

**MORPHOLOGICAL DIVERSITY OF MAIZE LANDRACES
OF NORTHERN TANZANIA**

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**A DISSERTATION SUBMITTED IN PARTIAL FULFILLMENT OF
REQUIREMENTS FOR THE DEGREE OF MASTERS OF SCIENCE IN CROP
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ABSTRACT

An experiment was conducted in the Northern Zone of Tanzania during the growing season 2014/2015. The aim of the study was to characterize the maize landraces collected at farm level and establish the diversity that exists in Northern Tanzania for landraces maize growers. The experiment with fifteen maize landraces was laid out in randomized complete block design (RCBD) with three replications. Data were collected on vegetative and reproductive variables. Data were subjected to Analysis of Variance (ANOVA) and Diversity Index by Shannon-Weaver for morphological traits using GenStat software and XLSTAT 2015 software. Pattern analysis for the relationship among landraces was achieved through cluster analysis; Dendrograms were developed using a hierarchical agglomerical clustering method. Associations among maize landraces were identified by principal component analysis and path coefficient for association among yield and yield components. Six principle components accounted for 84.23% of the total variation. Three clusters were generated where by cluster one comprised landraces DK-MB1, DM-KR1, MA-BB4, DA-MB4, AJ -MB3, JL-KR5, LE-MB2. Cluster two included landraces DQ-BB5, PD-KR2, JM-AR1, AD-KR3, AJ-BB2 and the third cluster comprised MP-BB1, TD-KR4, BN-BB3 landraces. High diversity index by Shannon-Weaver Index was obtained with pooling index of (0.99). High heritability for studied traits ranged from 67.09% (Number of primary branches) to 98.85 %(days to 50% silking). Genotypically 100 seed weight (0.87) and number of kernels per row (0.80) were significant and positive correlated with grain yield. Phenotypic plant height was significant positive correlated with ear height (0.93). Path coefficient analysis showed that 100 seed weight correlated significant positively with grain yield (0.87) indirect

effect via plant height (0.87), number of kernels per row correlated significant positively with grain yield (0.80) and indirect effect via plant height(0.82).

DECLARATION

I, Shida Mahenge Nestory do hereby declare to the Senate of Sokoine University of Agriculture that this dissertation is my own original work done within the period of registration and that it has neither being submitted nor being concurrently submitted in any other institution.

Shida Mahenge Nestory

(MSc. Candidate)

Date

The above declaration is confirmed

Prof. Reuben S.O.W.M

(Supervisor)

Date

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DEDICATION

This Dissertation is dedicated to my Father, Nestory Mahenge and my Mother, Paustina Pole who shaped my career with love and sacrificed much for value of my life. Almighty God brings joy for the rest of their life, Amen!

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LIST OF ABBREVIATION AND SYMBOLS

ANOVA	Analysis of Variance
DAP	Diammonium Phosphate
FAO	Food and Agricultural Organization of United Nations
GDP	Gross Domestic Product
KARI	Kenya Agricultural Research Institute
MAFC	Ministry of Agriculture, Food security and Cooperatives
QPM	Quality protein maize
RCBD	Randomized Complete Block Design
USD	United States Dollar

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background Information

Maize belongs to the family poaceae, the family has world-wide distribution and is economically the most important of all plant families. Members of this family are the three most important crops for human food: wheat, rice and maize (Jelena, 2009). Maize (*Zea mays L.*) is a staple food for millions of people in several African countries, Asia and South America (FAO, 2003). Important cereal crop in the world is maize and ranked the third after wheat and rice. It has high productivity potential compared to other Graminacea family members and referred to as a miracle crop (Subramanian and Subbaraman, 2010). Maize provides 60% of the dietary calories to the Tanzanian population (Nkonya *et al.*, 1998). One of the most important issues in maize evolution is how to explain the extraordinary morphological and genetic diversity that exist among the maize landraces (Matsuoka *et al.*, 2002). Major maize production areas are located in the United States, China, Brazil and Mexico and account for 70% of global production. Tanzania's economy is heavily dependent on agriculture, which accounts for about one third of the Gross Domestic Product (GDP). Agriculture provides 85% of exports and employs about 80% of the population. Maize is the major and most preferred staple food and cash crop in Tanzania. Popularity of maize is evidenced by the fact that it is grown in all the agro-ecological zones in the country (Rates, 2003). Maize market performance therefore has a significant impact on the welfare and food security especially of poor people. It is the most important staple food in Tanzania and in the East Africa region in general

and it is predicted that market demand for food staples will grow steadily to USD 11.2 billion in 2015 and USD 16.7 billion in 2030 (Match Maker Associates, 2010).

1.2 Problem Statement and Justification

The prolonged and significant loss of genetic variability in most crops seen in recent years has stimulated a growing interest in the preservation of biodiversity especially of endangered species (Myers *et al.*, 2000). In many countries, commercial maize hybrids have become widely accepted in agriculture and their expansion suppressed the cultivation of landraces (Shrestha, 2013). Morphological characterization was the first method used by researchers to select superior genotypes (Cadee, 2000).

A comparative morphological study of maize shows an important role in the management of crop diversity. Farmers working in traditional and subsistence agricultural communities use morphological traits to guide their use of germplasm in selecting superior traits (Perales *et al.*, 2005; Van Etten, 2006).

Erosion of plant genetic resources occurs in the country at intra-specific level of cultivated crops as loss of landraces or traditional cultivars and at the species level. The causes include use of modern varieties and land degradation. In degraded lands, farmers tend to concentrate on production of stress adapted species like cassava, sorghum and millets. Lifestyles have changed varieties to be cropped, due to different preferences in consumption habits and consequently market demand and crop utilization. Use of genetically uniform modern cultivars contributes to replacing and marginalizing the highly diverse local cultivars and landraces in traditional agro-

ecosystems though no research has been done to quantify the loss. Other threats include over-exploitation of land and other natural resources. Landraces within species seem to be threatened and they include maize, finger and pearl millets, yams, and local vegetable species (Tanzania Ministry of Agriculture Food Security and Cooperatives, 2009). Maize landraces are considered to be a valuable resource and because of their high genetic diversity, are most connected to the traditional agricultural practices. Preservation of the landraces and traditional agricultural practices is interconnected (Jelena, 2009). There is high expanding trend in developing countries to adopt improved maize varieties, primarily to meet market demand. The narrowing of genetic diversity in modern varieties emphasizes the importance of conserving genetic traits for future plant breeding work.

1.3 Objectives

1.3.1 Overall objective

To establish the available diversity of maize landraces to be used as gene donors in breeding programmes

1.3.2 Specific objectives

- (i) To evaluate the diversity that exists in maize landraces
- (ii) To determine heritability (broad sense) of maize traits

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Taxonomy

Maize is a monoecious species, which has separate staminate and pistillate flowers on the same plant. The male inflorescence (tassel) arises from the shoot apical meristem, while the female inflorescences (ears) originate from the axillary bud apices (Doriana *et al*, 2012). The number of chromosomes in *Zea mays* is $2n=2x = 20$. Maize or corn is a plant belonging to the family of grasses (*Poaceae*). Tribe Maydeae comprises genera which are recognized and included in Old and New World groups. Old World comprises Coix ($2n = 10/20$), Chionachne ($2n = 20$), Sclerachne ($2n = 20$), Trilobachne ($2n = 20$) and Polytoca ($2n = 20$), and New World group has *Zea* and *Tripsacum*. It is generally agreed that maize phylogeny was largely determined by the American genera *Zea* and *Tripsacum*, however it is accepted that the genus *Coix* contributed to the phylogenetic development of the species *Zea mays* (Tripath, 2011).

2.2 Geographic Origin and Distribution

Maize began to be domestically cultivated 6000 years ago, in regions of the Southwestern United States, Mexico, and Central America (Mangelsdorf, 1974). Maize landraces in South-Eastern Europe have different origins but suggested a common origin for all maize landraces present in Europe. The same authors have claimed that maize had been first introduced into the Balkans by the Turks during expansion of their empire. This presumption has been supported by the similarity of the names used for the maize by all nations in the region (Leng and Edwards, 1965).

2.3 Genomic Evolution

In the 1970s and 1980s a series of reports supporting the teosinte hypothesis were released. Teosinte is the ancestor of maize. The teosinte hypothesis was broadly accepted among biologists and evolutionists who were familiar with issues, data, and analytical methods.

2.4 Importance of Maize.

Maize is characteristically deficient in essential amino acids *vis-à-vis* lysine and tryptophan. To overcome this deficiency, quality protein maize (QPM) with sufficiently higher quantity of lysine and tryptophan has been developed (Tripath, 2011).

In Tanzania maize plays a crucial role in improving food security and livelihood of poor community as cash and food crop by selling the surplus (Makoye 2008). Although wide-spread occurrences of abiotic and biotic constraints keep pace with increasing population, need on crop evaluation and characterization will help to prevent these challenges and increase grain yield.

Table 1: Composition per 100g of edible portion of maize (dry)

Protein	11.1g	Carbohydrate	66.2g
Fat	3.6g	Calcium	10mg
Fibre	2.7g	Iron	2.3mg
Calories	342	Potassium	286mg
Phosphorus	348mg	Thiamine	0.42mg
Sodium	15.9mg	Carotene	90ug
Sulphur	114mg	Vitamin C	0.12mg
Riboflavin	0.10mg	Magnesium	139mg
Amino acid	1.78mg	Copper	0.14mg

Source: (Tripath , 2011)

2.5 Maize Production in Tanzania

Open pollinated seeds are produced in different environments with limited resources by small holders (Bigirwa *et al.*, 2003). Tanzania is composed of small holders who produce about 85% of the total production (Mbwaga, 1988).not refered

The major areas are lake zones, west zone, northern zone, southern zone, central, southern highlands and eastern zone. The southern zone occupies only 28% of the mainland, produces more than 50% of the total national maize production (Mdadila, 1995).

2.6 Diversity of Maize

Eighteen maize landraces of the Albanian Gene Bank collection were characterized by agro morphological descriptors. Results indicated significant morphological diversity in this study (Doriana *et al.*, 2012).

An experiment was conducted to analyze the genetic diversity among 38 maize accessions of the germplasm bank of Department of Millets, Coimbatore. Results

showed existence of maximum dissimilarity between the accessions which could be further evaluated for their breeding values as parents that have important value in maize crop improvement (Subramanian and Subbaraman, 2010).

Experiments on sixty inbred lines done at Rampur, Chitwan, Nepal in 2010/ 2011, indicated a wide range of variability among these inbred lines (Shrestha, 2013). Study of maize accessions done in 2013 in Sinola, Mexico, by microsatellite markers showed high number of alleles per locus and high genetic diversity found represents a gene reservoir useful in breeding programs (Karen *et al.*, 2013).

A study was done to determine differences in traits associated with resistance to the maize weevil in the field and in storage at the Kenya Agricultural Research Institute (KARI), Kiboko and Embu stations in seasons of 2010 and 2011. Resistant germplasm showed relatively long husk cover and shorter husk cover leading to poor covering of the maize cob among the susceptible landraces. The husk cover characteristics have been associated with controlling the level of field infestation of the maize cobs by post harvest pests such as the maize weevil and larger grain borer (Mwololo *et al.*, 2013).

Screening of Italian and foreign maize germplasm in 2009, identified genotypes to be used in breeding programmes, high contents of protein, lipid and carotenoid which have recently been introduced into high yielding maize varieties (Berardo *et al.*, 2009). Thirty quality protein maize lines were studied on agro-nutritional characters in 1999, 2000 and 2001 seasons at the Ahmadu Bellon University in Samaru, Zaria. The 30 quality protein maize separated into six groups (I-VI), show that group I and

V; II and IV; III and VI are similar in their days from planting to physiological maturity. Group VI are high yielders while groups III and IV are potential high yielders with high percentage protein content, hence groups V, III, I and VI are superior lines in crop improvement programmes (Showemimo and Yeye, 2005).

A study done in 2006, at Safi Abad Research Center in Iran showed from path analysis that characters including harvest index, total kernel number per ear, ear length, anthesis to silking interval had direct effects on kernel yield and accounted as the primary influential characters on kernel yield. These characters justified 82% of kernel yield variation and accounted as first class trait (Mehdi *et al.*, 2006). In the 1950s, the diffusion of maize (*Zea mays* L.) hybrids, characterized by a superior yield performance, brought a progressive substitution of local populations in almost all of the European maize-growing countries. As a consequence, the genetic variability of the cultivated maize germplasm was reduced over the past 50 years, in terms of both number of alleles and genetic diversity between hybrids (Reif *et al.*, 2005).

Experiment done in Eastern Serbia in 2009 to evaluate genetic diversity using morphological and molecular methods for ten collected maize landraces, showed significant differences on the characteristics measured hence variability was both within and between landraces, However, it showed cultivation of maize landraces has potentially gone down during the last two decades (Jelena, 2009).

Maize populations maintained by farmers were planted in experiment to evaluate the morphological and reproductive traits in 1999 to 2000 at Madeira and Porto Santo Island in Portugal, high morphological variability observed across maize landraces was useful for choosing the appropriate material for crop improvement in breeding programmes (Miguel *et al.*, 2007).

2.7 Heritability of Traits

Studies were done in Khozestan province in Iran during 2010 to assess the effects of drought stress on morphological characteristics of 18 new hybrids on yield and yield components, Results showed that heritability of grain yield was about 45% (Mostafavi *et al.*, 2013).

Experiments were conducted at the University of Agriculture in Pakistan in 2010 for estimation of genetic variability and trait association under drought stress of 40 maize accessions. Results indicated that high heritabilities were recorded for chlorophyll content and survival rate of seedlings, Higher values of heritability and genetic advance indicated that selection can be made on the bases of these traits (Mustafa *et al.*, 2014). A Study carried out in Zambia from 2004 to 2007 to determine heritability in broad sense of grain yield of maize under low nitrogen condition showed that grain yield of landraces was low meaning that selection basing on grain yield under low nitrogen conditions was not effective. However, anthesis silking interval and tassel size was high and landraces achieved high grain yield than checks under low nitrogen conditions should be used to breed for the low soil nitrogen conditions (Miti *et al.*, 2010). Experiment was carried out at Maize Research Centre, Rajendranagar, Hyderabad in 2012 to 2013 to determine the

various parameters of genetic variability, broad sense heritability and genetic advance estimates of maize genotypes. Results showed high values of heritability in broad sense indicating that characters are less influenced by environmental effects. Such characters were grain yield, plant height, ear height, number of kernels per row and 100 kernels weight. Heritability and genetic advance are very important parameters in genetic gain and are important criteria for effective use in selection (Kumar *et al.*, 2014).

A study was conducted at the department of genetics and plant breeding, Allahabad in India 2013, to estimate the genetic components of variance for grain yield and its related traits on broad sense heritability, and genetic advance in maize. High to moderate heritability, and genetic advance were recorded for biological yield, grain yield per plant, plant height and ear height, in which selection may lead for improvement for these traits in maize (Vashistha *et al.*, 2013).

A study was undertaken to study the gene action, broad and narrow sense heritability, and interrelationships among five selected traits of maize including, plant height, ear height, cob length, cob diameter, and number of rows per cob at Crops Research Institute at Fumesua, Kumasi in Ghana during season 2007 to 2010. Results indicated that heritability in broad sense was high for plant height, ear height, and cob length. Dominance genetic variation was the major component of genetic variation signifying effectiveness of selection in the early segregating generations for improving these traits (Tengan *et al.*, 2012).

A study was conducted in 2005 at Kharif Pakistan to evaluate phenotypic coefficient of variability, genotypic coefficient of variability, broad sense heritability, correlation and path coefficient on cobs per plant, plant height, cob height, days to 50% tasseling, days to 50% silking and grain yield. Results showed higher heritability for days to 50% tasseling, 50% silking and grain yield per plant and that these traits were more heritable in the materials studied (Akbar *et al.*, 2008).

An experiment was conducted in Shishi Lusht valley of Krakurm, District Chitral, in 2001 in Pakistan with an objective of achieving the level of self-reliance in food grains. Broad-sense heritability, coefficients of variability and genetic advance values were estimated. High values of broad sense heritability coupled with higher genetic advance in grain yield per plant, plant height, days taken to silking and days taken to tasseling provided the evidence that these variables were under the control of additive genetic effects, indicating that selection should lead to a fast genetic improvement of the material (Mahmood *et al.*, 2004).

An experiment was set at the University of Maiduguri, Nigeria during the cropping season of 2007 to evaluate broad sense heritability and correlations among number of stands per plot, anthesis silking interval, plant height, weight of cobs and grain yield. Results indicated that traits with high heritability and positive correlation with grain yield were important traits in selection with an objective of improving total yield in breeding programs (Aminu and Izge, 2012).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental Site and Materials

The study was conducted during the 2014/2015 cropping season at the Selian Agricultural Research Institute which is located in the Arusha region of Tanzania at 10° 22'S and 40° 10'E and 1378 m above sea level. Mean annual temperature and rainfall are 19.2°C and 1103 mm respectively. The soils are silty loams and volcanic in origin. Fifteen maize landraces collected from areas within the Arusha, Kilimanjaro and Manyara regions were used.

3.1.2 Methods

3.1.2.1 Experimental design

Randomized Complete Block Design (RCBD) was used to carry out the study and treatments arranged in three replications. Plots were of size 3m x 3m and each plot had 4 rows with 10 plants per row. Two seeds were sown in a hill and later thinned to one plant per hill. Rows were spaced 0.75m apart and hills spaced at 0.3m within a row. Fertilizer DAP (Diammonium Phosphate) were applied during planting at the rate of thirty(30) kg P/ha. Sixty(60)kg N/ha(Urea) was top dressed later at vegetative stage.

3.1.1 Materials

Fifteen maize landraces were used in this study. The maize landraces were obtained from Arusha and Manyara regions from farmer's fields (Table 2).

Table 2: Maize landraces used in this study

S/ N	Code	District	Village	Landraces name (Vernacular)	Meaning
1	DK- MB1	Mbulu	Bargish Uwa	-	-
2	LE- MB2	Mbulu	Bargish Uwa	-	-
3	AJ- MB3	Mbulu	Daudi	-	-
4	DA- MB4	Mbulu	Ants	-	-
5	MP- BB1	Babati	Bashnet	Kitombil	Early maturing
6	AJ- BB2	Babati	Endaw	Ikweto	Early maturing
7	BN- BB3	Babati	Gabadaw	Kitombil	Early maturing
8	MA- BB4	Babati	Endamanang	Ikweto	Our origin
9	DQ- BB5	Babati	Long	Erikwato	Our origin
10	JM- AR1	Arumeru	Olorien	-	-
11	DM- KR1	Karatu	Kilima Tembo	Mehhi	coloured
12	PD- KR2	Karatu	Rhotia Kati	Mehhi	coloured
13	AD- KR3	Karatu	Upper Kitete	Mehhi	coloured
14	TD- KR4	Karatu	Slahhamo Kambi Ya	Mehhi	coloured
15	JL-KR5	Karatu	Simba	Mehhi	coloured

3.2 Data Collection

Data on variables were collected according to the protocol developed by (IBGRI, 1991).

3.2.1 Days to 50% tasseling

Number of days were recorded by counting the duration from when seeds were planted to when half of plants in each plot had tasseled.

3.2.2 Days to 50% silking

Number of days were recorded by counting the duration from when seeds were planted to when half of plants in each plot had silked.

3.2.3 Plant height (cm)

Plant height was measured using 10 plants in a plot, from ground level to the point where the tassel of the plant started branching using a tape measure. The average measurement of 10 plants was recorded as plant height for the plot.

3.2.4 Ear height (cm)

Ear height was measured using 10 plants in a plot, from the ground level to the uppermost bearing ear. The average measurement of 10 plants was recorded as ear height for the plot.

3.2.5 Leaf length (cm)

Leaf length was assessed by measuring the length of a leaf, using a modified metric ruler from the ligule to apex of the leaf which subtends the uppermost ear, using 10 plants in a plot. The average measurement of 10 plants was recorded as leaf length of the plot.

3.2.6 Leaf width (cm)

Leaf width was assessed by measuring the width of a leaf, using a modified metric ruler from mid-way along its length for the leaf subtending the uppermost ear using 10 plants in a plot. The average measurement of 10 plants was recorded as leaf width.

3.2.7 Tassel length (cm)

Tassel length was measured, using 10 plants in a plot using metric ruler from the tassel base where it starts to branch to the tip of the tassel. The average measurement of 10 plants was recorded as tassel length of the plot.

3.2.8 Tassel branching space (cm)

Tassel branching space, the distance between the point where tassel starts to branch to end of tassel branching was measured using 10 plants in a plot. The average measurement of 10 plants was recorded as plant tassel branching space for the plot.

3.2.9 Tassel peduncle length (cm)

Tassel peduncle length, the length from the leaf sheath and tassel branch was measured in 10 plants in a plot using metric ruler. The average measurement of 10 plants was recorded as tassel peduncle length for the plot.

3.2.10 Number of primary branches on a tassel

Number of primary branches on a tassel was obtained from 10 plants in a plot, by counting the number of primary branches of a tassel in each plant. The average

measurement of 10 plants was recorded as number of primary branches on tassel of the plot.

3.2.11 Number of secondary branches on tassel

Number of secondary branches on tassel was counted using 10 plants in a plot, by counting the number of secondary branches of a tassel in each plant. The average measurement of 10 plants was recorded as number of secondary branches on tassel.

3.2.12 Number of tertiary branches on tassel

Number of tertiary branches on tassel were recorded using 10 plants in a plot by counting the number of tertiary branches of a tassel in each plant. The average measurement of 10 plants was recorded as number of tertiary branches on tassel.

3.2.13 Number of kernels rows

Number of kernels rows were recorded using 10 ears in a plot, by counting number of kernel rows in the central part of the uppermost ear. The average measurement of 10 ears was recorded as number of kernel rows for the plot.

3.2.14 Ear length (cm)

Ear length was measured using 10 ears in a plot using a metric ruler from lower level to the top level of the ear. The average measurement of 10 ears was recorded as ear length of the plot.

3.2.15 Ear diameter (cm)

Ear diameter from the central part of the uppermost ear was measured using 10 ears in a plot. The average measurement of 10 ears was recorded as ear diameter for the plot.

3.2.16 Cob diameter (cm)

Cob diameter was measured using 10 ear cobs in a plot, by measuring the diameter of the uppermost ear cob. The average measurement of 10 ear cobs was recorded as ear cob diameter of the plot.

3.2.17 Number of kernels per row

Number of kernels per row was recorded from 10 ears in a plot by counting the number of kernels per row of an. The average measurement of 10 ears was recorded as number of kernels per row in a plot.

3.2.18 100 seed weight (g)

100 seed weight was measured, using 5 groups of 100seeds measured in each plot. The average measurement of 5 groups of 100 seeds was recorded as 100 seed weight of the plot.

3.2.19 Grain yield (t/ha)

Grain yield was assessed, using two harvested rows in a plot after grain weight and moisture content recorded using the formula in equation.

$$\text{Grain Yield} \left(\frac{\text{t}}{\text{ha}} \right) = \frac{10}{\text{Pa}} \text{Pw} \frac{(\text{Sw} - \text{Cw})}{\text{Sw}} \frac{(100 - \text{Sm})}{86} \dots\dots\dots(1)$$

Where:

Pa=plot area (m²), Pw=grain yield from a plot (kg), Sw = sample weight (kg), Cw = cob weight of ear samples (kg) and Sm=grain sample moisture at harvest (%).

3.2.20 Leaf orientation

Leaf orientation was assessed by rating the leaf orientation of the plants in each plot using 5 plants in a plot. The most occurred frequency number was recorded as leaf orientation of the plot where 1 is erect, and 2 is pendant.

3.2.21 Kernel type

Kernel type was assessed by observing the type of kernel of 5 plants in a plot of the uppermost ear. The kernel type that appeared the most was recorded as kernel type of the plot and rated as 1 floury, 2 semi-floury, 3 dent, 4 semi-dent, 5 semi-flint, 6 flint, 7 pop, 8 sweet, 9 opaque, 10 tunicate, and 11 waxy .

3.2.22 Kernel colour

Kernel colour was assessed by observing colour of the kernels of 5 cobs in a plot of the uppermost ear. The kernel colour that appeared the most was recorded as kernel

colour of the plot where 1 is white, 2 yellow, 3 purple, 4 variegated, 5 brown, 6 orange, 7 mottled, 8 white cap, and 9 red.

3.2.23 Kernel row arrangement

Kernel row arrangement was assessed by observing the kernel row arrangement of the uppermost ear of 5 plants in a plot. Kernel row arrangement shape of the ears that appeared most was recorded as the kernel row arrangement of the plot and rated as 1 if regular, 2 irregular, 3 straight, and 4 spiral.

3.2.24 Husk cover

Husk cover was assessed by observing how good the ear leaves covered the cob of 5 plants in a plot, and rated as 3 if poor, 5 as intermediate, and 7 as good. The number that appeared most was recorded as husk cover of the topmost ear cob of the plot.

3.2.25 Stay green

Stay green was assessed in each plot at maturity by observing on plants that retained greenish colour and rated the intensity of greenish on 5 plants in a plot. The greenish retained was rated 3 if low, 5 as medium, and 7 as high. The number that appeared most was recorded as stay green of the landraces.

3.2.26 Ear damage

Ear damage was assessed in each plot after harvest by observing ears that were damaged by ear rot and insects in 5 ears and rated as 0 if no damage, 3 if little damaged, and 7 if severely damaged in a plot. The number that appeared most was recorded as ear damage of the plot.

3.2.27 Tassel type

Tassel type was assessed in each plot at milk stage by observing plant tassel arrangement of 5 plants and rated 1 as primary, 2 as primary-secondary, and 3 as primary-secondary-tertiary of 5 plants in a plot. The type which appeared the most was recorded as tassel type of the plot.

3.3 Data Analysis

Data collected was subjected to analysis of variance (ANOVA) using the GenStat Discovery 15th edition computer software. Treatment means separation was done using Turkey's test at the 5% level of significance. Diversity studies were assessed by Shannon Weaver Diversity Index, Principle Components Analysis and Cluster Analysis (Siopongco *et al*, 1999).

Heritability in broad sense analysis was done according to Hanson *et al.* (1956) procedures. Variance, covariance, correlations between important variables and path coefficient analysis were also done for the studied variables.

3.3.1 Specific Objective (i): To evaluate the diversity that exists in maize landraces

3.3.2 Analysis of variance

The analysis was performed using the statistical model for randomized complete block design (RCBD) as follows:

$$Y_{ijk} = U + T_i + B_j + E_{ijk} \dots \dots \dots (2)$$

Where;

Y_{ijk} = measured variable for the i^{th} treatment in the j^{th} block and k^{th} plot.

U = Overall mean of the experiment for the variable.

T_i = The effect of i^{th} treatment.

B_j = j^{th} block effect.

E_{ijk} = Random error effect to each observation in the i^{th} treatment, j^{th} block, and k^{th} plot.

3.3.3 Shannon-Weaver diversity index

Estimate of variability for each quantitative and qualitative character was computed by Shannon-Weaver Diversity Index, designated as H , using the formula

$$H = -\sum p_i (\log_2 p_i) \log n \text{ (Siopongco } et al, 1999).$$

Where H = Shannon-Weaver diversity index

p_i = i^{th} frequency proportion of each descriptor state

n = number of states

3.3.4 Principle component analysis

Raw data were first standardized to zero mean unit variance followed by computation of numerical measures of similarity and construction distance matrix using variance-covariance coefficients. Eigenvalues and Eigenvectors of the variance covariance matrix were then computed (Siopongco *et al.*, 1999).

3.3.5 Cluster analysis

Cluster analysis was performed using XLstat software 2015 for all variables, using standardized data. Numerical measures of likeness/similarity were computed and

distance matrix constructed using Euclidean Distance Coefficient. Clustering (Sequential, Agglomerative, Hierarchical, and Nested) by unweighted pair group of Arithmetic mean method was executed (Siopongco *et al.*, 1999).

3.3.6 Specific Objective (ii) To determine heritability (broad sense) of maize traits

Heritability (broad sense) was calculated as the ratio of genotypic variance to phenotypic variance using the formula (in equation) according to Hanson *et al.* (1956)

$$h^2_b = \frac{\sigma^2_g}{\sigma^2_{ph}} \times 100 \dots\dots\dots(3)$$

Where:

h^2_b = heritability in the broad sense,

σ^2_g = the component of variance due to landraces,

σ^2_{ph} = phenotypic component of variance.

3.3.7 Computation of phenotypic variance and genotypic variance

To estimate the extent of magnitude of variation among these traits, all data were subjected to analysis of variance; components of genotypic variance, phenotypic variance and error were computed by the formula in equation.

$$\sigma^2_g = \frac{MSG - MSE}{r} \dots\dots\dots(4)$$

$$\delta^2_{ph} = \frac{MSG}{r} \dots\dots\dots(5)$$

$$\delta^2_e = \frac{MSE}{r} \dots\dots\dots(6)$$

Where

MSG, MSE and r are the mean squares of landraces, mean squares of error and replication respectively (Baye, 2002).

3.3.8 Analysis of genotypic and phenotypic correlation coefficients

Covariance analysis was done using GenStat software to estimate genotypic and phenotypic variances, and covariance between two selected variables. The covariance components obtained were used to compute genotypic and phenotypic correlations between chosen characters using the formula in equation 4 (Makoye, 2008).

$$r = \frac{\delta g_{1.2}}{[\delta g_1 \times \delta g_2]^{1/2}}$$

Where

$\sigma_{g_{1.2}}$ = component of genetic covariance between the two variables

σ_{g_1} = component of genotypic variance of the first variable

σ_{g_2} = component of genotypic variance of the second variable

$$r = \frac{\delta ph_{1.2}}{[\delta ph_1 \times \delta ph_2]^{1/2}} \dots\dots\dots(8)$$

Where:

$\sigma_{ph_{1.2}}$ = component of phenotypic covariance between the two variables

σ_{ph_1} = component of phenotypic variance of the first variable

σ_{ph_2} = component of phenotypic variance of the second variable

3.3.9 Path coefficient analysis

Path coefficient analysis by Dewey and Lu (1959) describes the relationships between correlation coefficients, which was done to assess the level of paths influence among the correlated components. The formula arranged in matrix form was solved simultaneously to determine the direct effects. The model arranged in matrix is as shown in equations.

$$r_{15} = P_{15} + r_{12}P_{25} + r_{13}P_{35} + r_{14}P_{45} \dots \dots \dots (9)$$

$$r_{25} = P_{25} + r_{12}P_{15} + r_{23}P_{35} + r_{24}P_{45} \dots \dots \dots (10)$$

$$r_{35} = P_{35} + r_{13}P_{15} + r_{23}P_{25} + r_{34}P_{45} \dots \dots \dots (11)$$

$$r_{45} = P_{45} + r_{14}P_{15} + r_{24}P_{25} + r_{34}P_{35} \dots \dots \dots (12)$$

$$1 = P_x^2 + P_{15}^2 + P_{25}^2 + P_{35}^2 + P_{45}^2 + 2P_{15}r_{12}P_{25} + 2P_{15}r_{13}P_{35} + 2P_{15}r_{14}P_{45} + 2P_{25}r_{23}P_{35} + 2P_{25}r_{24}P_{45} + 2P_{35}r_{34}P_{45} \dots \dots \dots (13)$$

In the path model

r_{ij} = simple correlation coefficients for measuring the mutual association of the two variables

p_{ij} = path coefficients for measuring direct influence between variables to yield

$r_{ijp_{ij}}$ = indirect effects of variables upon another through the other variable

P_x = the residual effect in the path analysis model

i and j = (1, 2, 3 and 4)

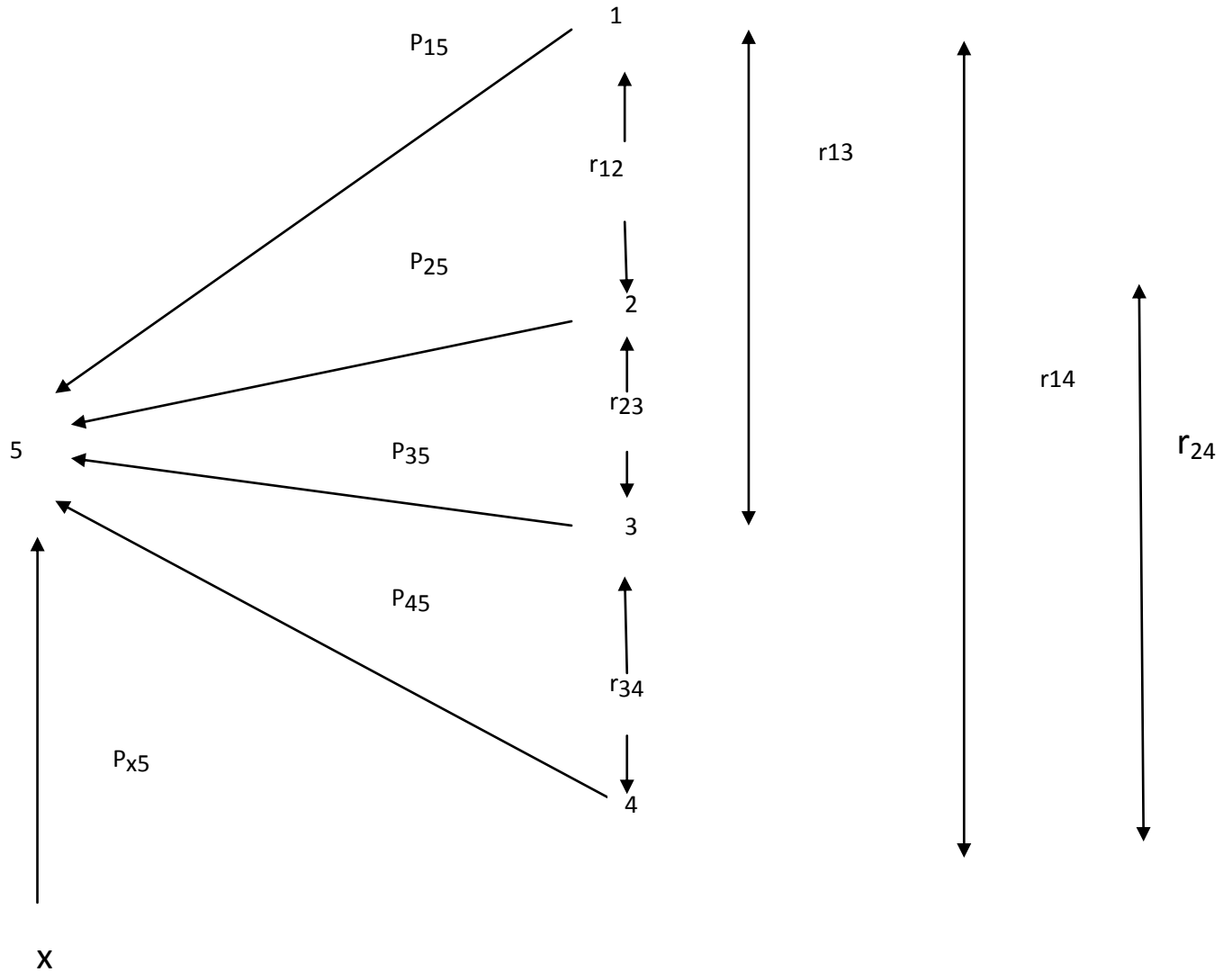


Figure 1: Paths of influence indicating the coefficients of factors

Key: 1 = plant height, 2 = ear height, 3=100 seed weight, 4 = number of kernels per row, 5= Grain yield, X = residual effects

3.3.10 Morphology of quantitative characters

Estimate of variability for the qualitative character was assessed according to (IBGRI, 1991) protocol. The analysis of variance was computed using Genstat discovery 15th edition computer software.

CHAPTER FOUR

4.0 RESULTS

4.1 Analysis of Variance and Basic Statistics Summary for Different Variables Studied

The results of analysis of variance for different variables studied showed that genotypic effects for some variables were significant while others were insignificant .

Differences were also observed by range, standard deviation, maximum and minimum values. Significances ($P \leq 0.05$) were noted in leaf length, tassel branching space, plant height, number of kernels per row, ear height, ear diameter, days to tasseling, days to silking, and cob diameter. Other variables did not show significant genotypic effects (Table 3) and (Table 4).

Table 3: Analysis of Variance(mean squares) of the studied variables

SV	DF	LL	100swt	Gy	TPL	TL	TBS	PH	NTBT	NSBT	NPB	NKR	NKPR	LW	EL	EH	ED	DTT	DTS	CD
Replication	2	104.80	63.50	0.20	25.30	31.10	25.80	10214.00	1.81	2.63	4.54	0.71	31.42	0.90	5.10	2916.00	0.01	5.64	8.71	0.17
Landraces	14	629.09*	324.00	2.90	343.00	680.35*	126.24*	16583.70*	8.44	19.40	90.40	24.22*	323.60	6.80	60.80	15341.91*	1.77*	377.24*	347.11*	2.05*
Error	28	518.90	371.00	4.30	330.00	705.00	153.00	6129.00	16.00	25.70	178.00	21.37	612.60	9.60	70.80	2611.00	1.55	26.40	24.00	1.62
Total	44																			

Table 4: Summary of basic statistics for different variables studied

	LL	100swt	Gy	TPL	TL	TBS	PH	NTBT	NSBT	NPB	NKR	NKPR	LW	EL	EH	ED	DTT	DTS	CD
Mean	95.90	52.50	2.38	29.20	45.10	20.70	297.20	1.61	2.18	14.00	13.18	39.94	11.80	21.20	163.10	4.98	72.29	74.20	2.88
Std. deviation	3.87	2.78	0.26	2.86	4.02	1.73	19.87	0.45	0.68	1.47	0.76	2.78	0.40	1.20	19.11	0.21	3.00	2.87	0.22
Range	11.00	9.00	0.90	8.80	16.30	7.30	61.50	1.80	2.30	6.10	2.70	9.20	1.20	3.80	60.70	0.70	10.70	9.30	0.80
Minimum	90.00	47.80	1.90	24.10	40.00	16.90	268.70	0.70	0.90	10.20	11.60	35.70	11.30	19.30	132.70	4.70	68.30	71.70	2.50
Maximum	101.00	56.70	2.90	32.90	56.30	24.20	330.20	2.40	3.20	16.30	14.30	44.80	12.50	23.10	193.30	5.40	79.00	81.00	3.30

Key: * = Significant at 5% level

SV = Sources of variation, DF = degree of freedom, 100SWT = 100 seed weight, Gy(t/ha) = Grain yield (tons per hectare

PH = Plant height, NKPR = Number of kernels per row, EH = Ear height, TPL = Tassel peduncle length, TL =

Tassel length, TBS = Tassel branches space, NTBT = Number of tertiary branches on tassel, NSBT = Number of secondary branches, NPB = Number of primary branches, NKPR = Number of kernels row, LW = Leaf width,

EL = Ear length , ED = Ear diameter, DTT = Days to 50% tasseling, DTS = Days to 50% silking, CD = Cob

diameter

4.2 Estimate of Variation Using Shannon-Weaver Diversity Index

The computed diversity indices for the qualitative character traits ranged from 0.95 (kernel row arrangement and kernel colour) to 0.99 (husk cover), with mean diversity value of 0.98.

The diversity value showed high variation in husk cover (0.99), ear damage (0.99), kernel type (0.99), stay green (0.98), leaf orientation (0.98), tassel type (0.98), kernel colour (0.95) and kernel row arrangement (0.95). The mean diversity index of 0.98 indicated existence of high variation within the collection, in terms of qualitative characters (Table 5).

Table 5: Computed diversity indices (H) for qualitative characters

Character	Diversity index (H)
Leaf orientation	0.98
Stay green	0.98
Husk cover	0.99
Ear damage	0.99
Kernel type	0.99
Kernel colour	0.95
Kernel row arrangement	0.95
Tassel type	0.98
Mean diversity index	0.98

All quantitative characters exhibited high diversity values of 0.99. High diversity values ranged from number of tertiary branches on tassel (0.96) to 100 seed weight (0.99). High degree of variation exists within the collection for the quantitative characters, as reflected by mean diversity value of 0.99.

Quantitative character traits gave overall diversity index of 0.99, indicative of high variability existing within the collection (Table 6).

Table 6: Computed diversity indices (H) for quantitative characters

Character	Diversity index (H)
100 Seed weight	0.99
Grain yield	0.99
Tassel peduncle length	0.99
Tassel length	0.99
Tassel branching space	0.99
Plant height	0.99
Number of tertiary branches on tassel	0.96
Number of secondary branches on tassel	0.97
Number of primary branches on tassel	0.99
Number of kernel row	0.99
Number of kernel per row	0.99
Leaf width	0.99
Leaf length	0.99
Ear length	0.99
Ear height	0.99
Ear diameter	0.99
Days to tasseling	0.99
Days to silking	0.99
Cob diameter	0.99
Mean diversity index	0.99

4.3 Principal Components Analysis

This analysis results in the identification of the major attributes that are responsible for the observed variation within the collection (Table 7). The first principal component is strongly correlated with seven of the variables. The first principal component increased with increased plant height (0.82), Number of primary branches (0.56), Number of kernels per row (0.53), Ear length (0.67), Ear height (0.91), Days to tasseling (0.96), Days to silking (0.95) and negative correlation for ear diameter (-0.59) the rest of traits contributed very low positively and negatively.

The second principal component increased with increased leaf length (0.59), 100seed weight (0.71), ear diameter (0.53) and cob diameter (0.56) while number of tertiary branches increased negatively (-0.62) other traits contributed very low. Third principal components increased with increased tassel length (0.56), tassel branches space (0.72), number of secondary branches (0.71) and cob diameter (0.56). The fourth principle component was explained by variation among landraces due to tassel peduncle length (0.60) and number of kernels per row (0.76).

High loading for grain yield (-0.56) and tassel peduncle length (-0.61) negatively contributed to increase in fifth principle component except leaf width (0.62) which contributed positively. The sixth component increased with increased number of tertiary branches (0.57).

Six principle components were produced and these principle components had cumulative explained variances of 84.23%. The first principle component accounted

for 29.40% of the total variation while principle components two and three accounted for 44.20% and 57.20% respectively.

Six principal components were extracted having Eigenvalue >1 out of fourteen (14). The computed eigenvalues for the variables subjected to principle component analysis together with the corresponding proportions and cumulative explained variance are given in (Table 7).

Table 7: Factor loadings and eigenvalue for component traits in principle component 1-6

Variables/components	F1	F2	F3	F4	F5	F6
Leaf length	-0.42	0.59	0.20	-0.31	-0.31	0.09
100seed weight	-0.34	0.71	-0.30	0.04	0.18	-0.23
Grain yield	-0.37	-0.13	-0.23	-0.06	-0.56	-0.09
Tassel peduncle length	-0.16	-0.02	-0.06	0.60	-0.61	-0.36
Tassel length	-0.12	0.07	0.56	-0.47	-0.39	-0.26
Tassel branches space	-0.34	-0.38	0.72	-0.18	-0.15	-0.20
Plant height	0.82	0.31	0.15	-0.04	-0.25	-0.18
Number of tertiary branches	-0.05	-0.62	0.08	0.07	-0.27	0.57
Number of secondary branches	-0.03	0.12	0.71	-0.29	0.09	0.39
Number of primary branches	0.56	-0.13	0.43	0.34	0.18	-0.27
Number of kernel row	-0.02	-0.31	0.39	0.76	-0.13	0.11
Number of kernel per row	0.53	-0.31	0.18	-0.41	0.09	-0.36
Leaf width	-0.43	-0.43	0.10	-0.03	0.62	-0.32
Ear length	0.67	0.49	0.02	-0.17	-0.10	0.19
Ear height	0.91	0.10	0.15	0.00	-0.26	-0.06
Ear diameter	-0.59	0.53	0.33	0.43	0.07	-0.06
Days to tasseling	0.96	0.01	-0.01	0.09	0.09	0.02
Days to silking	0.95	0.02	-0.02	0.17	0.13	0.06
Cob diameter	-0.14	0.56	0.56	0.37	0.26	0.15
Eigenvalue	5.58	2.82	2.45	2.11	1.79	1.23
Variability (%)	29.40	44.24	57.16	68.30	77.72	84.23
Cumulative %	29.40	44.24	57.16	68.30	77.72	84.23

Key: LL = Leaf length, 100wt = 100 seed weight(g), Gy(t/ha) = Grain yield ,TPL = Tassel peduncle length, TL = Tassel length, TBS = Tassel branching space, PH = Plant height, NTBT = Number of tertiary branches on tassel, NSBT = Number of secondary branches on tassel, NPB = Number of primary branches on tassel, NKR = Number of kernels row, NKPR = Number of kernels per row, LW = Leaf width, EL = Ear length, EH = Ear height, ED = Ear diameter, DTT = Days to tasseling, DTS = Days to silking, and CD = Cob diameter.

4.4 Cluster Analysis

Produced clusters by the cluster analysis conducted on fifteen landraces collected from different locations formed three (3) distinct clusters Figure 2.

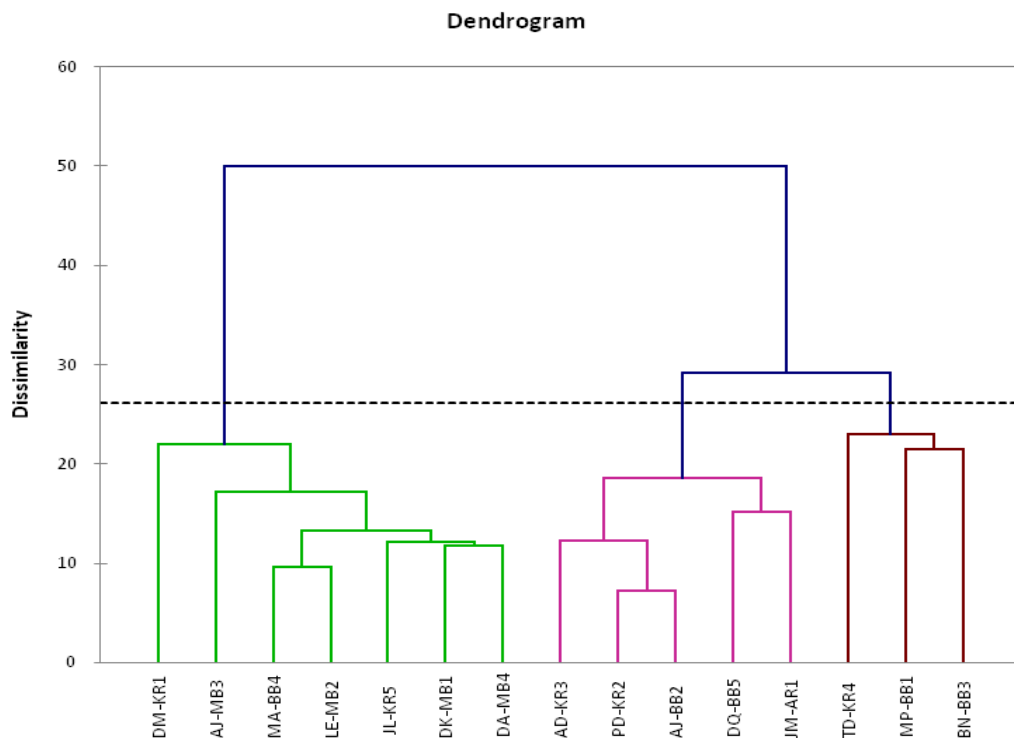


Figure 2: Dendrogram produced from cluster analysis of maize landraces using morphological data

In this analysis only three (3) clusters were formed, the first cluster was identified with seven landraces DK-MB1, DM-KR1, MA-BB4, DA-MB4, AJ-MB3, JL-KR5, and LE-MB2. The second cluster contained five (5) landraces DQ-BB5, PD-KR2, JM-AR1, AD-KR3, and AJ-BB2 and the third cluster was distinguished by three landraces MP-BB1, TD-KR4, and BN-BB3 (Table 8).

Table 8: Cluster membership of various maize landraces under this study

Cluster name	No. of landraces in each cluster	Name of landraces in each cluster
Cluster 1	7	DK-MB1, DM-KR1, MA-BB4, DA-MB4, AJ-MB3, JL-KR5, LE-MB2
Cluster 2	5	DQ-BB5, PD-KR2, JM-AR1, AD-KR3, AJ-BB2
Cluster 3	3	MP-BB1, TD-KR4, BN-BB3

The maize landraces in cluster 1 showed higher values of Gy (t/ha), TBS, NTBT, LW, and ED. The second cluster comprised of maize landraces having the highest values of LL, 100 SWT, and TPL. The members of the third cluster were characterized by higher value of TL, PH, NSBT, NPB, NKR, NKPR, EL, EH, DTT, DTS and CD (Table 9).

Table 9: Cluster analysis of various traits in maize landraces

Traits	Cluster 1	Cluster 2	Cluster 3
LL	96.03	97.50	92.88
100swt (g)	53.03	53.05	50.31
Gy (t/ha)	2.45	2.35	2.27
TPL	29.07	29.77	28.44
TL	45.55	42.88	47.59
TBS	20.95	20.26	20.77
PH	278.57	308.06	322.33
NTBT	1.65	1.64	1.48
NSBT	2.09	2.22	2.33
NPB	13.30	13.82	15.66
NKR	13.14	13.18	13.26
NKPR	39.11	38.84	43.71
LW	12.09	11.52	11.69
EL	20.58	21.36	22.43
EH	145.61	171.90	189.33
ED	5.04	4.98	4.83
DTT	70.23	72.53	76.66
DTS	72.28	74.46	78.33
CD	2.88	2.85	2.89

Key: LL = Leaf length, 100swt = 100 seed weight (g), Gy (t/ha) = Grain yield ,TP L= Tassel peduncle length, TL= Tassel length, TBS = Tassel branching space, PH = Plant height, NTBT = Number of tertiary branches on tassel, NSBT = Number of secondary branches on tassel, NPB = Number of primary branches on tassel, NKR = Number of kernels row, NKPR = Number of kernels per row, LW = Leaf width, EL = Ear length, EH = Ear height, ED = Ear diameter, DTT = Days to tasseling, DTS = Days to silking, and CD = Cob diameter

4.5 Heritability in Broad Sense, Genotypic Variance, Phenotypic Variance and Genotypic and Phenotypic Coefficients of Variation

Broad sense heritability for different characters varied considerably. Heritability obtained over traits ranged between 67.09% and 98.85%. Days to tasseling and days to silking had highest heritability of 98.85%, while number of primary branches had the lowest heritability of 67.09%. Ear height, leaf length, 100 seed weight, grain yield, tassel peduncle length, tassel length, tassel branching space, plant height, number of tertiary branches on tassel, number of secondary braches on tassel, number of kernel rows, number of kernels per row, leaf width, ear height, ear diameter, and cob diameter also recorded high broad sense heritabilities ranging from 67.09% (number of primary branches) to 98.85% (days to silking).

Phenotypic coefficients of variability (PCV) ranged from ear diameter (0.40%) to number of tertiary branches (15.20%) and genotypic coefficients of variability (GCV) ranged between leaf width (5.07%) and number of secondary branches (45.80%).

Genotypic variance varied considerably the highest was for plant height (1111.63%) and lowest was ear diameter (0.11%). Also phenotypic variance was recorded highest for plant height (394.87%) and lowest for ear diameter (0.04%) (Table 10).

Table 10: Variances and heritability estimates for the studied variables

Traits	GV	PV	GCV%	PCV%	h^2_b (%)
Leaf length	38.75	14.98	6.47	1.90	86.25
100seedweight	18.72	7.71	8.23	2.80	80.91
Grain yield	0.16	0.07	16.78	3.50	75.45
Tassel peduncle length	20.54	8.16	15.08	3.10	83.94
Tassel length	40.21	16.20	13.98	2.30	82.74
Tassel branches space	7.20	3.01	12.57	4.50	79.82
Plant height	1111.63	394.87	11.21	6.20	93.84
Number of tertiary branches	0.41	0.20	37.16	15.20	68.45
Number of secondary branches	1.08	0.46	45.77	13.50	77.92
Number of primary branches	4.33	2.15	14.91	2.80	67.09
Number of kernel row	1.48	0.58	9.10	1.20	85.29
Number of kernel per row	15.83	7.71	9.76	2.60	68.45
Leaf width	0.37	0.16	5.07	1.50	76.32
Ear length	3.50	1.45	8.49	1.90	80.60
Ear height	1064.77	365.28	19.99	6.00	97.16
Ear diameter	0.11	0.04	6.02	0.40	85.43
Days to tassel	26.63	8.98	7.06	0.60	98.84
Days to silking	24.51	8.26	6.60	0.70	98.85
Cob diameter	0.13	0.05	10.42	2.60	86.88

Key: Gv=Genetic variance,PV=Phenotypic variance,PCV=Phenotypic coefficients of variability,GCV=Genotypic coefficients of variability and h^2_b =Heritability broad sense

4.6 Estimates of Genotypic and Phenotypic Correlation Coefficients among Yield and Yield Components

The direction and magnitude of association between yield and yield components were found to differ in these traits of maize landraces. Genotypically plant height

showed significant positive correlation with ear height (0.99). This character had significant negative correlation with grain yield (-0.91) number of kernels per row (-0.89), and 100 seed weight (-0.95). Ear height showed significant negative correlation with grain yield (-0.91), 100 seed weight (-0.95), and number of kernels per row(-0.89). 100 seed weight and number of kernels per row indicated significant positive correlation with grain yield (Table 11).

Table 11: Genotypic Correlation coefficient among yield and yield components

	PH	EH	100SWT	NKPR	GY
PH	1.00				
EH	0.99*	1.00			
100SWT	-0.95*	-0.95*	1.00		
NKPR	-0.89*	-0.89*	0.82*	1.00	
GY	-0.91*	-0.91*	0.87*	0.80*	1.00

*Significant at 5% level

Key: PH = Plant height, EH = Ear height, 100SWT = 100 seed weight, NKPR = Number of kernels per row, GY = Grain yield.

Phenotypically plant height correlated significantly positive with ear height (0.93).

Other relations were not statistically significant (Table 12).

Table 12: Phenotypic correlation coefficient among yield and yield components

	PH	EH	100SWT	NKPR	GY
PH	1.00				
EH	0.93*	1.00			
100SWT	-0.10	-0.27	1.00		
NKPR	0.35	0.41	-0.40	1.00	
GY	-0.31	-0.27	0.08	-0.14	1.00

*Significant at 5% level

Key: PH = Plant height, EH = Ear height, 100SWT = 100 seed weight, NKPR = Number of kernels per row, GY = Grain yield.

4.7 Effects of Yield Components on Grain Yield

Results of associations among factors that influenced maize grain yield were described using path coefficient analysis (Table 13). The results indicated significant variability in causal relationships among maize grain yield influencing components. Correlation between plant height with grain yield was significant and negative (-0.91). This was mainly due to the strong negative direct effect (-0.91). The other relationships were too low to be of any significance value. Ear height had a significant negative correlation with yield (-0.91) mainly due to highly negative indirect effect via plant height (-0.91).

Hundred seed weight correlated significantly positively with grain yield (0.87). This was due to indirect effect via plant height (0.87). In this study number of kernels per row showed significant positive correlation with grain yield (0.80) which was greatly contributed by indirect effect via plant height (0.82).

Table 13: Direct and indirect effects of yield and yield components

	Source of variation	Effects
1	(PH) vs. grain yield (r_{15})	-0.91*
	Direct effect (P_{15})	-0.91
	Indirect effect via (EH) ($r_{12}P_{25}$)	0.05
	Indirect effect via (100SWT) ($r_{13}P_{35}$)	-0.01
	Indirect effect via (NKPR) ($r_{14}P_{45}$)	0.06
	Total	-0.91*
2	(EH) vs. grain yield (r_{25})	-0.91*
	Direct effect(P_{25})	-0.05
	Indirect effect via (PH) ($r_{12}P_{15}$)	-0.91
	Indirect effect via (100SWT) ($r_{23}P_{35}$)	-0.01
	Indirect effect via (NKPR) ($r_{24}P_{45}$)	0.06
	Total	-0.91*
3	(100SWT) vs. grain yield (r_{35})	0.87*
	Direct effect (P_{35})	0.01
	Indirect effect via (PH) ($r_{13}P_{15}$)	0.87
	Indirect effect via (EH) ($r_{23}P_{25}$)	0.05
	Indirect effect via (NKPR) ($r_{34}P_{45}$)	-0.06
	Total	0.87*
4	(NKPR) vs. grain yield (r_{45})	0.80*
	Direct effect (P_{45})	-0.07
	Indirect effect via (PH) ($r_{14}P_{15}$)	0.82
	Indirect effect via (EH) ($r_{24}P_{25}$)	0.05
	Indirect effect via (100SWT) ($r_{34}P_{35}$)	0.01
	Total	0.80*

Residual effect (R_{X5}) = 0.60

Key: PH = Plant height (EH) = Ear height, 100SWT = 100 seed weight (NKPR) = Number of kernels per row.

4.8 Analysis of Variance for Morphological Qualitative Traits

The results of analysis of variance for different morphological qualitative variables studied showed significant difference between landraces except for kernel row arrangement and husk cover (Table 14).

Table 14: Analysis of variances summary for the studied variables (mean squares)

Source of Variation	Df	SG	KT	KRA	KC	HC	LO
Replication	2	0.08	0.28	0.06	1.35	0.28	0.15
Landraces	14	4.16*	0.85*	1.80	12.18*	1.73	0.49*
Error	28	0.85	0.28	0.78	1.54	1.05	0.08
Total	44						

*Significant at 5% level

Key: SG = Stay green, KT = Kernel type, KRA = Kernel row arrangement, KC= Kernel colour, HC = Husk cover, and LO = Leaf orientation.

4.9 Mean Effects of Landraces for Different Qualitative Variables

Mean effects of landraces for the qualitative variables are shown in Table 15.

4.9.1 Kernel type

Mean effects for kernel type showed that different kernel types exist in maize landraces collected. Kernel type ranged from 3.70 (JM-AR1) to 2.00 (MP-BB1) and (AJ-BB2).

4.9.2 Stay green

Stay green was observed in maize landraces. MP-BB1 had the highest rating of 7.00 had statistically similar values with AD-KR3, AJ-BB2 and BN-BB3 with ratings of 5.00. The least rating was of 3.00 for JM-AR1, PD-KR2 and AJ-MB3.

4.9.3 Leaf orientation

DM-KR1, MA-BB4, and TD-KR4 did not differ significantly from each other with a score of 2.00. The lowest rating was 1.00 for JM-AR1, AJ-MB3, JL-KR5, LE-MB2, MP-BB1, AD-KR3, BN-BB3, and AJ-BB2.

4.9.4 Husk cover

Husk cover was assessed among the landraces with the highest mean effects rating score on JM-AR1 which was 7.00 and the lowest was 4.30 for TD-KR4 and LE-MB2. The mean effects did not show significant differences among the landraces collected.

4.9.5 Kernel colour

Kernel colour was observed in maize landraces to differ. DA-MB4 had the highest rating which showed significant difference from the rest of the landraces but not much from JM-AR1. DK-MB1 and DQ-BB5 displayed lowest ratings of 1.00.

4.9.6 Kernel row arrangement

Kernel row arrangement did not show significant difference among the collected maize landraces. It ranged from the highest score 3.30 for AJ-BB2 and lowest was

1.00 for AD-KR3, BN-BB3, DQ-BB5, LE-MB2, TD-KR4, DA-MB4, JL-KR5, DK-MB1 and PD-KR2 (Table 15).

Table 15: Mean effects of landraces on morphological qualitative traits

	Variables with varying scales					
	SG	KT	KRA	KC	HC	LO
Landraces	(3-7)	(1-11)	(1-4)	(1-9)	(3-7)	(1-2)
JM-AR1	3.00a	3.60b	2.00a	6.00bc	7.00a	1.00a
PD-KR2	3.00a	3.00ab	1.00a	4.00ab	5.60a	1.30ab
AJ-MB3	3.00a	2.60ab	3.00a	4.30ab	6.30a	1.00a
DK-MB1	3.60ab	3.30ab	1.00a	1.00a	5.60a	1.30ab
DM-KR1	3.60ab	3.30ab	2.00a	3.00ab	5.00a	2.00b
JL-KR5	3.60ab	2.30ab	1.00a	3.00ab	5.00a	1.00a
DA-MB4	3.60ab	3.60b	1.00a	9.00c	6.30a	1.60ab
MA-BB4	3.60ab	2.60ab	1.30a	4.00ab	5.30a	2.00b
TD-KR4	4.30abc	3.00ab	1.00a	4.60ab	4.30a	2.00b
LE-MB2	4.30abc	3.00ab	1.00a	3.00ab	4.30a	1.00a
DQ-BB5	4.30abc	2.30ab	1.00a	1.00a	6.30a	1.30ab
AJ-BB2	5.00abc	2.00a	3.30a	2.00a	5.60a	1.00a
BN-BB3	5.00abc	2.60ab	1.00a	2.00a	5.60a	1.00a
AD-KR3	6.30bc	2.60ab	1.00a	4.00ab	5.60a	1.00a
MP-BB1	7.00c	2.00a	1.30a	3.30ab	6.30a	1.00a
Mean	4.20	2.80	1.40	3.60	5.60	1.30
s.e.d.	0.70	0.40	0.70	1.00	0.80	0.20
CV (%)	1.80	4.90	4.50	8.30	2.50	7.80

Means within column with same letter(s) are not significantly from each other at 5%

Key: SG = Stay green, KT = Kernel type, KRA = Kernel row arrangement, KC = Kernel colour, HC = Husk cover, and LO = Leaf orientation. CV = Coefficient of variation, s.e.d = Standard error of differences.

Rating scale:

Stay green: 3 Low, 5 Medium, 7 High.

Husk cover: 3 Poor, 5 Intermediate, 7 Good.

Kernel row arrangement: 1 Regular, 2 Irregular, 3 Straight, and 4 Spiral. Kernel type:
1 Floury, 2 Semi-floury (morocho), with an external layer of hard endosperm, 3 Dent,
4 Semi-dent, intermediate between dent and flint but closer to dent, 5 Semi-flint, flint
with a soft cap, 6 Flint, 7 Pop, 8 Sweet, 9 Opaque 2/QPM, 10 Tunicate, 11 Waxy.

Kernel colour: 1 White, 2 Yellow, 3 Purple, 4 Variegated, 5 Brown, 6 Orange, 7
Mottled, 8 White cap, and 9 Red.

Leaf orientation: 1 Erect, 2 Pendant.

CHAPTER FIVE

5.0 DISCUSSION

5.1 Estimation of Variation of the Maize Landraces Collected

5.1.1 Variation from basic statistics and analysis of variances

Variation observed in maize landraces is indicated in measures of dispersion, range, standard deviation, minimum and maximum values of the variables. Significant differences in maize landraces in this study were observed for the studied variables which is similar with results of Makoye (2008) and Tanavar *et al.* (2014) on maize for days to tasseling, days to 50% silking, plant height, days to 50% maturity, ear height, percent of ear rot and grain yield.

The variation observed in maize landrace collections indicates selection potential in breeding programmes for combating agronomic challenges of abiotic and biotic stresses. From this collection, one could get landraces with genes of interest for improvement of adapted material in maize programmes to be used as donor parents. From this study breeders can make selection for early maturing landraces for ensuring earliness.

5.1.2 Diversity by Shannon-Weaver diversity index, principle components analysis, and cluster analysis

Estimation of variation of the collected maize landraces in the northern zone of Tanzania showed mean diversity index of (0.99) indicating existence of high variation within the collection.

Results are different from those obtained by Sioponco *et al.* (1999) which was (0.54) in maize, and low diversity index obtained by Manyasa *et al.* (2009) which was (0.32) in pigeon pea landraces. Contrasting findings could be due to differences in populations used. The variation in terms of qualitative and quantitative characters is important in selection and crop improvement (Yoshida, 1981).

High diversity index obtained in this study could be explained by the population itself having distinct genes different among and between the landraces. Environment could have contributed for expression of such diversity among and between the landraces collected. Conservation center for plant genetic resources could conserve this stock for further use of distinct genes in improvement work.

In this study first principle? component variations was contributed by days to tasseling, days to silking, plant height, number of primary branches, number of kernels per row, ear length, ear height and high negative loading was observed in ear diameter.

Second and third principle components were explained by cob diameter in common. However, 100 seed weight was high in the second and in the third the highest was tassel branches space. The fourth principle component had high loading on tassel peduncle length and number of kernel rows which differentiated with the fifth factor which had high loading on leaf width and high negative on grain yield and tassel peduncle length.

Lastly, sixth principle component had only one trait which contributed to variation among landraces with high loading on number of tertiary branches.

Six principle components obtained after data analysis are similar with results obtained by Ali *et al.*(2015) on wheat. Contrary results were obtained by Manyasa *et al.* (2009) and Ndiso *et al.*(2013) who found two principle components for maize and pigeon pea while Ali *et al.*(2011) obtained seven principle components on his study of sorghum. Beyene *et al.* (2005), Tanavar *et al.* (2014) and Mustafa *et al.*, (2015) reported four principle components from a study on maize.

The current study of maize landraces accounted for 84.23% of the total variation which coincides with the results obtained by Micic *et al.* (2013) which was (80.86%) on maize landraces of Yugoslavia. However a study done by Siopongco *et al.* (1999) showed 73.99% which is slightly lower on maize. Principle components produced account for the variation occurring at farm level which is attributed by environment. The broad trait diversity evident among the maize landraces suggests ample opportunity for genetic improvement of the crop through selection directly from the landraces and/or the development of inbred lines for future hybrid programs.

Results from this study produced three different clusters with few number of landraces in each cluster which signifies that the collection is very diverse and these clusters contain distinct characters from each other which is similar with results obtained by Beyene *et al.* (2005) and Khodarahmpour (2012) on maize. The predominant cluster with one to few landraces signifies diversity within a collection.

However these results do not support those obtained by Manyasa *et al.*(2009), Subramanian and Subbaraman (2010), Ali *et al.*(2011), Tanavar *et al.* (2014), Ali *et al.* (2015) and Mustafa *et al.*(2015), found four clusters on wheat, pigeon pea, maize ,and sorghum. Contrasting findings could be due to populations used.

The distribution of maize landraces in the study indicated that the geographical origin did not have any bearing on clustering pattern. Similar results were reported by Furat and Uzun (2010), Subramanian and Subbaraman (2010) on maize.

These landraces indicate that potential genes exist in Northern Tanzania for selection in maize crop improvement. Maize landraces are not static and continuously evolve due to the gene flow that farmers favor, their selection of maize characteristics for changing conditions, preferences and individual farmer selecting own maize type over time and farmers sharing seeds.

5.1.3 Morphological qualitative traits

5.1.3.1 Stay green

The findings indicate that landraces MP-BB1, AD-KR3, JL-KR5, BN-BB3, AJ-BB2, LE-MB2, DQ-BB5 and DA-MB4 can be used for livestock feeds and have genes for drought resistance due to their capability to retain greenish characteristic and is important trait in selection for landraces which use low nitrogen thus reduce inorganic fertilizer required (Arriola, 2006).

5.1.3.2 Kernel type

Evaluation on kernel type from this study indicated existence of different kernel appearance within and between landraces in which some were dent, semi dent, and semi floury. Similar observations were reported by Angelo *et al.* (2008). Landraces PD-KR2, DK-MB1, DK-KR1, DA-MB1, TD-KR4 and LE-MB2 can be used as gene donors on dent type since they are primarily used as animal feed, but also serves as a raw material for industry and as a staple worldwide (FAO, 2003; Brown and Darrah,1985).

5.1.3.3 Kernel row arrangement

Results from analysis of variance didn't show significant differences between the maize landraces collected. Similar results were reported by Angelo *et al.* (2008). DK-MB1, DM-KR1, MA-BB4, DA-MB4, DQ-BB4, MP-BB1, PD KR2, JM-AR1, TD-KR4, AD-KR3, JL-KR5, BN-BB4 and LE-MB2 showed regular type of kernel row arrangement which is a good trait in selecting maize cultivars for high kernel rows, high number of kernels per ear regarded as variables for high grain yield in maize crop production (Makoye, 2008).

5.1.3.4 Kernel colour

Rating of kernel colour displayed variation in this study. Some landraces were white, yellow, variegated, orange, and red. Studies conducted on maize displayed white, yellow and red colour (Angelo *et al.*, 2008). BN-BB3 and AJ-BB2 displayed yellow colour that can be used as gene donor. Increase in yellow color may reflect higher carotenoid content or lower fatty acid contents (Goldstein and Jaradat, 2013).

5.1.3.5 Husk cover

Husk cover didn't show significant difference between the landraces indicating less variation on this trait in the landraces under study. However there is need to increase diversity for this trait in future work. DK-MB1, DQ-BB5, MP-BB1, AJ-MB3, JM-AR1, AD-KR3 and AJ-BB2 showed good husk cover trait. This implies that the collection is good for avoiding ear rot disease and other post harvest insects. A similar observation was done by Warfied and Davis (1996) and Demissie *et al.* (2008) on maize. A good husk cover (husk going beyond the ear tip and tight husks) confers resistance to maize ears against the maize weevil (*Sitophilus zeamais*) in the field (Abadassi, 2015).

5.1.3.6 Leaf orientation

The scale indicated either erect or pendant and gave no room for other options. Most of the landraces were erect leaf orientation. Erect traits of maize landraces suits to be grown in any environment with little sun shine since they can capture easily sunshine for photosynthesis compared to pendant leaf orientation. Leaf orientation showed that the uprights/erect were considerably more productive. Factors other than more favorable light penetration through the canopies may be responsible for these results. Also upright leaf orientation on maize should favor ear formation (Pepper, 1974). In this study landraces that can be used as gene donors for erect orientation are JM-ARI, PD-KR2, AJ-MB3, DK-MB1, JL-KR5, DA-MB4, LE-MB2, DQ-BB5, AJ-BB2, BN-BB3, and AD-KR3, MP-BB1. Erect leaf orientation at the high plant population should provide more rapid canopy closure, enhance crop competition with weeds, and reduce dependence on herbicides while enhancing grain yields (Toler, 2013).

5.2 Genetic Variation of the Maize Landraces

5.2.1 Heritability broad sense

Results of heritability in the broad sense analysis for the studied variables showed that traits displayed high heritability values. The results are supported by Munawar *et al.* (2013), and Kumar *et al.* (2014) on maize respectively. High heritability for plant height was also reported by Khalil *et al.* (2011) and Kapoor and Chinka (2015) on wheat and maize. High heritability for grain yield had been reported by Shahrokhi *et al.* (2013) on maize. However Yagdi and Sozen (2009) reported low heritability for plant height in the study done on wheat. Miti *et al.* (2010) reported low heritability on grain yield for maize under low nitrogen experiment. Contrasting findings on this study could be attributed to differences in populations and environment

In this study the lowest heritability value was 67.09% for number of primary branches which is high according to standard classifications and the highest was 98.85% for days to silking. High heritability for plant height, grain yield and 100 seed weight in this study is similar to the results obtained by Majumder *et al.* (2008) on wheat and Devi *et al.* (2013) on maize. In the present investigation the heritability estimates were found to be high for grain yield per plant, plant height, ear height, 100 grain weight, days to 50 per cent silking which is similar to the results obtained by Vashistha *et al.* (2013) on maize. High broad sense heritability estimates were detected for plant height (95%), ear height (81%) as reported by Tengan *et al.* (2013) on maize.

The estimates of broad sense heritability values being high indicate that environmental factors did not greatly affect phenotypic variation of such characters

for the collected maize landraces and that selection can be effective in improvement programmes. This gives better idea on effectiveness of selection and predictability of trait transmission which can be made on the basis of these traits as observed by earlier scientists (Mustafa *et al.*, 2013).

5.2.3 Variances and coefficient of variation

The magnitude of genotypic coefficient of variation values for all traits were higher than the corresponding phenotypic coefficients of variation values indicating that these characters are influenced more by genetic effects. Similar results were reported by Munawar *et al.* (2013) in maize. However Kadri *et al.* (2010) observed that phenotypic coefficient of variation was higher than genotypic coefficient of variation in *Eruca* spp.

High genotypic coefficient of variation on plant height, ear height, number of kernels per row and 100 seed weight obtained in this study are similar to the findings observed by Kumar *et al.* (2014) on maize. Genetic variances and phenotypic variances were compared for the studied traits in this study and showed that relatively high genetic variances were observed for all variables indicating that the variables were highly influenced by genetic makeup among the maize landraces studied.

High genotypic coefficient of variation has also been reported by Vashistha *et al.* (2013) on anthesis silking interval, grain yield, ear height, harvesting interval, number of grains per cob, number of grains per row, and 100 seed weight thus offers

scope for genetic improvement through selection. The higher values of genotypic variance and genotypic coefficient of variance obtained in this study indicated that these traits can be used for selecting maize landraces for traits of interest.

5.2.4 Genotypic and phenotypic correlation coefficients for yield and yield components

Genotypic correlations among the traits studied showed that most of the traits were genotypically higher compared to phenotypic correlations implying these traits were associated genetically (Makoye, 2008). Genetic and phenotypic correlations help to know the relationship between phenotypic and genotypic relations on traits, these parameters are important in multi trait selection. Genotypically grain yield correlated significantly and positively with number of kernels per row (0.80) which agrees with findings of Wannows *et al.* (2010) who found positive significant genetic correlation of grain yield with number of kernels per row in maize.

Number of kernels per row showed significant positive correlation with 100 seed weight genotypically. Similar results were obtained by Yousuf and Saleem (2001) on maize. The trend of relationship of 100-grain weight with grain yield was positive and significant at genotypic level. Therefore selection based on these traits would be effective for increasing grain yield. Similar results were obtained by Reddy *et al.* (2013) on maize and rice respectively. Grain yield was significantly negatively correlated with ear height (-0.91) at genotypic level which is similar with results obtained by Olakojo and Olaoye (2011) in maize. Plant height displayed significant and positive correlation with ear height at genotypic and phenotypic levels. Similar

results were observed by Rafiq *et al.*(2010) on maize. This implies that these traits are inherent.

From this study the correlation coefficients of the pairs of characters revealed the presence of significant and positive genotypic correlation of grain yield with number of kernels per row and 100 seed weight. This indicated that increasing these attributes, could increase grain yield. The current study indicates that, number of kernels per row, 100 seed weight and grain yield were associated positively among themselves significantly, suggesting that selection for yield improvement can be done by selecting for number of kernels per row and 100 seed weight without compensation mechanisms among them.

5.2.5 Path coefficient analysis

Results on path coefficient analysis revealed that 100 seed weight correlated significantly positive with grain yield and indirect effects via plant height thus 100 seed weight interacts well with plant height in determining yield. Aslam *et al.*(1992) reported similar results on soybean. However the direct effect of 100 seed weight on grain yield was positive, but very low which do not qualify to be considered on yield increase.

Genotypic correlations between number of kernels per row and grain yield was significant and positive due to indirect effect of number of kernels per row via plant height. Therefore selection for more number of kernels per row will also increase grain yield. Similar results were reported by Ahmad and Saleem (2003) on maize.

This study suggests that selection for tall plants with high number of kernels per row and with heavier 100 seed weight will increase grain yield.

CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

Overall diversity index for all quantitative and qualitative traits for the studied materials showed that there was high variation ranging from 0.95 to 0.99. This indicated that we have potential material for breeding programmes at farm level. Cluster analysis also showed variation among maize landraces which signifies that some materials have distinct traits by forming clusters with few maize landraces in one cluster such as MP-BB1, TD-KR4, and BN-BB4 found in cluster three while six principle components were observed in this study. Genetic variation showed that the collection has high broad sense heritability for all traits studied indicating that environment has little influence on expression of these traits.

In path analysis, 100 seed weight and number of kernels per row had significant positive correlations with grain yield due to the strong positive interactions with plant height. 100 seed weight, grain yield and number of kernels per row were significantly positively related among themselves. Landraces such as DK-MB1, DQ-BB5, MP-BB1, AJ-MB3, JM-AR1, AD-KR3 and AJ-BB2 can be used as gene donors for resistance to ear rot disease and other post harvest insects. At farm level we still have diversity hence conservation strategy should be in place in order to conserve the existing diversity of maize in the Northern zone of Tanzania.

6.2 Recommendations

- (i) DK-MB1,DQ-BB5,MP-BB1,AJ-MB3,JM-AR1,AD-KR3, and AJ-BB2 are the best candidate for ear rot and post harvest insects due to its good husk cover trait.
- (ii) 100 seed weight and number of kernels per row were important trait for improvement of grain yield, therefore breeders should focus on these traits.

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