e	69ab	0.3a	10.7e	1.7abc	247.7 def	1.3 abc	17.7ijk	9.7d-g	2450 c-h	52.2def	547c-f
GBK 34278	1.8 a-f	80c-h	0.0a	4.0a-c	1.0a	312.5k-o	1.0 abc	17.7c-g	6.6abc	2130 b-h	44.2 b-f	561def
GBK 044667	2.5eh	81c-i	0.0a	1.7 abc	1.0a	286.4f-l	0.7ab	16.2 b-f	7.2a-d	1821 b-h	43.1 b-f	726f
GBK 033984	2.0 b-g	83c-j	0.0a	0.0a	1.0a	323.2l-p	0.7ab	17.8c-g	9.3c-g	1688b-f	35.2 b-e	600def
GBK 000365	1.8 a-d	87f-k	0.0a	1.3 abc	1.3ab	276.2e-k	1.0 abc	18.9e-i	8.7b-f	1943 b-h	40.9 b-c	473 b-f
Mean	1.8	82.1	0.3	3.0	1.8	273.4	2.2	20.3	8.1	2015	40.7	470
CV %	15.3	6.6	323.7	128.7	30.3	8.2	94.5	9.1	18.2	33.3	32.5	38.7
SE	0.161	3.147	0.563	2.252	0.205	12.87	1.173	1.074	0.86	387.2	7.63	104.9

4.2 Genetic Diversity

4.2.1 Cowpea

The agronomic traits analyzed using Shannon-weiner diversity index (H) for the 22 landraces of cowpea ranged from 3.975 pods per plant to 4.188 for days to maturity and number of seeds per pod. Hence days to maturity illustrated the highest diversity (4.188) among all accessions whereby number of pods per plant showed the lowest (3.975) (Table 11). The mean diversity index of 22 accessions calculated from the frequency of 12 quantitative traits was 4.153 indicating comparatively high diversity in cowpea.

Table 11: Shannon Weiner diversity index (H) estimates for 22 agronomic traits of cowpea accessions

Descriptor	Diversity index (H)
100Seed weight (g)	4.162
Days to flowering	4.184
Days to maturity	4.188
Pod length (cm)	4.186
Pods/plant	3.975
Pod width (cm)	4.185
Seed length (mm)	4.183
Seeds/pod	4.188
Seed width (mm)	4.183
Terminal leaf length (cm)	4.185
Terminal leaf width (cm)	4.183
Yield (g)	4.039
Mean	4.153

4.2.2 Pigeonpea

The agronomic traits of pigeon pea studied by using Shannon diversity index (H) having 32 accessions ranged from 4.562 to 4.274 (Table 12). Days for duration of flowering, days to maturity and leaf length indicated the highest diversity index (H) of 4.562. Pod length demonstrated the lowest diversity index of 4.274. The mean diversity index of accessions calculated from the frequency of 14 quantitative traits was 4.518 (Table 12). Indicating comparatively high diversity in pigeonpea.

Table 12: Shannon Weiner diversity index (H) estimates for 32 agronomic traits of pigeonpea accessions

Descriptor	Diversity index (H)
Days to flowering	4.558
Days to duration flowering	4.562
Days to maturity	4.562
Leaf length	4.562
Leaf width	4.558
100 seed weight	4.554
Raceme number per plant	4.456
Number of branches	4.527
Seed per pod	4.559
Pod bearing length	4.547
Pod length	4.274
Pod width	4.557
Yield	4.464
Mean	4.518

4.2.3 Sorghum

The quantitative traits of sorghum studied by using Shannon diversity index (H) having 31 accessions ranged from 2.180 to 4.527 (Table 13). Days to flowering showed the highest diversity index (4.527) and number of basal tillers per plot was the lowest (2.180) among the sorghum accessions. The mean diversity index of accessions obtained from the occurrence of 12 traits was 4.168 indicating high diversity of sorghum.

Table 13: Shannon Weiner diversity index (H) estimates for 31 agronomic traits of sorghum accessions

Descriptor	Diversity index (H)
Plant height	4.512
Number of flowering stem per plant	3.961
Days to flowering	4.527
Inflorescence length	4.480
Inflorescence width	4.505
Grain per panicle	4.437
Grain weight per panicle	4.452
Number of head per panicle	4.483
100 seed weight	4.505
Number of basal tiller per plot	2.180
Number of nodal tillers per plot	3.627
Grain yield	4.346
Mean	4.168

4.3 Correlations matrix for Cowpea, Pigeonpea and Sorghum Agro-Morphological Characters

4.3.1 Cowpea

4.3.1.1 Agronomic characters

The cowpea agronomic characters in correlation matrix showed that most characters had highly significant and positive correlation coefficients (Table 14). The terminal leaf length demonstrated highly significant and positive correlation with terminal leaf width ($r=0.899^{***}$), pod length with pod width ($r=0.823^{***}$), seed length, pod width and pods per plant with seed width ($r=0.770^{***}$ and 0.790^{***}) respectively. Pods per plant with yield ($r=0.712^{***}$), pods per plant with seed width ($r=0.696^{***}$) and seed width with yield ($r=0.688^{***}$) were also highly correlated. Days to flowering was significant and positively correlated with days to maturity ($r=0.636^{**}$), days to flowering with seed width ($r=0.672^{***}$), days to maturity with yield ($r=0.612^{**}$).

Table 14: Correlation matrix Pearson (n) between agronomic characters calculated from 22 cowpea accessions

Variables	DF	DM	P/PL	TLL	TLW	100SW	PL	PW	SPD	SL	SW	YLD
Days to flowering	1											
Days to maturity	0.636**	1										
Pods per plant	0.418	0.447*	1									
Terminal leaf length	0.489*	0.160	0.638**	1								
Terminal leaf width	0.504*	0.064	0.487*	0.899***	1							
100 seed weight (g)	0.142	0.288	0.204	0.153	0.205	1						
Pod length (cm)	0.235	0.155	0.326	0.457*	0.575**	0.278	1					
Pod width(cm)	0.423*	0.346	0.597**	0.635**	0.619**	0.200	0.823***	1				
Seeds per pod	0.093	0.210	0.238	0.079	0.112	-0.347	0.019	0.177	1			
Seed length(mm)	0.269	0.332	0.497*	0.359	0.418	0.147	0.728***	0.700***	-0.037	1		
Seed width(mm)	0.672***	0.494*	0.696***	0.641**	0.655**	0.227	0.645**	0.790***	-0.301	0.770***	1	-
Yield (g)	0.556**	0.612**	0.712***	0.316	0.193	-0.001	0.150	0.477*	0.456	0.415	0.688***	1

4.3.1.2 Morphological characters

The correlation matrix of morphological characters in table 15 indicates few associations being significant, though all associations were positive. The raceme position was strongly correlated ($r=0.558^*$) with immature pod pigmentation. Twinning tendency and growth pattern were significantly and positively correlated with immature pod pigmentation at ($r=0.524^*$, $r=0.513^*$) respectively. Correlations between twinning tendency with raceme position was ($r= 0.458^*$). Also for pod attachment to peduncle with pod curvature their significant correlation was ($r=0.425^*$).

Table 15: Correlation matrix Pearson (n) between morphological characters calculated from 22 cowpea accessions

Variables	GH	GP	TT	PP	TLS	RP	PAP	IPP	LC	PC	SS	Ttex.	RBSD
GH	1												
GP	0.335	1											
TT	0.143	0.162	1										
PP	0.241	0.244	0.160	1									
TLS	0.223	0.137	0.251	0.106	1								
RP	0.150	0.390	0.458*	0.046	0.000	1							
PAP	0.046	0.040	0.140	0.292	0.088	0.124	1						
IPP	0.045	0.513*	0.524*	0.011	0.019	0.558*	0.074	1					
LC	0.225	0.076	0.215	0.372	0.040	0.076	0.014	0.071	1				
PC	0.071	0.241	0.084	0.214	0.162	0.268	0.425*	0.249	0.179	1			
SS	0.118	0.001	0.191	0.210	0.168	0.040	0.063	0.073	0.065	0.116	1		
Ttex.	0.349	0.289	0.183	0.147	0.348	0.571	0.139	0.169	0.041	0.298	0.001	1	
RBSD	0.117	0.002	0.057	0.004	0.106	0.156	0.243	0.203	0.129	0.351	0.212	0.228	1

NB: GH=growth habit, GP=growth pattern, TT=twining tendency, PP=plant pigmentation, TLS=terminal leaf shape, RP=raceme position, PAP=pod attachment to peduncle, IPP=immature pod pigmentation, LC=leaf color, PC=leaf color, SS=seed shape, Ttex =tessa texture, RBSD=reaction to biotic stress (diseases).

4.3.2 Correlation between pigeonpea agro-morphological characters

4.3.2.1 Agronomic characters

The agronomic characters of pigeonpea in correlation matrix revealed to have significant and positive pair-wise correlation coefficients (Table 16). Days to flowering was highly significant and positively correlated with days to maturity ($r=0.90^{***}$), leaf width ($r=0.74^{***}$), leaf length ($r=0.57^{***}$), plant height ($r=0.75^{***}$) and pod length ($r=0.52^{**}$). Days to duration of flowering was associated with days to maturity ($r=0.72^{***}$), leaf width ($r=0.59^{***}$), leaf length ($r=0.49^{**}$) and plant height ($r=0.42^*$). Days to maturity had significant and positive correlation with leaf length ($r=0.58^{***}$) and leaf width ($r=0.69^{***}$). Correlations between leaf length and pod width was ($r=0.78^{***}$). Leaf width with plant height ($r=0.75^{***}$), raceme number per plant with yield ($r=0.56^{***}$) and pod bearing length with yield at ($r=0.59^{***}$) were highly significant and with positive correlation.

Table 16: Correlation matrix Pearson (n) between agronomic characters calculated from 32 pigeonpea accessions

Variables	DF	DDF	DM	LL	LW	SEW	100w	PHT	RNP	NB	SPD	PBL	PL	PW	Yield
DF	1														
DDF	0.69***	1													
DM	0.90***	0.72***	1												
LL	0.57***	0.49**	0.58***	1											
LW	0.74***	0.59***	0.69***	0.78***	1										
SEW	0.19	0.24	0.34	0.29	0.29	1									
100SW	0.01	0.08	0.16	0.23	0.09	0.34	1								
PHT	0.75***	0.42*	0.67	0.73	0.75***	0.29	0.27	1							
RNP	0.11	0.20	0.05	0.12	0.11	0.06	0.21	0.44*	1						
NBr	0.16	0.05	0.05	0.16	0.09	0.10	0.23	0.21	0.43	1					
SPD	0.09	0.08	0.06	0.17	0.05	0.02	-0.22	0.05	0.18	0.36	1				
PBL	0.00	0.23	0.06	0.34	0.20	0.15	0.32	0.47**	0.47**	0.04	0.11	1			
PL	0.52**	0.17	0.47**	0.21	0.36*	0.07	0.10	0.42*	0.11	0.04	0.15	0.28	1		
PW	0.14	0.10	0.21	0.20	0.21	0.35	0.26	0.03	0.24	0.02	0.22	0.31	0.18	1	
Yield	0.01	0.34	0.07	0.32	0.17	0.12	0.31	0.41*	0.56***	0.09	0.31	0.59***	0.19	0.09	1

Note: DF=days to flowering, DDF=days of duration to flowering, DM=days to maturity, LL=leaf length, LW=leaf width, SEW=seed eye width, 100 seed weight, PHT=plant height, RNP=raceme number per plant, NBr=number of branches per plant, SPD=seeds per pod, PBL=pod bearing length, PL=pod length, PW=pod width and Yield=yield per plot.

4.3.2.2 Morphological characters

The correlation matrix of qualitative characters showed that few of them were positively and significantly correlated (Table 17). The seed second color was strongly correlated with seed eye color ($r=0.97^{***}$), also seed color pattern was strongly correlated with seed eye pattern ($r=0.68^{***}$) and second seed color at ($r=0.68^{***}$), where growth habit was significantly correlated with leaf shape ($r=0.50^*$).

Table 17: Pearson correlation matrix (n) between morphological characters calculated from 32 accessions of pigeonpea

Variables	GH	STH	LC	LSH	VF	PF	FP	PC	SCP	SSC	SEC	SSH
GH	1											
STH	0.11	1										
LC	0.11	0.20	1									
LSH	0.50*	0.42	0.26	1								
VF	0.13	0.29	0.27	0.10	1							
PF	0.05	0.17	0.19	0.25	0.13	1						
FP	0.04	0.34	0.15	0.26	0.26	0.17	1					
PC	0.20	0.09	0.03	0.44	0.07	0.09	0.12	1				
SCP	0.19	0.23	0.08	0.24	0.24	0.20	0.21	0.19	1			
SSC	0.24	0.42	0.21	0.30	0.21	0.19	0.26	0.17	0.66***	1		
SEC	0.34	0.42	0.23	0.32	0.18	0.17	0.20	0.17	0.68***	0.97***	1	
SSH	0.14	0.10	0.39	0.23	0.01	0.12	0.31	0.15	0.07	0.04	0.03	1

Where: GH=Growth habit, STH=stem thickness, LC=Leaf color, LSH= leaf shape, VF=vigor at flowering, PF=pattern of flowering, FP=flowering pattern, PC=pod color, SCP=seed color pattern, SSC=seed second color, SEC=Seed eye color, SSH=seed shape.

4.3.3 Correlation between sorghum agro-morphological characters

4.3.3.1 Agronomic characters

The correlation matrix based on Pearson (n) for the variables studied in sorghum accessions indicated that the majority of these traits had positive and some with significant pair-wise correlation coefficients (Table 18). The grain weight per panicle was strongly positive and significantly correlated with yield ($r=0.794^{***}$). Grain number per

panicle with grain weight per panicle were strongly correlated ($r=0.780^{***}$). Plant height was significantly associated with days to flowering ($r=0.639^{***}$), inflorescence length ($r=0.522^{**}$), grain number per panicle ($r=0.468^{**}$) and grain weight per panicle ($r=0.505^{**}$). Inflorescence length had high significant correlation with grain number per panicle ($r=0.672^{***}$), inflorescence width correlated with grain weight per panicle ($r=0.552^{**}$), whereby grain number per panicle ($r=0.578^{***}$), inflorescence width ($r=0.579^{***}$), inflorescence length ($r=0.509^{**}$) were significant and positively correlated with yield.

Table 18: Correlation matrix Pearson (n) between agronomic characters calculated from 31 sorghum accessions

Variables	PH	NFSP	DF	IL	IW	GNP	GWP	NHP	100SW	NBTP	NNTP	GYLD
PH	1											
NFSP	0.234	1										
DF	0.639***	0.197	1									
IL	0.522**	0.305	0.279	1								
IW	0.180	0.006	0.216	0.117	1							
GNP	0.468**	0.264	0.183	0.672***	0.300	1						
GWP	0.505**	0.393*	0.432*	0.460*	0.552**	0.780***	1					
NHP	0.052	0.150	0.272	0.169	0.087	0.138	0.201	1				
100SW	0.020	0.279	0.142	0.343	0.035	0.352	0.118	0.133	1			
NBTP	0.083	0.495**	0.211	0.029	0.006	0.047	0.246	0.114	-0.166	1		
NNTP	0.126	0.243	0.199	0.340	0.162	0.492**	0.313	0.634***	-0.392	0.338	1	
GYLD	0.265	0.370*	0.364*	0.509**	0.579***	0.578***	0.794***	0.134	0.099	-0.109	0.177	1

Where: PH, NFSP, DF, IL, IW, GNP, GWP, NHP, 100SW, NBTP, NNTP and GYLD. Plant height, number of flowering stem per plot, days to flowering, inflorescence length, inflorescence width, grain number per panicle, grain weight per panicle, number of heads per plot, 100 seed weight, number of basal tillers per plot, number of nodal tillers per plot and grain yield respectively

4.3.3.2 Morphological characters

The qualitative characters of sorghum in correlation matrix revealed that all characters had positive and few of them showed significant correlation coefficients (Table 19). Grain color and grain covering were strongly positively and significantly correlated with bird attack ($r=0.57^{***}$ and $r=0.56^{***}$) respectively. Basal tillers were significant with nodal tillers at ($r=0.55^{**}$) and senescence with lodging ($r=0.56^{**}$). Also plant color was positive and significantly associated with leaf midrib color ($r=0.47^{**}$) and biotic reaction stress (diseases) ($r=0.53^{**}$).

Table 19: Correlation matrix Pearson (n) between morphological characters calculated from 31 sorghum accessions

Variables	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1.PLC	1														
2.JF	0.36	1													
3.LMC	0.47**	0.36	1												
4.ICL	0.10	0.23	0.16	1											
5.BRS	0.53**	0.31	0.47*	0.26	1										
6.IE	0.14	0.29	0.35	0.22	0.08	1									
7.GLC	0.30	0.02	0.02	0.18	0.27	0.08	1								
8.Senc	0.48	0.06	0.05	0.05	0.18	0.07	0.10	1							
9.GrCOV	0.00	0.31	0.00	0.38*	0.39*	0.01	0.05	0.12	1						
10.GrC	0.34	0.07	0.05	0.17	0.36	0.04	0.36	0.53**	0.39*	1					
11.B.att	0.42*	0.21	0.26	0.34	0.49*	0.05	0.30	0.41*	0.56***	0.57***	1				
12.Wblo	0.28	0.00	0.08	0.27	0.00	0.14	0.17	0.30	0.21	0.17	0.11	1			
13.LODG	0.14	0.01	0.18	0.38*	0.07	0.14	0.56**	0.03	0.14	0.05	0.13	0.35	1		
14.Bfil	0.18	0.14	0.18	0.37	0.01	0.16	0.07	0.33	0.15	0.23	0.16	0.10	0.20	1	
15.Nfil	0.33	0.05	0.33	0.28	0.34	0.02	0.32	0.26	0.15	0.52	0.41*	0.03	0.18	0.55**	1

4.4 Principal Component Analysis (PCA)

4.4.1 Cowpea

4.4.1.1 Agronomic traits

Twelve quantitative traits were analyzed using PCA method to determine their relative importance. The first two PCs explained 63.168% of total variation contributed by datasets (Table 20). The PC1 accounted the highest proportion of 47.642% of total agronomic trait variations and had largest eigenvalue of 5.717. The PC2 had 15.526% variability with 1.863 eigenvalues. The importance of PC1 was highly contributed by seed width, pod width, pods per plant, terminal leaf length, terminal leaf width, seed length, yield and days to flowering. The variables that contributed heavily to PC2 were only days to maturity (0.541) and 100 seed weight (0.451).

Table 20: Squared cosines of the variables and eigenvalues of agronomic traits

	PC1	PC2	PC3	PC4	PC5
Days to flowering	0.459	0.089	0.010	0.068	0.303
Days to maturity	0.257	0.541	0.028	0.022	0.093
Pods per plant	0.598	0.097	0.006	0.022	0.185
Terminal leaf length	0.579	0.046	0.018	0.297	0.008
Terminal leaf width	0.554	0.135	0.030	0.228	0.000
100 seed weight (g)	0.032	0.451	0.159	0.018	0.245
Pod length (cm)	0.488	0.187	0.110	0.119	0.000
Pod width(cm)	0.763	0.036	0.016	0.035	0.008
Seeds per pod	0.058	0.038	0.778	0.001	0.052
Seed length(mm)	0.549	0.013	0.044	0.249	0.011
Seed width(mm)	0.915	0.000	0.008	0.011	0.004
Yield(g)	0.466	0.231	0.217	0.015	0.003
Eigenvalue	5.717	1.863	1.424	1.084	0.914
Variability (%)	47.642	15.526	11.865	9.032	7.613
Cumulative %	47.642	63.168	75.033	84.065	91.679

PC- principal component

NB. Values in bold correspond for each variable to the factor for which the squared cosine is the largest.

4.4.1.2 Quantitative and observation scatter plot matrix

The first two biplots PC1 and PC2 for quantitative traits explained 63.17% of the total variation which was associated with twelve traits of cowpea accessions (Figure 5). Some of the observations appear to be clustered together on the origin like TZA 256, TZA 2694, TZA 264, TZA 263, TZA 2314, TZA 3681, TZA 130, TUMAIN etc, indicating that they have common characteristics. Other accessions are situated far from the origin (TZA 3085, TZA 3625, TZA 3847, GBK 013187 and TZA 3998), a sign of having different unique characters from the other. From the first quadrant accessions are assumed to be the best candidates since they are positive contributors of the given characteristics than in either of the rest three quadrants which mostly are negative contributors of characters (Figure 5).

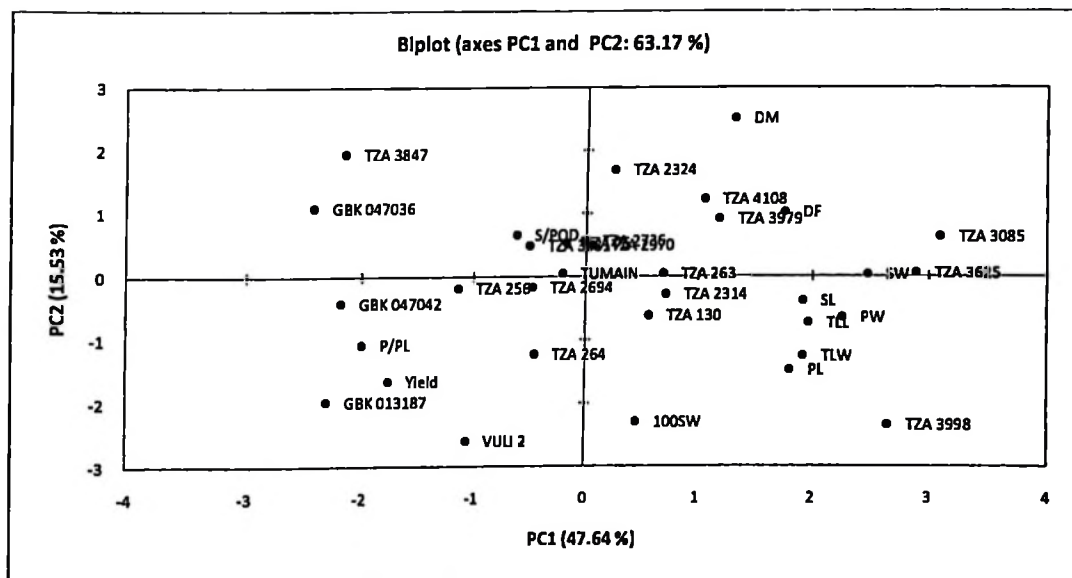


Figure 5: Distribution of accessions in PC1 and PC2 for quantitative trait similarities

4.4.1.3 Morphological traits

Thirteen qualitative traits were analyzed to determine their relative variability. The total variability in first PC, second PC and third PC was 22.443%, 16.079% and 13.251%

respectively. More than 51% of qualitative traits variability in PC1-PC3 contributed for divergence between the accessions (Table 21). The PC1 that explained the proportion (22.443%) of total morphological variance with eigenvalue of 2.918 was contributed highly by raceme position followed by immature pod pigmentation, testa texture and growth pattern as shown in bold values. However, PC2 which explained (16.079%) of the total variation with eigenvalue of 2.090 was attributed greatly by plant pigmentation and twinning tendency and in the other PCs the variance was contributed as shown.

Table 21: Squared cosines of the variables and eigenvalues of morphological traits

	PC1	PC2	PC3	PC4	PC5
Growth habit	0.136	0.175	0.196	0.000	0.005
Growth pattern	0.444	0.014	0.064	0.029	0.004
Twinning tendency	0.245	0.354	0.032	0.028	0.017
Plant pigmentation	0.045	0.460	0.002	0.196	0.005
Terminal leaflet shape	0.022	0.218	0.029	0.526	0.001
Raceme position	0.611	0.065	0.034	0.005	0.003
Pod attachment to peduncle	0.027	0.234	0.326	0.024	0.000
Immature pod pigmentation	0.485	0.152	0.002	0.014	0.002
Leaf color	0.000	0.176	0.195	0.092	0.327
Pod curvature	0.305	0.023	0.386	0.063	0.025
Seed shape	0.001	0.163	0.005	0.001	0.611
Testa texture	0.477	0.055	0.003	0.163	0.006
React to biotic stress(D'ses)	0.119	0.000	0.448	0.069	0.127
Eigen value	2.918	2.090	1.723	1.210	1.133
Variability (%)	22.443	16.079	13.251	9.304	8.717
Cumulative %	22.443	38.522	51.773	61.077	69.794

PC-Principal component

4.4.1.4 Qualitative and observation scatter plot matrix

Figure 6 shows the distribution of 22 accessions of cowpea. The first two biplots resulted to 38.52 of the total variation. Most of the accessions seem to be clustered together at the

origin indicating that they have familiar qualitative characters in common, for instance TZA 2694, TZA 264, TZA 130, TZA 256, TZA 75, GBK 047042, GBK 047036, TUMAIN, TZA 3979, TZA 3681 (Figure 2). Accessions in the first quadrant with TZA 2314 and fourth quadrant (TZA 2324) distributed separately so that are assumed to have unique morphological make up from the other genotypes.

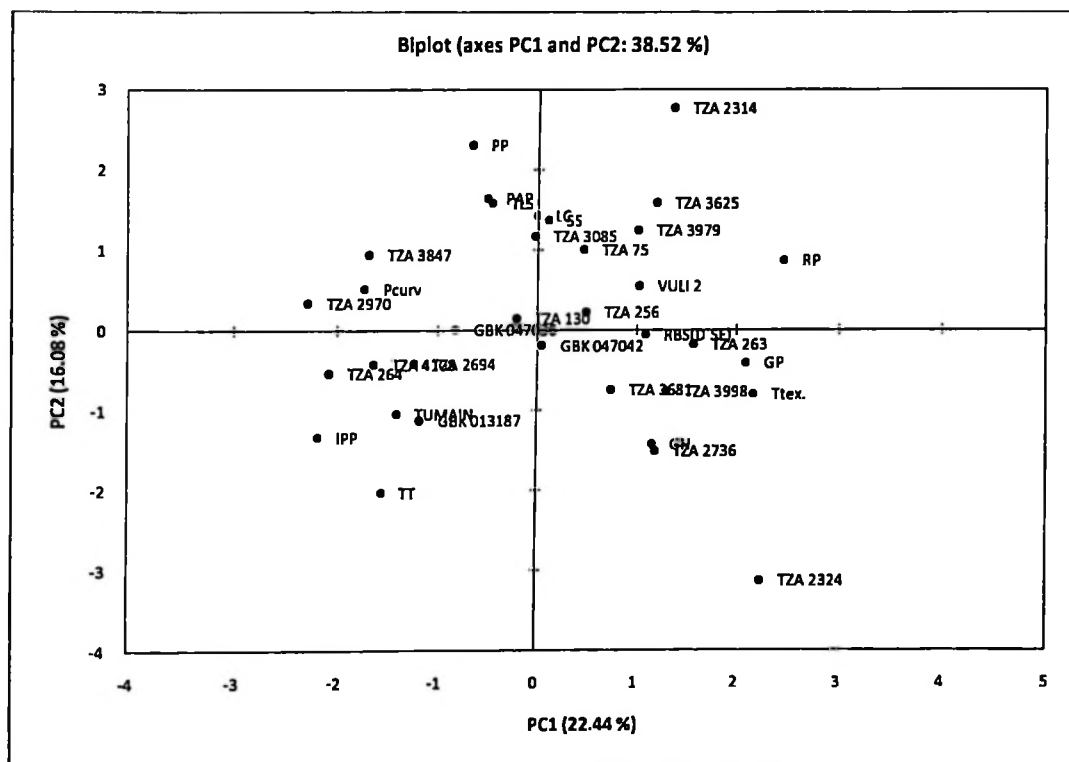


Figure 6: Distribution of varieties among accessions in PC1 and PC2 for qualitative trait similarities

4.5 Cluster Analysis

4.5.1 Quantitative traits

The data collected from quantitative traits and illustrated by the agglomerative un-weighted pair-group average, showed the relationship among the accessions (Figure 7). Based on Pearson correlation coefficient, the dendrogram at similarity distance 0.985424

was divided into four major clusters (A, B, C and D) according to the agronomical characters associated with them. Variability between clusters was 77.63% and within clusters was 22.37%. Majority of study accessions was under cluster D and C with 10, and 9 accessions respectively. Clusters B and A were composed of 2 and 1 accessions respectively. The dendrogram shows a comparatively high similarity among accessions, with exceptional of A and B which was distinct from the others displayed in the clusters. Each sub group had many similarities. A clear separation among accessions was found ranging from 0.985 to 0.999 units. The landraces were dispersed all over the dendrogram which indicates diversity among these populations.

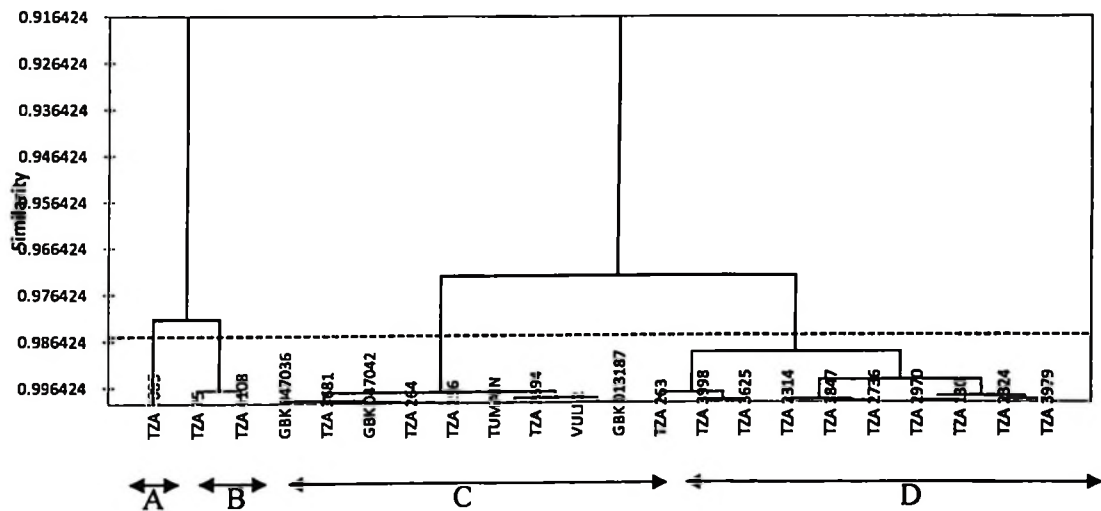


Figure 7: Dendrogram obtained by cluster analysis showing the agronomic similarity rate of 22 cowpea landraces

4.5.2 Qualitative traits

The qualitative traits illustrated by the agglomerative un-weighted pair-group average, showed the relationship among the accessions (Figure 8). The dendrogram at similarity distance 0.780 000 was divided into four major clusters (A, B, C and D) according to the

qualitative characters correlated with them. Variability between clusters was 37.04% and within clusters was 62.96%. The greater part of study accessions in similarity was under cluster D and B with 11 and 8 accessions respectively. Clusters A and C were composed of 2 and 1 accessions respectively. The dendrogram shows a relatively high similarity among accessions with outstanding of A and C which were distinct from the other put on view in the clusters. Each sub group had many similarities. A clear separation among accessions was found ranging from 0.780 to 0.950 units. The landraces were dispersed all over the dendrogram being a sign of divergence among these populations.

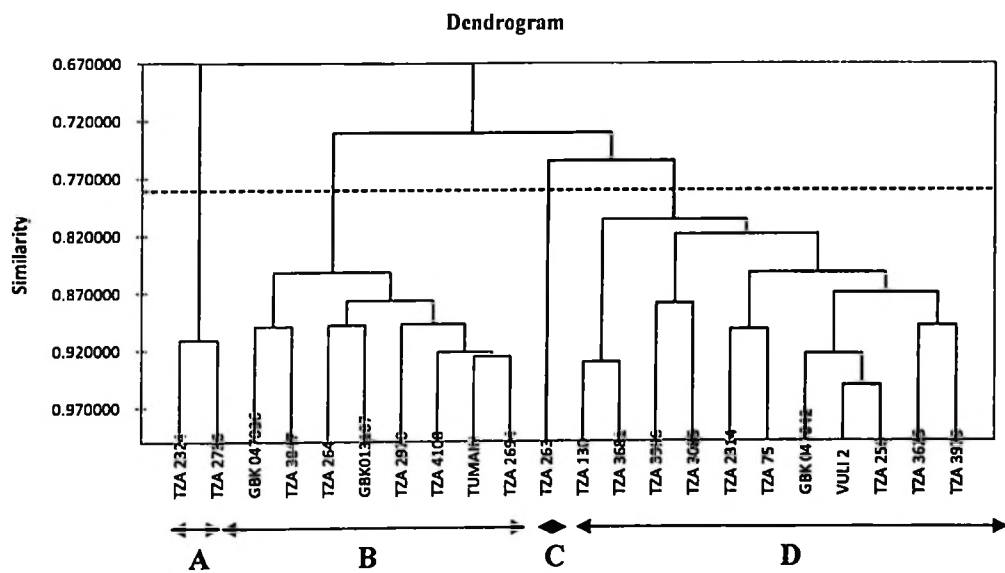


Figure 8: Dendrogram obtained by cluster analysis showing the similarity rate of 22 cowpea landraces

4.6 Principal Component Analysis

4.6.1 Sorghum

4.6.1.1 Agronomic traits

In principal component, twelve quantitative traits were analyzed. The total variability in first PC and second PC was 34.756% and 19.206% respectively; more than 53% of

quantitative traits in PC1-PC2 contributed for divergence between the accessions (Table 22). The PC1 that explained the highest proportion 34.756% of total variation with eigenvalue of 4.171 was attributed highly by grain weight per panicle followed by grain number per panicle, inflorescence length, grain yield and plant height. However, the PC2 which explained 19.206% of the total variance and 2.305 eigenvalues were contributed by number of nodal tillers per plot, number of basal tillers per plot, number of flowering stems per plant, 100 seed weight and number of heads per plot.

Table 22: Squared cosines of the variables and Eigen values of agronomic traits

	PC1	PC2	PC3	PC4	PC5
Plant height	0.427	0.015	0.030	0.188	0.249
Number of flowering stem/ plant	0.152	0.444	0.081	0.000	0.105
Days to flowering	0.332	0.029	0.064	0.390	0.048
Inflorescence length	0.529	0.021	0.230	0.001	0.000
Inflorescence width	0.265	0.001	0.270	0.203	0.040
Grain per panicle	0.683	0.044	0.092	0.064	0.000
Grain weight per panicle	0.811	0.032	0.026	0.029	0.005
Number of head per plot	0.098	0.266	0.147	0.158	0.231
100 seed weight	0.013	0.419	0.281	0.010	0.001
Number of basal tiller per plot	0.020	0.440	0.021	0.035	0.192
Number of nodal tiller per plot	0.211	0.559	0.018	0.015	0.047
Grain yield	0.630	0.034	0.043	0.119	0.004
Eigen value	4.171	2.305	1.304	1.212	0.921
Variability (%)	34.756	19.206	10.870	10.098	7.673
Cumulative %	34.756	53.961	64.831	74.928	82.601

PC-Principal component

4.6.1.2 Quantitative and observation scatter plot matrix

Figure 9 shows the distribution of 31 accessions of sorghum. The two biplots (PC1 and PC2) for quantitative traits explained 53.96% of the total variation (Figure 9). The accessions shown in the first quadrant have the strongest contribution variation of characters. For instance TZA 4226, TZA 3205, TZA3147 showed the characters number

of nodal tillers per plot (NNT/PLT), number of heads per panicle (NH/P) and grain number per panicle (GN/P) contributing to great variation. Majority of the observations were clustered at the origin showing that they have common makeup. Few of the accessions were positioned far from the origin indicating great variation of characters from the other landraces. The former include TZA 4226, TZA 3991, GBK 000387, TZA 471 and TZA 2702.

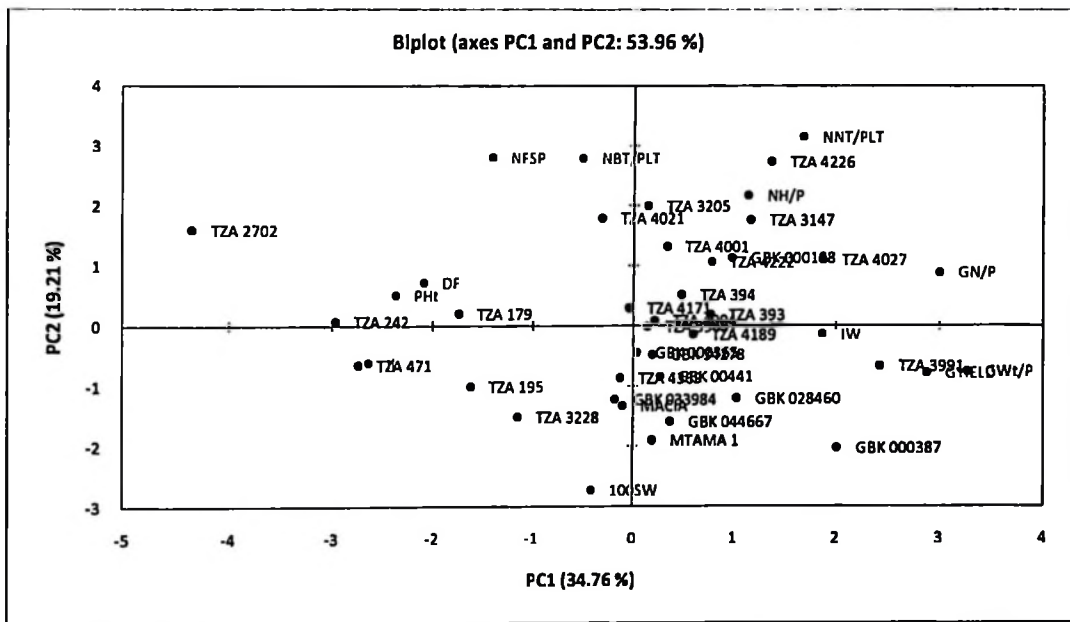


Figure 9: Distribution of varieties among accessions in PC1 and PC2 for quantitative trait similarities

4.6.1.3 Morphological traits

Fifteen qualitative traits were analyzed to find out their relative variability. The total variability in first PC and second PC was 25.311% and 16.392% respectively. In the two PCs 41.705% of qualitative traits in PC1-PC2 contributed to variance between the accessions (Table 23). The PC1 that explained the highest proportion (25.311%) of total morphological variance with eigenvalues 3.797 was highly donated by bird attack, grain

color, nodal tiller and biotic reaction stress and plant color. However, the second PC which explained (16.392%) of the total variance and eigenvalues of 2.459 was greatly contributed by inflorescence compactness and shape and juice flavor and in the other PCs the variance was contributed as indicated.

Table 23: Squared cosines of the variables and eigenvalues of morphological traits

	PC1	PC2	PC3	PC4	PC5
Plant color	0.420	0.304	0.005	0.006	0.000
Juice flavor	0.002	0.363	0.232	0.001	0.040
Leaf midrib color	0.180	0.195	0.299	0.003	0.059
Infloresc.comp.and shape	0.116	0.489	0.012	0.002	0.079
Biotic reaction tress	0.478	0.043	0.053	0.116	0.065
Inflorescence exertions	0.000	0.096	0.311	0.060	0.033
Glume color	0.151	0.175	0.330	0.000	0.000
Senescence	0.351	0.002	0.006	0.034	0.414
Grain covering	0.200	0.202	0.000	0.424	0.016
Grain color	0.569	0.012	0.051	0.003	0.072
Bird attack	0.640	0.018	0.038	0.083	0.002
Waxy bloom	0.014	0.257	0.106	0.011	0.370
lodging	0.001	0.239	0.536	0.021	0.011
Basal tiller	0.173	0.059	0.001	0.612	0.003
Nodal tiller	0.501	0.004	0.000	0.156	0.065
Eigen value	3.797	2.459	1.982	1.532	1.232
Variability (%)	25.311	16.392	13.211	10.213	8.212
Cumulative %	25.311	41.703	54.914	65.126	73.338

PC-Principal component

4.6.1.4 Qualitative and observations scatter plot matrix

The first two PC1 and PC2 for quantitative traits explained 41.70% of the total variation which was associated with twelve traits of sorghum accessions (Figure 10). The most effective characters and observations in the first quadrant were plant color and leaf midrib color traits with MACIA, MTAMA 1, TZA 471, GBK 000441 and TZA 3965 observations. Greater part of the observations was clustered together at the origin

illustrating that they have common composition of characters. Few of the accessions were located far from the origin signifying great variation of characters from the other landraces, for instance MACIA, MTAMA 1, TZA 2702, TZA242 and TZA 3228.

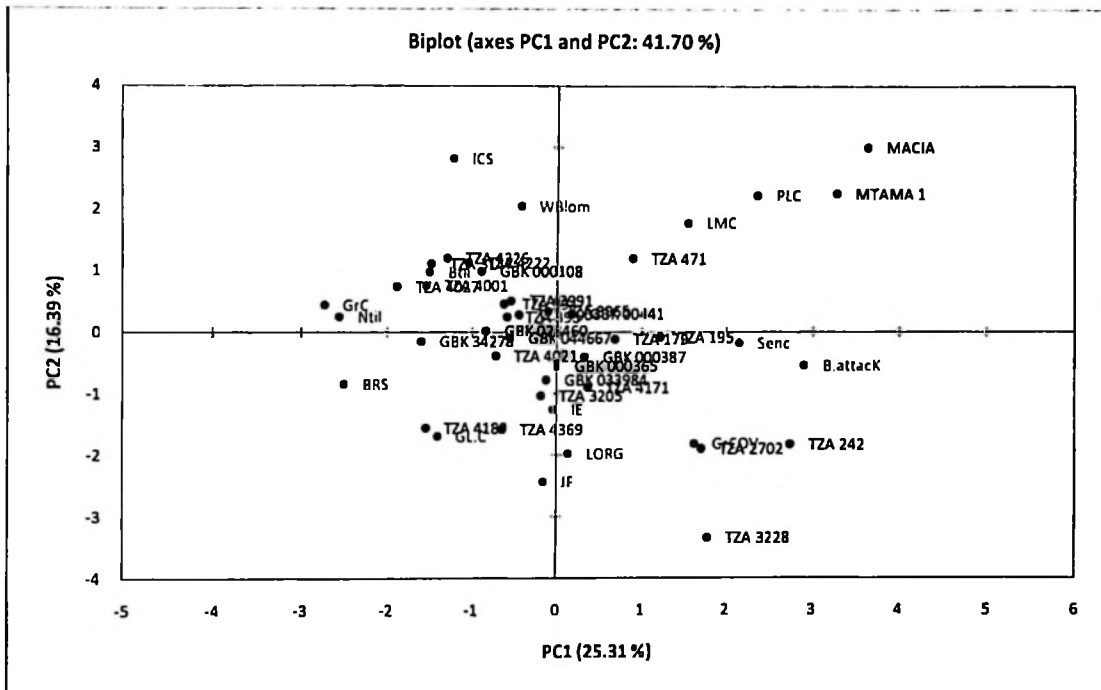


Figure 10: Distribution of varieties among accessions in PC1 and PC2 for trait similarities

4.7 Cluster Analysis

4.7.1 Quantitative traits

The dendrogram based on agronomic data, genetic diversity of sorghum accessions ranged from 0.99513 to 1.0 (Figure 11). The highest genetic similarity (1.0) was found. The results showed that lowest genetic distance was recorded in majority of the accessions for example TZA 4001 and MACIA. The dendrogram at similarity distance of 0.99513 was divided into six clusters (I, II, III, IV, V and VI) according to the quantitative characters associated with them (Figure 11). Variability between clusters was

37.24% and within clusters was 62.76%. The major part of accessions in similarity was under cluster III and the smallest was under I and V. Each sub group had many similarities. The landraces were distributed all over the dendrogram which indicates divergence among these populations.

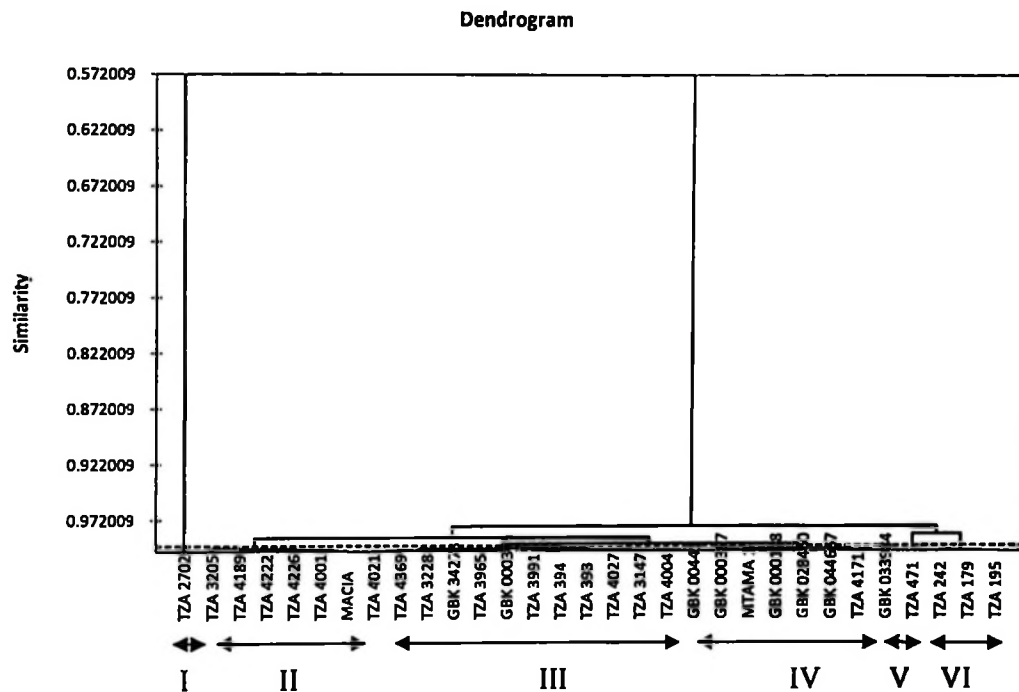


Figure 11: Dendrogram obtained by cluster analysis showing the similarity rate of 31 sorghum landraces

4.7.2 Qualitative traits

The agglomerative un-weighted pair-group average illustrated the association of qualitative traits among the accessions (Figure 12). The dendrogram at similarity distance of 0.675310 was divided into four major clusters (A, B, C and D) according to the qualitative characters correlated with them. Variability between clusters was 37.32% and within clusters was 62.68%. The greater part of study in accessions similarity was under cluster D with 25 accessions. Cluster A and C were composed of 1 and 2 accessions respectively. The dendrogram shows a relatively high similarity among accessions

diversity with exceptional of A sub cluster which was divergent from the other displays in the clusters. A clear separation among accessions was found ranging from 0.675310 to 0.988208 units. The accessions were distributed all over the dendrogram an indication of divergence among these populations.

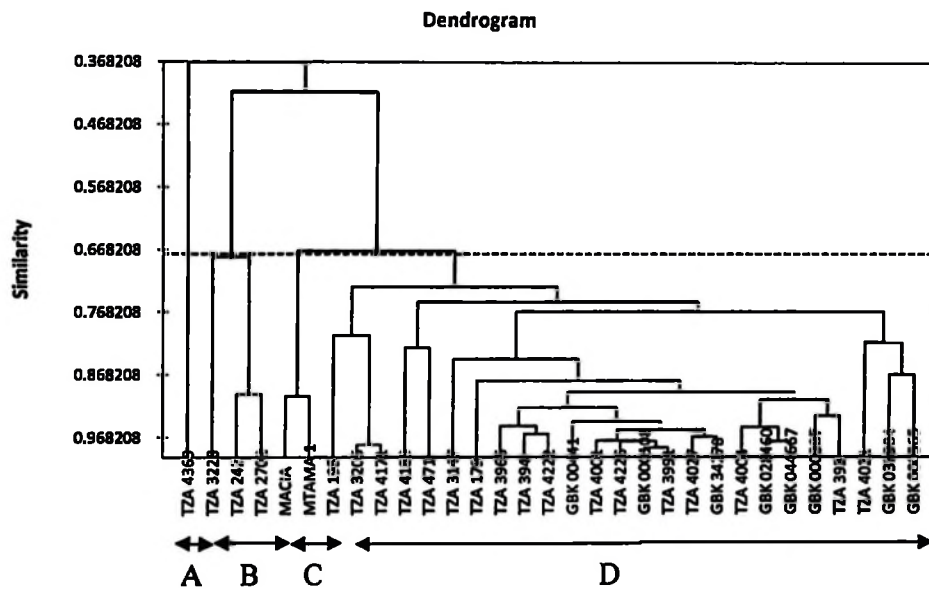


Figure 12: Dendrogram obtained by cluster analysis showing the similarity rate of 31 sorghum landraces

4.8 Principal Component Analysis

4.8.1 Pigeon pea

4.8.1.1 Agronomic traits

In pigeonpea, the entire quantitative traits variability in first PC was 32.919 % and second PC was 17.865% where more than 50% of quantitative traits in PC1 and PC2 donated deviation between the accessions (Table 24). In PC1 32.919% of total agronomic variance with 4.938 eigenvalue mostly was attributed by plant height, leaf width and days to 50% flowering etc. Nevertheless the PC2 which explained 17.865% of the total variation and

2.680 eigenvalue was contributed by yield, pod bearing length and raceme number per plant.

Table 24: Squared cosines of the variables and eigenvalues of agronomic traits

	PC1	PC 2	PC 3	PC 4	PC 5
Days to 50% flowering	0.760	0.080	0.000	0.054	0.035
Days to duration of flowering	0.411	0.332	0.036	0.007	0.035
Days to maturity	0.728	0.141	0.001	0.004	0.003
Leaf length	0.657	0.001	0.053	0.035	0.082
Leaf width	0.764	0.012	0.003	0.000	0.001
Seed eye width	0.177	0.001	0.045	0.258	0.003
100 seed weight	0.078	0.131	0.184	0.257	0.063
Plant height	0.817	0.066	0.002	0.014	0.002
Raceme number per plant	0.059	0.570	0.067	0.049	0.030
Number of branches/plant	0.022	0.059	0.517	0.026	0.239
Seeds per pod	0.005	0.000	0.630	0.067	0.126
Pod bearing length	0.092	0.595	0.063	0.003	0.106
Pod length	0.251	0.005	0.081	0.206	0.060
Pod width	0.039	0.070	0.002	0.619	0.146
Yield	0.078	0.615	0.071	0.055	0.047
Eigenvalue	4.938	2.680	1.753	1.655	0.977
Variability (%)	32.919	17.865	11.686	11.031	6.515
Cumulative %	32.919	50.784	62.470	73.501	80.016

PC-Principal component

4.8.1.2 Observations and quantitative scatter plot matrix

The first two PC1 and PC2 for agronomic traits revealed 50.78% of the entire variation which was related with traits of pigeonpea accessions (Figure 13). The most useful characters and observations in the first part of the biplot were yield, plant height, number of branches, and leaf length with valuable observations in GBK 041787, TZA250, TZA 2456, TZA 2466, MALI and GBK0459993. Most of the observations were clustered at the origin demonstrating that they have common characteristics. Few of the accessions were situated far from the origin suggesting great variation of characters from the other landraces such as GBK 045991, TZA 2672 and KOMBOA.

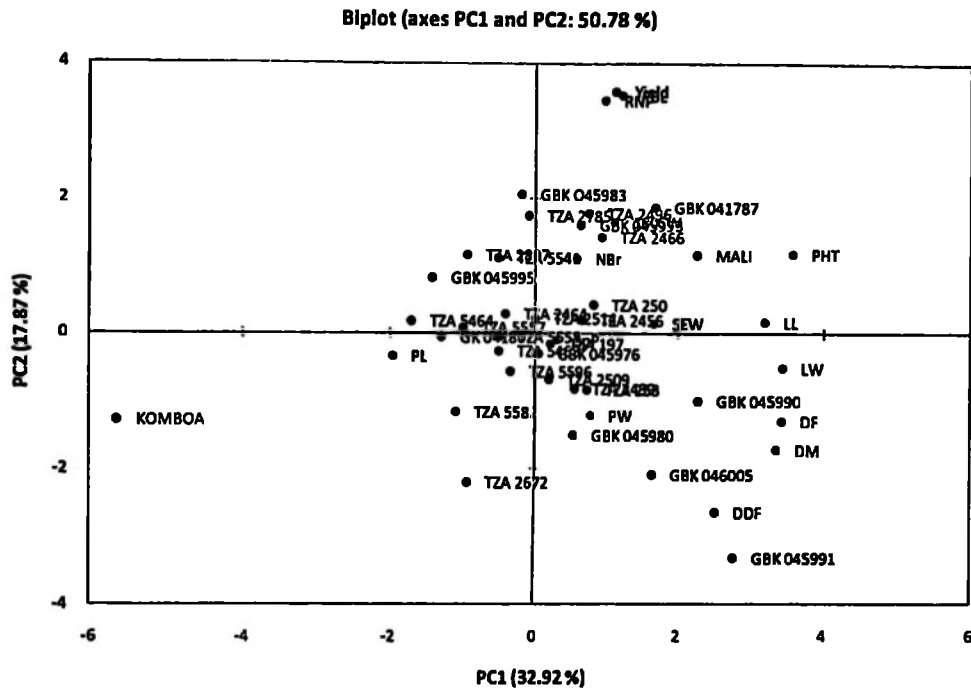


Figure 13: Distribution of varieties among accessions in PC1 and PC2 for trait similarities

4.8.1.3 Morphological traits

The total variability in first PC (29.791%) and second PC (14.923%) of twelve qualitative traits was analyzed where more than 57 % of qualitative traits in PC1-PC3 contributed for divergence between the accessions (Table 25). The PC1 that explained the highest proportion (29.791%) of total qualitative variation and significant with eigenvalue of 3.575 was contributed by seed eye color, seed second color, seed color pattern, stem thickness and leaflet shape (Table 25). However, the second PC which explained (14.923%) of the total variance and 1.791 eigenvalue was attributed by seed shape, pattern of flowering, leaf color and leaflet shape. In the other PCs the variation and significance was contributed as shown.

Table 25: Squared cosines of the variables and eigenvalues of morphological traits

	PC1	PC2	PC3	PC4	PC5
Growth habit	0.169	0.109	0.269	0.063	0.075
Stem thickness	0.385	0.002	0.067	0.041	0.026
Leaf color	0.138	0.251	0.131	0.072	0.180
Leaflet shape	0.372	0.298	0.080	0.064	0.008
Vigor at flowering	0.137	0.011	0.245	0.133	0.207
Pattern of flowering	0.022	0.393	0.081	0.000	0.226
Flowering pattern	0.205	0.014	0.241	0.105	0.149
Pod color	0.116	0.014	0.229	0.413	0.003
Seed color pattern	0.506	0.124	0.011	0.014	0.010
Seed second color	0.744	0.088	0.005	0.055	0.007
Seed eye color	0.761	0.068	0.017	0.085	0.006
Seed shape	0.019	0.418	0.174	0.081	0.092
Eigenvalue	3.575	1.791	1.551	1.126	0.990
Variability (%)	29.791	14.923	12.925	9.386	8.254
Cumulative %	29.791	44.714	57.639	67.025	75.279

PC-Principal component

4.8.1.4 Qualitative and observation scatter plot matrix

The first two PC1 and PC2 for qualitative traits explained 44.714% of the total variation which was associated with twelve traits of pigeonpea accessions (Figure 14). The most effective characters and observations in the first component were seed color pattern, seed second color and seed eye color traits with accessions GBK 045995, TZA 5596, TZA 5582 and KOMBOA used as checks. Most of the accessions appeared to be clustered at the origin indicating that they have common characteristics. Other accessions were situated far from the origin signifying great variation of characters from the other landraces, for instance GBK 045995, TZA 5582, TZA 2672, TZA 5541 and TZA 197.

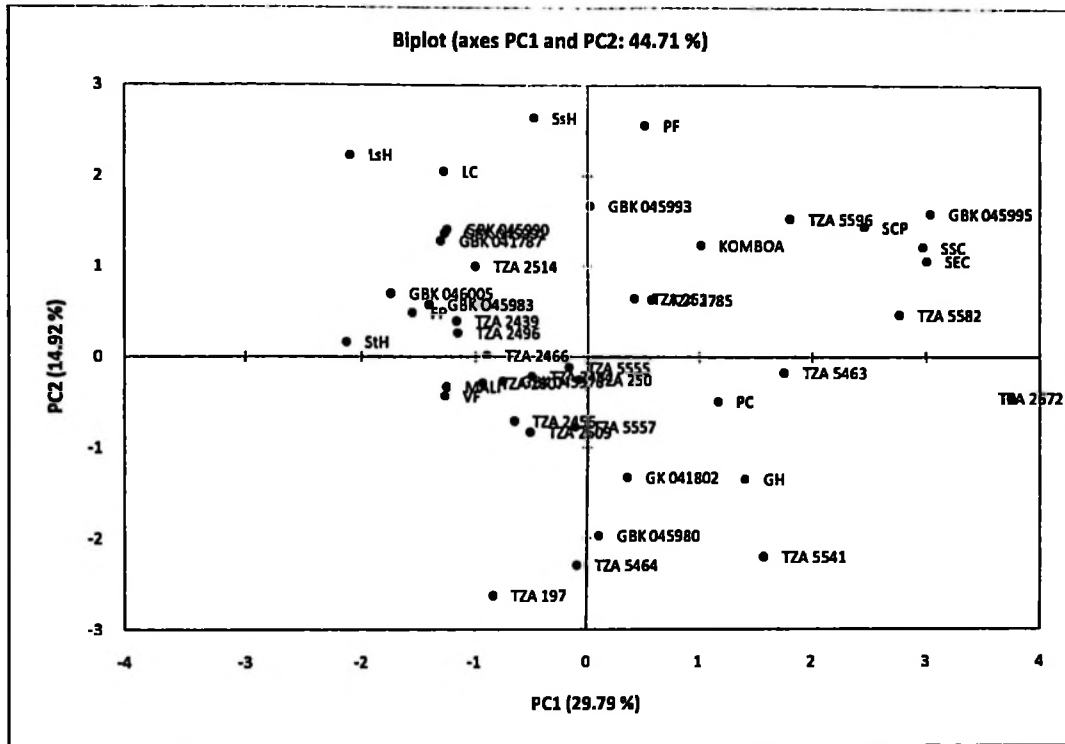


Figure 14: Distribution of varieties among accessions in PC1 and PC2 for trait similarities

4.9 Cluster Analysis

4.9.1 Quantitative traits

The dendrogram at similarity distance of 0.968303 was divided into three major clusters (I, II and III) according to the agronomic characters interrelated (Figure 15). Variability between clusters was 62.66% and within clusters was 37.34.68%. The majority of study in accessions similarity was under cluster I with 24 accessions. Clusters II and III were composed of 1 and 7 accessions respectively. A clear separation among accessions was found ranging from 0.968 to 0.999 units. The accessions were isolated all over the dendrogram which was an indication of divergence among these populations.

found ranging from 0.7745 to 0.9988 units. The accessions were separated all over the dendrogram which was an indication of divergence among accessions.

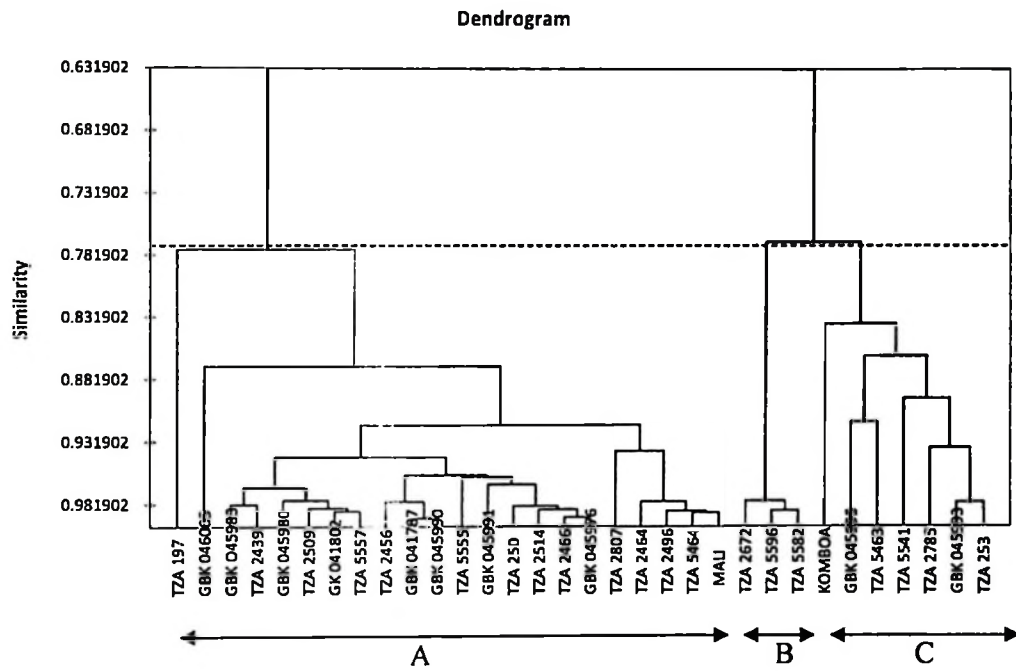


Figure 16: Dendrogram obtained by cluster analysis showing the similarity rate of 32 pigeonpea landraces

CHAPTER FIVE

5.0 DISCUSSION

Knowledge about genetic diversity of cultivated crops has become a very important and fundamental tool in breeding programmes worldwide especially in the current situation of climate changes (Tanzania report on genetic resource, 2009). This tool helped to determine the efficiency of sorghum, cowpea and pigeonpea when used in breeding, which eventually may result in enhanced food production (Khodadadi *et al.*, 2011). Therefore this study intended to assess genetic diversity of locally adapted sorghum, cowpea and pigeonpea landraces using agro-morphological approach and superior materials of these crops obtained from the study will assist in breeding programmes.

5.1 Analysis of Variance

From the results obtained, analysis of variance revealed that, most of the traits showed highly significant ($p < 0.001$) differences among the accessions of cowpea, pigeonpea and sorghum in all measured agronomic field traits (Tables 5, 7 and 9) respectively, which indicated the presence of sufficient variability that can be exploited through selection. The existence of high variability for different characters among cowpeas, sorghum and pigeonpea varieties had been reported by Idahosa *et al.* (2010) and Teshome *et al.* (1997). For example, the accessions with the highest values for yield were GBK 013187 (cowpea) from Kenya, TZA 2496 (pigeonpea) and TZA 3991 (sorghum) landraces from Tanzania (Tables 6, 8 and 10) respectively. However, in terms of yield components, accession GBK 013187 (cowpea) had highest value may be due to mean comparisons which illustrated better results in 100 seed weight, pods per plant, days to flowering and days to maturity. Similar findings have been reported by Ibrahima *et al.* (2013) on those traits. The results

in Table 6 showed early maturing landraces, so they could probably managed to escape or tolerate the scarcity or poor distribution of rainfall which can be used to solve the issue of climate change when used in breeding programs.

In pigeonpea, TZA 2496 accession was superior for grain yield and had high values for leaf length, leaf width and 100 seed weight. Similar results were reported by Rupika and Bapu, (2014) on grain yield and 100 seed weight. This accession had a high 100 seed weight pod bearing length which might be a cause for good performance in yield (Table 8). On the contrary MALI variety had highest 100 seed weight among all accessions but did not give the highest yield. Also TZA 5541 observed the lowest 100 seed weight among accessions but was not the lowest in terms of yield. Also even though there was a positive correlation between 100 seed weight with yield, it was not significant. This indicates that not only 100 seed weight may contribute better on yield performance; some accessions might have high yield due to 100 seed weight and others not (Table 8). Plant height, raceme number per plant, pod bearing length were highly positive correlated with yield and explained yield differences between accessions (Table 16). For example TZA 2496 and 2466 have high yield but they differ both in terms of pod bearing length, raceme number per plant, This point out that, not only one yield component can contribute high yield.

TZA 3991 sorghum accession had the highest yield, grain weight per panicle and inflorescence width among all sorghum accessions and high number of grains per panicle followed by GBK 000387 having higher yield with grain weight per panicle and inflorescence width (Table 10). This indicates that when used in breeding to improve accessions with low traits of grain number per panicle and grain weight per panicle like TZA 2702, TZA 471 etc they are seen to diverge from other accessions as shown in figure

7. They latter can contribute much in genetic diversity and improvement of the inferior accessions. Inflorescence length, days to maturity and number flowering stem per plot are high correlated to contribute in yield, but yield differs among accessions.

5.2 Diversity Analysis

The values measured for genetic diversity based on agronomic traits exhibited the differences in cowpea, pigeon pea and sorghum accessions (Tables 11, 12 and 13) respectively. This helped to identify the genetic variation in each of the population. A High diversity index indicates unbiased occurrence of classes for an individual trait and genetic diversity (Magurran, 2004). The rate of diversity was from 0 to 4, where 0 is no divergence and more than 4 means have high diversity according to Magurran, (2004) findings where focuses on multiple levels of types of diversity within and among species of plants and how they evolved and maintained their roles in generating and maintaining biodiversity. From the results obtained, most of accessions in quantitative traits exhibited divergence .Nevertheless, days to maturity for cowpea, pod length for pigeonpea and days to flowering in sorghum showed highest variation of traits among their accessions (Table 11, 12 and 13) respectively. These traits therefore, contributes much to differences among accessions. Thus if these were used in breeding they would contribute to genetic advance.

5.3 Phenotypic Traits Correlation

In correlation matrix, the results attained showed that majority of the agro-morphological characters of cowpea, pigeonpea and sorghum accessions had high positive pair-wise correlation coefficients (Tables 14 - 19). For instance in cowpea, terminal leaf length and terminal leaf width, as well as pod length and pod width for quantitative traits were very strongly correlated (Table 14). These characters appeared to have the highest values in TZA 3085 and TZA 3998 and TZA 3625 accessions (Table 6). This indicated that the

accessions contained broad leaves and large seeds since they resulted to have long terminal leaf length, pod length with wide terminal leaf width and pod width than other accessions.

For qualitative values, raceme position (upper canopy), intermediate twinning tendency, indeterminate growth pattern were highly correlated with pattern of immature pod pigmentation (Table 15). Porter *et al.* (1974) had also documented on positive and significant correlation between raceme positions, twinning tendency with immature pod pigmentations in cowpea. Traits can be effectively used with other correlated vegetative characters in improvement programmes.

In pigeonpea, the agronomic traits correlation coefficients results obtained between leaf length with leaf width, days to 50% flowering with plant height appeared to have high significant and positive relationships (Table 16). Some similar results were reported on significant correlations between days to 50% flowering with plant height by Rupika and Bapu, (2014) in their assessment of genetic diversity in pigeonpea collections using morphological characters. GBK 045990 was taller than all pigeonpea accessions (224.5 cm) and spent many days before flowering stage (151.7) compared to KOMBOA which was the shortest (107 cm) and showed the lowest number of days to flowering (86.3) (Table 8).

Therefore, there might be some strong association between plant height with number of days to flowering of the accessions suggesting that there was early (KOMBOA) and late maturing (GBK 045990) accessions where due to climate change which causes poor distribution of rainfall the early flowering can be suitable for those environments which receive relatively low rainfall. These can also be used in breeding programmes to improve

phenological traits in other accessions. The correlation matrix of morphological characters resulting from 32 pigeonpea accessions exhibited a great link between seed second color (light-brown, reddish-brown, light-grey and dark-purple), seed color pattern (mottled, speckled and mottled and speckled) with seed eye color (orange, reddish-brown, light- grey and dark-purple) (Table 17). Upadhyaya *et al.* (2007) and Manyasa *et al.* (2008) had documented similar observation of significant correlation of seed coat dark color, seed coat light color with seed color pattern when evaluating phenotypic diversity in pigeonpea. In this study it was observed that, seed second color and seed eye color were significant and positively correlated with seed color pattern. These agromorphological traits imply that they can be used for future characterization and selection programs.

In sorghum phenotypic values, the study revealed that grain weight per panicle was strongly correlated with grain yield; inflorescence length, inflorescence width and grain number per panicle illustrated strong associations with yield. Grain number per panicle was correlated with grain weight per panicle (Table 18). Bucheyeki *et al.* (2009) also reported that inflorescence width and grain number per panicle had significant and positive correlations with grain yield. On contrast this study revealed that grain weight per panicle and inflorescence length had significant correlation with yield. This most likely demonstrated a possibility that, inflorescence size in accessions may cause a change or variation in number of grains and yield.

The qualitative characters observed were evident that, the grain colors, grain covering with grain bird attack were strongly correlated. Teshome *et al.* (1997) had found similar findings on grain color and grain covering correlation in sorghum. Results obtained in this study showed that senescence was significantly correlated with bird attack and senescence

correlated with grain covering. From results obtained in this study, the cause of bird attack may be influenced by color and length of glume grain coverage. For instance TZA 2702 revealed that yellow color was the most attractive to birds since it recorded Therefore, variation in the morphological character (color) may be used in breeding programs to improve the accessions or varieties which are susceptible to bird attack.

5.4 Principal Component Analysis

Principal components analysis (PCA) was used to establish the comparative importance of the categorization of traits (Jackson, 1991). The associations between the agro-morphological traits of cowpea, pigeonpea and sorghum eigenvalues were used as a basis for the identification of the principal components in this study (Panthee *et al.*, 2006).

5.4.1 Cowpea

In cowpea, the first two principal components explained the highest proportion (63.168%) of total agronomic variance and were linked with seed width, pod width, pod length, seed length, yield, 100 seed weight, number of seeds per pod and days to maturity (Table 20). These traits were highest in accessions TZA 3625, TZA 3998, TZA 3085, TZA 2314, TZA 2324, GBK 013187, TZA 130, and TUMAIN respectively and also TZA 3625 matured late among all cowpea accessions (Table 6). Some findings in cowpea were observed by Obeisesan (1985), that 100 seed weight, number of seeds per pod, were the primary components for predicting grain yield in cowpea. Also Shwe *et al.* (1972) found that number of days to maturity and grain yield in soybean had the highest contributions to the genetic variability. Comparative study on the yield components of ten cowpea varieties done by Manggoel and Uguru, (2011) showed that seed width, pod width and seed length had high variation which contributed for divergence between the accessions.

In contrast to study, number of pods per plant, terminal leaf length and terminal leaf width were also observed to contribute much on diversity.

In qualitative traits, the total variance of 51.773% obtained from PC1-PC3 was associated with raceme position, growth habit, testa texture, immature pod pigmentation, plant pigmentation, twinning tendency, pod curvature and pod attachment to peduncle. Findings on immature pod pigmentation, pod attachment to peduncle and plant pigmentation were similarly been reported by Ibrahima *et al.* (2013) as they contributed more in divergence among 16 accessions evaluated. This study, also observed that raceme position, growth habit, testa texture, twinning tendency and pod curvature contributed highly in divergence. Some of the accessions illustrated in figure 2 showed to contribute positive divergence in raceme position means was characterized with upper canopy like TZA 3625, TZA2314 and GBK013187, TZA264, TZA 2694 contributed on twinning tendency that is have intermediate twinning system; immature pod pigmentation this means accessions were characterized with pigmented valves and green sutures. TZA 2970 had curved pods and moderate plant pigmentation at the base and tips of petioles, where the majority of cowpea landraces like TZA 3998 showed smooth to rough seed texture. This therefore indicates a high variability in relation to the traits correlated with first two principal components.

5.4.2 Pigeonpea

PCA is the most valuable statistical tool for screening multivariate data with significantly high correlations reported by Johnson (1998). This information may help plant breeders to identify adequate traits for using in hybridization and selection programs. Therefore the results obtained from agro-morphological characters in pigeonpea, the PC1 and PC2 revealed the highest amount (50.784%) of total agronomic variance associated with plant

height, leaf width, days to flowering (DF), days to maturity (DM), pod width, pod bearing length, raceme number per plant, pod length and yield (Table 24). These quantitative traits were found highest in MALI, GBK 045991 (DF and DM), TZA 2509 and GBK 045990, GBK 045995, GBK 041787, TZA 2466 and TZA 2496 pigeonpea accessions respectively (Table 8). Some similar findings had been reported by Muniswamy *et al.* (2014) on leaf width, raceme number per plant and pod bearing length as they contributed divergence in pigeonpea.

Manggoel and Uguru. (2011) observed that, days to flowering and days to maturity characters contributed to genetic variability between comparative studies of cowpea varieties. Mehetre *et al.* (1997) found that pod length and grain yield in soybean genotype contributed to high diversity. Accessions diverged from each other based on the contribution of some reproductive traits and pod components (days to 50% flowering, days to 50% maturity, pod length, pod width, raceme number per plant) whereby results of this study are close to those of Manggoel and Uguru (2011) and Sulnathi *et al.* (2007) who found that days to 50% flowering and days to 50% maturity contributed much for the divergence between cowpea accessions.

Duration of flowering also was observed to contribute high divergence among pigeonpea accessions. Even though, some traits had been seen to contribute high divergence as reported by authors in soybean (Mehetre *et al.* (1997) and cowpea (Manggoel and Uguru, (2011) and Sulnathi *et al.* (2007), this study also reported contribution of the traits as mentioned above to high divergence among pigeonpea accessions for example TZA 5582 has the lowest plant height whereby MALI as check is the highest (Table 8). Therefore characters like days to 50% flowering, days to 50% maturity, number of pods per plant,

pod length, raceme number per plant and plant height should be considered while selecting parents for hybridization program in yield improvement of pigeonpea.

In the observations, KOMBOA revealed the highest correlation of variance (0.828). This improved variety was used as a check, but its results were very different from other from accessions. For example it was the lowest in yield, plant height, and days to maturity (Table 8). It grouped far from others thus being an indicator of having distinct characteristics among from other accessions (Figure 13). Others also including MALI were the highest and vigorous improved varieties grouped a bit far from the others as shown in scatter plot matrix (Figure 13), whereby also had been used as check. GBK 045991 had great divergence among pigeonpea accessions on days to 50% flowering, days to maturity, illustrating as late maturing accession.

The PCs illustrated a total variance of 44.714% of morphological traits contributed by seed eye color, seed second color, seed color pattern, seed shape and pattern of flowering (Table 25). Some results were reported by Upadhyaya *et al.* (2007) and Manyasa *et al.* (2008) on seed color pattern, seed shape and pattern of flowering in pigeonpea. In this study, morphological traits leaf color, stem thickness were observed to contribute to divergence in pigeonpea accessions. Some of these traits can be used for identifying individual germplasm in breeding programs. The accessions having these traits were highly variable and among them was GBK 045995 with mottled and speckled color pattern, light grey seed second color and seed eye color. TZA 5582 had mottled seed color pattern, dark purple second seed color and seed eye color. Seed shape, stem thickness, leaflet shape and leaf color illustrated their variation in figure 10 second quadrant. For instance GBK 046005 showed high divergence with broad – elliptic leaflet shape, angular seed shape and thick stem among pigeonpea accessions.

5.4.3 Sorghum

The first two PCs in sorghum revealed the highest comparative total quantitative variance (53.961%) which was contributed by grain weight per panicle, grain number per panicle, grain yield, inflorescence length, plant height, number of nodal tillers per plot, number of flowering stems per plant, number of basal tillers per plot, 100 seed weight and number of heads per panicle (Table 22). Some similar documented findings in grain weight per panicle, grain number per panicle, grain yield, inflorescence length, and number of tillers per plant, contributing higher variation were reported by Bucheyeki *et al.* (2009), where 14 traits were used to classify sorghum variability in Tanzania. The remaining traits like number of basal tillers per plot, 100 seed weight and number of heads per panicle were complementary agronomic traits that were found to contribute to divergence.

The majority of these traits were grouped in a negative association i.e. quadrants II, III and IV (Figure 5), means that those grouped together have the same character compared to other one. For example the number of nodal tillers per plot and heads per panicle that clustered in quadrant I. This implies that most of the agronomical traits had high divergence and few were having the strongest divergence among the accessions. For example observations obtained to have strong variation were TZA 2702 with association of (0.730), had highest plant height and greatest number of basal tillers per plot. TZA 4226 with correlation of variance (0.656), had the greatest number of nodal tillers per plot and heads per plot, TZA3991 with 0.688 correlation showed the highest grain weight per panicle and yield among all the sorghum landraces (Figure 5 and Table 22). These should be the best accessions to be used in future breeding programmes. However, the principal components demonstrated a total variance of (41.703%) of qualitative characters related with bird attack, grain color, biotic reaction stress (disease severity), plant color and nodal tillers (Table 23), also in biplot, their distribution illustrated in figure 6 showed

to vary greatly. This indicates that, there was a strong divergence amongst accessions of the traits. Plant color showed highest diversity since it was in positive correlation. MTAMA I and MACIA as improved varieties used as checks differed greatly (0.552 and 0.557 respectively) with the accession evaluated by having tan (grey-yellow) plant color and were illustrated in positively associated quadrant. Some accessions associated with high variation but located in negatively related quadrant were TZA GBK 034278 and TZA 3228 which also had low bird attack while TZA 4189 had medium susceptibility to disease.

5.5 Cluster Analysis (Dendrogram)

Cluster analysis presents guides to relationships between accessions and hierarchical jointly special grouping such that similar descriptions are mathematically gathered into same cluster (Hair *et al.*, 1995) and (Aremu, 2005) where genetic relationship on agromorphological traits among and within breeding materials can be identified and classified. In this study a fundamental inquiry relating to genetic relationship among 85 accessions (cowpea 22, pigeonpea 32 and sorghum 31) was addressed to identify genetic diversity information which is very significant in breeding programs. The cluster analysis method (un-weighted pair group method arithmetic (UPGMA) using centroids was used to divide accessions under study into phenotypic groups (Figures 3 and 4, 7 and 8, 11 and 12).

5.5.1 Cowpea

For example in cowpea the dendrogram of similarity distance 0.985424 was divided into four major clusters (A, B, C and D). In cluster A it was composed only of TZA 3085 accession and B were TZA 75 and TZA 4108. These three accessions from groups A and B illustrated in the phylogenetic tree diverged greatly from the other two clusters, since C (GBK047035 –GBK013187) and D (TZA 263-TZA3979) showed great phylogenetic

relationship of similarity of quantitative traits among them (Figure 3). Aremu *et al.* (2007) reported that UPGMA provides more accurate grouping information of phylogenetic relationship on breeding materials than other clusters.

In figure 4, dendrogram of similarity distance 0.780000 was divided into four groups (A, B, C and D) of accessions according to qualitative characters. TZA 2324, TZA 2736 (A) and TZA 263 (C) had greater divergence from other group of B (GBK 047036 – TZA 2694) and D (TZA 130 – TZA3979) as shown in the phylogenetic tree. The landraces were dispersed all over the dendrogram being a sign of divergence among the populations.

5.5.2 Pigeonpea

In pigeonpea the dendrogram at similarity distance of 0.968303 was divided into four clusters (I, II, III and IV) of interrelated agronomic characters (Figure 11). These showed great phylogenetic differences of accessions between (62.66%) and within (37.34%) clusters.

Most of the pigeonpea accessions in terms of quantitative characters seem to be similar cluster I (TZA 2496 – TZA 5596), with the exception of cluster II (KOMBOA) and III (GBK 045991 – TZA 2672). The accessions were isolated all over the dendrogram branches depending on their phylogenetic similarities which is an indication of divergence among the population.

In qualitative traits the dendrogram was divided at 0.774564 distances in three major clusters (A, B. and C) (Figure 12). The variation between groups was 66.55% and within groups was 33.45%. These results demonstrate that there was a great divergence between groups of accessions in terms of their measured qualitative traits. For instance TZA 2672,

TZA 5596 and TZA 5582 composed in group B were more divergent from the other display of accessions in the clusters A (TZA 197 – MALI) and C (KOMBOA – TZA 253). A and C groups in the dendrogram showed a relatively high similarity among accessions, although the accessions were separated all over the phylogenetic tree as a sign of variation. TZA 197, GBK 046005, TZA 2807 in cluster A and KOMBOA, TZA 5541, TZA 2785 in group C seem to have unique qualitative characters simply because they are isolated from the others of the same group.

5.5.3 Sorghum

The genetic diversity of sorghum accessions ranged from 0.99513 to 1.0. The phylogenetic tree showed the highest similarity at 1.0 distance (Figure 7). The variability between was 37.24% and within clusters was 62.76%, this shows that there was a lower divergence between accessions than within accessions of sorghum.

The dendrogram was divided into six clusters I (TZA 2702), II (TZA 3205 – MACIA), III (TZA 4021 - GBK 00441), IV (GBK 000387 – GBK 033984), V (TZA 481) and VI (TZA 242-TZA 295). TZA 2702, TZA 481 and TZA 242-TZA 295 in clusters I, V and VI respectively indicating greater variation from the other accessions in terms of quantitative characters. Cluster III of accessions contained more similarities compared to II and IV. The landraces were isolated all over the phylogenetic tree which is a sign of divergence in their phylogenetic relationships among them.

The phylogenetic tree at similarity distance of 0.67531 broken into four major clusters A (TZA 4369), B (TZA 3228 – MACIA), C (MTAMA I and TZA 195), D (TZA 3205 – GBK 000365) according to their qualitative characters (Figure 8). TZA 4369 illustrated to have the highest divergence from the other accessions followed by MTAMA I, TZA 195

and TZA 3228 – MACIA compared to TZA 3205 – GBK 000365 which showed relatively high similarity among them. The variability between clusters was low at 37.32% than within clusters at 62.68%; this indicates that, there was lower diversity between one accession to another than within sorghum accessions in accordance to their qualitative traits. However in the dendrogram obtained by cluster analysis of similarities TZA 3228, TZA 195, TZA 3145, TZA 179 and TZA 4021 resulted to have unique qualitative characters, since they are separated from their groups as shown in Figure 8.

Therefore the results obtained for all three crops for their agronomic and morphological characters indicated that the total phenotypic variation among the accessions was comparatively high. These values which are assumed to reflect the genetic diversity of agro-morphological characters among the accessions make it possible to obtain broad segregated characteristics when diverse accessions are used.

These findings demonstrated that the use of cluster analysis of quantitative and qualitative characters graphically describes similarity and differences among accessions. Diversity data findings on cluster analysis of quantitative and qualitative character have also been reported by Marjanovic-Jeromela *et al.* (2003), Mahasi and Kamundia (2007) on varietal populations and inbred lines assessed by cluster analysis in genetic diversity of rapeseed (*Brassica napus*).

CHAPTER SIX

6.0 CONCLUSION AND RECOMMENDATIONS

6.1 Conclusions

Genetic diversity was studied among 85 accessions of three crops using agro-morphological characters. Higher level of genetic diversity of agro-morphological traits observed in this study will enable efficient utilization and improvement of cowpea, pigeonpea and sorghum accessions in breeding programs for increased productivity. The study will have particular importance in areas of Tanzania growing these three crops, where their productivity are considerably low due to biotic and abiotic constraints such as diseases, low rainfall, high temperature (climate change) due to use of unimproved varieties and other stresses.

The analysis of variance revealed highly significant differences among the accessions for most of the documented quantitative traits except few of them in all three crops. Also by using principal components and phylogenetic tree, the agro-morphological variation within and between the studied accessions suggests a relatively high divergence. This implies that, these traits were highly linked for most of the divergence in these accessions. Based on the results, the analysis of variance revealed GBK 013187 in cowpea, TZA 2496 (pigeonpea) and TZA 3991 for sorghum had highest yield among other accessions. These were some of the best accessions based on their yields and some yield components identified which can be used in future breeding for developing high yielding hybrids to increase productivity.

The study identified accessions having unique characteristics in their PCA and phylogenetic relationships such as TZA 3085 (C) A), TZA 263 (C) A, TZA 2324 (C) B,

TZA 2314 (Q)I, TZA 2979 (Q) II, VULI 2 (Quadrant (Q) III),TZA 3998 (Q IV),TZA 3847 and GBK 047038 (Q II) for cowpea landraces; KOMBOA (Q III and C II), GBK 041787 (Q I), GBK 045991 (Q IV) and TZA 2672 (QIII and C IV), TZA 197 (Q III) for pigeonpea.

In sorghum accessions with unique characteristic were TZA 4226 (Q I), TZA 2702 (Q II and C I), TZA 4369 (C) I, TZA 471 Q III and C V) and GBK 000387 (Q IV) and MACIA and MTAMA 1 (QI and C III). In summary, the best accessions having unique characters and highest divergence obtained their phylogenetic relationships were TZA 3085 and TZA 2324 in cowpea; KOMBOA and TZA 2672 in pigeonpea and TZA 2702,TZA 471,MACIA and MTAMA 1 for sorghum. These showed a good indicator of having highest genetic divergence among their groups.

6.2 Recommendations

- i) Based on the results obtained, accessions TZA 3998, TZA263, TZA 2324, TZA 2314, GBK 013187 and GBK 047038 for cowpea landraces; GBK 041787, GBK 045991, TZA 2672, TZA 2496, and TZA 197 for pigeonpea and for sorghum accessions TZA 4226, TZA 471, TZA 4189, GBK 000387 and TZA 3991 should be used as parents in crossing programmes because they have high genetic divergence. For those accessions mature early like GBK 013187 (cowpea), GBK 045995 (pigeonpea) and TZA 3205 and GBK 000387 (sorghum) can be used to escape drought.
- ii) The quantitative traits (days to 50% flowering, days to maturity, seed width, pods per plant in cowpea; grain weight per panicle, grain number per panicle, grain yield, number of nodal tillers per plot) in sorghum; days to maturity, plant height,

raceme number per plant in pigeonpea and qualitative characters (raceme position in cowpea, grain color, bird attack) in sorghum and seed color pattern in pigeonpea showed to have high divergence, so that breeders are advised to emphasize on the use of these traits in breeding in order to improve the accessions which may result to high productivity with good quality to combat food insecurity in Tanzania since they demonstrated high divergence.

- iii) Best accessions identified should be further evaluated on some yield components and some qualitative traits in order to come up with more conclusive information on their diversity using of molecular markers.

- iv) More landraces/accessions should be collected and evaluated for genetic diversity.

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APPENDICES

**Appendix 1: Qualitative data studied in 31sorghum accessions grown at SUA
during the 2014 growing season**

ep	Plot No.	Acc. No.	PC	JF	ICS	BRS	IE	GLC	Senc	GrC OV	Gr C	B.att acK	W Blo m	LO RG	Btil	N til
1	1	TZA 3205	1	2	4	4	3	4	3	5	4	2	5	1	0	1
1	2	GBK 000108	1	1	8	5	2	4	3	3	3	1	5	1	1	1
1	3	GBK 000387	1	2	7	6	1	5	5	3	2	1	3	1	0	0
1	4	TZA 4189	1	2	7	6	2	6	3	3	5	1	3	5	0	1
1	5	GBK 028460	1	2	8	6	2	4	5	1	4	2	5	1	0	1
1	6	TZA 3991	1	1	7	5	2	4	3	3	3	1	5	1	0	1
1	7	TZA 3147	1	1	8	5	2	4	1	5	4	1	7	1	1	1
1	8	TZA 179	1	2	8	4	4	2	3	3	2	2	5	1	0	0
1	9	TZA 4001	1	2	10	6	2	4	3	5	4	1	7	1	1	1
1	10	TZA 4004	1	1	8	6	2	5	5	3	3	1	5	1	0	1
1	11	MACIA	2	1	8	2	2	4	5	5	2	5	7	1	0	0
1	12	TZA 4171	1	2	4	5	3	4	3	5	4	3	5	1	0	0
1	13	TZA 4021	1	1	6	2	3	6	3	5	4	1	5	3	1	1
1	14	TZA 242	1	2	3	3	3	2	5	9	2	5	3	1	0	0
1	15	TZA 4369	1	1	1	5	2	6	3	3	4	1	3	5	0	1
1	16	TZA 394	1	1	8	4	2	4	3	3	3	1	3	1	1	1
1	17	GBK 00441	1	1	8	6	2	4	3	3	3	3	5	1	0	0
1	18	TZA 471	1	1	9	3	1	4	3	3	4	2	3	5	0	0
1	19	TZA 3965	1	1	10	5	3	4	5	5	3	1	3	1	0	1
1	20	TZA 195	1	2	5	5	2	2	3	3	2	4	5	1	0	0
1	21	TZA 2702	1	2	5	4	2	5	5	9	2	8	3	1	1	1
1	22	TZA 4222	1	1	10	4	2	4	3	5	4	1	5	1	1	1
1	23	TZA 3228	1	2	4	5	2	6	5	9	1	3	3	7	0	0
1	24	TZA 4226	1	1	9	5	2	4	3	3	4	1	5	1	1	1
1	25	TZA 393	1	1	8	6	2	4	5	3	3	1	3	3	1	1
1	26	MTAMA 1	2	1	8	2	2	2	7	3	2	4	5	1	0	0
1	27	TZA 4027	1	2	11	8	3	4	3	3	4	1	5	1	1	1
1	28	GBK 34278	1	2	9	8	3	5	3	3	4	1	5	1	0	1
1	29	GBK 044667	1	2	9	6	4	5	5	1	3	2	5	1	0	1
1	30	GBK 033984	1	1	5	6	3	5	5	3	4	1	5	2	0	0
1	31	GBK 000365	1	2	6	4	3	5	3	3	3	1	7	4	0	0

Note: Bird Attack Score Scale Was 1-9, 1=Not Attacked, 9=Very Susceptible To Bird Attack.

Abbreviations.

Acc. No = Accession number, PC = pod color, JF=juice flavor, ICS=inflorance compactness and shape, BRS=biotic reaction stress, IE=inflorance exertion, GLC=gloom color, Senc= senescence, GrCOV.= grain coverage, GrC=grain color, Battack= bird attack, WBloom=waxy bloom, LORG= lodging, Btil= basal tillers, and Ntil=nodal tillers.

Appendix 2: Quantitative traits studied in three crops

Cowpea	Pigeonpea	Sorghum
100Seed weight (g)	Days to flowering	Plant height
Days to flowering	Days to duration flowering	Number of flowering stem per plant
Days to maturity	Days to maturity	Days to flowering
Pod length (cm)	Leaf length (cm)	Inflorescence length
Pods/plant	Leaf width (cm)	Inflorescence width
Pod width (cm)	100 seed weight	Grain per panicle
Seed length (mm)	Raceme number per plant	Grain weight per panicle
Seeds/pod	Number of branches	Number of head per panicle
Seed width (mm)	Seed per pod	100 seed weight
Terminal leaf length (cm)	Pod bearing length (cm)	Number of basal tiller per plot
Terminal leaf width (cm)	Pod length (cm)	Number of nodal tillers per plot
Yield (g)	Pod width (cm)	Grain yield
	Yield (g)	

Appendix 3: Qualitative traits studied in three crops

Cowpea	Pigeonpea	Sorghum
Growth habit	Growth habit	Plant color
Growth pattern	Stem thickness	Juice flavor
Twinning tendency	Leaf color	Leaf midrib color
Plant pigmentation	Leaflet shape	Inflorescence. compactness and shape
Terminal leaflet shape	Vigor at flowering	Biotic reaction stress
Raceme position	Pattern of flowering	Inflorescence exertions
Pod attachment to peduncle	Flowering pattern	Glume color
Immature pod pigmentation	Pod color	Senescence (Abiotic reaction)
Leaf color	Seed color pattern	Grain covering
Pod curvature	Seed second color	Grain color
Seed shape	Seed eye color	Bird attack
Testa texture	Seed shape	Waxy bloom
Reaction to biotic stress		lodging
		Basal tiller
		Nodal tiller