DIVERSITY OF FINGER MILLET (*Eleusine coracana* (L.) Gaertn.) GENOTYPES ON DROUGHT TOLERANCE AND YIELD IN TANZANIA

ROBERTSON MICHAEL SIMBAGIJE

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ABSTRACT

Studies were conducted to assess the morphological, physiological and genetic diversity of finger millet genotypes with respect to yield and drought tolerance in Tanzania. Alpha lattice field experimental design was used in morphological characterization of 169 Tanzania finger millet genotypes and complete randomized design for drought and yield evaluation experiments. Morphological descriptors used were plant height, number of productive tillers per plant, number of fingers per panicle, number of leaves per plant, time to plant maturity, yield per plant and thousand grain weights. Data were analyzed using descriptive statistics and correlation matrix, dendrogram and cluster analysis techniques. Plant yield was found to be significant ($P \leq 0.05$) and positively correlated with number of productive tillers, plant maturity, and number of fingers per panicle, finger length and thousand grain weights. Analysis for principal component was done to determine contributing factors to finger millet diversity. The number of tillers, thousand grain weight, plant maturity and number of fingers per panicle were identified as important traits contributing to diversity and yield variability among finger millet genotypes in Tanzania. Thirteen SSR markers recovered polymorphic information content ranging from 0.31 to 0.79, indicating very high genetic diversity of the finger millet genotypes. The Markers detected 114 private alleles, which can help in advancing molecular breeding using techniques such as next generation sequencing to identify the genotypes possessing those identified private alleles. Principal coordinate analysis showed 42% genotypes' variations within and 55% genotypes variations across locations and 3% genotypes' variations between locations. Cluster analysis discriminated 169 finger millet genotypes into a phylogeny tree of 13 distinct clusters. Drought phenotyping using yield stability, drought resistance and stress tolerance indices identified genotypes TFA 77, TFA 169 and TFA 11 to be superior drought tolerant and high yielding genotypes under terminal drought

stresses. Determination of adaptation and stability of finger millet genotypes across finger millet production agro-ecologies targeting release of improved varieties for immediate farmers' use in Tanzania is recommended. Integrated physiological, molecular and morphological characterization is recommended for large number of genotypes screening for drought tolerance using morphological and physiological traits associated with grain yield for finger millet variety development in Tanzania.

DECLARATION

I, ROBERTSON MICHAEL SIMBAGIJE, do hereby declare to the Senate of Sokoine University of Agriculture that this thesis is my own original work done within the period of registration and that it has neither been submitted nor being concurrently submitted for a degree award in any other institution.

_____ _____

Robertson Michael Simbagije Date

(PhD Candidate)

The above declaration is confirmed by;

_____ _____

Prof. Susan Nchimbi-Msolla Date

(Supervisor)

_____ _____

Prof. .A.J.P Tarimo Date

(Supervisor)

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DEDICATION

This work is dedicated to my Mother Dorothy Ntirabampa and the late Sr. Julia Ndayitwayeko who laid the foundation stone of my career to this level of education.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

LIST OF ABBREVIATIONS AND SYMBOLS

µg	Micro grams = 10^{-6} gram
ABI	Applied Biosystems
BecA	Bioscience East and Central Africa
BME	ß-Mercaptoethanol
bp	base pair
C	Chloroform
Ca	Calcium
Cdna	complementary DNA
CGIAR	Consultative group of Agricultural Research
cM	centi Morgan
CTAB	Cytyltrimethyl Ammonium Bromide
DAR-win	Dissimilarity Analysis and Representation for windows
DNA	Deoxyribose Nucleic Acid
dNTPs	Deoxynucleoside Triphosphates
EDTA	Ethylene Diamine Tetra Acetic acid
F	Forward
FAM	6-Carboxy-Fluorescine (Blue)
FAO	Food and Agriculture Organization
Fe	Iron
Hi-Di	Highly Deionized dye
IBPGR	International Board of Plant Genetic Resources
Kb+	Kilobase and above (1000base pair and above)
KOAc	Potassium Acetate
LIZ	Five dye labeled high density size standard

M	Molar
m.a.s.l.	Meter above sea level
MAFS	Ministry of Agriculture, Food Security and Coorperatives
Max	Maximum
MW	Molecular Weight
Nacl	Sodium Chloride
NaOAc	Sodium Acetate
NED	6-Carboxy-X-Rhodamine (Yellow/Black)
ng	Nanograms = 10^{-9} gram
nm	Nanometer = 10^{-9} meter
P	Phosphorus
PCA	Principal Component Analysis
PCoA	Principal Coordinate Analysis
PCR	Polymerase Chain Reaction
PET	Tetrachloro -6-Carboxy-Fluorescene (red)
PGRC	Plant Genetic Resources centre
PIC	Polymorphic Information Content
R	Reverse
rDNA	Ribosomal Deoxyribose Nucleic Acid
REML	Restricted Maximum Likelihood
RNA	Riboxy nucleic Acid
RNase	Ribonuclease
rpm	Revolutions per Minute
Sec	Seconds
SSR	Simple Sequence Repeats
TAE	Tris Acetate EDTA (buffer)
Taq	Thermus aquaticus

TBE	Tris Borate EDTA
TE	Tris Ethylenediaminetetraacetate
TM	Trade Mark
U	Units
UPGMA	Unweighed Pair Group Method based on Arithmatic Average
UV	Ultraviolate
v	Volts
v/v	volume by volume
VIC	Tetrachloro-6-carboxy-fluorescine (Green)
vol	volume
W	Watt
w/v	weight by volume
Zn	Zinc
µg	microgram
µl	Microlitres = 10^{-6} litres
µM	micromolar

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background Information on Finger Millet Production

Finger millet (*Eleusine coracana* (L.) Gaertn.) sub species c*oracana*, belongs to family Poaceae. The cultivated *Eleusine coracana* is a tetraploid (2n=4x=36). The crop is grown for food and cash in semi-arid and arid areas under rain-fed conditions. The crop may have originated from Uganda or neighbouring highlands of Ethiopia (CGIAR, 2001; Bennetzen *et al*., 2003). In Eastern and Central Africa, it is produced in Uganda, Kenya, Tanzania, Rwanda, Burundi, Eastern Democratic Republic of Congo, Ethiopia, Sudan and Somalia (Obilana *et al*. 2002).

In Tanzania, it is traditionally produced in Rukwa, Mbeya, Iringa, Ruvuma, Mara, Kagera, Kigoma, Kilimanjaro, Singida, and Dodoma (Marandu and Ntundu, 1995). The crop is grown mainly by subsistence farmers under rain fed cropping system within the semi arid and arid regions of Tanzania which are drought prone areas (Mgonja *et al*., 2007). Despite its importance as a low input, food security and nutritious crop, its productivity is low ranging from 0.4 to 2 tons/ha (Dida *et al*., 2007). The production potentials are estimated to be as high as 4 tons per hectare (Mgonja *et al*., 2005). The average grain yields on farmers' fields are low, ranging from 500 kg/ha to 750 kg/ha (Mitaru *et al*., 1993) due to lack of improved varieties and poor agronomic practices (Mgonja, 2005; URT, 2006). Farmers obtain local cultivar seeds from local markets and recycle seeds from their previous harvests (Obilana *et al*., 2002). Tanzania crop census report has shown that there has been a considerable decline in yield over the years (URT, 2008).

Morphological diversity determination and characterization involving observation, measurement and documentation of visible and heritable traits is needed in finger millet (Ferreira, 2005). Genetic diversity study involves generation of information on variability among individuals or population for use in conservation and cultivar improvement. Deoxyribose Nucleic Acid (DNA) polymorphisms have been used to characterize and identify novel germplasms for use in the crop breeding (O'Neill *et al*., 2003). The information on genetic variability has been used in identifying and developing genetically unique variety to the existing cultivars (Chakravarthi and Naravaneni, 2006). Genetic diversity may refer to the sum of characteristics within any species or genus (Rao and Hodgkin, 2002). Among other values of genetic diversity is counteracting biotic and abiotic stresses and have been reported to be important in insect pests and diseases management (Hajjar *et al.*, 2008). Nisar *et al.* (2008) suggest the determination of genetic diversity information and its relationship as a strategy for utilization of the germplasm and crop management.

Species genetic diversity is important for sustainable crop existence by increasing a chance of species to survive biotic and abiotic stresses (Trethowan and Kazi, 2008). Moisture deficit is a significant challenge to the future survival and production of plant and animal species on earth. A plant responds to a lack of water by halting growth and reducing photosynthesis and other plant processes in order to survive to next generation. When water loss increases progressively, leaves begin to wilt and fall off or die together with mother plant. Drought stress may affect rainfall distribution, duration and intensity, temperature regimes, soil characteristics, plant growth and alleviated food and income insecurity in many countries (Sadras, 2002). The shift in rainfall frequency and intensity has led to severe drought causing negative impact on crop productivity in semi arid and arid regions of Tanzania (Kijazi and Reason, 2009). Drought in this context refers to a

condition in which the amount of water available to plant is insufficient to meet the transpiration needs of the crop. It entails deficiency in precipitation over an extended period, usually a season or more, resulting in a water shortage causing adverse impacts on vegetation, animals, and people (Araus *et al.,* 2002). It therefore hinders agricultural development by encouraging unsustainable land use.

1.2 Economic Importance of Finger Millet in Tanzania

Finger millet is a cereal crop grown for its nutritious grain production. It serves as a sustainable and food security crop that is especially important for its nutritive and cultural values and excellent storage qualities (Dida *et al*., 2007). Finger millet contains essential amino acids including leusine, tryptophan, cystine, methionine, phenylalanine and tyrosine all with high biological values. Finger millet grains are reported to contain large quantities of iron, calcium, dietary fibre, polyphenols and proteins (Devi *et al.,* 2011). FAO (2009) reported finger millet to be rich in fat content, vitamins and minerals than maize, rice and sorghum. It is an important preventive tool against protein-energy malnutrition and has an excellent nutritive value by containing 7 to 14 per cent protein (Oryokot, 2001). The two sulphur-containing amino acids namely, methionine and cystine are deficient in other cereals and most of starchy foods such as cassava and maize (Oryokot, 2001). This makes it an ideal crop in the control of protein-energy malnutrition in communities living on starchy food, particularly in semi arid and arid regions.

The crop has fewer storage pests than other cereals (Obilana and Manyasa, 2002). Grain quality deterioration is delayed making the crop an important food security crop in famine prone areas (Upadhyaya *et al*., 2007). It provides raw material for the local brewing industries and is used in formulation of weaning foods (Obilana *et al.,* 2002). FAO (2012)

reports finger millet to be staple food in many African countries and to have saved many lives during famine period. Its ability to store for years with less insect pest damage and little deterioration in nutritional quality make an ideal crop for food security. It has several health benefits which are attributed to its polyphenol and dietary fiber contents. It has high content of calcium (0.38%), dietary fiber (18%) and phenolic compounds (0.3-3%) (Goron and Raizada, 2015).

1.3 Importance of Finger Millet in Drought Stress Adaptation

Finger millet is the first most important among millets grown in many regions of Tanzania under diversified situations of soil, temperature and rainfall. It's early maturing, low input and less affected by major pests and diseases; high rejuvenation capacity after alleviated stress conditions makes this crop ideal for dry land farming.

Finger millet growth, development and the subsequent yields are influenced by soil moisture, solar radiation, temperature, soil nutrients and other many factors. The crop is mainly grown under poor environmental conditions such that their potential productivity is rarely achieved. Inadequate soil moisture content and low nutrient fertility are the biggest limitations to the crop production.

The cro is robust, tufted, tiller producing grass, growing up to 170 cm tall (FAO, 2012; De Wet 2006). Finger millet panicle has florets which grow into fingerlike structures ranging from 4 to 19cm. The name finger millet is named after these fingerlike structures (de Wet, 2006; Quattrocchi, 2006). Finger millet under good crop growing conditions matures after 3 to 6 months (Dida *et al.*, 2006). It performs well at altitudes between 1000 and 2000m above sea level and at the average temperature of 23°C (FAO, 2012). It requires well

distributed rainfall ranging from 500 to 1000 mm per growth cycle (Dida *et al.,* 2006). Finger millet is adapted to a wide range of soil conditions though it prefers fertile, well-drained sandy to sandy loam soils with pH ranging from 5 to 7 units. It is a small seeded cereal which undergoes C_4 photosynthetic pathway with minimum photorespiration, a process which runs antagonistically with photosynthesis. It keeps leaf pores shut for longer periods thereby avoiding water loss through evapotranspiration (Araus *et al.,* 2002).

The drought phenotyping of finger millet targeting drought tolerant variety development is a pre requisite for sustained grain yield in semi arid and arid regions (Araus, *et al.,* 2002). Proper recording of meteorological data on rainfall, temperatures, wind, evapo-transpiration and light intensity will help in identification, understanding and interpretation of events of drought stress and associated environmental factors and thus plan for climate resilience crop development (FAO, 2012). Sufficient genetic variability for the target traits is prerequisite to effective breeding and landraces and wild genotypes provide valuable opportunities to enhance the variability for drought adaptive traits and yield (Talamè *et al.,* 2004).

1.4 Statement of the Problem and Justification

Finger millet production in Tanzania is also limited by numerous biotic and abiotic constraints. Finger millet is often cultivated in semi-arid and arid agro-ecology, where it is frequently affected by drought. The production constraints associated with drought need drought tolerant varieties adapted to low inputs in semi arid and arid areas. Current and predicted climate change will likely result in increased temperatures and unreliable rainfall, and may lead to a larger diversity of insect pests and diseases attacking these crops. Therefore, finger millet production is expected to continue facing the impacts of

climate change and food insecurity threatening livelihoods of people arid regions. Development of resilient and drought tolerant genotypes adapted to the effects of climate changes is necessary to sustain the lives of people in Tanzania (Mgonja *et al*., 2007).

Water availability is the most important environmental factor that reduces crop production. In Tanzania, regions that are highly and frequently affected by drought in include Kilimanjaro, Arusha, Manyara, Shinyanga, Simiyu, Singida and Dodoma (Kijazi and Reason, 2009). Severe drought stresses which inflicted Tanzania from 1998 to 2005 have drastically affected crop yields in arid and semi arid regions to the extent that cereal crops like sorghum and pearl millet which are relatively drought tolerant attained only about 25% of their yield potential (Kijazi and Reason, 2009). Soil moisture deficit due to increased frequencies and severity of drought is likely going to exacerbate crop yield reduction and lead to food insecurity in Tanzania.

There are major challenges to breeding under water-limited conditions of semi arid and arid regions. First crop drought tolerance is influenced by multi-factorial trait repertoires requiring integrated breeding strategy (Blum, 2005). Secondly, there is lack of effective phenotyping method to concisely identify quantitative traits responsible for yield and yield related traits across different water régimes. Thirdly, drought stress is highly variable in its timing, duration and severity. Fourthly, the whole-plant response to drought stress is complex because it is determined by component traits that interact and differ in their individual responses to the intensity and duration of water deficits and temperature (Passioura, 2010).

Finger millet breeding has been limited to selection methods basing on morphological traits. Mgonja (2005) reports on Few agronomic and yield evaluation trials limited to mass selection techniques because of time and financial constraints. Farmers' dependence on local finger millet cultivars' seeds have lead to decline in the crop production in Tanzania. Mgonja *et al.* (2005) reported finger millet yield on farmers' fields of 675 kg ha^{-1}on average which is far below the crop yield potential in Tanzania. Furthermore, the crop production has been on a declining trend in farmer's fields from 147,700.0 tons to 77,890.0 tons with an averaging decline of 0.234 tons ha^{-1} per year from 2001 to 2005 (URT, 2006). Factors which contributed to such a decline were lack of improved varieties, poor agronomic practices and severe drought.

There is scant information on finger millet diversity and agronomic recommendations for yield improvement (Fakrudin *et al*., 2011). The lack of information on plant diversity and information on drought tolerance traits has led to poor breeding programs which in turn have led to limited availability of improved seeds and drought tolerant varieties. Moose and Mumm (2008) suggests collection of genotypes with genetic variability as pre-requisite for both conventional and molecular breeding. Upadhyaya *et al*. (2008) also suggested assessment of genetically diverse resource base as a pre-requisite for crop yield improvement. Then phenotypic information can be used in crop selection for desired traits (Ayana and Bekele, 1999). Genotype collections followed by selection for superior phenotypes will enable application of efficient and more effective methods of variety development and crop improvement.

Finger millet has been neglected by mainstream research, policy makers and at the production level. Although difference in cultivars grown by farmers can clearly be

observed in the field, meager funds and insignificant research work has been committed to assess the diversity of these finger millet cultivars (Fakrudin *et al*., 2011). The assessment of genetic diversity using DNA markers is one of the key tools of crop improvement and germplasm conservation (Fakrudin *et al.*, 2011). Molecular genetics techniques using DNA polymorphism have been used to characterize and identify elite breeding lines for uses in the crop breeding processes (O'Neill *et al*., 2003) and the same techniques can help improve finger millet production in Tanzania.

After intensive review, need for determination of diversity of finger millet genotypes aimed at screening for drought tolerance and greater yield was identified. The current study, therefore, was set to evaluate phenotypic diversity and yielding potential of finger millet genotypes in Tanzania. In addition to phenotyping, the research also involved screening finger millet genotypes using SSR molecular markers to determine genetic diversity. Evaluation of genotypes to determine the genetic diversity among genotypes was reported by Ferreira (2005) to have improved crop variety development with respect to yield and yield components.

1.5 Objectives

1.5.1 Overall objective

To characterize Tanzania finger millet accessions (TFA) for future use in the crop improvement in Tanzania.

1.5.2 Specific objectives

1.5.2.1 To evaluate phenotypic diversity of local finger millet genotypes using morphological, phenological and physiological characteristics

1.5.2.2 To determine genetic diversity of local genotypes of finger millet using molecular characterization

1.5.2.3 To establish drought tolerance and yield levels of finger millet genotypes collected from major growing districts of Tanzania

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Finger Millet Phenotyping

The availability of diverse genetic resource base, their morphological and genetic variability and characterization are reported by Upadhyaya *et al*. (2008) as an essential activity for the effective utilization in crop improvement programs. Bedis *et al.* (2006) identified phenotypic diversity among thirty seven finger millet genotypes and reported significant variation in time to flowering, time to maturity, plant height, panicle length, number of panicles per plant, number of fingers per panicle and grain yield. Their study was based on plant phenotypic characteristics developed by IBPGR (2011); which enabled them to determine the highly heritable morphological characters. Quantitative traits are the cumulative resultant of polygenic actions through interaction and are influenced by the environment and contribute towards the overall phenotype (Sham *et al.,* 2002). For example, yield component traits such as plant height, plant maturity, and number of tillers, finger length, drought resistance, root density and disease resistance are quantitative traits that are widely used in the selection of superior cultivars in finger millet (Sham *et al*., 2002). Quantitative traits vary among individuals across different environments (Sham *et al.,* 2002). Bedis *et al*. (2006) reported genetic variability of 37 finger millet genotypes with respect to diversity and showed maximum genetic variability in the number of time to flowering, time to maturity, plant height, and number of fingers per panicle and grain yield. The phenotypic coefficient of variation was highest for fodder yield, number of productive tillers per plant and grain yield per plant (Bedis *et al*., 2006). Mgonja *et al*. (2007b) also reported a considerable range of morphological and genetic diversity among Eastern and Central Africa finger millets and recommended for extensive collections,

characterization and careful evaluation across regions for the effective utilization of genetic base in the crop improvement programs. According to All India Coordinated Small Millets Improvement Project report (1996) the acquisition of primary information about plant genetic diversity is an important fundamental work to sustain genetic conservation. Evaluation of genotypes to determine the genetic diversity among genotypes will improve crop variety development with respect to yield and yield components (Ferreira, 2005).

2.2 Finger Millet Genotyping

The availability of diverse genetic resources is very important for genetic improvement of finger millet and Bennetzen *et al*. (2003) confirmed the availability of genetic diversity among finger millets of East and Central Africa. Haider *et al*. (1994) reported genetic variation and characters associated with 11 yield components of 46 genotypes of finger millet. Sherchan (1989) also reported genetic variation of finger millet in terms of plant pigmentation, panicle type and time to plant maturity.

Breeders use information on genetic diversity to directly select individual plants with traits of interest and serve time and recourses in breeding programs. Dida *et al.* (2008) were able to discriminated population structure of 79 finger millet accessions using 45 simple sequences repeats (SSR) markers and identified significant distinction of plant architecture and yield in Asian and African finger millet populations in one experiment.

Several molecular markers have been utilized for characterizing the germplasm. Salimath *et al.* (1995) suggested SSR markers to be the most promising for the analysis of plant diversity. SSR markers are characterized by their abundance and are unaffected by

environmental factors (Ram *et al.*, 2007). They are powerful tools for assessing genetic variation and relationships within and among species. They are born from regions in which variants of simple repetitive DNA sequence motifs are already over represented (Tautz *et al.*, 1986). They often present high levels of inter and intra specific polymorphism, particularly when tandem repeat number is ten or greater (Queller *et al.*, 1993). The SSRs are mostly co-dominant markers, and are indeed excellent for studies of population genetics and mapping (Jarne and Lagoda, 1996; Goldstein and Schlotterer, 1999).

The SSRs are used in molecular genetics studies because they are highly polymorphic, require low amount of DNA, easily automated for high throughput screening and exchanged between laboratories (Gupta *et al.*, 1999). They are characterized by their abundance, reproducibility and rarely affected by environmental conditions (Sergio and Gianni, 2005). In a nutshell, molecular markers provide unambiguous estimates of genetic variability of populations (Sinha and Pande, 2010).

2.3 Crop Morphological and physiological Mechanisms of Adaptation to Drought

Overall, three strategies can help a crop to mitigate the effect of drought stress: (a) drought escape (b) drought avoidance (c) drought tolerance (Araus *et al.*, 2002). Drought escape strategy refers to proper timing of life cycle such that completion of the most sensitive developmental stages is achieved before drought sets in. In drought avoidance the plant root system is well developed to extract water from deep soils and shoots system reduces evapotranspiration thus maintaining grain yield (Araus *et al.*, 2002). Drought tolerance involves mechanisms such as osmotic adjustment which enable the plant to maintain turgor pressure under reduced soil water potential and drought avoidance mechanisms can

be expressed even in the absence of stress and are then considered constitutive (Araus *et al.,* 2002). Drought tolerances mechanisms are the result of a response triggered by drought stress itself and are therefore considered adaptive (Araus *et al.,* 2002). When the stress is terminal and predictable, drought escape through the use of shorter duration varieties is often the preferable method of improving yield potential. Drought avoidance and tolerance mechanisms are required in situations where the timing of drought is mostly unpredictable.

Tuberose (2012) reported two basic drought tolerance mechanisms as dehydration avoidance and dehydration tolerance in dehydration avoidance plants use morphophysiological features such as deep root system, early flowering, exudation of waxes, osmotic adjustment to maintain hydration status. Dehydration tolerance is defined as the relative capacity to sustain or conserve plant function in a dehydrated state (Blum, 2005) and is regarded a second line of defense after dehydration avoidance. However, dehydration tolerance mechanism in crop plants is rare, less effective and it only exists in the seed embryo and is lost after germination (Blum, 2005). Tuberose (2012) again reported that in dehydration tolerance plants undergo biochemical process of remobilization of stem water-soluble carbohydrates and accumulation of molecular oxidants to maintain physiological functions despite the severity of drought. However, there is no unified drought tolerance mechanism either at plant level or at gene level (Blum, 2005). Moreover, the traits associated with avoidance and tolerances differ between genotypes and vary with the stage of the plant life cycle (Araus *et al.,* 2002). Blum (2005) observed that natural selection and farmers' selection have been targeting dehydration avoidance as the major strategy in coping with drought stress.

There are also two physiological processes involved in drought tolerance which include sustained leaf photosynthesis during grain-filling contributing to increased dry matter accumulation, and increased grain number per panicle due to higher partitioning of assimilates during fertilization and grain filling stages (Blum, 2004). Tollenaar and Lee (2006) ascertained that such an increase in dry matter accumulation and grain during grain filling period are in direct proportional. However, Tambussi *et al.*, (2005) reported photosynthetic efficiency and performance under water stress to favour panicle development to leaves in wheat and other small grain cereals. Finger millet is believed to be drought resilient crop that can be used as a coping strategy to counteract the effects of drought stress (FAO, 2012). Phenotyping for drought tolerance and yield stability should be carried out across a broad range of environments within the target population environment (Tuberose, 2012) and understanding patterns of adaptive diversity is essential in identifying genotypes which are resilient to drought stress (Mercer and Perales, 2010).

The morphological and physiological traits that affect yield in drought conditions are either expressed under well-watered or drought stress conditions. However, drought-responsive traits are expressed only under pronounced water shortage (Blum, 2006). Constitutive traits affect yield under drought stress conditions and breeders have used these traits to breed for dehydration avoidant varieties (Blum, 2005, 2006,) in drought phenotyping for enhanced yield (Blum, 2009). Potential traits for selection targeting yield improvement under drought conditions are casually correlated genetically with yield. They are of greater heritability than yield and genetic variability is useful when no yield penalties under favorable conditions and their measurements are done in non-destructive, rapid, accurate, and inexpensive way (Blum, 1998; Monneveux and Ribaut, 2006).

2.4 Grain Yield and Drought Adaptation in Finger Millet

Grain yield remains an appropriate way to gauge the overall phenotypic value of any genotype (Tuberose, 2012). Yield is a complex quantitative trait influenced by multiple genes. It is with low heritability and high genotype-environment (GxE) interaction (Jackson *et al.*, 1996) such that, breeding for drought tolerance using grain yield traits as indicator need to be conducted in stress environment (Bänziger *et al*., 2006; Lafitte *et al*., 2006). To facilitate drought tolerance breeding, evaluation of various yield components is necessary. Availability of genetic variability in yield influencing traits and understanding of the associations among traits are important towards the crop improvement because simultaneous improvement in drought tolerance and yield traits depends on the nature and degree of association between traits (Mnyenyembe and Gupta, 1998). This is because the ultimate expression of yield in crop plants is usually dependent upon the action and interaction of a number of important traits (Tuberose, 2012). Grain yield is a product of integrated different plant processes upon limited resources like solar radiation, water and soil nutrients (Blum, 2004). The processes involves production of photo-assimilates and transformation of assimilates into harvestable component. As such direct selection for high yielding is a strategy that has been commonly used in cereal breeding to improve yield in water limited environments. For example Kumar *et al.* (2007) reported high heritability of grain yield under severe terminal drought stress in rice. They also reported low heritability for secondary traits and integrative drought resistance traits such as harvest index, floret sterility, flowering delay, root pulling force, root dry weight all under field condition. Direct selection for yield under managed stress, when combined with concurrent selection for yield potential, is an effective but underutilized approach to developing stress tolerant finger millet (Bernier *et al.,* 2008). Babu *et al.* (2003) reported high heritability for leaf rolling, harvest index and panicle fertility in drought affected

fields. Because plant changes their resource partitioning according to the growing conditions. Babu *et al.* (2003) suggested selection of plants with high capacity of remobilizing non structural carbohydrates from stems to grains. Drought stress allows clear differentiation between resistance and susceptible genotypes on the bases of yield.

Improved breeding for greater yield potential and better adaptation to drought stresses requires full understanding of physiology in order to properly perform drought phenotyping. Such understanding will enable efficient and effective physiological breeding. Physiological breeding entails use of secondary traits to determine higher yield potential and improved behavior of the crop when grown in a stressful environment. There are several means to determine phenotypic traits that can help speed up physiological breeding for drought tolerance (Araus *et al*., 2002). Physiological understanding of G x E interactions help to conduct multi-environmental experiments to evaluate performance of an elite cultivar and interpreting the nature and magnitude of G x E interactions for use in future yield improvements. Genetic improvement through selection for primary trait like grain yield in a target environment have been achieved in wheat, rice and maize and can be achieved in finger millet (Ceccarelli and Grando, 1996). Araus *et al*. (2002) identified the plant adaptation as a key factor that will determine the future severity of the effects of drought on the crop production.

2.5 Phenological Changes and Drought Avoidance in Finger Millets

Phenology is the most widely used secondary trait because of ease of measurement and relatively high heritability (Bänziger *et al*., 2000). Selection for a flowering date that does not coincide with the period of water deficit is a highly effective way to improve drought adaptation (Araus *et al*., 2002). A phenological change of finger millet at the onset of drought is another factor to consider when breeding for drought tolerance (Tuberose,

2012). The time to flowering is a major trait related to the adaptation of genotypes to water deficit stress (Passioura, 2002; Araus, 1998). Review by Slafer (2003) identified time to flowering as the first attribute that has been optimized by breeders to achieve drought avoidance adaptation. Passioura (1996) and Slafer and Whitechurch (2001) all reported early maturity to be the most effective means to increase yield in semi arid and arid areas. The number of days to flowering is normally measured under both stress and non stress conditions. However, under severe drought stress finger millet flowering is delayed due to vegetative growth dormancy. Finger millet yield improvement can therefore be realized when selection is done on duration to plant physiological maturity and genotypes maintaining panicle fertility under drought stress rather than time to flowering. Apart from drought adaptation advantage, phenological changes of the crop allows for augmented cropping intensity for cereals and intercropping with other crops in cereal-based farming systems (IRRI, 1996). Relatively inexpensive changes, such as shifting planting dates or switching to an existing crop variety, may moderate the negative impact of climatic change.

2.6 Plant Height Influence on Biomass and Grain Yield Production

Royo *et al*. (2007) reported plant height to be negatively correlated to the harvest index (HI) and Slafer *et al*. (2005) identified minimum height below which yield limitation is obvious. Selection for reduced height is therefore done when the breeding materials exceeds a threshold of 70–100 cm (Richards, 1992; Miralles and Slafer, 1995). There is no increase in biomass associated with increase in tallness, but proportional reduction in the harvest index (Royo *et al*., 2007). Below the threshold, any gain in the harvest index does not compensate for the loss in biomass due to poor solar radiation distribution within the canopy and consequent reductions in resource use efficiency (Miralles and Slafer, 1997).

2.7 Finger Millet Root Biomass for Drought Adaptation

Selection for faster growing and deeper roots could enhance water harvest and help stabilize yield under drought conditions (Zhu *et al.,* 2011). The importance of well developed root system for higher yield has been reported in maize (Tuberosa *et al.*,2003; Hammer *et al.*,2009; Landi *et al.*,2010; Hund *et al.,* 2011), barley (Forster *et al.*,2005), wheat (Manschadi *et al.,* 2006; Wasson *et al.*,2012), and rice (Steele *et al.*,2006; Kamoshita *et al.*, 2008; Witcombe *et al.,* 2008; Bernier *et al.,* 2009; Henry *et al.,* 2011). The effects of root density on yield will depend on soil moisture distribution and competition within the plant population (King *et al.,* 2009). Kimurto *et al.* (2005) reported to have successfully measured plant grown under controlled conditions and recommended it as a quick and accurate method for determination of root characteristics and prediction of yield potentials in finger millet.

2.8 Drought Tolerance Indices Application in Determination of Terminal Drought Tolerant Finger millet Genotypes

Severity of drought depends on the development phase of plant (Gupta *et al.,* 2001). Post anthesis stage of cereal plants has a critical importance on drought tolerance. This is because dry matter production after heading is the determinant of grain yield (Schnyder, 1993; Saidi *et al.,* 2008). Selection breeding in cereals based on yield performance under drought stress conditions has therefore become a common approach. Drought tolerant genotypes selection indices in dry condition have been developed and used to identify drought tolerant genotypes in wheat and maize (Talebi *et al.,* 2009; Pireivatlou *et al*., 2010). Rosielle and Hamblin (1981) suggested use of drought tolerance index (DTI) to select genotypes for drought tolerance in wheat and rice. Fernandez (1992) reported to have selected high yielding wheat genotypes under water deficit conditions using DTI.

Kumar *et al.* (2008) reported that selection under severe drought stress at reproductive stage led to yield reduction of 65% than did under non stressed conditions. Drought tolerance index techniques were adopted in selecting drought tolerant genotypes of finger millet in this study.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Collection Locations and Experimental Sites

3.1.1 Collection Locations

The study involved four major finger millet producing districts of Singida rural in the wards of Mtinko, Ntuntu, Mughamo, Hongelo, and Ilongelo; Kondoa in wards of Itaswi, Hondomairo,Goima, Pahi and Changaa; Mpanda rural in wards of Bulamata, Ifumbula, Ilangu, Busongola and Kamjela. Collection in Ngara was done in wards of Rusumo, Kabanga, Mugoma, Ntobeye and Muruvyagira. Earlier finger millet germplasm collections were sourced from National Plant Genetic Resources Centre (NPGRC) at Tropical Pest Research Institute (TPRI) in Arusha. Collection of seeds of the genotypes was done from five wards, three villages per wards and five farmers per village in each of the districts (Fig.1).

3.1.2 Experimental Site

The experiment was conducted between March and July in 2014 at the crop Museum of Sokoine University of Agriculture (SUA).The experimental site is located at 6° 50' 55" S / 37° 39' 22" E at about 500-600 meters above sea level. Rainfall received for the season 2013/2014 averaged 565.7mm per annum (SUA Meteorological data, 2014). The area is dominated by soils which are well drained, dark reddish brown, clay loams and sandy clays with moderate structure and low natural fertility.

Table 1: Summary of Weather parameters recorded on weekly bases during drought phenotyping period (See appendix 1 for daily weather parameters)

Weeks	**Max T (ºC)**	**Min T (ºC)**	**Net SR (Wm^{-2} day^{-1})**	**RH (%)**	**Rainfall (mm)**	**Evaporation (mm)**
1-7 March	31.04	21.49	14.24	53.29	25.10	21.80
8-14 March	30.67	21.83	26.00	62.71	24.80	27.30
15-21 March	31.73	22.07	24.55	55.29	2.80	18.20
22-28 March	31.76	22.09	25.54	51.43	56.80	18.90
29Mar-4Apr	29.47	21.46	21.03	69.71	75.90	21.35
5-11Apr	29.83	22.00	17.69	67.14	91.20	1.75
12-18Apr	28.07	20.59	15.94	79.14	60.50	16.70
19-25Apr	29.40	20.99	16.01	87.43	65.30	24.35
26Apr-2May	29.97	20.36	22.15	77.29	27.70	23.65
3-9May	27.74	20.77	159.65	66.14	64.60	12.80
10-16May	29.16	19.69	159.75	62.71	26.30	7.65
17-23May	27.64	19.60	75.94	66.14	3.70	5.50
24-30May	28.01	19.39	127.21	67.29	2.00	6.85
31May -6 June	28.93	18.37	133.36	65.29	0.00	5.90
7-13 June	27.56	18.33	97.02	61.00	0.00	5.00
14-20June	28.14	17.23	94.92	57.71	23.30	6.00
21-27June	27.23	18.09	143.88	54.43	0.70	4.00
28June-4July	27.66	15.74	140.67	54.57	0.00	5.00
5-11July	27.87	16.30	95.94	53.00	0.00	6.00
12-18July	27.37	15.11	139.27	51.43	0.00	6.80
19-25July	27.93	16.37	127.55	55.14	0.00	6.90

Max T = Maximum temperature, Min T = Minimum temperature, Net SR = Net solar radiation and RH = Relative humidity

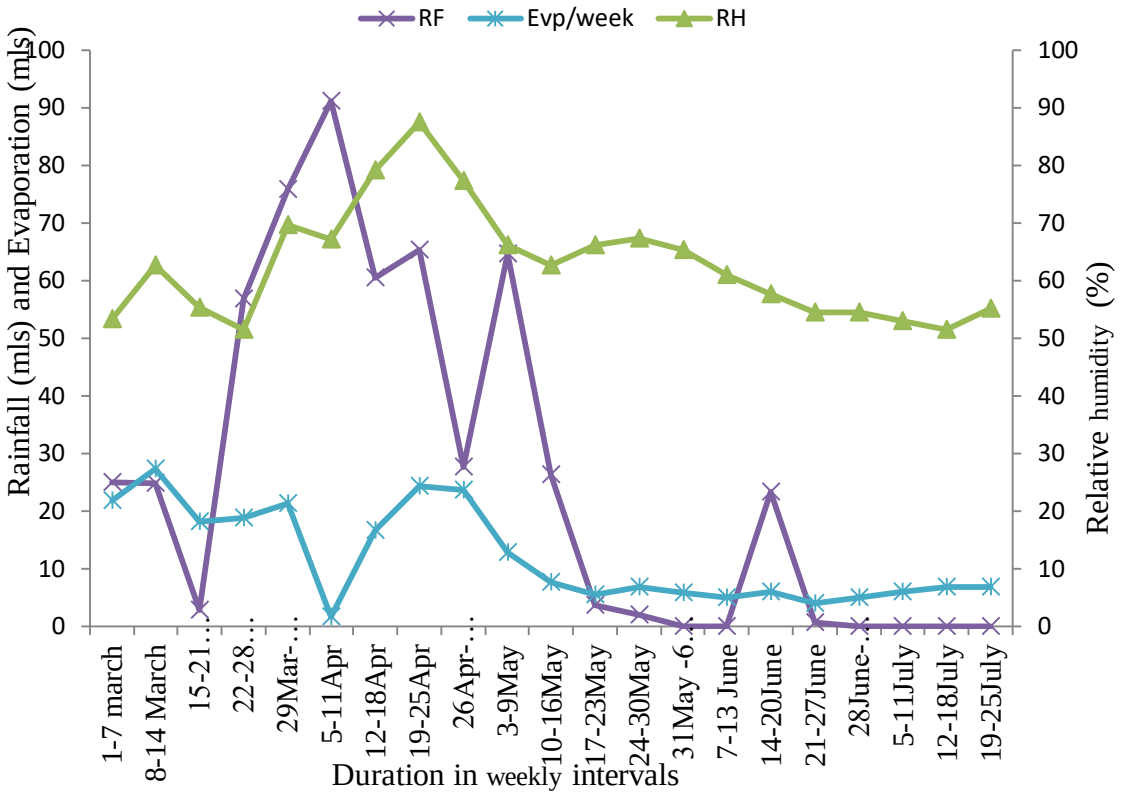

Figure 13: Rainfall, evaporation and relative humidity recorded during drought phenotyping period

RF = Rainfall, Evap/week = Evaporation rate recorded in week interval

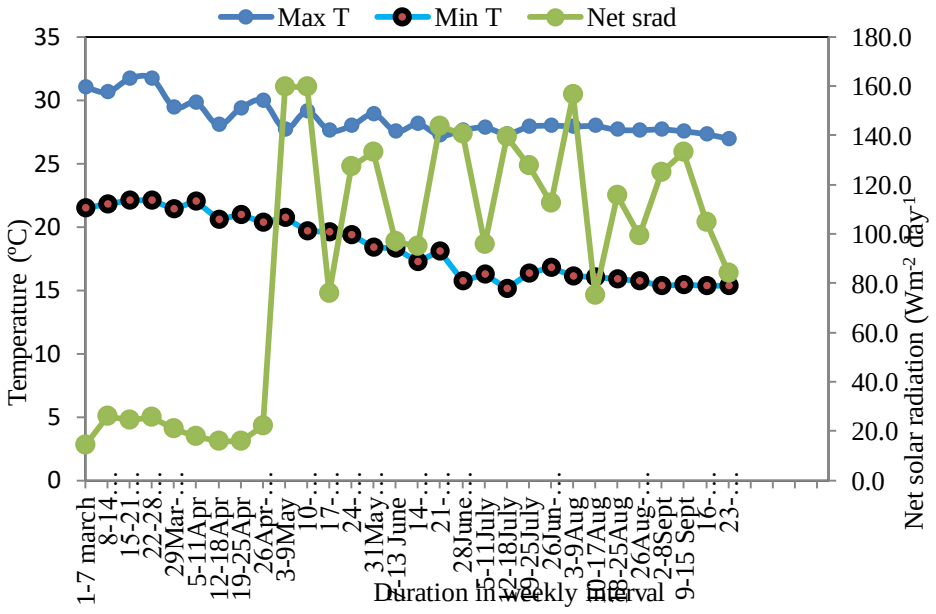

Figure 24: Temperatures and solar radiation recorded during drought phenotyping period

Max T= Maximum temperature, Min T= Minimum Temperature, Net srad = Net solar radiation=8

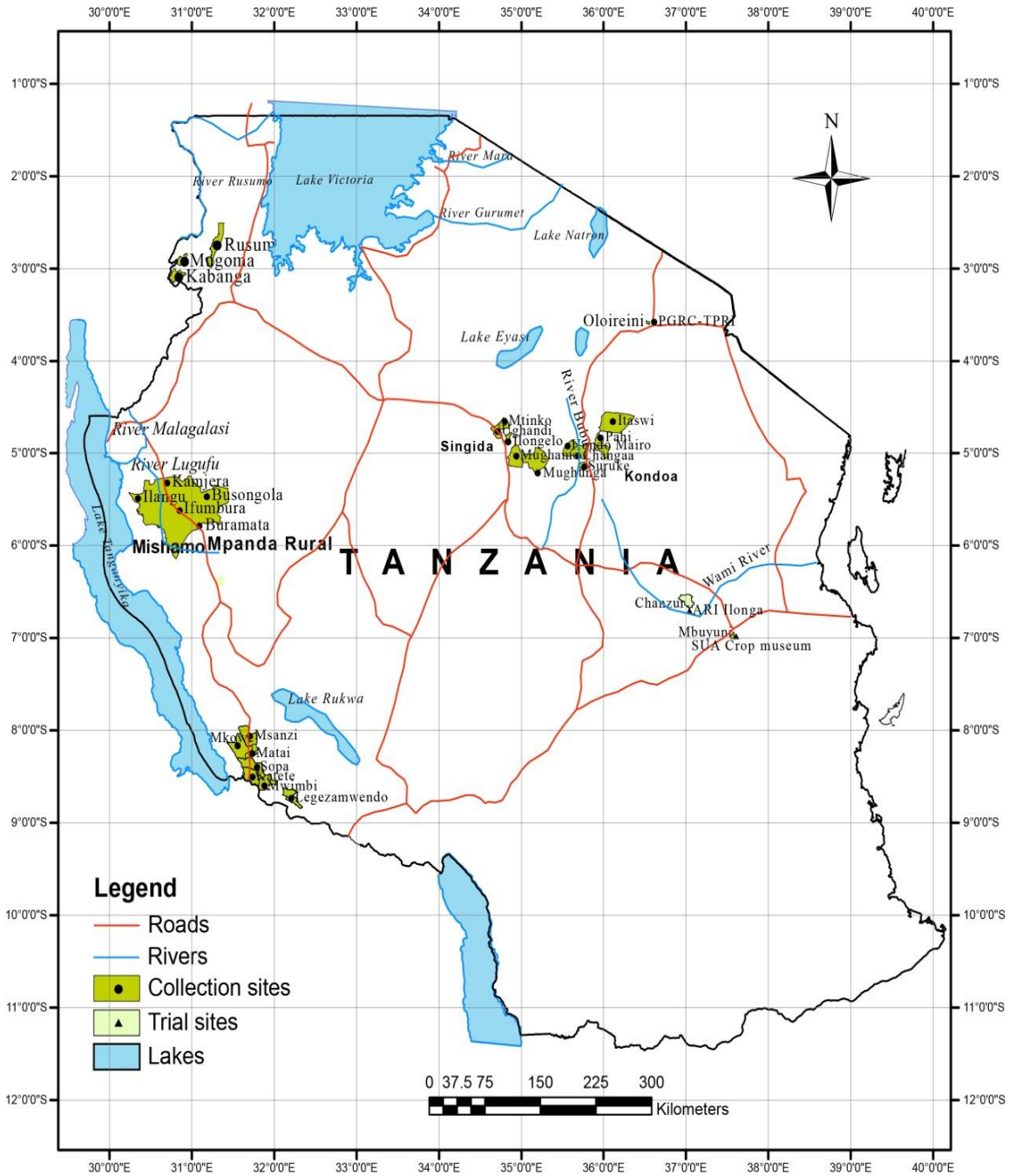

Figure 3~~1~~: Tanzania map showing collection and experimental sites of finger millet genotypes

3.2 Materials and Sampling Procedures

A total of 120 Tanzania finger millet accession samples in the form of seeds were collected from farmers' fields and 46 accessions from NPGRC in 2012. A total of 166 Accessions were collected and planted at ARI Ilonga under irrigation during 2012 for single plant selection. Some accessions contained more than one genotype and based on phenotypic differences 169 local genotypes were selected for this study. Seeds and leaf samples of each genotype were harvested, dried, packed in polyethylene bags, labeled and transported to the International Livestock Research Institution laboratories (ILRI) in Nairobi for molecular characterization.

Forest soil characterized by reddish clay loam with moderate structure and moderate natural fertility was collected from uncultivated land of horticulture unit at Sokoine University of Agriculture and used in pot and PVC column experiments. NPK in 23:10:5 fertilizers was applied at the rate of 60.53%N, 26.32%P and 13.16%K per ha and an organophosphate systemic insecticide (Dimefarm 40EC) with contact and stomach actions against wide range of insects pests was used in insect control.

3.3 Evaluation of phenotypic diversity of finger millet genotypes using morphological characteristics

3.3.1 Experimental design

To determine morphological diversity and yield potentials of finger millets, the 169 genotypes were evaluated in 2013/14 cropping season. A 13 X 13 α- lattice experimental design with three replications and a plot size of 5 m length single row with plant spacing of 20 cm by 75 cm was used. Two weeks after seedlings emergence, plants were thinned to single plant per hill. Crop husbandry and post harvest management practices were done according to recommendations by the ministry of Agriculture (URT, 1998).

3.3.2 Data collection

The list of descriptors used and scoring were done according to IBPGR (2011) and Technical Bulletin on Biodiversity (2007) respectively with minor modification by leaving out traits of less economic importance (Appendix1). Ten plants per plot were randomly selected, labeled and phenotypic traits assessed. Data on the quantitative traits such as plant height (cm) (PH), number of productive tillers (NT), finger numbers (NF), finger length (cm) (FL), duration to plant maturity in days (PM), thousand grain weight in gm/1000seeds (SM) and plant yield in grams per plant were determined. The qualitative traits including panicle shape (PS), plant pigmentation (PP) and finger branching (FB) were assigned numerical codes as follows: - Panicle shape in a scale of 1 to 5; 1 for droopy (fingers lax and drooping), 2 for open (fingers straight), 3 for semi-compact (tops of fingers curved), 4 for compact (fingers close to each other and incurved at the tips) and 5 for fist-like (fingers very closely and incurved). De Wet (2006) recommended the use of inflorescence spreading characteristics to group finger millet genotypes and the same was used in this study. Plant pigmentation and finger branching were assessed in a binary scale of 0 for absent and 1 for present.

3.3.3 Data analysis

Analysis of variance for quantitative and qualitative traits was performed using Genstat software 15th edition software. Principal component analysis (PCA) with varimax rotation (University of Illinois at Chicago, 2009) was performed by using statistical package for social sciences version 16.0 (SPSS version 16) by factor reduction method to determine

the nature and source of observed variation. Factors with Eigen values greater than one were selected as major contributors to the observed variations among the finger millet genotypes. The genotypes were classified based on similarities into a dendrogram using agglomerative hierarchical clustering (AHC) according to Pearson correlation coefficient and unweighted pair group method with arithmetic mean (UPGMA) using XLSTAT 2015 version. The decisive correlation coefficients ($P \leq 0.05$) range adopted was from -1.00 to +1.00; where - 1.00 was the perfect negative correlation while +1.00 was the perfect positive correlation and 0.00 value implying lack of correlation between traits. Skinner *et al.,* (1999) reported the correlation values of ± 0.707 to be biologically meaningful to explain variation between correlated variable by 50 percent. Genotyped data analysis was done using GenALEX.6.4, Power marker and DARwin5 software (Peakall and Smouse, 2012).

3.4 Determination of Genetic Diversity of Finger Millet Genotypes by Molecular Characterization

Seeds of 169 finger millet genotypes were grounded using mortar and pestles with addition of liquid nitrogen and finger millet flour samples kept in refrigerator at negative 20 degree centigrade prior to genomic DNA extraction.

DNA extraction was achieved using ZR Plant/Seed DNA Miniprep™ (D6020) Kit, DNA quantification by NanoDrop200 and DNA quality was checked through Agarose gel electrophoresis. Polymerase chain reaction (PCR) was performed using AccuPower® -dye PCR Premix Bionner kit. DNA de-naturalation by HI-DI™ Formamide genetic analysis grade and alleles sizing using GeneScan™ -500 LIZ®. Genotyping using ABI 3730 genetic analyzer and scoring was done using Genemapper® Software Version 6.4.

The polymorphic information content (PIC) analysis was done using GenAlex. 6.5 (Peakall and Smouse, 2012) to identify markers with high polymorphic information for discriminating individual finger millet genotypes among Tanzania finger millet accessions. Decision was guided by Wright, S. (1951), suggestion that F_{ST} between 0.15 – 0.25 indicate great degree of genetic divergence and F_{ST} > 0.25 = very great degree of genetic divergence.

3.5 Establishment of drought tolerance and yield levels of finger millet genotypes collected from major growing districts of Tanzania

An evaluation of finger millet genotypes for water deficit tolerance due to terminal drought was conducted by studying above ground and bellow ground plant characteristics. Thirty high yielding finger millet genotypes selected based on high performance in yield, number of productive tillers and thousands grain weights were used in drought phenotyping. These genotypes were investigated under terminal drought conditions based drought tolerance index (Fernandez, 1992) for two consecutive growing seasons under field conditions at Sokoine University of Agriculture crop museum during cropping season from March 2014 to July 2015.

3.5.1 Above ground drought phenotyping of finger millet genotypes

Twelve traits of economic importance for sustained yield under terminal drought conditions were identified and used in finger millet drought tolerance screening. These included shoot traits namely shoot biomass (SB), plant height (PH), leaf area index (LAI), finger length (FL), number of productive tillers (NT), harvest index (HI), root to shoot ratio (R: S ratio), grain yield potential (Yp), grain yield under stress (Ys), yield stability index (YSI), harvest index (HI) and drought tolerance index (DTI).

3.5.2 Bellow ground drought phenotyping of finger millet genotypes

PVC tubes were filled with forest soil to three quarter volume and planted one genotype per pot and PVC tube in three replications. Two weeks after emergence, seedlings were thinned down to retain 1 seedling per pot. NPK in 23:10:5 fertilizers was applied using spot placement method at the rate of 60.53%N, 26.32%P and 13.16%K per ha at sowing and band placement at 45 days after emergence and second fertilizer application was done at flowering.

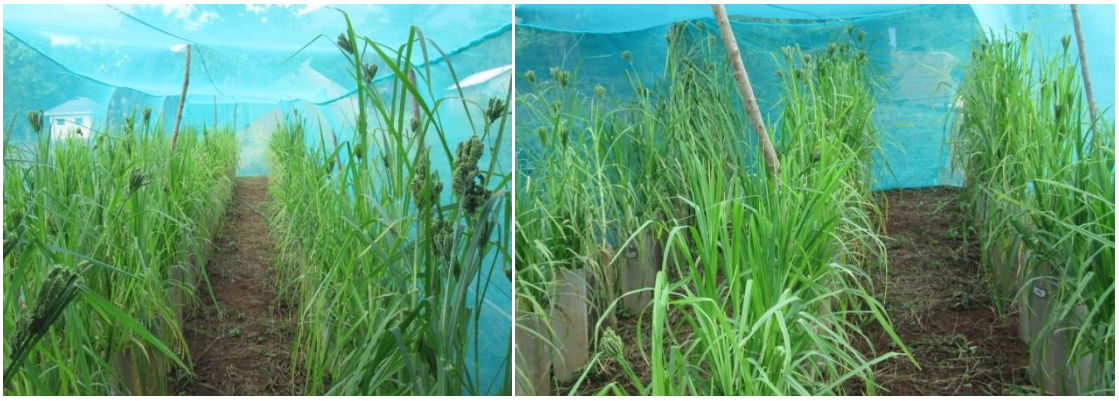

Plate 1: PVS Experiment to assess bellow ground properties of finger millet

The 8mm square knotted netting mesh was used to create an impassible barrier that excluded both small and large pest birds. An organophosphate systemic insecticide (Dimefarm 40EC) with contact and stomach actions against wide range of insects pests including aphids, crickets, leafhoppers, bollworms and whiteflies was applied at the rate of 1.5 L per ha. Supplemental irrigation was supplied from planting to 50% flowering after which the crops were subjected to terminal drought stress at the anthesis stage to the point of physiological maturity.

3.5.1 Characterization of finger millet shoot traits which influence yield and drought adaptation

The experimental design adopted was complete randomized design (CRD) (Gomez and Gomez, 1984) with thirty experimental plastic pots of 4 liters volume arranged in three replications. Data were recorded for quantitative traits at different growth stages as per plant descriptors for finger millet (IBPGR, 2011). Data on shoot biomass, yield, number of days to 50% flowering, number of days to maturity, number of productive tillers per plant, number of panicles per plant, number of fingers per panicle, length of the longest finger, number of leaves per plant, average leaf length per plant, plant height, counted from seedling emergence to crop physiological maturity. One thousand grain weights and grain yield per plant were determined after harvest, threshing and winnowing. Flowering was observed visually and recorded in all pots when stigmas were visible on the 50% panicles of productive tillers of the plant on each pot.

At maturity, panicles were cut from all plants and oven dried at 70°C to constant weight. Panicles were weighed, mechanically threshed and the grain weighed. 1000 grains of each genotype were counted and weighed to determine grain size (seed mass). Following panicle harvest, the stover of all genotypes was cut at soil level and oven dried at 70°C to constant weight and weighed. Shoot biomass was determined as sum of the stover dry

weight, panicle dry weight and total grain yield per plant and were expressed on single genotype basis. Grain size was estimated from the one thousand grain weights and the grain yield per plant was used to estimate yield per area using the plant (pot) spacing.

The finger millet leaf and leaf area linear measurements were established following Kemp (1960) and Pereira (1977) recommendations as was reconfirmed by Wang and Zhang (2012). A finger millet leaf shape factor of 0.3 (a) as recommended by Rajappa *et al.* (1972) was used to determine actual leaf area (A) using the following formula,

$A = a\ x\ Lx\ W$ .....(1)

Where: A = Actual leaf area, a = leaf shape factor, L =Maximum leaf length and W = maximum leaf width.

The leaf area index (LAI) was determined by dividing the product of actual leaf area (m^2) (A) and leaf number per plant to the ground area (m^2) covered by the plant which in turn was

$LAI = A\ x \frac{NL}{GA} per\ plant$ .....(2)

Where LAI = Leaf area index, NL = number of leaves per plant, A = Actual leaf area (m^2) GA= ground area per plant (m^2).

The ground area was determined as product of plant spacing (0.75m by 0.25m). The shape factor was derived as the slope of the regression of the observed area of mature leaves on the product of the observed values of length and maximum width of mature leaves.

Harvest index (HI) was calculated by dividing grain dry weight to plant total biomass. HI provided a general estimate of the success of individual entries in maintaining dry mass allocation to grain yield under post-flowering stress (Bidinger, 2002).

3.5.2 Characterization of finger millet root traits which influence yield and terminal drought adaptation

The experimental design adopted was complete randomized design (CRD) with thirty experimental PVC tube of 90 cm length arranged in three replications (Gomez and Gomez, 1984). PVC tube of 90 cm length and diameter of 20cm and polyethelene tube of 95 cm length and 19.5cm diameter were used.

The bellow ground was constitutive root traits namely root biomass, root length (RL), root density (RD), root volume (RV) and total biomass (TB). Gravimetric technique for root volume determination was used (Harrington *et al.,* 1994). After plant physiological maturity roots and stems were harvested by destructive method. Roots bounds were removed from their mother plants by cutting at soil level. The root bounds were rinsed free of medium under running water. The washed roots were blotted dry. Root volumes of 30 finger millet plants were determined using the volume displacement technique whereby root bound was immersed in a 1000ml beaker and overflowing water was measured using 1000ml measuring cylinder to determine the volume of plant roots. Displaced volume of water was estimated to be equivalent to root volume in milliliters. Root length was measured through the longest root from stem to the tip in centimetres; harvested roots after volume and length determination were oven dried at 70°C to constant weight and root biomass was determined by weighing the dried root samples in grams. Root density (g/ml) was calculated by dividing root biomass to root volume (formula).

3.6 Overall Data Analysis

One way analysis of variances with no blocking and coefficient of determination (R^2) by regression analysis were performed using Genstat software 15th edition software. Means separation was done by Turkey test at least significant difference test (LSD) of 0.05 probability level. Different **c**orrelation coefficient analysis and Principal component analysis with varimax rotation was performed by using statistical package for social sciences (SPSS) version 16.0 by factor reduction method to determine major factors contributing to observed variations. Factors with Eigen values greater than one were selected as major contributors to the observed variations among finger millet genotypes. Weather parameters were obtained from SUA meteorological station and were analyzed and graphs plotted using excel computer software window 7 version.

Drought tolerance index (DTI) is the difference in yield between stress and non-stress genotypes and was used to determine high yielding genotypes and drought tolerance potential of each genotype (Fernandez, (1992). The variation in potential yield and phenology can be corrected for by calculating a DTI (Pantuwan *et al.,* 2002; (Lafitte, 2004), and drought-tolerant genotypes may be selected by using DTI. The cutoff point was set at 25percent yield decline as maximum allowable for a genotype to be grouped as drought tolerant.

The average grain yield data obtained from the drought stressed crops and non stressed crops experiments were used to calculate drought tolerant levels here after called relative yield decline (RYD) for each genotype (Rosielle and Hamblin, 1981) using the following equations:- $\text{Relative yield decline, RYD} = 100 - \left(\frac{Ys}{Yp}\right) x100$…….(3)

Yield stability index, $YSI = \frac{Ys}{Yp}$……..……....(4)

Stress tolerance index, $STI = Yp\ (\frac{Ys}{MYp^2})$……..……....(5)

Drought tolerance index, $DTI = \left[Ys\ x\ \left(\frac{Ys}{Yp}\right) \div MYs\right]$……..……...(6)

Where:-

Yp: Yield under non-stress conditions

Ys: Yield under the stress conditions

MYp: mean yield over all genotypes evaluated under non-stress conditions

MYs: mean yield over all genotypes evaluated under stress conditions

CHAPTER FOUR

4.0 RESULTS AND DISCUSSION

4.1 Diversity of Finger Millet Genotypes Based on Morphological Traits

4.1.1 Qualitative phenotypic traits

Qualitative characters like pigmentation in plant parts, panicle shape, grain shape and colour have been used in the past for classifying finger millet collections. The qualitative characters are useful in varietal identification during participatory varietal selection and breeding involving farmer's participation (Witcombe *et al.,* 1996).

4.1.1.1 Panicle types

The study identified five finger millet panicle types namely compact, semi compact, open, droopy and fist-likeamong the 169 finger millet genotypes. Results showed their distribution among the 169 genotypes as shown in Table 2 and plate 1A-1E. Among the 169 genotypes, open panicle type showed the highest frequency (40.8%) followed by semi-compact (32.0%). Droopy panicle type, compact panicle and fist-like panicle accounted for 23.1%, 3.6% and 0.6%, respectively (Table2).

Table 22: Distribution of different panicle shapes of finger millet in Tanzania

Panicle shapes	Frequencies	Percent
Semi compact	54	32.0
Open	69	40.8
Droopy	39	23.1
Compact	6	3.6
Fist-like	1	0.6
Total	**169**	**100**

Some genotypes, which had highly proliferated fingers that clumped together loosely and firmly were classified as compact and fist-like panicles, respectively. The most commonly grown cultivars had much smaller inflorescences with more or less spreading fingers that were either incurved or relaxed have been classified as semi compact and open respectively. Others were loose and droopy at maturity (Rao and de wet, 1997; Upadhyaya *et al.*, 2007).

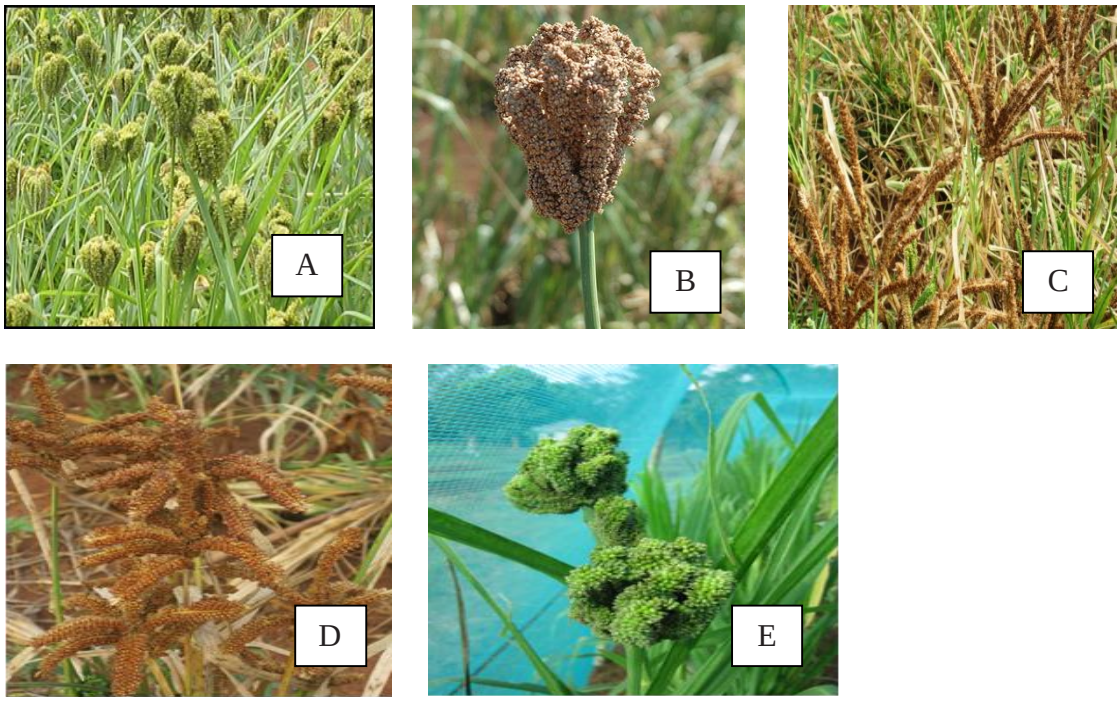

Plate 1: Different panicle shapes of finger millet genotypes in Tanzania

A = Compact, B = Semi compact, C = Open, D = Droopy and E = Fist-like panicle types.

4.1.1.2 Plant pigmentation

The one hundred and sixty nine (169) finger millet genotypes were classified in binary format as 0 for green and 1 for pigmented at the node, leaf sheath and/or inflorescence. Two colours, whitish (Table 3 Plate 2A) and purple (Table 3 and Plate 2B) were observed.

Table 3: Different plant pigmentation in finger millet genotypes in Tanzania

Plant pigmentation	Frequencies	Percent
White (plants green with white panicles)	10	5.92
Purple(both nodes, sheaths and panicles)	32	18.93
Green (whole plant green)	127	75.15
Total	**169**	**100**

The white colour was observed only on the inflorescence with no colouration on the other parts of the respective plant. The purple colour was observed either on the internodes, inflorescence, and leaf sheath or flag leaf. The 42 genotypes with white and purple were classified as pigmented while the other 127 genotypes were green and classified as non-pigmented (Table 3 and Plate 3C). These genotypes were found to be highly variable in qualitative traits i.e. panicle shape and pigmentation.

Plate 2: **Different panicle colours among finger millet genotypes in Tanzania**

A = White, B = Purple and C = Green

The plant pigmentation is influenced by anthocyanin, reddish brown or brown pigments and chlorophyll, green or yellow pigments. The colour character expressed by anthocyanin is more conspicuous when plants are full grown and colour intensity diminishes with maturity.

4.1.1.3 Panicle abnormalities

While normal physiological well being of finger millet include production of fingerlike florets, when these florets in turn produce profusely rudimentary miniature of florets it is an abnormality. Field observations indicated three types of panicle abnormalities:- finger branching, goose necked and crazy head panicles (Plate 3 A, B and C). These abnormalities affect crop productivity through reduction in florets fertilization, poor seed

setting and reduction in seed size, thereby reducing thousand grain weights and eventually yield per plant.

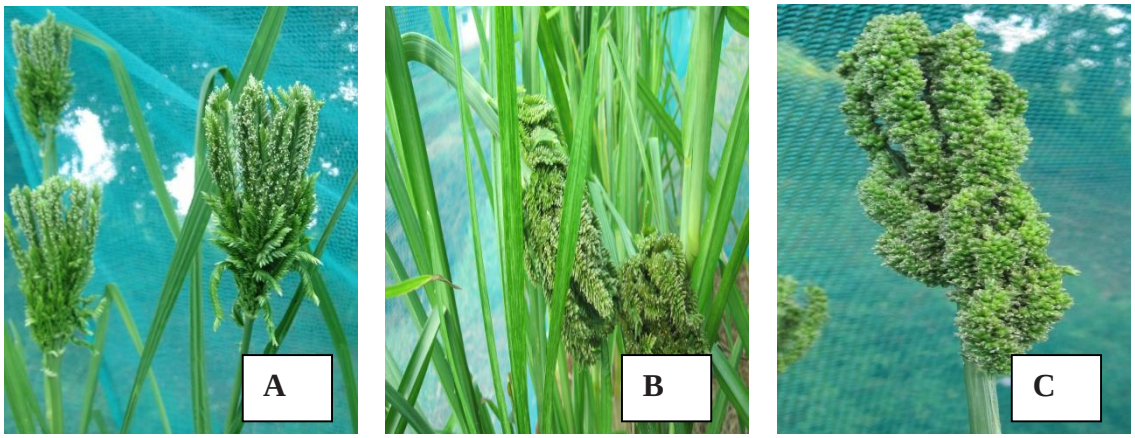

Plate 3: Finger millet panicle abnormalities

A = Finger branching B = Goose neck C = Crazy head types

4.1.2 Quantitative traits

Eight quantitative traits, including plant height, number of productive tillers, number of fingers, finger length, plant maturity, thousand grain weights and plant yield were determined (Table 6).

Table 46: Analysis of variance for 169 finger millet genotypes using eight quantitative traits

Source of variation	Df	Min	Max	Mean	Range	LSD	EMS	Std.dev.	F-value	F.pr.
Yield per plant	168	4.546	5.798	5.168	1.25	1.653	1.060	6.676	1.082	<.001
1000grains wt	168	1.77	3.74	3.74	1.97	0.5677	0.12	0.41	3.45	<.001
Productive tillers (#)	168	2.00	19.00	6.16	16.71	2.1811	1.84	1.47	2.60	<.001
Number of fingers	168	4.00	14.00	7.35	9.54	2.1031	1.71	1.44	3.12	<.001
Finger length (mm)	168	48.83	110.57	74.04	61.74	19.408	145.90	14.13	3.84	<.001
Plant height (cm)	168	66.68	127.367	94.94	60.69	19.357	145.10	10.08	1.96	<.001
Plant maturity (days)	168	75	140.00	112.54	65.38	16.378	103.90	14.70	5.54	<.001

Df = Degree of freedom, EMS = error mean square, F.pr = F probability, LSD = least significant deference and std.dev = Standard deviation.

All quantitative traits showed highly significant variations among them and thus variation among genotypes. These included number of productive tillers which ranged from 2 (TFA 23) to 19 (TFA139), time to maturity from 75 days (TFA 39) to 140 days (TFA 118), plant height ranged from 67 cm (TFA 16) to 127 cm (TFA 51), fingers number per panicle ranged between 4 (TFA 7) to 14 (TFA 94) and panicle length ranged from 49mm (TFA 127) to 111mm (TFA 84), thousand grain weight average ranged from 1.77g (TFA 113) to 3.74g (TFA 18), and average plant yield per genotype ranged from 4.546g/per plant to a maximum of 5.798g/plant (Table 6).

These results are supported by Odelle (1993) who reported yield potential of 4,265 kg ha^{-1} in Uganda, Kebede (2007) who reported 3,700 kg ha^{-1} in Ethiopia and Bondale (1993) who also reported yield 4,789 kg ha^{-1} in India. Malambane and Jaisil (2015) reported that high variation in grain yield per plant could be attributed to high variation in genetic make-up of the genotypes. However, grain yield may be influenced by multiple traits and environmental factors. Ahmad *et al.* (2011) and Lang *et al.* (2009) reported similar variations among quantitative traits, suggesting diversity among the finger millet genotypes. Mishra *et al*. (1980) evaluated the performance of 480 indigenous finger millets along with standard varieties and observed a wide range of variation between time to heading, time to maturity, number of productive tillers, height at maturity, number of fingers per panicle, finger length and grain yield per plant.

4.1.2.1 Phylogenic relationships among finger millet genotypes in Tanzania

The cluster analysis of morphological data using phylogeny tree method (Fig.4) grouped 169 finger millet genotypes into thirteen clusters based on variations in number of productive tillers, time to physiological maturity, plant height, number of fingers, finger length, panicle type, thousand grain weight and plant yield.

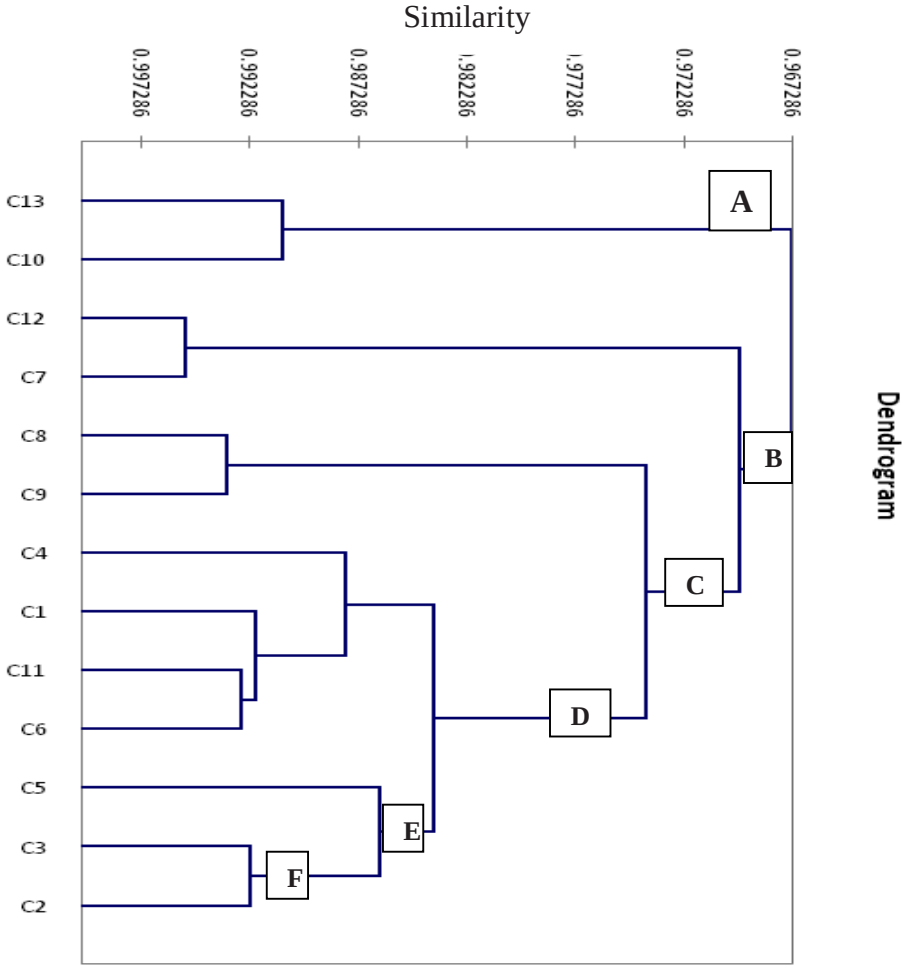

Figure 45: A phylogeny tree showing genetic divergence and ancestors lineages of Tanzania finger millet genotypes

Key: C1 to C13 = Finger millet genotype clusters

A to F = Finger millet ancestral lineage

The 13 clusters are as follows: 1st cluster which had 27genotypes, 2nd cluster had 36, 3rd cluster had 27, 4th cluster had 16, 5th cluster had 1, 6th cluster had 37, 7th cluster had 2, 8th cluster had 7, 9th cluster had 7, 10th cluster had 4, 11th cluster had 1, 12th cluster had 1 and

13thcluster had 1genotype (Fig. 4 and Table 7). Based on the magnitude of divergence the genotypes were grouped into two major ancestral lineage A with clusters 10 and 13 and ancestors lineage B consisting of clusters 1 to 9, 11 and 12. The clusters 10 and 13 have close proximity but wider divergence from other clusters (Table 7 and Fig. 4). Some genotypes (TFA9, TFA102, TFA151 and TFA167) were solitary, each standing alone in clusters 5, 11, 12, and 13, respectively. These have significant genetic divergence, suggesting that they are different species in the genus *Eleusine Gaertn*. Phylogenic method is used for morphological and molecular data to determine similarities and differences among plant species or between populations of plants (Hall *et al.*, 2002a; Doyle *et al.*, 2003). The genotype grouping into clusters based on ancestral lineage was very useful in planning for drought phenotyping and in screening for high yielding genotypes.

Table 57: Clusters of finger millet genotypes based on genetic divergence and similarities

Clusters	Tanzania Finger Millet Genotype	Genotypes
1	TFA1, TFA8, TFA24, TFA26, TFA33, TFA36, TFA40, TFA44, TFA48, TFA56, TFA65, TFA67, TFA68, TFA71, TFA87, TFA90, TFA98, TFA100, TFA105, TFA106, TFA107, TFA125, TFA129, TFA131, TFA134, TFA138, TFA163.	27
2	TFA2, TFA3, TFA5, TFA7, TFA10, TFA11, TFA14, TFA19, TFA20, TFA21, TFA23, TFA25, TFA28, TFA29, TFA30, TFA42, TFA43, TFA45, TFA46, TFA50, TFA53, TFA60, TFA63, TFA70, TFA73, TFA75, TFA79, TFA82, TFA91, TFA97, TFA99, TFA113, TFA122, TFA135, TFA143, TFA144.	36
3	TFA4, TFA12, TFA13, TFA17, TFA18, TFA22, TFA34, TFA35, TFA49, TFA52, TFA55, TFA57, TFA66, TFA72, TFA76, TFA89, TFA95, TFA96, TFA103, TFA104, TFA108, TFA120, TFA121, TFA123, TFA141, TFA142, TFA158.	27
4	TFA6, TFA27, TFA37, TFA38, TFA59, TFA69, TFA77, TFA83, TFA84, TFA86, TFA94, TFA101, TFA117, TFA128, TFA139, TFA140.	16
5	TFA9.	1
6	TFA15, TFA31, TFA32, TFA39, TFA41, TFA47, TFA51, TFA54,	37

	TFA61, TFA62, TFA74, TFA78, TFA80, TFA81, TFA85, TFA92, TFA93, TFA109, TFA110, TFA111, TFA112, TFA114, TFA115, TFA116, TFA118, TFA119, TFA126, TFA127, TFA132, TFA136, TFA137, TFA146, TFA149, TFA152, TFA154, TFA155, TFA162.	
7	TFA16, TFA145.	2
8	TFA58, TFA147, TFA148, TFA150, TFA153, TFA161, TFA166.	7
9	TFA64, TFA124, TFA156, TFA159, TFA160, TFA164, TFA165.	7
10	TFA88, TFA130, TFA133, TFA157.	4
11	TFA102.	1
12	TFA151.	1
13	TFA167.	1

These findings are supported by several authors who indicated that different phenotypic traits for the different crops have contribution to the overall variability observed among studied genotypes (Lule *et al*., 2012; Negash *et al*., 2005 and Assefa *et al.*, 1999, 2003). Bezaweletaw *et al.* (2006) indicated that finger millet genotypes collected from neighbouring regions and countries had some degree of similarities and differences. Tsehaye and Kebebew (2002) reported variations within and between genotypes collected in neigbouring regions and from different locations. The similarities observed, could be due to similar climatic and edaphic factors in the geographical locations and selection by farmers focused on same traits, or same primary seed sources.

It is common to informal seed systems in Tanzania involving farmers' seed exchanges in the local markets and farmers selecting the same traits based on their interest. Ayana and Bekele (2000) reported that genotypes from bordering regions had close genetic background possibly due to movement of seed between regions. The observed variation and similarity among finger millet genotypes is not correlated with geographical distribution, but attributed to inherent genetic variations among and between genotypes. Bezaweletaw *et al.* (2007) reported that similarity and differences in finger millet genotypes were beyond their geographical location.

4.1.2.2 Diversity of Finger millet genotypes based on principal component analysis

Principal component analysis confirmed the existence of high genetic diversity among finger millets genotypes. All traits studied had variable degrees of variation in every component and entire variation was explained in five principal components (Tables 8 and 9).

Table 68: Cumulative percentage of five components of variation contributing to diversity of finger millet in Tanzania

Components	TV	V %	C V %
1 Productive Tillers	2.81	56.13	56.13
2 Thousand grain weight	1.15	22.97	79.11
3 Yield	0.55	11.06	90.17
4 Number of Fingers	0.31	6.19	96.35
5 Plant Maturity	0.18	3.65	100.00

TV = Total variances, V% = percentage of variation and CV% = cumulative percentage of variation

Results in Table 8 showed five components contributing to diversity in the finger millet genotypes. However, based on the Eigen-value of 1, two principal components (Table 9) were extracted because they had Eigen value greater than one and they explained cumulative variability among finger millet genotypes by 79.11% (Table 8 and Fig. 6) (Stevens, 2002).

Table 79: Factors of variation among 169 finger millet genotypes and the two extracted components contributing to diversity of finger millet in Tanzania

Factor of Variation	Components	
	1	2
Productive Tillers	0.93	0.11
Thousand grain weight	0.90	0.06
Yield	0.81	0.43
Number of Fingers	0.04	0.88
Plant Maturity	0.25	0.78

Results in Table 9 and Fig. 6 showed five factors of variation to have influenced principal components and are ranked according to magnitude of their contributions to the variation. The highest contributor to component one was number of productive tillers, followed by thousand grain weight and yield. Number of fingers and plant maturity contributed least to component one but they are the major contributors to component two. This means that the two components are inversely proportional and improvement in one component will lead to decline in the other.

Figure 5~~6~~: Principal components contributing to diversity in Tanzania finger millet genotypes extracted based on Eigen value of one

Key; 1= Productive Tillers, 2 = Thousand grain weight, 3 = Yield, 4= Number of Fingers and 5= Plant Maturity

4.1.2.3 Association of finger millet grain yields and yield components

The degree of correlations between different quantitative traits for 169 Tanzania finger millet genotypes was estimated through correlation coefficient analysis. Table 10 shows the correlation coefficient ($P \leq 0.05$) among the nine descriptors influencing variation, hence diversity in the finger millet genotypes.

Grain yield is a complex character influenced by many yield components. The understanding of the association between yield and yield components is useful in improving the efficiency of selection. This study identified number of tillers, plant height, time to plant maturity, number of fingers, finger length, finger branching, panicle shape and thousand grain weights to have biological significance on the variation in plant yield. The results (Table 10) showed that yield was significantly and positively correlated with number of productive tillers, thousand grain weight, time to plant maturity, number of fingers, finger length and panicle shape.

Table 8~~10~~: Correlation matrix of quantitative traits influencing yield of Tanzania finger millet genotypes

Variables	Yield	NT	PH	PM	NF	FB	FL	PS	1000gwt
Yield	**1**								
NT	**0.768*** **	**1**							
PH	0.076	0.073	**1**						
PM	**0.529*** **	**0.294*** **	**0.159***	**1**					
NF	**0.520*** **	**0.227** **	**0.197***	**0.567*** **	**1**				
FB	0.035	-0.009	0.086	0.031	0.108	**1**			
FL	**0.463*** **	**0.201** **	0.070	**0.429*** **	**0.357*** **	**-0.210** **	**1**		
PS	**0.165***	**0.190***	0.007	**0.334*** **	**0.153***	**0.353*** **	**-0.168***	**1**	
1000gwt	**0.714*** **	**0.775*** **	0.127	**0.287*** **	**0.213** **	-0.051	**0.219** **	0.132	**1**

*significant at p value ≤ 0.05, **significant at p value ≤ 0.01, ***significant at p value≤ 0.000, NT = Number of tillers, Yield = Grain yield, PH = Plant height, PM= Plant maturity, NF=Number of fingers, FB = Finger branching, FL=Finger length, PS = Ear shape and 1000gwt = Thousand grain weights.

The observed strong positive correlation between thousand grain weight, number of productive tillers, and number of fingers per panicle; finger length and grain yield per plant; pave the way for plant breeders to make the crop improvements with respect to these yield components. This indicates that increase in these characters may result into

increase in grain yield. Singh *et al*. (1990) and Tazeen *et al.* (2009) also reported that grain yield correlated positively with biomass, and harvest index of finger millet. Nandini *et al.* (2013) reported yield to have positively correlation with plant height, tiller number and 1000 grain weights in finger millet. Similarly, Bezaweletaw *et al.* (2006) found finger millet grain yield per plant to be significantly and negatively correlated with time to heading and time to maturity. However, Singh *et al*. (1990) observed positive correlation between time to 50% heading and time to maturity with grain yield. Equally, this study showed that grain yield per plant had positive and significant correlation with plant height, number of tillers per plant, number of fingers per panicle, finger length, and 1000 grain weights. The positive and significant correlation of grain yield with plant height, number of panicles per plant, number of fingers per panicle, finger length and time to maturity imply that improvement in any of these traits will lead to improvements in grain yield.

Results in Table 10 show number of productive tillers to be significantly correlated with 1000 grain weight and plant maturity. Productive tillers also had positive but weak correlation with number of fingers and finger length (Table 10). This means that selection for increased number of productive tillers will have small increase in number of fingers and finger length. Dagnachew *et al.* (2012) reported productive tillers per plant to be highly correlated with yield and since breeders final target is yield selection for high tillering ability will lead to improved yield.

4.1.2.4 Phenological changes and their contribution to finger millet drought tolerance or avoidance

The time to plant maturity (Table 10) was found to be highly and positively correlated with yield, number productive tillers; and number of fingers, finger length, panicle shape and thousand grain weights. This is scientifically justified because given an ideal growing

condition and the optimum growth duration actually involves a balance of growth processes throughout the life of the plant. This balance should result in the production of maximum number of tillers, panicles and fingers, large grain size and high 1000 grain weight. The balance may result in high grain yields but also one yield component associated with such increment may be to the expense of other yield component (Vergara *et al.*, 1966). These results are similar to those of Kadam *et al.* (2009) who reported significant positive association of grain yield per plant with time to flowering and 1000-grain weight in finger millet.

This characterization led to grouping of individual genotypes into early maturing (75 to 100days) with 42 genotypes; medium duration (101 to 120days) with 79 genotypes and late maturing above 120 days with 48 genotypes. The understanding of variations in time to maturity provided opportunity for developing improved varieties according to agro-ecological suitability and help plan successive cropping systems. Selecting for early maturing varieties is an important copping strategy against the effects climate change. These will ensure that farmers realize a crop harvest through terminal drought escape which is experienced frequently.

Plant height showed significant and positive correlation with time to plant maturity and number fingers. Significant variation in plant height was observed among the Tanzania finger millet genotypes (Tables 6 and 10). When there is optimal growing conditions vegetative growth is encouraged and maturity is delayed due to luxurious growth associated with increased plant height. There were weak positive correlation among plant height, yield, number of productive tillers, finger branching, finger length, 1000-grain weight and panicle shape. This weak and positive correlations does not contradict the

breeders' objective of selection for shorter and higher yielding varieties because plant height affects the ability of the plant to resist a lateral force and tall plants tend to lodge easily than short plants (Harris, 2007). Lodging alters plant growth and development by interfering with flowering, thereby reducing photosynthetic capabilities through reduced carbohydrate assimilation. Severe lodging also affects the transport of nutrients and moisture from the soil hence poor grain development. The variation in plant height gives chance to breeders to use the diversity potentials in breeding for necessary height to address lodging problem. This is because selection for height was found to be more effective in improving yield than direct selection for yield (Mnyenyembe and Gupta, 1998). The study identified number of productive tillers to be the major contributor to finger millet diversity and yield; tiller production traits would be useful in screen finger millet genotypes for improved crop yield.

Number of fingers per panicle was highly significant and positively correlated with yield, time to plant maturity, and finger length. Number of productive tillers, time to plant maturity, plant height, and time to 50% flowering, panicle and fingers length showed high positive and significant correlation with seed yield per plant (Table 10).

Table 9~~11~~: Simple linear regressions coefficient of determination (R^2) for phenotypic traits in relation to finger millet yield in Tanzania

	Yield (g per plant)				
Traits	**Regression coefficient**	**Standard error**	**R - squared**	**t-value**	**F-probability**
Productive Tillers	0.329	0.025	0.499	13.189***	0.000
Plant height	-0.005	0.002	0.008	-2.239*	0.044
Panicle shape	-0.038	0.072	0.040	-0.528ns	0.000
Finger branching	-0.030	0.037	0.011	-0.801ns	0.016
Finger length	0.206	0.062	0.000	3.299**	0.673
number of Finger	0.013	0.002	0.132	6.553***	0.000
Plant maturity	0.121	0.019	0.141	6.303***	0.000

1000-gwt	0.012	0.002	0.179	5.449***	0.000

The study has proven finger millet yields to be influenced by multiple traits which are integrative in nature. Number of productive tillers, number fingers, days to plant maturity and thousand grain weight (Table 11) were the traits identified to have contributed significantly to variation in yield and diversity in finger millet. The results of this study are in agreement with those by Gowda *et al.* (2008) and Priyadharshini *et al.* (2011) who reported reliability of phenotyping results and its importance in identifying a suitable source/donor for the trait, and planning for selection of plants/progenies for advanced breeding. They also recommended phenotying technique as a reproducible, robust, cost-effective, non-destructive and desirable in broader sense of breeding programs. These findings are also supported by IBPGR (2011) that reported that most of genetic resources collections are made up of populations or genotypes that are genetically variable and screen for desirable trait remain a prerequisite of plant breeding. The evaluation of finger millet phenotypic traits is very important for breeding program because farmers use these traits before adopting a new variety. The major criterion used by farmers is yield but other phenotypic characteristics of plants like seed color, pigmentation and lodging susceptibility influence their decision to adopt or not. Jarvis et al. (2005) reported that, farmers use different phenotypic features of plants for selection and identification during on farm evaluation of farmers' preferred cultivars. Breeding programs concentrating efforts and resources on identified yield component traits can simultaneously improve finger millet yields. Since major yield component traits are phenotypic and easy to measure, mass selection for these traits can lead to subsequent improvement in the crop grain yield

4.2 Diversity of Finger Millet Genotypes Based on Molecular Characteristics

4.2.1 DNA concentration and quality assessment

DNA quality and quantity checking were performed and leaf samples produced poor quality and low DNA concentration as shown in Plate 4 for genotype 19 and 130 while all seed samples produced good quality and quantity of genomic DNA (Plate 5) .Leaf samples were collected from aerial tillers which might have had less meristem cells/tissues due to advance stage of lignifications. Seed genomic DNA was therefore found useful and informative in the molecular characterization of finger millet genotypes.

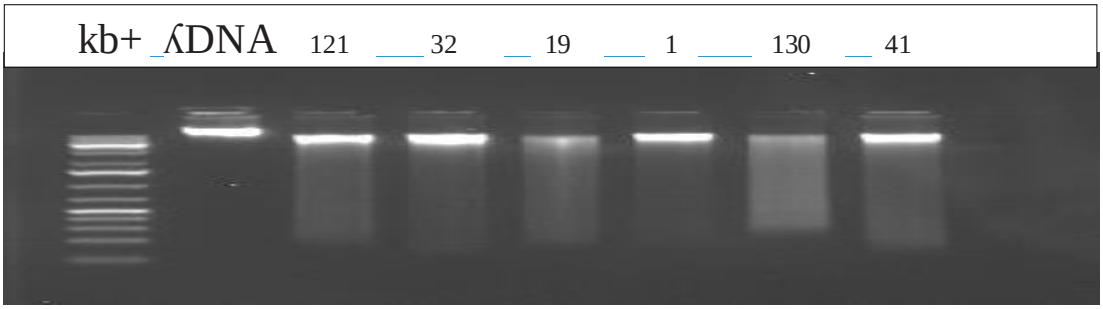

Plate 4: **Seed and leaf Genomic DNA quality and quantity checking**

(Seeds = 121, 32, 1 and 41, Leaf = 19 and 130)

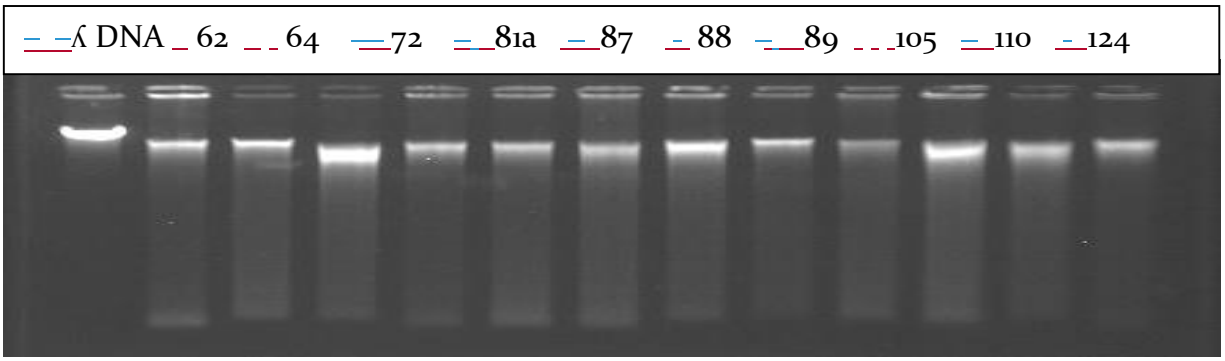

Plate 5: Image of Gel electrophoresis showing genomic DNA from finger millet seed samples

4.2.2 Polymorphic information content (PIC) analysis

Markers with alleles of equal allelic frequencies and those with multiple alleles within the population have higher PIC values. The markers 107 and 11 had the highest PIC value and had equal allelic frequencies of 0.77. Markers 10, 81, 56, 77, 11, 12, 15, 104, and 53 had high PIC and have multiple alleles (Table 12). Based on PIC and F-statistics values in Table 12 the study identified 13 SSR markers which were able to recover polymorphic information content (PIC) ranging from 0.33 to 0.79 F_{ST} values, indicating extremes in the degree of genetic divergence among finger millet genotypes.

Table 10~~12~~: Summary statistics on significance of the SSR markers used in finger millet genotyping in Tanzania

Primers	Allele frequency	Genotype	Allele No.	Genetic diversity	Heterozygosity	PIC	Fst
UGEP10	0.47	19.00	10.0	0.63	0.18	0.56	0.72
UGEP76	0.50	2.00	4.00	0.51	1.00	0.38	-0.97
UGEP81	0.89	5.00	4.00	0.20	0.05	0.18	0.77
UGEP56	0.98	5.00	4.00	0.04	0.02	0.04	0.57
UGEP53	0.29	37.00	16.00	0.82	0.48	0.79	0.42
UGEP77	0.55	20.00	11.00	0.64	0.24	0.60	0.62
UGEP11	0.77	11.00	8.00	0.39	0.06	0.36	0.86
UGEP12	0.60	11.00	7.00	0.58	0.25	0.53	0.56
UGEP15	0.46	23.00	10.00	0.70	0.15	0.67	0.79
UGEP26	0.98	3.00	3.00	0.03	0.02	0.03	0.33
UGEP65	0.81	9.00	7.00	0.33	0.21	0.31	0.37
UGEP104	0.92	6.00	5.00	0.16	0.04	0.15	0.76
UGEP107	0.77	8.00	6.00	0.38	0.04	0.35	0.90
UGEP90	0.74	17.00	11.00	0.44	0.45	0.42	-0.03
UGEP18	0.44	13.00	8.00	0.68	0.39	0.63	0.43
Means	0.68	12.60	114*	0.43	0.39	0.24	0.40

114* = Detected number of private alleles, PIC = Polymorphic information content and Fst = F-statistics

4.2.2.1 Gene frequencies

Allele frequencies, private alleles, heterozygosity and PIC results for finger millet genotyping (Table 12) were highly informative, indicating high gene diversity and

existence of abundance of heterozygous finger millet genotypes. It implies that substantial crop improvement can be achieved through integration of conversional and molecular breeding techniques in a shortest time possible using finger millet accessions collated from Tanzania farmers. Simple sequence repeats (SSR) Markers detected 114 private alleles which can help in advancing molecular breeding using techniques such as next generation sequencing to identify the genotypes possessing these identified private alleles. In turn, the identified genotypes will be useful in drought phenotyping for improved production through marker assisted selection in multi-environmental evaluation experiments. Molecular SSR markers have been useful tools in this study by measuring the diversity of 169 finger millet in relatively short time using very few funds and since finger millet whole genome is not sequenced, SSR markers offers great opportunity for the crop improvement.

4.2.2.2 Inbreeding coefficient

All markers identified inbreeding coefficient of 0.33 to 0.90 except markers UGEP 90 and UGEP 76 which indicated absence of inbreeding (Table12). This is in accordance with the analysis of molecular variance (AMOVA) (Fig. 6) from PCoA and phylogeny trees (Fig. 7), which show scattered groupings of genotypes across all populations without defined trends according to sampling areas. (The 97% observed similarities (Fig. 6) between studied finger millet genotypes might have been contributed by the seed supply system. There is farmers' exchange of seeds, peoples' migration taking seed from one region to another. This in turn leads to high gene flow among populations. Farmers might have been exchanged seed from same ancestries and most likely from same genetic base. The accessions might have had same ancestries and adaptive role of the traits in the

environment that may have led to dominance of superior genotypes. However, since the plant is known to be self pollinating, with possibility of 3-5% crossing pollination, the observed heterozygosity confirms that the genotypes have been naturally maintaining their genetic makeup and remained true to type despite the gene flow movement exist through informal seed supply systems.

Genetic variation between genotypes based on districts of collection was found to be 3%, genetic variation between genotypes within a district was 42% and Genetic variation between finger millet genotypes regardless of districts of collection was found to be 55% (Fig. 6).

4.2.4 Principal coordinates analysis (PCoA) based on genetic distance to

determine gene flow between studied populations

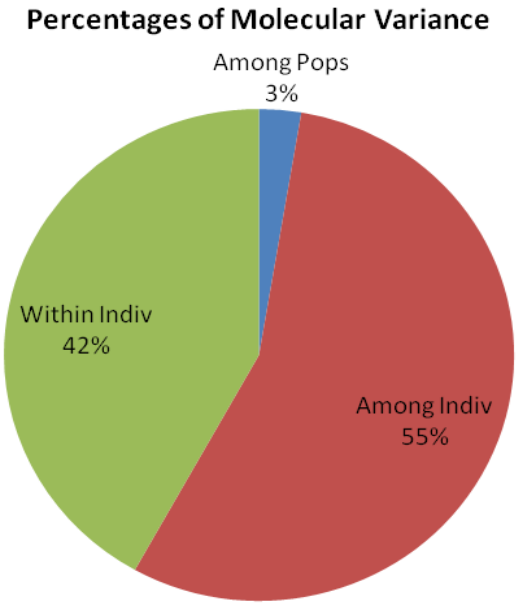

Figure 67: Analysis of molecular variance (AMOVA) for finger millet genotypes in Tanzania

4.2.3 Cluster analysis

The phylogeny tree shows variations between individual accessions and groups them into four major distinct clusters and 13 sub clusters (Fig. 7). The variation between individual accessions is very important for breeders' use in crop improvement. This clustering is based on differences and similarities useful in discriminating for and against desirable and undesirable traits or genotypes respectively.

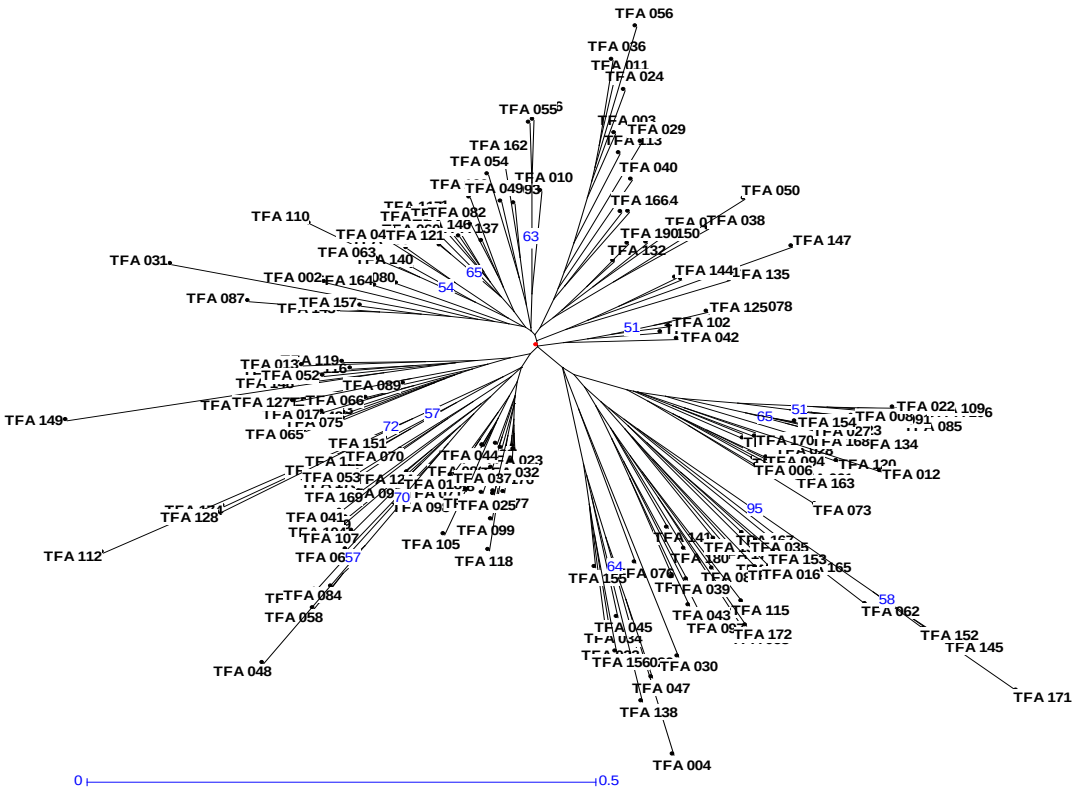

Figure 78: Population structure and genetic variation of Tanzania finger millet accessions

The study of finger millet accessions using 25 SSR markers showed that the greatest variability was within finger millet genotypes than among populations of districts of collection. Results in Fig. 7 and Table 12 showed that the studied genotypes had equal

contribution to the overall genetic diversity across populations. The findings are similar to that of Dida *et al.* (2008) who discriminated population structure of 79 finger millet accessions using 45 SSR markers and identified significant distinction of plant architecture and yield in Asian and African finger millet population in a single experiment.

The importance of these findings is confirmed by Trethowan and Mujeeb-Kazi (2008) who report increased genetic diversity as important in pests and disease control through resistance and tolerance and for ensured sustainable production in crop species. Hajjar *et al.* (2008) also confirmed value of genetic diversity to include provision of genetic barriers against different biotic and abiotic stresses. Diverse genetic base provides desirable allelic variation for production of improved breeding lines and elite candidate for advanced breeding programs (Tar'an *et al*., 2005). Molecular markers are indispensable tools for measuring the diversity of plant species and characterization of larger number of germplasm when time and resources are limited (Govindaraj et al., 2015). Cordeiro *et al*. (2002) indicated that SSR markers have the advantage of being inexpensive than other molecular markers. Evaluation of genotypes to determine the genetic diversity among genotypes was reported by Ferreira (2005) to have improved crop variety development with respect to yield and yield components.

4.3 Terminal Drought Tolerant Finger Millet Genotypes based on yield and tolerance indices

Post anthesis stage of cereal plants is important in drought tolerance

phenotyping. Dry matter production after heading is the determinant of grain yield (Schnyder, 1993; Saidi *et al.*, 2008) and it has been the base for evaluation of cereals grain yield performance under drought stress conditions. Drought tolerant genotypes selection indices in dry condition have been developed and used to identify drought tolerant genotypes (Talebi *et al.*, 2009.

4.3.1 Shoots characteristics contributing to terminal drought adaptation and grain yield

The results shown that total biomass (TB), root density, root length, plant height, number of tillers, leaf area index, grain yield and harvest index were statistically significant at ($p \leq 0.001$) in determining plant response to drought stress (Table 2 and 3). The regression analysis showed that average yield per genotype had positive and significant correlation with shoot biomass (Fig. 4), harvest index (Fig. 5) and root length under drought stress conditions (Fig. 6).

4.3.1.1 Total biomass

Total biomass (TB) is the sum of all the above ground parts of the plant and root characteristics of the plant. The highest individual plant TB recorded was of 442.3g for genotype TFA 44 and the lowest was 165.7g for genotype TFA171. The overall mean TB for all genotypes was found to be 269g with variation between genotypes of 8.9 percent, mean difference of 39.3g and the range of 276. 6g. The TB was found to be positively and significantly correlated with root volume (RV), root density (RD), root length (RL), number of tillers (NT), number of leaves (NL), leaf aqrea index (LAI), and root to shoot (R:S) ratio. It was also found to be negatively and significantly correlated with plant HI and weak correlation with PH (Table 2, 3 and 4). Although grain yield had positive relationship with shoot biomass, delayed maturity and high plant height led to grain yield reduction in favour of vegetative growth. The relation is in agreement with findings by Royo *et al*. (2007) who observed no increase in biomass associated with increase in PH,

but proportional reduction in the harvest index. Miralles and Slafer (1997) reported biomass accumulation to a point beyond which the gain in the HI does not compensate for the loss in biomass due to poor solar radiation distribution and associated reduction in resource use efficiency. Photosynthetic efficiency and performance under water stress have been reported for genotypes able to maintain green tissues in wheat and other small grain cereals but panicle being better adapted to drought than leaves (Tambussi *et al*., 2005).

4.3.1.2 Shoot biomass

The shoot biomass (SB) refers to all above ground plant parts including leaves, panicle, stalk, and tillers. Results showed that shoot biomass contributed to diversity of finger millet genotypes by 9 percent, with least significant difference means of 26.3g and difference in individual genotype performance ranging from 130 to 236.3g with a range of 106.3g.(**Table)**

Simple linear regression coefficient indicated positive relationship between shoot biomass and grain yield (Fig. 8). This implies that efforts to improve shoot biomass will contribute to an equal improvement in finger millet grain yield. Large seed size will ensure improved seedling emergence and initial biomass establishment through early plant growth with large foliage and prostrate growth habit will lead to increased ground cover, thus conserving soil moisture and potentially increasing radiation use efficiency (RUE).

Table 1113: Summary statistics of morphological and physiological characteristics of finger millet genotypes

Traits	Range	Minimum	Maximum	Sum	Mean	Std. Dev
Root density (RD)	0.53	0.17	0.70	12.79	0.43	0.14

Root :Shoot ratio (RS)	0.92	o.14	1.06	14.80	0.49	0.21
Leaf area index (LAI)	4.81	1.38	6.19	91.64	3.05	1.08
Number of tillers (NT)	10.00	7.33	17.33	382.33	12.75	2.80
Harvest index (HI)	23.25	8.90	32.15	510.55	17.02	6.67
Yield per plant (Y)	37.84	24.87	62.71	1282.22	42.74	10.79
Root length (RL)	74.00	55.33	129.33	2553.63	85.12	18.76
Root biomass (RB)	201.03	26.00	227.03	2717.68	90.59	46.50
Plant height (PH)	46.00	72.33	118.33	2883.34	96.11	11.89
Shoot biomass(SB)	106.30	130.00	236.30	5356.00	179	28.56
Root volume (RV)	316.60	66.70	383.30	6422.00	214	81.87
Total biomass	**276.60**	**165.70**	**442.30**	**8073.50**	**269**	**69.22**

Tuberose (2012) reported that in drought tolerance, plants undergo biochemical process of remobilization of stem water-soluble carbohydrates and accumulation of molecular oxidants to maintain physiological functions despite the severity of drought.

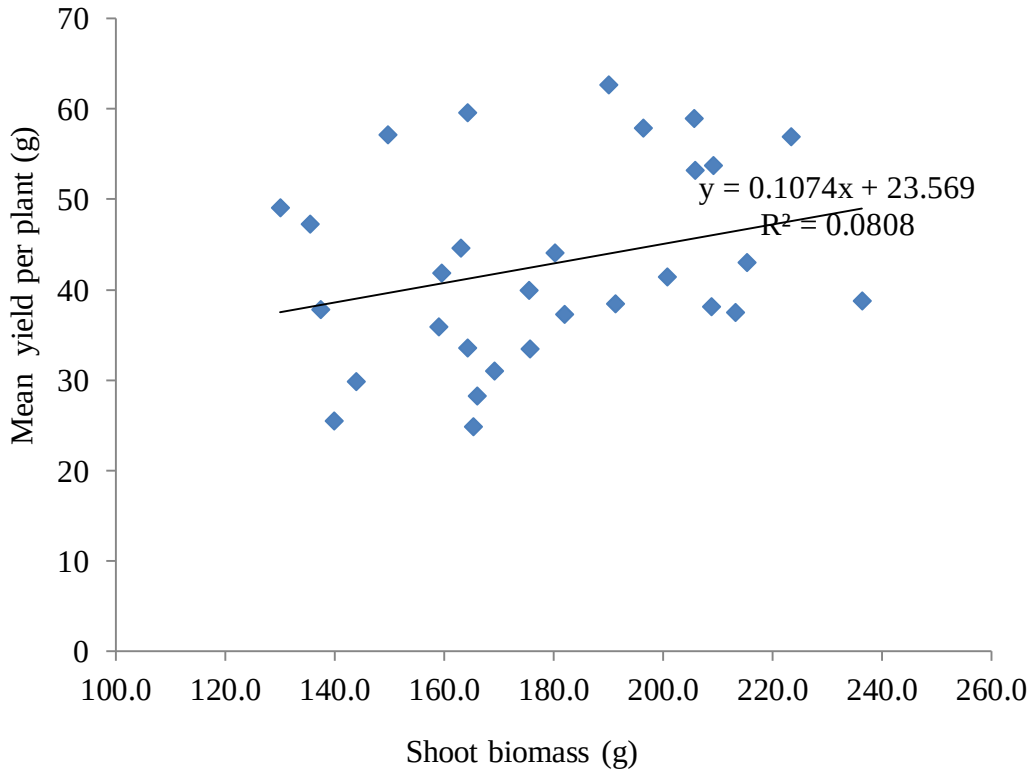

Figure 89: Relationship between shoot biomass and grain yield of finger millet in Tanzania

These findings are supported by Blum (2004) who reported sustained leaf photosynthesis during grain-filling contributing to increased dry matter accumulation, and increased grain

number per panicle due to higher partitioning of assimilates during fertilization and grain filling stages. Tollenaar and Lee (2006) also confirm such an increase in dry matter accumulation and grain during grain filling period to be in direct proportional. Tambussi *et al*., (2005) reported photosynthetic efficiency and performance under water stress to favour panicle development to leaves in small grain cereals. FAO (2012) recommend finger millet as potential drought resilient crop for use as coping strategy to counteract the effects of drought stress.

4.3.1.3 Productive tillers

The maximum NT recorded was 17 for genotype TFA 118 and the lowest were 7 for genotype TFA 102. Average number of tillers was 12 per genotype (Table 13). There was a variation of 16 percent, between means across genotypes of 3 tillers and a range of ten tillers (Table 14). Correlation coefficient analysis revealed positive and significant correlation between productive tillers and SB, RB, TB, RV, RL, R: S ratio and LAI. NT and HI had negative but significant correlation at significance of 0.01 alpha levels (Table 14). HI inversely correlation with NT may be attributed to resultant competition for space, light and nutrients in higher tillering plants than in medium or low tillering plants. High tillering plants grew into very thin plants that produced small panicles and some panicles were with seedless fingers. Therefore negative correlation between NT and HI is justified because large number of tillers led to yield reduction through reduced seed mass since HI is a ratio of grain yield to total plant biomass.

4.3.1.4 Plant height influence on biomass and grain yield

The highest plant height measured was 118.4cm for genotype TFA 100 and the shortest genotype was TFA 91 measuring 72.3cm.The overall average height for all finger millet genotypes in this study was 96.1cm (Table 13). The analysis of variance revealed PH to have a variation of 6.3 percent between genotypes' height and a grand mean of about 96 cm with significant difference between means of 9.9cm. These results showed that variation in plant height was highly significant within **0.001 F probabilities** (Table 13). There were positive and weak correlation among PH and SB, TB, RV, RL, LAIbut significant positive correlation was with finger (panicle) length (Table 14). Taller genotypes had longer duration to maturity due to prolonged vegetative growth to attain potential plant height, thereby partitioning more of its assimilates to shoot biomass than grain biomass. Taller plants also had thin stalks and showed lodging characteristics, which can predispose panicles to insect pest and demage contaminate grain yield. Taller genotypes were found to have smaller panicles and poorly fertilized fingers and hence, small seed size (Pereira and Lee, 1995).

These results comply with those of Slafer *et al*. (2005) who identified the minimum height below which yield limitation occurs. Based on this plant height limitation on yield and when the breeding materials exceed a threshold of 70–100 cm, selection for reduced height is recommended (Richards, 1992; Miralles and Slafer, 1995). Otherwise, there is no increase in biomass associated with increase in tallness, but proportional reduction in the harvest index (Royo *et al*., 2007). These results are also supported by Royo *et al*. (2007) who recommended breeding for reduction in plant height to an optimum range to increase

yield potential through increased biomass partitioning into grains and simultaneously reducing the risk of lodging.

4.3.1.5 Leaf area index and its influence on grain yield and drought stress adaptation

The results showed that Leaf area index development increased progressively during vegetative growth and reached its climax at the physiological maturity from which it reduced at an increasing rate. The highest LAI of 6.9 was recorded from genotype TFA 125, followed by TFA 58 with LAI of 4.95. Other genotypes with large LAI were TFA 77, TFA 102 and TFA 95, which had 4.59, 4.21 and 4.02, respectively. The lowest LAI of 1.38 was obtained from genotype TFA 86 and the average LAI was 3.05 (Table 13). The LAI coefficient of variation across the all genotypes was 15.4 with least significant difference of 0.777 between means. (Table13). LAI was positively and significantly correlated with SB, TB, RV, NT, and NL. However, there was a weak positive correlation between LAI and plant height (Table 14).

Plants use leaves to intercept photons an essential electromagnetic particles or waves for water, heat and CO_2 utilization in biochechmical processes (Soltani and Sinclair, 2012). To accomplish this function, LAI of finger millet consists of photo-synthetically active green and senescent leaves at different plant growth stages. The retained old leaves of finger millet play an important role of intercepting precipitation (Soltani and Sinclair, 2012). LAI is one of the most important biometeorological variables to assess in plant breeding and is a measure of the population of plants as they interact with the environment (Araus *et al.,* 2003). It has been found that LAI varies due to rainfall, evaporation and plant nutritional status (Morison *et al*., 2008). Timing the phenological development of the

crop is therefore important such that it coincides with rainfall season to maximize LAI, photosynthesis and hence grain yield in drought prone areas (Araus *et al.,* 2003). To continue to avoid drought, the finger millet leaves roll up to reduce water loss, but this avoidance strategy is only a last resort and the farmer is advised to irrigate soon after leaf-rolling begins.

Table 1214: Morphological and physiological traits Analysis of variance for finger millets genotypes

Variables	GM	SS	MS	EMS	LSD	SE	CV	F-value	F. prob
Shoot biomass	178.5	70950.9	2446.6	259.9	26.33	16.12	9.0	9.41	< 0.001
Root biomass	90.6	188144.1	6487.7	262.8	26.47	16.21	17.9	24.69	< 0.001
Total biomass	269.1	416836.5	14373.7	576.8	39.22	24.02	8.9	24.92	< 0.001
Root volume	214.1	583240.3	20111.7	348.6	30.49	18.67	8.7	59.69	< 0.001
Root density	0.43	1.703	0.587	0.085	0.15	0.0923	21.6	6.89	< 0.001
Root length	85.1	30631	1056.2	214.5	23.92	14.65	17.2	4.92	< 0.001
Plant height	96.11	12301.56	424.19	36.69	9.893	6.057	6.3	11.56	< 0.001
Tillers	12.74	682.456	23.533	4.144	3.325	2.036	16	5.68	< 0.001
Finger length	9.33	170.126	5.8664	0.8234	1.482	0.907	9.7	7.12	< 0.001
LAI	3.055	101.288	3.4927	0.2225	0.771	0.4717	15.4	15.69	< 0.001
HI	17.02	3869	133.41	12.11	5.684	3.48	20.5	11.02	< 0.001
Root:shoot ratio	0.4939	3.755	0.129	0.008	0.1444	0.88	17.9	16.56	< 0.001
Yield	42.74	10119.84	348.96	74.36	14.084	8.623	20.2	4.69	< 0.001

GM = Grand Means, SS = Sum of squares, MS = Mean sum of squares, EMS = Error mean squares, LSD = Least significant difference, SE= Standard error, CV= Coefficient of variation, F. Prob= F probability, LAI= Leaf area index and HI= harvest index.

All the thirteen traits used in finger millet drought tolerance screening showed highly significant variations at significance ($p \leq 0.001$) (Table 2 and 3).

4.3.1.6 Harvest index

The highest harvest index (HI) of 32.15was recorded for genotype TFA 111 and the lowest HI was 8.9for genotype TFA 58 (Fig. 9). The overall mean HI index was 17.02 across genotypes (Table 2 and 3). HI was negatively and significantly correlated with SB, RB, TB, RV, RL and NT. However, it had positive and significant correlation with grain yield ($p \leq 0.001$) of (Table 4). It had weak negative correlation with PH, NL and

insignificant correlation with LAI and FL. The finding is also supported by Royo *et al.* (2007) who observed plant height to be negatively correlated with harvest index These relationships are justified by the fact that grain yield is a fraction of the dry matter accumulated by the crop during the growing season (Duvick, 1999). The genetic increase in grain yield have been due to modifications in the HI and associated reductions in plant height and increase in stress tolerance (Tollenaar *et al.*, 2000).

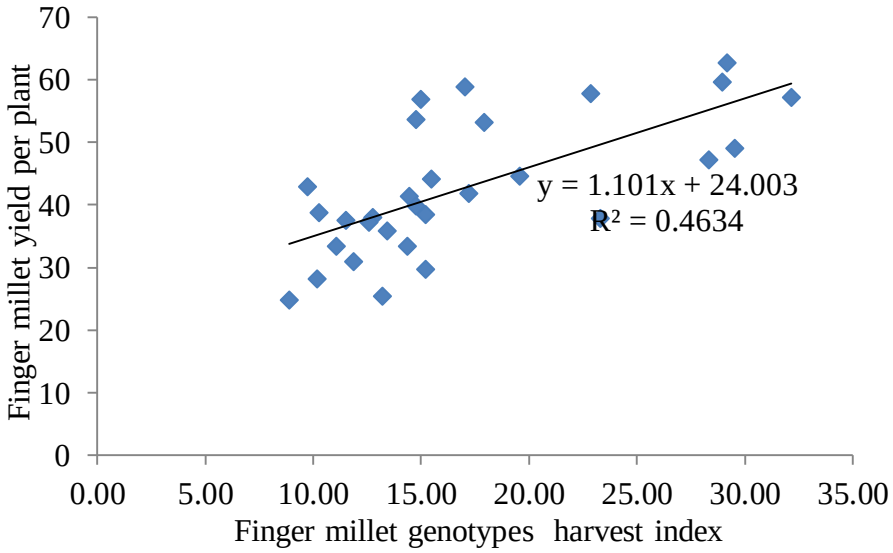

Figure 9~~10~~: Terminal drought stressed finger millet plant yield and harvest index

Table 13~~15~~: Morphological and physiological traits correlations of finger millet under drought stress

VAR	S B	R B	T B	R V	R D	R L	PH	N T	F L	N L	LAI	Y/P	HI	R:S
S B	1													
RB	0.61**	1												
T B	0.85**	0.94**	1											
R V	0.62**	0.69**	0.74**	1										
R D	0.17	0.60**	0.48**	-0.07	1									
R L	0.51**	0.41**	0.50**	0.45**	0.22*	1								
PH	0.27*	0.17	0.23*	0.22*	-0.01	0.24*	1							
N T	0.46**	0.39**	0.46**	0.40**	0.129	0.39**	0.02	1						
F L	0.11	0.15	0.15	0.05	0.23*	0.17	0.30**	-0.13	1					
N L	0.53**	0.35**	0.47**	0.32**	0.13	0.31**	0.09	0.78**	-0.06	1				
LAI	0.39**	0.17	0.28**	0.28**	-0.08	0.17	0.21*	0.53**	-0.13	0.73**	1			

Y/P	0.31**	-0.09	0.07	-0.06	-0.14	0.07	-0.06	-0.04	-0.01	0.08	0.08	1	
HI	-0.35**	-0.67**	-0.61**	-0.57**	-0.40**	-0.32**	-0.24*	-0.30**	-0.14	-0.22*	-0.10	0.71**	1
R:S	0.36**	0.95**	0.80**	0.62**	0.63**	0.31**	0.13	0.29**	0.15	0.23*	0.06	-0.26*	-0.71**	1

* Correlation is significant at alpha level of 0.05 **Correlation is significant at alpha level of 0.01.

Key: S B= Shoot biomass, RB = Root biomass, TB = Total biomass, RV = Root volume, RD = Root density, RL= Root length, PH= Plant height, NT = Number of tillers, FL= Finger length, NL= Number of Leaf, LL= Leaf length, LW=Leaf width, LAI= Leaf area index, Y/P = yield per plant, HI= harvest index, R: S = Root to shoot ratio

4.3.2 Finger millet root characteristics contributing to terminal drought adaptation and yield

4.3.2.1 Root biomass

Genotype FTA 44 produced the highest root biomass of 227.03g per plant. The lowest root biomass production was 26g per plant from genotype TFA 103. The average biomass production was found to be 90.59g per plant across genotypes (Table 14 and 15). Root and shoot biomass had positive and significant correlation ($p \leq 0.001$) with total biomass, root volume, root length, number of productive tillers, number of leaves and root to shoot ratio (Table 14). Finger millet plants survive drought stress by using a couple of strategies including well developed and extensive fibrous root system capable of extracting water from deep soil layers when the surface water dries off (Plate 6).

A poorly developed root system will accelerate the rate at which drought stress affects crop growth and presence of competing root systems by site conditions such as compacted soils or high water tables, or by container size. A plant with a large mass of leaves in relation to the root system is prone to drought stress because the leaves may lose water faster than the roots can supply it. Poorly established plants may be especially susceptible to drought stress because of the limited root system or the large mass of stems and leaves in comparison to root density.

Plate 6: **Fibrous root system of finger millet genotypes**

4.3.2.2 Root length

The genotype 169 had the longest root (129.33cm) and the shortest root was 55.33cm from genotype TFA 103. The root length overall average was 85.12cm. The variation in root length was found to be 17.2 percent and means difference was 23.92cm. RL correlated positively with SB, RB, TB, RV, NT, NL, RD and R: S ratio. However, it had significant negative correlation with HI. Linear regression analysis results showed RL to be positively correlated with yield (Fig.10)

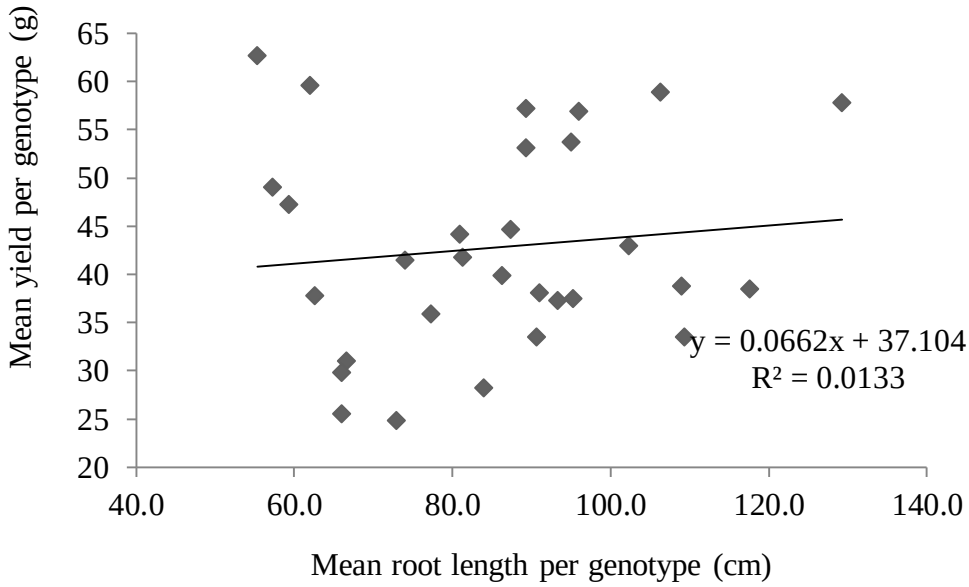

Figure 10~~11~~: Terminal drought stressed finger millet plant yield and root length

These findings are supported by Blum (2006) who identified primary factors responsible for superior performance of drought adapted cereal genotypes to include ability of the plant to capture deep soil moisture. Lorens *et al*. (1987) testified deep rooted genotypes to have yield advantage under drought stress over shallow rooted crops. Osmont *et al*. (2007) reported continued low crop productivity on farmer's fields despite lavish research reports on drought tolerance and adaptation to have been due to breeding programs not exploring the role of root architecture in drought adaptation experiments. The ongoing uncertainty in rainfall frequency, distribution and intensity compelled this study to undertake these tedious activities of using root characteristics in screening finger millet genotypes for drought adaptation.

4.3.2.3 Root density

The root density varied from a maximum of 0.7g/ml for genotype TFA 89 to a minimum of 0.17g/ml for genotype TFA 169. The overall average of finger millet root density was found to be 0.43g/ml. RD correlated positively and highly significantly with RB, TB, and R: S ratio. There were also significant correlation between RD, RL and FL. However, RD had highly significant negative correlation with HI and yield.

4.3.2.4 Root to shoot ratio

The highest R: S ratio obtained for genotype TFA 44 was 1.06 and the lowest was 0.14 for genotype TFA 103. The average R: S ratio was found to be 0.49 (Table 14 and 15). Root to shoot ratio had positive and significant correlation with shoot biomass, root biomass, total biomass, root volume, root density, root length, number of productive tillers and number of leaves. However, it had negative and weak correlation with harvest index and grain yield (Table 14). These results provide strong evidence for genotypic variation in root morphology, density and root extension.

4.3.3 Determination of major traits contributing to finger millet diversity on drought tolerance and yields

Grain yield had positive significant correlation with ($p \leq 0.01$) and positive regression coefficient with SB and HI. It had weak correlation with LAI, NL, RL, TB and negative correlation with PM, PH, NT, RB, RD, R: S ratio. The observed appreciable LAI indicated that plants invested more of it's assimilated in to vegetative biomass since there was an equal increment in grain biomass. From the above relationships it is not clear which trait contributed substantially to final grain yield. Obviously, high LAI, RB, NT, PH, PM, RD, NL, RL have high contribution to finger millet diversity but had little contribution to final grain yield and therefore would suffice as criteria for selection of finger millet drought tolerant genotypes.

Principal Components refers to the principal components model in which items are assumed to be exactly in linear combinations of factors. The Principal components method assumes that components ("factors") are uncorrelated. It also assumes that the communality of each item sums to 1 over all components (factors), implying that each item has 0 unique variance. The factor extraction method allows the variance of each variable to be a function of both item communality and nonzero unique variable variance (Reyment and J¨oreskog, 1993).

Principal components analysis and Factor analysis are used to identify underlying constructs or factors that explain the correlations among a set of variables. They are often used to summarize a large number of variables with a smaller number of factors. Eigen value is a unique standardized variance associated with a particular factor and is used to assess the communality among variables. For a variable to be considered as significant determinant of variation it should have an eigen values of greater than one. It follows that any variable with the eigen value less than one is disregarded and all variable with eigen value greater than one are chosen as major contributor to the observed variations (Kline, 1994).

Principal component analysis and coefficient of determination were performed to ascertain which traits contributed more to finger millet diversity and yield variations. Five principal components were extracted based on the Eigen value of 1 unit (Table 16 and Fig.12) and thirteen traits contributing to drought tolerance were ranked according to their level of contributions as shown in table 16.

Table 1416: Principal components influencing finger millet diversity and yield under terminal drought stress conditions

Components	Total variance	% variance	Cum % of variance
1 Total biomass	5.690	35.562	35.562
2 Root volume	2.736	17.103	52.665
3 Shoot biomass	1.635	10.217	62.882
4 Root biomass	1.462	9.138	72.019
5 Root: shoot ratio	1.132	7.073	79.093

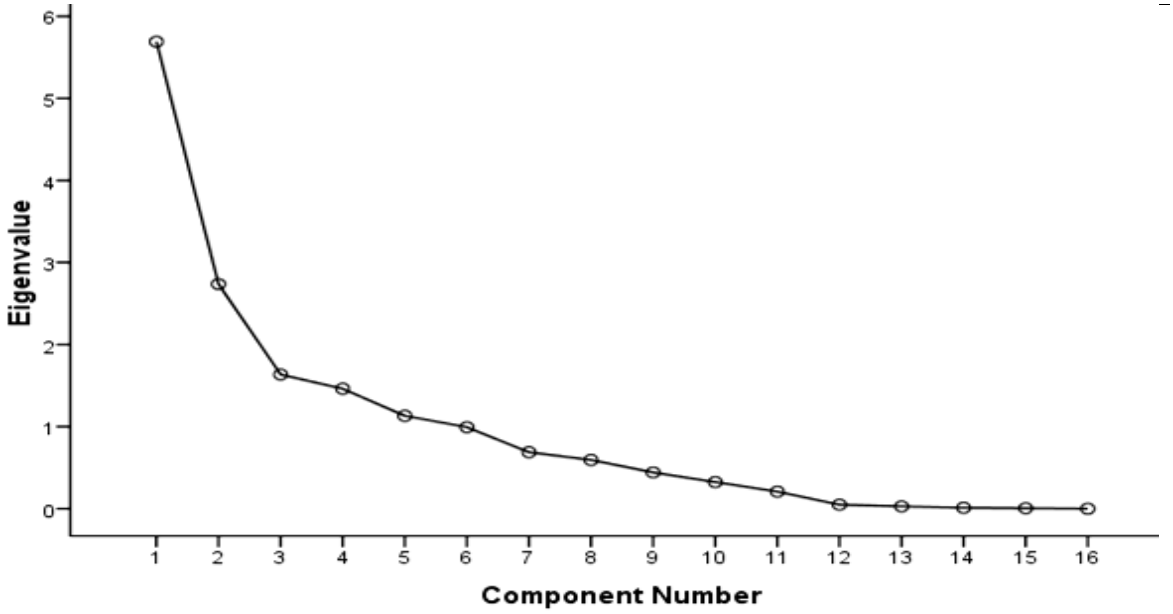

Figure 1112: Screed graph to show contribution of different traits to diversity and yield of finger millet under drought stresses

Key: 1 = Total biomass, 2 = Root volume, 3 = Shoot biomass, 4 = Root biomass, 5 = Root: shoot ratio, 6 = Root length, 7 = Leaf area index, 8 = Number of leaves, 9 = Number of productive tillers, 10 = Leaf width, 11 = Yield per plant, 12 = Harvest index, 13 = Leaf length, 14 = Root density, 15 = Finger length, 16 = Plant height

Table 15~~17~~: Determination of Factors contributing to finger millet diversity

		Component				
Serial No.	**Traits**	**1**	**2**	**3**	**4**	**5**
1	Total biomass	0.900	0.223	-0.126	0.246	0.104
2	Root volume	0.864	0.081	-0.214	-0.240	-0.022
3	Shoot biomass	0.835	0.285	0.228	0.028	0.078
4	Root biomass	0.795	0.147	-0.336	0.348	0.104
5	Root : shoot ratio	0.646	0.060	-0.515	0.379	0.109
6	Root length	0.625	0.121	0.088	0.094	0.118
7	Leaf area index	0.161	0.883	-0.015	-0.366	0.131
8	Number of leaves	0.334	0.830	0.048	0.147	-0.137
9	Number of productive tillers	0.379	0.723	-0.066	0.155	-0.272
10	Leaf width	-0.118	0.589	0.021	-0.333	0.467
11	Yield per plant	0.151	0.051	0.930	0.001	0.039
12	Harvest index	-0.520	-0.051	0.796	-0.119	-0.071
13	Leaf length	-0.104	0.207	-0.075	-0.779	0.160
14	Root density	0.179	0.106	-0.282	0.776	0.222
15	Finger length	0.069	-0.121	0.040	0.315	0.774
16	Plant height	0.288	0.015	-0.087	-0.275	0.640

The coefficient of determination identified major five traits to have contributed significantly to finger millet diversity with respect to drought tolerance and yield. Shoot biomass, harvest index and root to shoot ratio were identified to be positively, highly significant and contributed greatly to drought tolerance and finger millet yield under terminal drought stress conditions. Root biomass contributed significantly but in opposite direction (Table 17).

Table 1618: Coefficient of determination of traits contributing to finger millet yield per plant under terminal drought stress and their level of significance

	Traits	SE	R^2	t-values
1	Shoot biomass	0.034	0.809	9.885***
2	Root biomass	0.057	-0.758	-3.562**
3	Root volume	0.014	0.123	1.395
4	Root density	6.086	0.093	1.243
5	Root length	0.021	0.014	0.402
6	Plant height	0.031	-0.005	-0.153
7	Productive tillers	0.189	-0.037	-0.786
8	Finger length	0.273	0.037	1.095
9	Leaf number	0.031	-0.014	-0.109
10	Leaf length	0.123	0.059	0.678
11	Leaf width	3.916	-0.056	-0.758
12	Leaf area index	3.070	-0.019	-0.104
13	Harvest index	0.080	1.264	28.085***
14	Root : shoot ratio	11.963	0.953	4.679***

****

4.3.4 Flowering, physiological maturity and associated phenological and physiological changes

A proper timing of lifecycle, resulting in the completion of the most sensitive developmental stages while water is abundant is recommended for drought escape strategy. Flowering time is recognized as the most critical factor to optimize adaptation to drought prone environments with poor rainfall intensity and distribution over the growing season (Richards, 2006). Phenological traits of significance in drought phenotyping are days to flowering and days to physiological maturity (Benjamin *et al*., 2012). This is because the correlation between time to flowering, plant height, biomass production and partitioning, yield components and grain yield is at maximum during anthesis thereby making this stage of diagnostic importance to breeders (Bänziger *et al*., 2000).

The result of this study (Fig. 12) showed that genotypes TFA 171 and 130 took 102 days to flower and 121days to physiological maturity. Genotypes TFA 100, 90, and 89 took 104 days to flower and 123days to physiological maturity. Other genotype is TFA 77 which took 105 days to flowering and 124 days to physiological maturity. The difference between days to flowering and physiological maturity averaged at 19 days.

Based on the results above backup by extensive review of other scholar's works, six genotypes TFA 171,130, 100, 90, 89 and 77 were identified as early maturing compared to the other genotypes in the study. The latest maturing genotypes were found to be TFA 139, 94, 88, 86, 82, 74, 67 and 58.

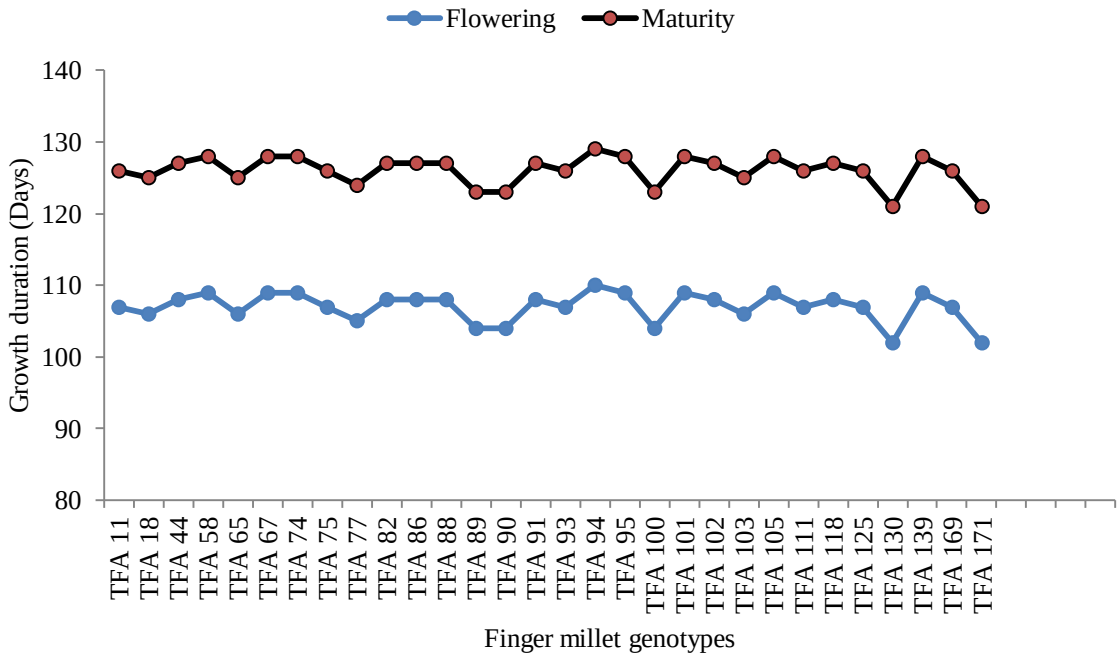

Figure 12~~13~~: Duration to 50% flowering and physiological maturity

Selection for early flowering genotypes is a simple and effective way of increasing yield under terminal drought and increase the chance of escaping terminal drought (Sadras *et al.*, 2009). Lafitte and Courtois (2002) showed the advantages of earlier flowering over later flowering in terms of higher spikelet fertility, higher harvest index, and higher yield

in rice experiment involving diverse germplasm. Positive associations between variation in yield and flowering time across different levels of water availability have been reported in different crops (Sadras *et al.,* 2009). As photosynthesis becomes inhibited by drought, grain filling process becomes increasingly reliant on stem reserves. Thus soluble carbohydrate reserves contribute to superior performance under drought stress (Blum, 1988; Reynolds *et al*., 2005). High pre-anthesis biomass accumulation and post anthesis remobilization play a crucial role during terminal drought stress conditions (Blum, 1988; Reynolds *et al*., 2005). Shearman *et al*. (2005) reported indicated that reserves accumulated in the stem increased yield potential in wheat. Drought escape through the use of shorter duration varieties is often the preferable method of improving yield potential (Benjamin *et al*., 2012).

4.3.5 Finger millet terminal drought tolerance level explained in terms of grain yield

Two or more stresses may have common physiological effects on different traits and may be an indicator of overall plant health. Abiotic and biotic stresses can result in similar physiological response from which tolerant plant can be separated from sensitive ones.

To determine the most desirable drought tolerant genotypes, four quantitative indices of drought tolerance and relative yield decline due to drought stress were calculated. Drought tolerance indices for screening finger millet genotypes included stress intensity, yield stability index, stress tolerance index and drought tolerance index (Table 19, 20 and 21).

The yield potentials of genotypes used in this section were adopted from the results of objective one of this research and are used to compare performance of the thirty selected high yielding genotypes under terminal drought stress conditions (Table 19). Genotype with high yield potential was TFA 105 which had 90.56g and genotype with lowest yield potential was TFA 94 which had yield of 56g per plant before yield evaluation under terminal drought stress conditions.

After terminal drought tolerance yield evaluation, the maximum finger millet grain yield was 62.71g per plant for genotype TFA 103 and the minimum grain yield of 24.87g per plant was recorded for genotype TFA 58. The average grain yield obtained was 42.74g per plant. There was 90.30 percent variation in relative yield decline between genotypes. Severe yield decline were observed among genotypes TFA 102, 58, 93,94,82, 100, 95, 18, 171, 75, 88, 91 139, 118,67, 44,89 and 101 all of which had a yield decline of above 50 percent (Table 19 and Fig. 13). Genotypes which had yield decline of less than 50% include TFA 11, 130, 105, 90, 74, 86, 111, 125,103,169 and 77. Out of all the studied genotypes, genotype 169 and 77 were stable and had only 6 and 4 percent yield decline under drought respectively (Table 19 and Fig. 13).

Table 1719: Calculated tolerance indices of finger millet genotype under terminal drought stress and non-stress conditions

Genotypes	YP	YS	RYD	%RYD	MYP	MYS	SI	YSI	STI	DTI
TFA 105	90.56	56.94	48.43	41.00	88.60	56.94	0.36	0.63	0.66	0.63
TFA 18	82.85	37.56	68.88	65.98	82.60	37.56	0.55	0.45	0.46	0.45
TFA 44	77.72	43.03	66.56	57.43	79.78	43.03	0.46	0.55	0.53	0.55
TFA 67	76.04	39.92	69.64	62.47	77.47	39.92	0.48	0.52	0.51	0.52
TFA 101	75.76	44.14	66.56	55.09	77.03	44.14	0.43	0.58	0.56	0.58
TFA 125	70.73	59.62	57.83	22.21	75.80	59.62	0.21	0.84	0.73	0.84
TFA 103	73.06	62.71	54.18	19.39	74.33	62.71	0.16	0.86	0.83	0.86
TFA 130	69.14	49.06	66.08	42.00	74.21	49.06	0.34	0.71	0.62	0.71
TFA 58	70.66	24.87	82.43	91.71	73.93	24.87	0.66	0.35	0.32	0.35
TFA 11	62.86	44.64	71.94	46.11	52.75	44.64	0.15	0.71	1.01	0.71
TFA 88	72.33	38.13	72.42	65.37	72.35	38.13	0.47	0.53	0.53	0.53
TFA171	71.29	37.84	73.02	65.82	72.30	37.84	0.48	0.53	0.52	0.53
TFA 139	65.19	38.48	74.92	62.85	71.91	38.48	0.46	0.59	0.49	0.59
TFA 90	71.86	53.76	61.37	35.05	71.89	53.76	0.25	0.75	0.75	0.75
TFA 65	68.51	41.48	71.58	57.59	71.79	41.48	0.42	0.61	0.55	0.61
TFA 118	66.57	38.79	74.18	62.69	71.65	38.79	0.46	0.58	0.50	0.58
TFA 111	73.32	57.2	58.06	29.99	71.36	57.20	0.20	0.78	0.82	0.78
TFA 100	69.19	33.48	76.84	74.59	70.46	33.48	0.52	0.48	0.47	0.48
TFA 82	69.01	31.07	78.56	79.67	69.03	31.07	0.55	0.45	0.45	0.45
TFA 86	66.44	53.19	64.66	30.01	66.46	53.19	0.20	0.80	0.80	0.80
TFA 75	64.56	37.29	75.92	65.43	65.99	37.29	0.43	0.58	0.55	0.58
TFA 93	64.65	28.28	81.72	87.02	65.92	28.28	0.57	0.44	0.42	0.44
TFA 89	65.78	41.83	72.48	55.35	65.81	41.83	0.36	0.64	0.64	0.64
TFA 102	61.26	25.54	84.36	95.18	62.53	25.54	0.59	0.42	0.40	0.42
TFA 77	60.77	58.97	64.16	4.87	62.21	58.97	0.05	0.97	0.93	0.97
TFA 169	60.28	57.86	65.12	6.67	61.29	57.86	0.06	0.96	0.93	0.96
TFA 74	57.23	47.25	72.96	30.47	58.66	47.25	0.19	0.83	0.79	0.83
TFA 95	56.57	33.53	81.03	71.99	57.84	33.53	0.42	0.59	0.57	0.59
TFA 94	56.33	29.82	83.20	83.55	57.60	29.82	0.48	0.53	0.51	0.53
TFA91	57.39	35.94	79.38	65.12	57.41	35.94	0.37	0.63	0.63	0.63

Key: YP = Yield potential, YS = Yield under stress, RYD = Relative yield decline, MYP = Mean Yield Potential, MYS = Mean yield under stress, SI = Stress Intensity, YSI = Yield Stability Index, STI = Stress Tolerance Index, DTI = Drought Tolerance Index

These results are supported by Andrade *et al*. (1996) who reported decreases in gross photosynthetic rate, water potential, plant height, grain filling duration, number of panicle per plant, number of fingers, 1000-grain weight, total biomass, grain yield and harvest index as drought stress severity increased.

Table 1820: Summary statistics to show variations among different drought tolerance indices

Indices	Range	Minimum	Maximum	Mean	Std. Error	Std. Deviation	Variance	t^2
RYD	35.93	48.43	84.36	70.6157	1.62984	8.92702	79.692	-0.552
MYP	35.85	52.75	88.60	69.3653	1.49616	8.19479	67.155	0.015
Yp	34.23	56.33	90.56	68.2637	1.43162	7.84133	61.486	0.676
MYS	37.84	24.87	62.71	42.7407	1.96907	10.78502	116.317	0.268
Ys	37.84	24.87	62.71	42.7407	1.96907	10.78502	116.317	0.268
DTI	0.62	0.35	0.97	0.6297	0.02928	0.16035	0.026	0.520
YSI	0.62	0.35	0.97	0.6297	0.02928	0.16035	0.026	0.520
STI	0.69	0.32	1.01	0.6160	0.03168	0.17354	0.030	0.657
SI	0.61	0.05	0.66	0.3777	0.02962	0.16222	0.026	-0.481

YP = Yield potential, YS = Yield under stress, RYD = Relative yield decline, MYP = Mean Yield Potential, MYS = Mean yield under stress, SI = Stress Intensity, YSI = Yield Stability Index, STI = Stress Tolerance Index, DTI = Drought Tolerance Index

Table 1921: Correlation analysis between grain yield and drought tolerance indices for screening the best finger millet genotype was done using SPSS 16.0 version

Indices	Yp	Ys	RYD	MYP	MYS	SI	YSI	STI	DTI
Yp	1								
Ys	0.254	1							
RYD	-0.606**	-0.918**	1						
MYP	0.936**	0.207	-0.538**	1					
MYS	0.254	1.000**	-0.918**	0.207	1				
SI	0.193	-0.875**	0.633**	0.282	-0.875**	1			
YSI	-0.201	0.892**	-0.643**	-0.222	0.892**	-0.980**	1		
STI	-0.171	0.823**	-0.601**	-0.325	0.823**	-0.979**	0.918**	1	
DTI	-0.201	0.892**	-0.643**	-0.222	0.892**	-0.980**	1.000**	0.918**	1

YP= Yield potential, YS = Yield under stress, RYD = Relative yield decline, MYP = Mean Yield Potential, MYS = Mean yield under stress, SI = Stress Intensity, YSI = Yield Stability Index, STI = Stress Tolerance Index, DTI = Drought Tolerance Index

Yield under stress condition (Ys) was significantly and positively corrected with STI, MP, YSI, YSI and DTI implying that these indices were very effective in identifying high

yielding genotypes under drought conditions. Dehghani *et al.* (2010) reported that STI was significantly and positively correlated with yield under stress conditions.

To determine the most desirable drought tolerant cultivar according to all indices, mean rank and standard deviation of ranks of all drought tolerance indices were calculated and based on these indices the most desirable drought tolerant cultivars were identified.

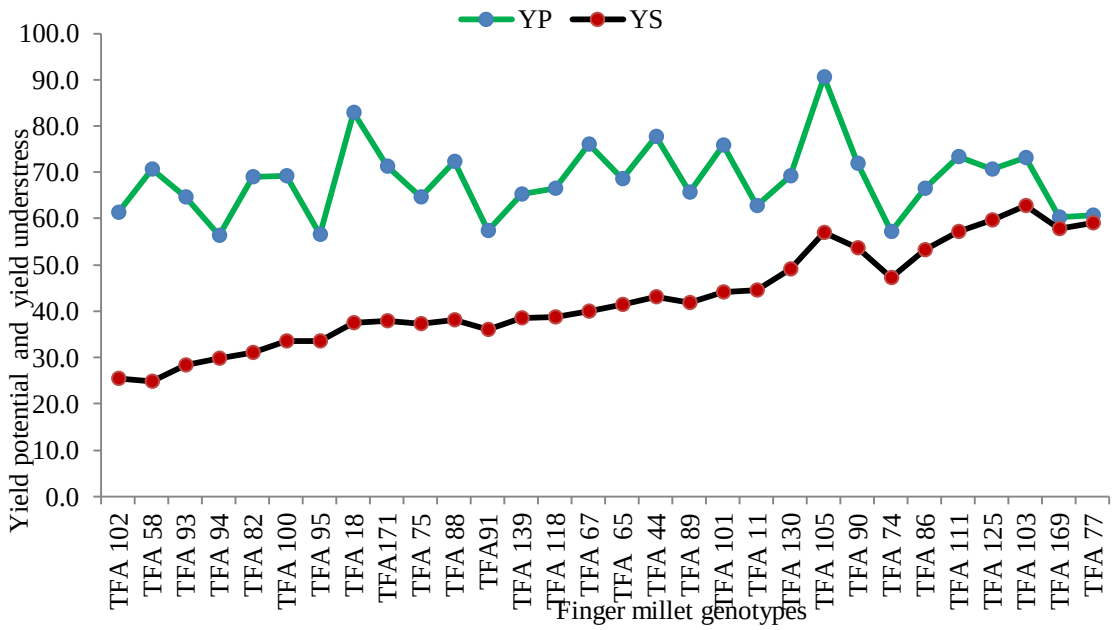

Figure 13~~14~~: Finger millet yield potential and yield under terminal drought stress

Genotype FTA 11 had the highest STI, followed by 169 and 77 genotypes. Genotype TFA 58 had the lowest STI (Table 19 and Fig. 14). Based on the applied relative yield decline, yield stability, drought resistance and stress tolerance indices, Genotypes TFA 77, 169 and 11 were selected as superior drought tolerant and high yielding genotypes under terminal drought stresses.

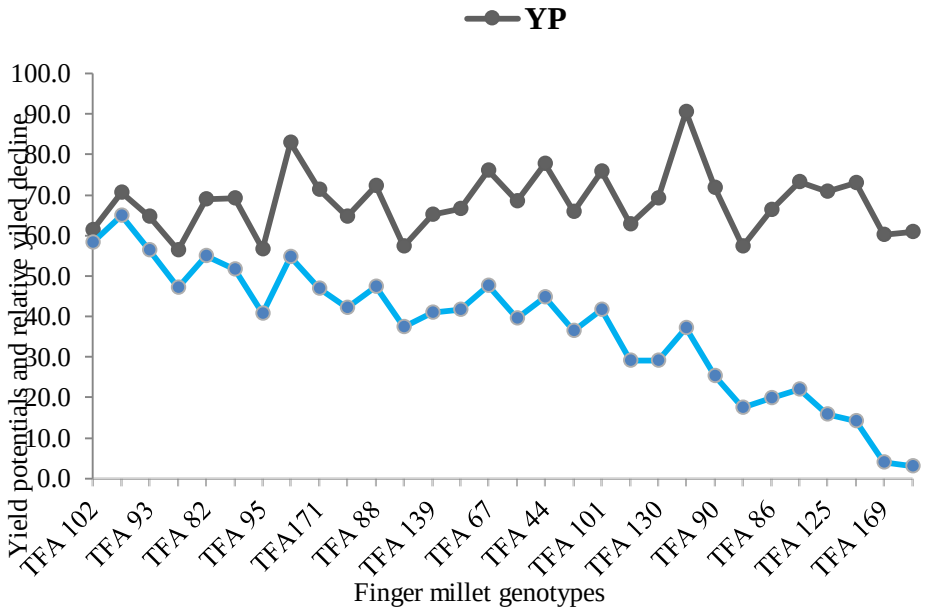

Figure 14~~15~~: Finger millet yield potentials and relative yield decline due to terminal drought stress

Figure 15~~16~~: Drought tolerant finger millet genotypes selection using stress tolerance index

These findings justified the benefits of continued use of conventional breeding. It is in line with Bänziger and Araus (2007) and Reynolds and Tuberosa (2008) suggestions that conversional breeding can still offer an opportunity for significant and predictable improvements in the crop drought tolerance. For example, in maize significant progress in grain yield under drought stress has been made through selection in multi-environment experiments for yield component traits (Campos *et al.*, 2004). Appropriate stress management is effective for selection than a conventional large multi-experiment testing scheme. Thus Bänziger *et al*. (2006) reported that hybrids selected under managed stress using similar protocols have significantly out-yielded commercial hybrids in southern and eastern Africa, particularly under severe and moderate water-stress conditions. Advanced practical solutions for drought-prone farming need concerted effort of multidisciplinary to fully contribute to the morphological and physiological understanding and skills for amelioration of plant stress impacts (Kumar and Singh, 1998). The breeding progress depends on accurate selection of elite genotypes with improved attributes in the context of target population environments (Sorrels, 2007). This implies that precise phenotyping will remain one of the cornerstones of future breeding.

CHAPTER FIVE

5.0 CONCLUSIONS AND RECOMMENDATIONS

5.1 Conclusions

Results on morphological characterization of finger millet genotypes identified number of productive tillers, plant maturity, and number of fingers, finger length and one thousand grain weights as the major determinant of finger millet plant yield and contribute largely to the crop diversity.

The phenotypic variability and traits of economic importance identified will allow for direct selection of individual genotypes with traits of interest in the early stages of crop improvement. The study has generated important information on the traits of economic importance in finger millet cultivar development and its utilization in breeding programs will improve crop production and food security in Tanzania.

From the study on genetic diversity of finger millet genotypes higher number of private alleles (68%) was identified suggesting high genetic diversity among finger millet genotypes in Tanzania. SSR markers therefore, have been very useful in discriminating finger millet genotypes.

Drought phenotyping was very much revealing, based on the applied relative yield decline, yield stability, drought resistance and stress tolerance indices, Genotypes TFA 77, 169 and 11 were selected as superior drought tolerant and high yielding genotypes under terminal drought stresses.

5.2 Recommendations

Genetic resource collection, conservation and varietal development depends upon the presence of genetic variability in the trait of interest. The wider genetic variability among Tanzania finger millet genotypes revealed through descriptive statistics analysis, proximity and similarities observed from cluster analysis and principal component analysis provide guidance to the recommendation that extensive genotype collections and characterization be done by breeders to exploit genetic variability from distinct clusters for the development of improved varieties. The molecular characterization detected existence of great number of private alleles which can be a foundation for the crop improvement with respect to yield and stress adaptation.

Integrated physiology, molecular characterization and plant breeding programs are recommended for more genotypes screening for drought tolerance using morphological and physiological traits associated with gains in grain yield for finger millet variety development in Tanzania.

Multi environmental experiments under drought stress and non stress conditions be planned and conducted by multidisciplinary team of scientists to evaluation the identified potential drought tolerance and high yielding genotypes for more comprehensive, effective, accurate drought phenotyping and varietal development targeting official variety release and seed multiplication for immediate farmers' use in Tanzania.

This characterization led to grouping of individual genotypes into early maturing (75 to 100days) with 42 genotypes; medium duration (101 to 120days) with 79 genotypes and late maturing above 120 days with 48 genotypes. The understanding of variations in time to maturity provided opportunity for developing improved varieties according to agro-

ecological suitability and help plan successive cropping systems. Selecting for early maturing varieties is an important copping strategy against the effects climate change. These will ensure that farmers realize a crop harvest through terminal drought escape which is experienced frequently.

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APPENDICES

Appendix: 1.Weather recorded on daily bases in Morogoro 2013 and 2014

Year	Months	Dates	Max Temp (℃)	Min Temp(℃)	RH (%)	RF (Mm)
2013	March	1	34.5	21.0	40	0.0
2013	March	2	34.2	22.8	45	0.0
2013	March	3	35.2	22.6	42	0.0
2013	March	4	34.1	23.0	44	0.0
2013	March	5	32.9	23.0	56	7.6
2013	March	6	32.3	22.9	52	0.0
2013	March	7	32.7	23.5	52	0.0
2013	March	8	30.8	23.5	88	1.2
2013	March	9	33.5	21.5	46	0.0
2013	March	10	33.0	21.2	51	0.0
2013	March	11	31.2	23.4	48	17.4
2013	March	12	32.4	21.1	59	0.0
2013	March	13	33.0	22.0	49	0.0
2013	March	14	33.7	21.0	38	0.0
2013	March	15	33.8	21.0	49	0.0
2013	March	16	33.7	22.0	48	0.0
2013	March	17	32.2	22.3	75	3.1
2013	March	18	32.0	22.0	54	1.4
2013	March	19	31.8	22.9	87	4.3
2013	March	20	32.8	21.0	54	9.1
2013	March	21	30.5	21.3	62	1.5
2013	March	22	32.4	22.5	56	9.6
2013	March	23	32.0	22.5	52	TR
2013	March	24	28.4	22.6	92	2.2
2013	March	25	29.0	21.0	68	0.0
2013	March	26	32.2	22.0	57	8.4
2013	March	27	30.7	22.3	80	9.6
2013	March	28	30.9	21.0	62	0.0
2013	March	29	31.2	21.3	69	0.4

2013	March	30	29.6	22.0	65	20.7
2013	March	31	28.7	22.0	80	2.9
2013	April	1	27.3	22.0	78	5.2
2013	April	2	31.0	21.0	60	1.5
2013	April	3	31.1	20.4	60	0.0
2013	April	4	32.2	22.3	58	1.0
2013	April	5	30.7	22.5	60	16.9
2013	April	6	28.0	22.3	75	9.9
2013	April	7	30.2	22.0	68	0.0
2013	April	8	29.9	22.9	66	TR
2013	April	9	31.7	22.2	61	1.7
2013	April	10	32.0	22.6	60	2.4
2013	April	11	27.5	23.2	79	1.5
2013	April	12	30.7	22.4	71	0.8
2013	April	13	29.0	22.4	74	2.6
2013	April	14	28.1	21.4	69	0.0
2013	April	15	31.0	20.8	59	1.0
2013	April	16	29.0	21.8	70	0.5
2013	April	17	30.1	19.7	63	11.6
2013	April	18	30.0	21.1	75	4.9
2013	April	19	30.4	21.0	64	4.4
2013	April	20	30.6	21.0	65	0.0
2013	April	21	31.1	19.6	57	11.0
2013	April	22	31.7	20.7	54	0.0
2013	April	23	31.1	20.1	63	0.7
2013	April	24	31.1	21.8	60	16.6
2013	April	25	29.0	21.4	64	1.0
2013	April	26	29.0	21.3	62	TR
2013	April	27	29.0	19.1	59	0.8
2013	April	28	30.0	19.3	57	0.0
2013	April	29	28.6	21.0	67	1.7
2013	April	30	29.3	21.5	70	28.6
2013	May	1	27.0	20.7	75	0.3
2013	May	2	26.8	20.8	71	3.9
2013	May	3	29.9	20.3	55	4.5
2013	May	4	26.7	21.2	73	2.8
2013	May	5	28.5	21.3	65	1.2
2013	May	6	30.2	20.6	53	4.1

2013	May	7	27.7	21.5	59	0.0
2013	May	8	28.8	18.8	60	0.0
2013	May	9	29.8	18.4	58	0.0
2013	May	10	29.7	19.6	60	1.7
2013	May	11	31.0	21.1	55	2.6
2013	May	12	30.0	21.2	55	TR
2013	May	13	30.7	19.6	47	0.0
2013	May	14	28.2	20.3	61	0.0
2013	May	15	29.1	19.7	55	0.0
2013	May	16	29.0	20.2	54	0.0
2013	May	17	30.4	19.0	47	0.0
2013	May	18	30.5	18.8	55	0.0
2013	May	19	30.0	20.1	47	0.0
2013	May	20	30.1	17.3	53	0.0
2013	May	21	29.6	18.0	55	0.0
2013	May	22	29.7	17.1	55	0.0
2013	May	23	29.0	18.4	61	0.0
2013	May	24	30.1	19.4	52	0.0
2013	May	25	31.2	18.4	54	0.0
2013	May	26	30.0	18.7	58	0.0
2013	May	27	29.1	18.9	60	1.7
2013	May	28	30.5	20.7	56	0.0
2013	May	29	31.3	20.2	42	0.0
2013	May	30	31.1	17.0	53	TR
2013	May	31	31.0	19.2	43	0.0
2013	June	1	30.8	17.4	43	0.8
2013	June	2	30.5	19.1	45	0.0
2013	June	3	29.4	13.8	35	0.0
2013	June	4	29.8	14.2	44	0.0
2013	June	5	29.8	17.8	47	0.0
2013	June	6	29.5	14.2	39	0.0
2013	June	7	29.9	16.2	42	0.0
2013	June	8	28.6	14.2	39	0.0
2013	June	9	27.7	14.1	48	0.0
2013	June	10	29.4	16.4	43	0.0
2013	June	11	28.2	15.0	47	0.0
2013	June	12	29.6	14.8	41	0.0
2013	June	13	29.8	14.4	44	0.0

2013	June	14	30.2	16.5	53	0.0
2013	June	15	29.0	18.4	59	0.0
2013	June	16	29.5	17.3	46	0.0
2013	June	17	28.2	16.0	37	0.0
2013	June	18	29.1	16.8	46	0.0
2013	June	19	29.1	15.8	45	0.0
2013	June	20	27.6	16.7	49	0.0
2013	June	21	28.8	16.9	35	0.0
2013	June	22	28.7	16.9	46	0.0
2013	June	23	28.2	18.4	51	0.0
2013	June	24	29.2	17.1	48	0.0
2013	June	25	28.2	17.5	49	0.0
2013	June	26	29.5	15.6	41	0.0
2013	June	27	28.8	16.1	45	0.0
2013	June	28	29.7	16.4	42	0.1
2013	June	29	29.0	16.8	50	0.0
2013	June	30	29.3	15.7	42	0.0
2013	July	1	29.2	15.3	43	0.0
2013	July	2	29.0	15.4	42	0.0
2013	July	3	28.0	15.6	45	0.0
2013	July	4	30.4	17.8	53	0.0
2013	July	5	29.8	15.8	46	0.0
2013	July	6	29.7	14.6	41	0.0
2013	July	7	29.2	13.7	36	0.0
2013	July	8	27.4	16.0	47	0.0
2013	July	9	29.5	13.6	32	0.0
2013	july	10	30.0	12.9	30	0.0
2013	July	11	28.3	13.1	39	0.0
2013	July	12	28.7	13.0	34	0.0
2013	July	13	29.5	13.2	35	0.0
2013	July	14	30.5	12.5	37	0.0
2013	July	15	31.1	13.4	38	0.0
2013	July	16	30.0	16.0	43	0.0
2013	July	17	29.3	15.5	46	0.0
2013	July	18	28.1	16.8	45	0.0
2013	July	19	28.7	14.6	47	0.0
2013	July	20	28.7	15.6	43	0.0
2013	July	21	30.0	18.6	43	0.3

2013	July	22	28.5	14.4	46	0.0
2013	July	23	28.7	14.0	41	0.0
2013	July	24	30.1	14.0	67	0.0
2013	July	25	29.4	16.9	44	TR
2013	July	26	30.9	19.4	37	0.0
2013	July	27	30.0	16.5	44	0.0
2013	July	28	29.2	16.0	77	0.0
2013	July	29	30.6	15.3	38	1.2
2013	July	30	29.6	19.2	42	0.0
2013	July	31	28.1	19.0	45.0	0.2

Appendix: 2.

YEAR	**MONTHS**	DATES	MAX TEMP(℃)	MIN TEMP(℃)	R.H (%)	RF(mm)
2014	March	1	32.5	20.4	39	0.0
2014	March	2	32.7	21.4	42	2.5
2014	March	3	32.2	21.7	53	0.3
2014	March	4	31	22.7	47	5.2
2014	March	5	31.5	21.8	56	3.6
2014	March	6	26.3	21.7	78	13.5
2014	March	7	31.1	20.7	58	0.0
2014	March	8	32.3	22.0	50	0.0
2014	March	9	28.9	22.4	63	1.9
2014	March	10	30.3	20.8	47	15.7
2014	March	11	29	21.3	65	0.2
2014	March	12	32.1	20.0	56	0.3
2014	March	13	30.5	23.8	78	4.5
2014	March	14	31.6	22.5	80	2.2
2014	March	15	28.4	20.0	80	2.8
2014	March	16	31.4	20.4	57	0.0
2014	March	17	32.1	22.0	53	0.0
2014	March	18	32.2	22.8	49	0.0
2014	March	19	32.6	23.5	49	0.0
2014	March	20	32.8	23.8	47	0.0
2014	March	21	32.6	22.0	52	0.0
2014	March	22	32.2	22.4	58	0.3
2014	March	23	32.6	22.2	52	0.2
2014	March	24	32.8	23.2	64	TR

2014	March	25	33.1	21.8	38	7.1
2014	March	26	31.6	21.8	46	9.2
2014	March	27	31.3	22.5	33	30.2
2014	March	28	28.7	20.7	69	9.8
2014	March	29	29.4	21.0	69	0.1
2014	March	30	24.9	21.5	96	71.9
2014	March	31	29	21.2	62	1.2
2014	April	1	31	20.9	67	TR
2014	April	2	29.7	21.4	66	0.0
2014	April	3	30.8	21.2	58	2.5
2014	April	4	31.5	23.0	70	0.2
2014	April	5	31.4	22.5	61	1.2
2014	April	6	31.2	22.1	56	0.0
2014	April	7	31.6	22.0	54	2.4
2014	April	8	29.2	22.5	70	TR
2014	April	9	29.1	22.0	66	1.4
2014	April	10	29.1	21.9	74	9.6
2014	April	11	27.2	21.0	89	76.6
2014	April	12	22.9	20.7	95	34.6
2014	April	13	27.3	19.9	68	5.9
2014	April	14	28.3	20.6	74	0.0
2014	April	15	29.4	21.0	70	16.6
2014	April	16	30	20.6	80	0.4
2014	April	17	29.2	21.5	80	3.0
2014	April	18	29.4	19.8	87	0.0
2014	April	19	29.1	22.0	90	0.0
2014	April	20	30.1	21.9	87	16.3
2014	April	21	28.4	20.7	98	12.5
2014	April	22	28.3	21.0	79	16.9
2014	April	23	29.8	21.4	94	19.2
2014	April	24	29.9	19.9	84	0.0
2014	April	25	30.2	20.0	80	0.4
2014	April	26	30.9	21.0	90	1.6
2014	April	27	30.9	21.0	87	0.0
2014	April	28	30.2	20.5	90	0.0
2014	April	29	30.7	19.0	63	0.0
2014	April	30	28.8	20.0	84	9.7
2014	May	1	29.1	21.1	63	9.7

2014	May	2	29.2	19.9	64	6.7
2014	May	3	28	20.9	68	4.8
2014	May	4	27	21.3	67	5.6
2014	May	5	27.3	20.5	64	4.7
2014	May	6	29.8	21.0	54	7.7
2014	May	7	26.7	20.4	85	26.5
2014	May	8	27	20.6	67	12.7
2014	May	9	28.4	20.7	58	2.6
2014	May	10	29.2	20.0	58	0.0
2014	May	11	30.3	18.9	60	0.0
2014	May	12	30.3	20.1	61	0.0
2014	May	13	28.7	21.6	76	17.9
2014	May	14	29.1	20.5	52	8.4
2014	May	15	28	18.4	68	0.0
2014	May	16	28.5	18.3	64	0.0
2014	May	17	28.6	19.0	65	0.0
2014	May	18	28.7	21.0	60	0.0
2014	May	19	28.1	20.0	54	0.2
2014	May	20	27.8	17.4	54	0.0
2014	May	21	25.4	19.8	66	0.8
2014	May	22	27.5	20.0	68	0.3
2014	May	23	27.4	20.0	96	2.4
2014	May	24	27.7	17.1	47	0.0
2014	May	25	26	19.5	72	0.8
2014	May	26	29.3	20.0	58	1.2
2014	May	27	28.4	20.5	62	0.0
2014	May	28	27.1	20.2	73	0.0
2014	May	29	28.8	19.2	63	0.0
2014	May	30	28.8	19.2	96	0.0
2014	May	31	28.5	15.9		0.0
2014	June	1	28.5	15.5	56	TR
2014	June	2	29.2	19.0	64	0.0
2014	June	3	30	19.2	61	0.0
2014	June	4	29.4	20.5	67	0.0
2014	June	5	27.9	19.6	67	0.0
2014	June	6	29	18.9	66	0.0
2014	June	7	27.8	19.8	68	0.0
2014	June	8	26.6	20.0	67	0.0

2014	June	9	28.3	18.5	54	0.0
2014	June	10	29.3	16.0	55	0.0
2014	June	11	27.5	17.9	66	TR
2014	June	12	26.7	19.5	57	0.0
2014	June	13	26.7	16.6	60	0.0
2014	June	14	26.4	15.6	57	0.0
2014	June	15	28.8	16.5	55	0.0
2014	June	16	29	18.2	64	0.0
2014	June	17	26.9	18.8	72	0.0
2014	June	18	28.3	18.5	62	0.0
2014	June	19	28.9	16.5	52	0.0
2014	June	20	28.7	16.5	42	23.3
2014	June	21	26.9	19.3	54	0 .0
2014	June	22	27.2	19.2	47	0.7
2014	June	23	26.8	19.3	60	0.0
2014	June	24	26.4	17.5	61	0.0
2014	June	25	27.5	17.8	53	0.0
2014	June	26	27.5	16.5	57	0.0
2014	June	27	28.3	17.0	49	0.0
2014	June	28	27.9	16.4	56	0.0
2014	June	29	29	13.0	43	0.0
2014	June	30	28.2	17.7	60	0.0
2014	July	1	28	13.8	54	0.0
2014	July	2	26.5	16.5	47	0.0
2014	July	3	26.2	16.0	70	0.0
2014	July	4	27.8	16.8	52	0.0
2014	July	5	28.7	14.9	49	0.0
2014	July	6	26.8	16.9	62	0.0
2014	July	7	27.9	17.9	57	0.0
2014	July	8	28.6	18.0	57	0.0
2014	July	9	28.7	16.4	47	0.0
2014	july	10	28.3	14.0	50	0.0
2014	July	11	26.1	16.0	49	0.0
2014	July	12	26.7	12.5	46	0.0
2014	July	13	28	14.0	48	0.0
2014	July	14	26.6	14.6	58	0.0
2014	July	15	26.1	16.7	54	0.0
2014	July	16	28.3	13.4	43	0.0

2014	July	17	28.6	17.2	54	TR
2014	July	18	27.3	17.4	57	0.0
2014	July	19	28.2	19.0	60	0.0
2014	July	20	29.8	17.0	56	0.0
2014	July	21	27.7	17.5	59	0.0
2014	July	22	28.6	14.8	37	0.0
2014	July	23	27.2	14.0	47	0.0
2014	July	24	26.4	17.2	70	0.0
2014	July	25	27.6	15.1	57	0.0
2014	July	26	28.2	16.3	55	0.0
2014	July	27	29.3	19.1	51	TR
2014	July	28	29.5	17.9	47	0.0
2014	July	29	29.8	19.0	42	13.0
2014	July	30	28.2	19.0	48	0.0
2014	July	31	29.5	19.2	50	0.0

Appendix 3: Morphological quantitative and qualitative traits for finger millet diversity studies (IBPGR, 2011)

I	Quantitative traits	Description
1	Time to Plant Maturity (PM)	Number of days from sowing to 50% of the plants in the plot reaching maturity stage (readiness for harvest)
2	Plant height (PH)	Average length of 10 plants from ground level to tip of inflorescence (ear) recorded at dough stage
3	Productive tillers (NT)	Average number of basal tillers from 10 plant samples which bear mature ears
4	Panicle Length (PL)	Average length of 10 plants in centimeter from base to tip of longest spike (finger) on main tiller at dough stage
5	Number of fingers (NF)	Average number of finger counted from 10 plant samples per main plant ear
6	Panicle weight (PW)	Average weight of 10 fingers from main plants in a plot at harvest in gram
7	Finger length (FL)	average length of peduncles of 10 plant samples taken from top most node to base of the thumb finger in centimeter
8	Thousand grain weight	weight of thousand seeds in gram
9	Grain yield per plant (GY)	Average yield of ten plants in gram
10	Harvest index (HI)	The ratio of grain yield to biological yield per plant times 100
11	Biomass weight (GW)	Total weight of biomass at harvest
II	**Qualitative traits**	
21	**Plant pigmentation**	Visual observation and classification Recorded binary format as 0= Not pigmented and 1= Pigmented

22	**Panicle shape**	Panicle shape observed at dough stage and recorded as:- 1 Droopy (fingers lax and drooping) 2 Open (fingers straight) 3 Semi-compact (tops of fingers curved) 4 Compact (fingers incurved) 5 Fist-like (fingers very incurved)

Appendix 4: DNA extraction protocol used

For optimal performance, add beta-mercaptoethanol (user supplied) to the **Plant/Seed DNA Binding Buffer** to a final dilution of 0.5% (v/v) i.e., 250 µl per 50 ml *or* 500 µl per 100 ml.

Before Starting: **Zymo-Spin™ IV-HRC Spin Filters** (*green tops*) need to be prepared prior to use by: 1) snapping off the base, 2), inserting into a **Collection Tube**, and 3), spinning in a microcentrifuge at exactly 8,000 x *g* for 3 minutes.

1. Add up to 150 mg of finely cut plant or seed sample to a **ZR BashingBead™ Lysis Tube**. Add 750 µl **Lysis Solution** to the tube.

2. Secure in a bead beater fitted with a 2 ml tube holder assembly (e.g., Disruptor Genie™) and process at maximum speed for 10 minutes.

Processing times may be as little as 40 seconds when using high-speed cell disrupters (e.g., the portable ***Xpedition*™ Sample Processor**, page 6, FastPrep□-24, or similar). See manufacturer's literature for operating information.

3. Centrifuge the **ZR BashingBead™ Lysis Tube** in a microcentrifuge at ≥10,000 x *g* for 1 minute.

4. Transfer up to 400 µl supernatant to a **Zymo-Spin™ IV Spin Filter** (orange top) in a **Collection Tube** and centrifuge at 7,000 rpm (~7,000 x *g*) for 1 minute.

5. Add 1,200 µl of **Plant/Seed DNA Binding Buffer** to the filtrate in the **Collection Tube** from Step 4 and mix.

6. Transfer 800 µl of the mixture from Step 5 to a **Zymo-Spin™ IIC Column** in a **Collection Tube** and centrifuge at 10,000 x *g* for 1 minute.

7. Discard the flow through from the **Collection Tube** and repeat Step 6.

8. Add 200 µl **DNA Pre-Wash Buffer** to the **Zymo-Spin™ IIC Column** in a new **Collection Tube** and centrifuge at 10,000 x *g* for 1 minute.

9. Add 500 µl **Plant/Seed DNA Wash Buffer** to the **Zymo-Spin™ IIC Column** and centrifuge at 10,000 x *g* for 1 minute.

10. Transfer the **Zymo-Spin™ IIC Column** to a clean 1.5 ml microcentrifuge tube and add 50-100 µl (25 µl minimum) **DNA Elution Buffer** directly to the column matrix. Centrifuge at 10,000 x *g* for 30 seconds to elute the DNA.

11. Transfer the eluted DNA from Step 10 to a prepared **Zymo-Spin™ IV-HRC Spin Filter** (green top) (see above) in a clean 1.5 ml microcentrifuge tube and centrifuge at exactly 8,000 x *g* for 1 minute.

Appendix 5: Table means

TFA	Yield/ton	NT	PH	PM	NF	FB	FL	ES	SM
105	4.725331	7.145957	113.0848	129.7732	8.548323	0.449704	92.36292	2.402367	3.436312
18	4.405593	8.453649	97.00789	121.568	8.907298	-0.08876	91.33728	2.017751	3.74144
44	4.254917	7.889546	92.7002	126.3116	8.061144	-0.08876	91.33728	1.786982	3.228876
67	4.131969	7.069034	96.85404	120.927	7.086785	1.013807	80.05523	1.761341	2.860927
101	4.10827	8.658777	99.62327	125.1578	9.4714	0.295858	94.4142	2.120316	3.336824
125	4.042875	7.99211	83.44379	110.0296	7.291913	1.013807	50.82446	3.838264	3.111183
103	3.964433	7.325444	90.62327	131.8245	9.138067	-0.03748	97.74753	2.120316	2.853491
130	3.957838	8.658777	100.1105	106.6963	6.95858	0.680473	78.82446	2.838264	3.351183
58	3.94311	7.684418	86.13609	116.0552	7.932939	0.065089	106.2091	1.915187	3.030671
159	3.892462	7.299803	89.57199	118.7475	8.21499	-0.06312	95.18343	2.120316	3.070927
88	3.858799	7.581854	108.7771	132.8501	8.932939	1.09073	100.568	2.658777	3.126055
171	3.855765	7.966469	87.90533	115.4142	8.881657	0.936884	71.8501	3.120316	3.40426
139	3.835437	9.017751	93.54635	139.9014	8.112426	-0.08876	86.9783	2.069034	3.245542
90	3.834295	7.915187	97.44379	116.1834	8.932939	0.424063	90.56805	1.99211	3.066055
65	3.82868	8.351085	101.1361	126.0552	7.266272	0.065089	69.54241	2.248521	3.350671
118	3.821142	7.325444	82.44379	140.0296	7.95858	0.680473	82.15779	2.171598	3.024517
111	3.806102	7.145957	86.08481	113.1065	9.881657	1.116371	72.36292	1.7357	3.416312
100	3.757915	7.658777	97.62327	128.4911	9.138067	0.295858	84.4142	2.120316	3.156824
82	3.681777	7.581854	92.44379	116.1834	8.599606	0.09073	93.90138	2.325444	3.179389
86	3.544784	8.248521	90.11045	126.1834	7.932939	0.09073	97.23471	1.658777	3.366055
75	3.519703	6.7357	86.85404	120.927	8.753452	0.34714	90.05523	2.428008	3.047594
93	3.515841	7.658777	102.2899	135.1578	9.4714	0.295858	87.74753	3.120316	3.110158
89	3.509762	7.581854	87.44379	109.5168	7.266272	0.09073	83.90138	1.99211	3.079389
102	3.334759	7.658777	112.2899	125.1578	7.4714	0.295858	84.4142	2.120316	3.290158
77	3.317658	6.7357	110.1874	134.2604	10.42012	0.680473	96.72189	2.094675	3.207594
169	3.268713	8.299803	102.9053	98.74753	8.21499	0.270217	75.18343	1.120316	3.450927
126	3.170712	8.325444	88.44379	120.0296	6.291913	0.013807	55.49112	2.504931	3.331183
74	3.12868	7.402367	100.1874	127.5937	6.086785	0.013807	103.3886	1.761341	3.19426
95	3.084878	6.325444	92.95661	125.1578	9.138067	-0.03748	97.74753	2.120316	2.976824
94	3.072166	6.99211	85.95661	121.8245	13.80473	0.962525	91.08087	2.453649	2.996824
91	3.061925	7.248521	94.11045	106.1834	8.266272	1.09073	63.90138	2.658777	2.939389
63	3.011806	7.017751	114.4694	132.7219	9.599606	0.731755	76.20907	2.915187	2.950671
69	3.001199	7.069034	102.5207	124.2604	9.420118	0.013807	80.05523	1.761341	3.460927
132	2.985215	7.017751	94.54635	119.9014	6.112426	0.911243	80.31164	2.069034	2.312209
96	2.948878	8.658777	84.95661	131.8245	9.138067	-0.03748	87.74753	2.453649	3.250158
147	2.938938	7.658777	90.21302	109.2604	6.984221	1.013807	72.61933	4.069034	3.032209
23	2.925134	6.120316	90.67456	138.2347	9.907298	0.244576	71.33728	2.017751	3.334773
61	2.911436	7.017751	86.13609	119.3886	6.599606	1.065089	66.20907	2.915187	3.030671
51	2.898725	5.889546	127.3669	132.9783	8.727811	0.244576	84.67061	2.453649	2.922209
124	2.89686	7.325444	96.11045	100.0296	7.291913	1.013807	78.82446	2.504931	3.031183
143	2.868119	8.351085	106.213	116.568	8.445759	0.911243	56.9783	3.069034	3.178876
154	2.852153	6.99211	86.87968	99.26036	6.984221	1.013807	85.95266	1.069034	2.792209
71	2.85154	5.402367	101.5207	127.5937	7.420118	0.680473	100.0552	1.094675	2.71426
11	2.813369	6.530572	115.8028	131.4398	8.932939	1.142012	87.49112	2.658777	3.168876

165	2.801988	6.299803	87.90533	98.74753	7.21499	0.936884	78.51677	1.120316	2.937594
83	2.758058	6.915187	99.11045	119.5168	9.932939	0.09073	90.56805	1.99211	3.139389
47	2.751525	8.556213	95.03353	96.31164	5.727811	-0.08876	64.67061	1.786982	2.968876
97	2.732418	7.658777	95.62327	115.1578	8.4714	0.962525	74.4142	3.120316	3.176824
25	2.722541	6.453649	91.67456	138.2347	9.240631	-0.08876	81.33728	2.017751	3.448107
145	2.716494	6.658777	85.21302	109.2604	6.317554	0.680473	82.61933	2.069034	3.025542
78	2.695999	6.7357	110.1874	110.927	7.420118	1.013807	73.38856	2.428008	2.920927
153	2.687738	8.325444	86.87968	122.5937	5.317554	0.013807	72.61933	4.069034	3.445542
66	2.678206	5.7357	91.85404	117.5937	8.420118	0.34714	93.38856	1.094675	2.847594
121	2.676179	8.325444	110.1105	113.3629	6.625247	1.013807	58.82446	3.171598	3.051183
57	2.670606	5.684418	90.13609	132.7219	8.266272	0.065089	86.20907	1.581854	2.684004
112	2.670205	8.812623	102.7515	109.7732	6.21499	1.116371	82.36292	3.069034	3.449645
73	2.648755	6.7357	83.52071	110.927	7.753452	1.013807	66.72189	2.761341	3.347594
115	2.632472	7.47929	122.7515	113.1065	7.881657	0.783037	79.02959	2.7357	3.169645
133	2.598845	6.684418	87.87968	113.2347	7.445759	0.577909	56.9783	3.7357	3.265542
41	2.596829	5.889546	91.7002	112.9783	7.394477	0.244576	81.33728	1.786982	2.875542
114	2.587109	7.47929	99.41815	109.7732	6.881657	1.116371	62.36292	3.7357	3.336312
76	2.583347	6.7357	91.85404	110.927	7.086785	0.680473	60.05523	3.094675	3.11426
64	2.571629	6.684418	87.80276	102.7219	6.599606	1.065089	89.54241	1.581854	2.777337
60	2.559806	7.684418	119.4694	112.7219	7.266272	1.065089	52.87574	3.248521	3.044004
45	2.511658	6.556213	88.36686	99.64497	6.394477	0.244576	64.67061	0.786982	2.748876
122	2.463142	7.325444	91.77712	120.0296	7.625247	0.680473	82.15779	2.171598	2.944517
80	2.460132	4.915187	110.7771	116.1834	10.59961	1.09073	83.90138	2.99211	2.539389
109	2.453035	7.47929	94.08481	113.1065	5.21499	1.116371	72.36292	2.7357	3.429645
98	2.443529	7.325444	111.6233	138.4911	8.804734	0.629191	61.08087	2.786982	2.930158
107	2.341168	5.47929	99.41815	123.1065	8.548323	0.449704	89.02959	2.069034	2.942978
110	2.335346	7.812623	106.7515	119.7732	8.21499	0.783037	75.69625	2.069034	3.409645
158	2.320642	5.658777	80.21302	112.5937	7.650888	1.013807	75.95266	3.7357	2.572209
62	2.288443	5.017751	87.80276	119.3886	7.266272	0.065089	99.54241	1.915187	2.290671
137	2.247733	6.351085	96.21302	123.2347	8.779093	0.244576	66.9783	2.7357	2.352209
163	2.240165	6.966469	79.57199	105.4142	6.548323	0.60355	81.8501	2.120316	2.790927
68	2.227125	6.402367	85.18738	107.5937	6.420118	0.680473	66.72189	2.428008	3.09426
72	2.201495	7.069034	88.52071	120.927	6.753452	0.680473	53.38856	2.761341	3.03426
119	2.147646	6.99211	115.1105	120.0296	7.625247	0.013807	65.49112	3.171598	3.104517
155	2.134138	6.658777	91.87968	105.927	6.317554	0.013807	99.286	2.069034	3.005542
17	2.121875	5.453649	95.00789	114.9014	7.240631	0.244576	68.00394	2.351085	3.568107
177	2.11421	5.966469	109.572	108.7475	8.21499	0.936884	65.18343	3.120316	2.550927
81	2.10428	7.915187	87.44379	99.51677	5.266272	0.09073	77.23471	0.99211	3.499389
149	2.094864	6.658777	99.54635	139.2604	7.650888	0.34714	79.286	2.402367	2.818876
99	2.054641	6.325444	90.95661	121.8245	9.4714	0.629191	57.74753	2.786982	2.510158
120	2.050505	6.99211	100.1105	113.3629	7.625247	0.680473	65.49112	2.838264	2.61785
19	2.038453	5.786982	85.00789	124.9014	6.907298	0.244576	61.33728	2.351085	2.934773
162	2.032965	7.966469	91.23866	108.7475	6.881657	0.60355	75.18343	1.453649	3.32426
134	1.983704	5.351085	87.87968	89.90138	7.112426	0.577909	86.9783	1.402367	2.238876
146	1.974242	7.325444	81.87968	119.2604	6.650888	1.013807	75.95266	2.7357	3.092209
27	1.973062	4.684418	92.57199	97.9783	5.856016	0.577909	72.61933	2.248521	2.783491

54	1.97194	3.684418	92.80276	112.7219	8.932939	1.065089	82.87574	2.581854	2.090671
140	1.937778	7.684418	101.213	111.568	7.779093	-0.08876	60.31164	3.069034	2.545542
108	1.935257	6.145957	101.0848	113.1065	7.881657	1.116371	65.69625	3.7357	2.909645
131	1.930979	6.99211	90.11045	126.6963	5.95858	0.013807	65.49112	2.171598	2.664517
37	1.91441	4.684418	86.90533	127.9783	7.189349	0.244576	75.95266	2.581854	2.483491
170	1.894343	5.633136	74.90533	100.4142	7.21499	-0.06312	66.8501	1.120316	2.870927
92	1.8679	5.99211	84.62327	121.8245	8.138067	0.295858	87.74753	2.786982	2.043491
28	1.854484	5.351085	107.572	104.645	7.522682	0.244576	75.95266	2.581854	2.490158
13	1.847517	4.863905	95.80276	111.4398	5.932939	0.808679	84.15779	0.99211	2.555542
50	1.838577	3.889546	96.7002	102.9783	11.06114	0.911243	68.00394	2.786982	2.142209
15	1.811875	5.120316	85.00789	114.9014	7.240631	0.577909	61.33728	3.684418	3.114773
127	1.768979	6.658777	100.1105	113.3629	7.625247	1.013807	48.82446	2.838264	2.864517
12	1.765517	5.530572	90.80276	121.4398	6.266272	1.142012	77.49112	2.658777	2.768876
172	1.761425	5.633136	92.90533	132.0809	8.21499	0.270217	91.8501	2.786982	2.617594
168	1.726639	6.299803	98.90533	105.4142	8.881657	-0.06312	71.8501	1.120316	2.817594
70	1.726177	6.7357	105.1874	105.927	6.420118	1.013807	83.38856	1.761341	3.020927
5	1.681695	5.530572	108.4694	128.1065	7.599606	0.142012	90.82446	2.325444	2.928876
141	1.681215	7.017751	69.54635	99.90138	6.112426	0.911243	60.31164	3.069034	2.245542
123	1.667542	6.325444	101.7771	106.6963	6.625247	1.013807	65.49112	1.838264	2.691183
48	1.666458	5.556213	102.7002	111.3116	6.727811	-0.08876	58.00394	1.453649	2.635542
22	1.651534	4.453649	90.67456	104.9014	6.240631	0.911243	58.00394	2.684418	2.56144
142	1.648978	7.351085	96.21302	99.90138	6.112426	0.911243	60.31164	1.7357	2.352209
87	1.62948	6.248521	99.11045	119.5168	7.932939	0.09073	100.568	1.99211	2.446055
59	1.609792	6.017751	107.8028	111.0552	8.266272	0.065089	59.54241	2.915187	2.890671
43	1.566992	5.22288	101.7002	112.9783	6.394477	0.577909	58.00394	2.786982	2.672209
53	1.552784	4.684418	91.13609	109.3886	9.266272	1.065089	62.87574	2.581854	2.224004
106	1.549094	4.47929	93.75148	126.4398	8.548323	0.449704	69.02959	2.7357	2.716312
136	1.515645	5.017751	99.87968	116.568	6.445759	0.911243	70.31164	2.402367	2.332209
167	1.492121	5.966469	93.90533	108.7475	6.21499	0.60355	65.18343	3.120316	2.567594
144	1.438637	7.017751	69.54635	99.90138	6.112426	0.911243	60.31164	3.069034	2.345542
104	1.421381	6.325444	92.28994	138.4911	7.804734	0.629191	91.08087	2.120316	2.723491
34	1.414544	4.684418	85.90533	94.64497	6.522682	0.244576	79.286	1.915187	2.683491
148	1.395086	4.99211	94.87968	125.927	10.98422	1.013807	75.95266	2.7357	2.245542
56	1.388473	6.017751	99.46943	89.38856	7.599606	0.731755	49.54241	0.915187	2.650671
79	1.338251	4.915187	97.44379	109.5168	9.266272	0.757396	73.90138	0.99211	2.372722
26	1.330408	4.453649	93.34122	94.90138	7.907298	0.577909	54.67061	3.017751	2.20144
52	1.330147	4.889546	95.03353	116.3116	5.394477	0.244576	64.67061	3.120316	2.775542
85	1.318829	6.248521	92.11045	119.5168	6.599606	1.09073	60.56805	2.99211	2.812722
135	1.317615	6.017751	94.54635	109.9014	6.112426	0.244576	73.64497	2.7357	2.352209
20	1.307327	4.453649	98.34122	98.23471	6.240631	-0.08876	91.33728	2.017751	2.794773
31	1.269329	3.351085	92.57199	94.64497	6.189349	0.577909	75.95266	2.248521	2.703491
8	1.22528	4.197239	90.80276	111.4398	6.599606	1.142012	60.82446	2.99211	2.535542
33	1.191758	4.351085	87.57199	87.9783	5.189349	-0.08876	92.61933	1.915187	2.903491
152	1.187219	5.99211	88.54635	92.59369	5.317554	0.013807	72.61933	2.069034	2.665542
84	1.143303	3.248521	91.11045	139.5168	7.932939	0.09073	110.568	1.99211	1.839389
21	1.140601	5.120316	76.67456	98.23471	6.573964	0.577909	54.67061	1.017751	2.594773

138	1.137556	6.684418	86.21302	89.90138	4.779093	0.244576	56.9783	3.069034	2.518876
129	1.12612	6.325444	107.7771	120.0296	7.95858	0.34714	85.49112	2.171598	2.31785
9	1.090198	3.863905	92.46943	121.4398	7.599606	1.142012	64.15779	2.99211	2.282209
175	1.066847	5.299803	95.57199	118.7475	6.21499	0.936884	55.18343	3.120316	2.94426
4	1.063976	5.197239	87.46943	126.4398	7.599606	0.142012	80.82446	2.99211	2.688876
6	1.046939	3.530572	99.13609	131.4398	6.599606	0.808679	77.49112	2.325444	2.395542
16	1.043001	5.453649	66.67456	78.23471	6.573964	-0.08876	58.00394	1.351085	2.634773
55	1.041169	4.017751	76.13609	86.05523	5.599606	0.065089	66.20907	0.915187	2.350671
113	0.987805	2.812623	82.75148	139.7732	8.21499	1.116371	72.36292	3.069034	1.769645
150	0.897753	5.325444	91.87968	102.5937	5.650888	0.680473	59.286	1.7357	2.598876
166	0.885232	6.966469	99.57199	85.4142	5.548323	0.270217	68.51677	1.786982	2.897594
40	0.859806	5.22288	111.7002	99.64497	6.394477	-0.08876	68.00394	1.453649	2.448876
42	0.849303	5.556213	90.03353	92.9783	4.727811	-0.08876	51.33728	1.453649	2.582209
49	0.829436	4.22288	110.0335	99.64497	7.727811	-0.08876	71.33728	1.786982	2.075542
151	0.808953	2.99211	73.54635	139.2604	6.650888	0.013807	62.61933	3.069034	1.865542
116	0.714783	5.812623	92.75148	99.77318	6.21499	0.449704	52.36292	1.069034	2.722978
14	0.70066	5.120316	105.0079	91.56805	5.240631	0.577909	61.33728	1.684418	2.78144
36	0.623477	4.351085	90.90533	94.64497	6.856016	0.244576	49.286	1.581854	2.396824
156	0.62199	5.325444	91.87968	92.59369	5.984221	0.34714	52.61933	2.402367	2.705542
24	0.58823	4.120316	103.3412	91.56805	7.240631	0.577909	54.67061	1.017751	2.394773
117	0.568413	6.47929	87.75148	79.77318	5.21499	0.116371	82.36292	2.069034	2.876312
1	0.566421	4.530572	75.80276	98.10651	5.932939	0.808679	60.82446	3.325444	2.302209
46	0.550103	3.22288	103.3669	86.31164	6.727811	0.244576	51.33728	0.786982	2.068876
38	0.510336	4.351085	94.23866	87.9783	5.189349	0.244576	52.61933	2.248521	2.396824
35	0.503758	4.684418	94.23866	87.9783	4.856016	-0.08876	59.286	1.248521	2.530158
3	0.465102	4.530572	100.8028	104.7732	5.599606	0.475345	57.49112	0.99211	2.152209
32	0.454988	2.351085	99.90533	107.9783	6.189349	0.911243	75.95266	2.248521	1.963491
10	0.382776	3.530572	119.1361	108.1065	5.932939	1.142012	67.49112	1.658777	2.402209
29	0.282114	3.351085	100.9053	91.31164	5.856016	0.577909	49.286	1.248521	2.123491
39	0.231788	4.017751	95.90533	74.64497	5.189349	-0.08876	59.286	1.915187	2.336824
30	0.193625	3.351085	99.23866	77.9783	5.856016	0.577909	79.286	1.248521	2.070158
7	0.030468	3.863905	99.13609	84.77318	4.266272	0.142012	80.82446	1.658777	2.322209
2	0.057091	3.863905	90.80276	101.4398	5.599606	0.142012	82.49112	1.658777	2.242209

NT = Number of tillers, Yield = Grain yield, PH = Plant height, PM= Plant maturity, F=Number of fingers, FB = Finger branching, FL=Finger length, PS = Ear shape and 1000gwt = Thousand grain weights.

Appendix 1: The 169 finger millet genotypes into 13 clusters based cluster analysis

Appendix 6: Summary spastics

Appendix 7: The 169 finger millet genotypes into 13 clusters based cluster analysis results

Cluster	1	2	3	4	5	6	7	8	9	10	11	12	13
	TFA1	TFA2	TFA4	TFA6	TFA9	TFA15	TFA16	TFA58	TFA64	TFA88	TFA102	TFA151	TFA167
	TFA8	TFA3	TFA12	TFA27		TFA31	TFA145	TFA147	TFA124	TFA130			
	TFA24	TFA5	TFA13	TFA37		TFA32		TFA148	TFA156	TFA133			
	TFA26	TFA7	TFA17	TFA38		TFA39		TFA150	TFA159	TFA157			
	TFA33	TFA10	TFA18	TFA59		TFA41		TFA153	TFA160				
	TFA36	TFA11	TFA22	TFA69		TFA47		TFA161	TFA164				
	TFA40	TFA14	TFA34	TFA77		TFA51		TFA166	TFA165				
	TFA44	TFA19	TFA35	TFA83		TFA54							
	TFA48	TFA20	TFA49	TFA84		TFA61							
	TFA56	TFA21	TFA52	TFA86		TFA62							
	TFA65	TFA23	TFA55	TFA94		TFA74							
	TFA67	TFA25	TFA57	TFA101		TFA78							
	TFA68	TFA28	TFA66	TFA117		TFA80							
	TFA71	TFA29	TFA72	TFA128		TFA81							
	TFA87	TFA30	TFA76	TFA139		TFA85							
	TFA90	TFA42	TFA89	TFA140		TFA92							
	TFA98	TFA43	TFA95			TFA93							
	TFA100	TFA45	TFA96			TFA109							
	TFA105	TFA46	TFA103			TFA110							
	TFA106	TFA50	TFA104			TFA111							
	TFA107	TFA53	TFA108			TFA112							
	TFA125	TFA60	TFA120			TFA114							
	TFA129	TFA63	TFA121			TFA115							
	TFA131	TFA70	TFA123			TFA116							
	TFA134	TFA73	TFA141			TFA118							
	TFA138	TFA75	TFA142			TFA119							
	TFA163	TFA79	TFA158			TFA126							
		TFA82				TFA127							
		TFA91				TFA132							
		TFA97				TFA136							
		TFA99				TFA137							
		TFA113				TFA146							
		TFA122				TFA149							
		TFA135				TFA152							
		TFA143				TFA154							
		TFA144				TFA155							
						TFA162							

Appendix 8: Shoot and root biomass characteristics mean separation in finger millet genotypes

Genotype	T B (g)	R D (g/ml³)	R L (cm)	PH (cm)	N T	LAI	Y/P (g)	HI
TFA11	230.6a-f	0.31a-e	87.33a-f	108.33e-f	8.00ab	2.26e-j	44.64a-g	19.56a-f
TFA 18	331.6g-j	0.46a-h	95.33a-f	90.33a-e	16.00d-g	1.17a-c	37.56a-g	11.51a
TFA 44	442.3k	0.59e-h	102.33a-f	102.33c-g	17.33g	2.29e-k	43.03a-g	9.74a
TFA 58	275.6d-h	0.59e-h	73.00a-e	87.33a-c	15.00c-g	2.10c-j	24.87a	8.90a
TFA 65	288.1e-h	0.34a-f	74.00a-e	108.67e-g	12.67b-g	3.063jk	41.48a-g	14.45a-c
TFA 67	268.7c-h	0.40a-h	86.33a-f	111.67fg	10.67a-f	1.43a-f	39.92a-g	14.74a-c
TFA 74	168.1a	0.49b-h	59.33ab	92.00b-e	9.67a-d	1.23a-d	47.25a-g	28.31d-g
TFA 75	295.9f-i	0.48b-h	93.33a-f	99.00c-g	13.67b-g	2.01c-i	37.29a-g	12.57a-c
TFA 77	345.6h-j	0.53c-h	106.33b-f	96.00c-f	11.00b-g	2.06c-j	58.97fg	17.03a-c
TFA 82	265.2c-g	0.38a-g	66.67a-d	107.67d-g	15.00c-g	2.47g-k	31.07a-e	11.85ab
TFA 86	296.5f-i	0.35a-f	89.33a-f	104.67c-g	16.67fg	3.30kl	53.19b-g	17.92a-e
TFA 88	298.6f-i	0.25a-c	91.00a-f	93.67c-f	13.00b-g	2.02c-i	38.13a-g	12.76a-c
TFA 89	241.6a-f	0.70h	81.33a-e	86.33a-c	10.00a-e	1.52a-g	41.83a-g	17.21a-d
TFA 90	367.4i-k	0.55d-h	95.00a-f	91.67a-e	10.00a-e	1.09ab	53.76c-g	14.74a-c
TFA 91	269.9c-h	0.52b-h	77.33a-e	72.33a	10.33a-f	0.92a	35.94a-g	13.42a-c
TFA 93	277.5d-h	0.39a-g	84.00a-f	88.67a-d	15.00c-g	2.14c-j	28.28a-c	10.17a
TFA 94	194.6a-c	0.22ab	66.00a-d	73.33ab	14.00b-g	2.44f-k	29.82a-d	15.18a-c
TFA 95	234.3a-f	0.66gh	109.33d-f	102.67c-g	12.00b-g	1.51a-g	33.53a-f	14.37a-c
TFA 100	301.6f-j	0.49b-h	90.67a-f	118.33g	14.67c-g	2.68h-k	33.48a-f	11.08a
TFA 101	287.2e-h	0.47b-h	81.00a-e	102.00c-g	10.33a-f	1.40a-e	44.14a-g	15.48a-c
TFA 102	193.2a-c	0.40a-h	66.00a-d	105.67c-g	7.33a	0.98a	25.54ab	13.20a-c
TFA 103	216.0a-e	0.23a-c	55.33a	102.00c-g	10.00a-e	2.181d-j	62.71g	29.15fg
TFA 105	377.3jk	0.56d-h	96.00a-f	93.67c-f	16.33e-g	2.80i-k	56.94d-g	14.98a-c
TFA 111	178.6ab	0.44a-h	89.33a-f	74.00ab	14.00b-g	2.10c-j	57.2d-g	32.15g
TFA 118	378.6jk	0.63f-h	109.00c-f	104.67c-g	17.33g	4.13l	38.79a-g	10.26a
TFA 125	205.5a-d	0.27a-d	62.00a-c	74.00ab	13.33b-g	2.47g-k	59.62fg	28.95e-g
TFA 130	166.5a	0.31a-e	57.33a	99.00c-g	9.00a-c	1.73b-h	49.06a-g	29.52fg
TFA 139	257.7c-g	0.36a-f	117.67ef	104.00c-g	15.00c-g	1.64a-g	38.48a-g	15.20a-c
TFA 169	253.5b-f	0.17a	129.33f	101.00c-g	13.00b-g	2.16c-j	57.86e-g	22.84b-g
TFA 171	165.7a	0.25a-c	62.67a-d	88.33a-d	12.00b-g	1.82b-i	37.84a-g	23.31c-g
LSD(P<0.001)	**39.22****	**0.15****	23.92**	**9.983****	**3.325****	**0.5136****	**14.084****	**5.684****
CV%	**8.9**	**21.6**	17.2	**6.3**	**16**	**15.4**	**20.2**	**20.5**

TFA= Tanzania finger millet accession, GM= grand mean, SE= Standard error, LSD Least significant difference, F.pro= F probability, CV%= coefficient of variation.