# ADAPTATION OF COMMONLY GROWN KENYAN POTATO CULTIVARS TO DIVERSE AGRO-ECOLOGICAL ZONES

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### (BPHIL BIOTECH. TUK)

Thesis submitted in partial fulfillment for the requirements of the degree of Master of Science in Plant Breeding and Biotechnology in the department of Plant Science and Crop Protection in the University of Nairobi.

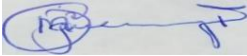**Department of Plant Science and Crop Protection, Faculty of Agriculture**

**University of Nairobi**

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# DECLARATION

This thesis is my original work and has not been presented for a degree in any other University
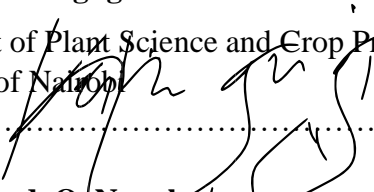
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## DEDICATION

I dedicate this work to the God Almighty, my strong pillar, my wife Beatrice and children Tessy Bosibori Maobe and Anthony Maobe for inspiring support. I also dedicate this thesis to my Mum The late Teresia Bosibori and the late sister Dorothy Consolata for their love. Finally, to my Dad who tireless supported me and my siblings with parental love.

# ACKNOWLEDGMENT

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# LIST OF ABBREVIATIONS

**CIP**-  International potato center

**COI**- Crossover Interactions

**FAO**- Food and Agriculture Organization

**GDP**- Gross Domestic Product

**GGE**-Genotype, Genotype-Environment

**GREG**- genotype regression

**KALRO**- Kenya Agricultural and Livestock Research organization

**MLND**-Maize Lethal Necrosis Disease

**PCA**- Principal Component Analysis

**RCBD**- Randomized Complete Block Design

**SREG** - Site Regression

**SVD**- Single Value Decomposition

# GENERAL ABSTRACT

Potato (*Solanum tuberosum L.*) grows best in cool areas where there is reliable water supply. Inadequate supply of water and elevated temperatures during growth and tuber formation significantly reduces tuber yield. Identification of potato genotypes that have a wider adaptation to different production environments that vary in temperature and humidity is increasingly becoming an important objective for potato variety development. The lack of stable and widely adapted potato varieties that can withstand the effects of unpredictable weather is a major contributor food and nutritional insecurity. Unstable and poorly adapted varieties are major limiting factors to potato production. This study aimed at evaluating and selecting genotypes that have broad adaptability, specific adaptation and stable for tuber yields across diverse environments. The approach was to test elite genotypes in different environments under conventional or farmers' practices and intensive management (high input production) systems.

Twenty-seven elite potato genotypes that were genetically diverse comprising of ten Table type genotypes and twenty-three Processing type genotypes were used in this evaluation. The genotypes were sourced from Kenya Agricultural and Livestock Research Organization (KALRO) and International Centre for Potato Improvement (CIP). The experimental design was Randomized Complete Block Design (RCBD) and replicated thrice. Genotypes, G5 G4 G6 G7 G9 G15 G16G18 G19 G21G23 G25 and G27 of the Table type and G1, G2, G3, G10, G12, G13, G14, G17, G22, G26 of the Processing type were screened in climatically diverse potato producing regions in Kenya during the long rainy seasons of 2015 and 2016**.** Each block measured, 35M by 11M with 1M spacing between blocks, 27 plots measuring 3 M by 3 M, and 1M foot path between plots. The genotypes were randomly allocated to plots and tuber yield data was scored at harvesting. The results indicated that genotypes interacted differently with the different environments. The genotypes and environments were also significantly different. The diversity in the genotypes and environments was the main factor that influenced variations in yield. This was an indication that the environments have elements that either favor potato tuber yield or act as limiting factors for tuber yields. These factors were mainly humidity and temperature. This was evident in the tuber yield variation across environment for each genotype. Regions with higher rainfall intensity and cooler temperatures during the growing period had higher yields compared to warmer regions with low and poorly distributed rainfall during the growing period. The levels of genotype by environment interactions were

considered to be the main causes of the yield inconsistencies that were observed between genotypes and within genotypes in different environments.

In conventional management, the genotypes and the environments were significantly different and, the genotypes also significantly interacted with the environment at (P<0.001). Narok location proved to be conducive for production of both Table and Processing type genotypes. The location had average yields of 29.26 t ha$^{-1}$ 28.15 t ha$^{-1}$ for Table and Processing type genotypes respectively. These yields were significantly above the yields from other evaluation environments.

During the intensive management evaluation, the Table type genotypes had a higher average tuber yield of 33.54 t ha$^{-1}$ whereas the Processing type genotypes that had an average tuber yield of 26.1 t ha$^{-1}$. Table type genotype, Kenya Karibu with 47.35 t ha$^{-1}$ mean yield and Processing type genotype, G2 with 37.8 t ha$^{-1}$ were the highest yielding genotypes. The least yielding Table type genotype was Sherehekea with 27.36 t ha$^{-1}$ whereas for the Processing type genotype, G5 had 19.5 t ha$^{-1}$ was the least yielding. Table type, genotype, G4 and Processing type, genotype, G22 were the most stable.

The environmental influence was responsible for the yield diversity. Narok and Suera locations provided conducive environment for the two types of potato genotypes whereas Kibirichia was not favorable for potato production. The intensive management practices influenced marginal tuber yield gain for both the Table and Processing types. The implementation of the intensive management can be best applied when the economic value of the yield under intensive management is well established.

## CHAPTER ONE: INTRODUCTION

### 1.1 Background information

The human population is on a rapid rise causing a huge demand on food supply systems (Clover, 2003). Sub-Saharan Africa (SSA) is experiencing a huge food decline due to climate change and other food production challenges (FAO, 2009). This has greatly contributed to the food insecurity situation of the sub-region. To adopt new varieties and crop production technologies designed to enhance productivity is a more feasible approach (Margaret and Kariuki, 2015). Therefore, special attention is given to productivity by way of using suitable varieties (Donkor et al., 2016).

Twenty-five percent of Kenyan's Gross Domestic Product (GDP) is obtained from Agriculture. This makes it the leading employer of approximately 75% of the country's workers (Muriuki et al., 2001). Improvement of the quality of agricultural inputs will uplift the living standards of many Kenyans who depend on agriculture both directly and indirectly (Patrick and Rosemary, 2006). Many people in the developing countries are food insecure and the prices of the stables are steadily rising but, the prices of potatoes have remained fairly stable (Hoffler and Ochieng, 2008). Potato therefore is a major crop that is a reliable source of food and can provide dependable employment to a major proportion of the population.

Limited attention has been given to tuber crops whereas great emphasis has been on cereals crops (Njuki, 2011). Food and Agriculture Organization (FAO), (2016) stated that Kenya's grain yields dropped by 6% due to abiotic and biotic production stress factors.  In order to boost food production, there is need then to also consider alternative crops such as tuber crops. For example, potatoes   which are highly nutritious, have short production cycle and about 85% of the crop is consumed in comparison to cereal crops which take a longer period to mature and less than 50% of it is consumed (Robertson et al., 2018). Potato is also a food security crop and thus it can be a major contributor in ensuring food and nutritional self-reliance for the country.

 Potato (*Solanum tuberosum L.*) is a major food crop globally with an annual global harvest of 320 million metric tons and ranked fourth after rice, wheat and maize. Like in many countries, potato is fast transforming into a cash crop in Kenya.  Potato production in the region is still

below the potential level of 22 tons per ha$^{-1}$ (Muthoni et al., 2013). Potato breeders have developed several of cultivars with an aim of improving it's production (http://cipotato.org/potato/facts/), but quite old varieties are still being grown (Michiel et al., 2016). The main reason why the yields are low is because of the effects of environmental factors. These factors are responsible for the genotype by environment interaction in the production locations. The preferred strategy is to evaluate new cultivars and the introductions in the target productions areas in order to select the most adapted and stable ones. The amount of land under potato production globally has been increasing in the last two decades but the yields per hectare are still low (FAOstat, 2016). The small scale farmers in East Africa have increased the amount of land that is under potato production mainly with the International Potato Center (CIP) cultivars (Gildemacher et al., 2009). However, there is no equivalent yield increase. The major reason for this low yield, is the insufficient production and distribution of quality seed (Tierno et al., 2014).

Kenya's potato yields are far below the potential levels of above 22 t ha$^{-1}$and above. The consumer demand is high especially in the urban centers (Wang'ombe and Meine, 2014). The low potato production is due to a number of challenges in the production and post-harvest handling processes that include lack of disease and pest free seeds, inefficient pest and disease management practices, unreliable marketing structures, lack of well adapted and stable varieties and a lack of clear policies along crop production chain (Riungu, 2011). Globally potato is a source of food and income to farmers and other players, such as wholesalers, retail traders and processors in the value chain (Nyankanga et al., 2004).

## 1.2. Potato production and consumption in Kenya

In Kenya, potato is ranked second after maize (Mutunga, 2014) and also the second widely grown crop (Muthoni et al., 2013). Potato has attracted between 500,000 to 800,000 farmers with productivity of 7.7 t ha$^{-1}$ (Nyankanga. et al., 2004). Among these farmers, 500,000 are small scale farmers producing potatoes on approximately 120,000 hectares and contributing more than KSh.50 billion to the Kenyan economy annually (USAID-KAVES, 2014). A few large scale commercial farmers practice mono-cropping while the majority small scale farmers,

practice mixed cropping where common beans / potato intercrop is the most widespread practice (Nyankanga, et al., 2004).

Kenyan farmers in the potato production regions grow different varieties for different markets. Some of these varieties are: Kenya Karibu, Kenya Mpya, Sherekea, Unica, Tigoni and Shangi among others (NPCK, 2017). There exist two market types, the market that converts harvested tubers to products like crisps and chips and utilizes Processing type of potato and the one that directly cooks the tuber locally which utilizes the Table types.

Kenya produces about 790,000 metric tons per year and is the leading producer in Sub-Saharan Africa (FAO, 2008). Potato is normally consumed as chips, boiled or mixed with bean and many other recipes (Nyankanga et al., 2004). Potato production in Kenya is low because of different factors such as inadequate and high cost of farm inputs, low soil fertility, pest and diseases among others (Muthoni et al., 2013).

In Kenya, potato is mainly produced in the highlands (1500-3000m) of Central, Eastern and Rift valley regions (Kaguongo et al., 2008; FAO, 2008). These regions are densely populated which has led to land fragmentation and hence most farmers grow potatoes in 0.5-2.5 acres of land (Fatunbi, 2018). This triggers the need to develop varieties that can be grown in other region to expand the production area by introducing well adapted varieties. Development of potato cultivars adapted to the environments available for potato production is one of the important steps towards increase of yield and profitability in farming (Gadum et al., 2003).

## 1.3. Problem statement and justification

The world population by the year 2013 had reached 7.2 billion and is projected to increase to 9.6 billion by the year 2050. The current food deficit will be expanding and the diversity in nutritional demands will be on the increase. As the population increases also new demands for agricultural land arise straining food production (Fatunbi, 2018). The available potato cultivars are not well adapted to the available production environments. Climate change has led to unpredictable weather patterns for example, low levels of precipitation has led to massive crop failure due to low soil moisture and atmospheric humidity (Cairns et al., 2012). There is need

to develop varieties that are adapted these diverse environments, to satisfy this demand (Fischer et al., 2014).

The East African potato market is on the increase with various consumer qualities for both Table and Processing types emerging (Fischer et al., 2014). This calls for breeding of potato varieties which are adapted to the production environments, stable and have consumer preferred properties such as color and taste (Ghislain et al., 2019). To address this, multi-locational trials were carried out to evaluate the effect of the environment on Table and Processing potato genotypes tuber yield performance (Gedif and Yigzaw, 2014).

Potato has not received much improvement attention largely due to its tetraploid genetic nature (Taylor, 2018) and this why, old cultivars with low yields are still grown. With this slow rate of improvement, the crop is vulnerable to both biotic and abiotic production constraints. The existing germplasm lacks sufficient levels of adaptability, resistance or tolerance to biotic and abiotic constraints (Li et al., 2010a). The triploid nature of potato presents unfavorable alleles which largely remain in the genome and become noticeable at each breeding cycle. These innate traits slow the improvement process. It takes long to select a genetically fit clones from triploid generations (Tang et al., 2017). Success in the search of well adapted and stable genotypes is also dependent on the use of reliable methods of analysis for stability and adaptability of genotypes.

Currently maize, the main food crop in Kenya is maize and is plagued by several biotic and a biotic stress factors (FAO, 2008). This has resulted in low yields being recorded in maize production fields with losses of between 34% and 100% (Lima et al., 2014; Manono, 2014). This drop in maize yields, has led to the need to evaluate alternative food crops such as potato for food security.

## 1.4. OBJECTIVES
### 1.4.1 Broad objective
To improve potato production in Kenya through screening and releasing of potato varieties that are stable and adapted to various potato producing regions.

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**1.4.2 Hypothesis**

High yielding potato cultivars, do not depend on production region and management practice.

**1.4.3   Specific objectives**

i. To determine potato genotypes adaptability and stability based on tuber yield in different selected potato growing regions under subsistence farmer management system.

ii. To evaluate the potato genotypes for tuber yield adaptability and stability under intensive management across selected potato growing regions.

**Hypothesis**

i)      Low input potato production system does not enhance the adaptability and stability of stability of potato genotypes.

ii)       High input potato production management system does not affect the adaptability and stability of potato genotypes.

# CHAPTER TWO: LITERATURE REVIEW

## 2.1 Origin of potato

The domestication of potato was first done in South America in the highlands of Andes and lowlands of South Central Chile (Hardigan et al., 2017). The crop then diffused from South America to Europe at around 16th century, after which it spread to the entire world. Potato cultivation started in Africa around 1830 in South Africa and in 1880 in East Africa by The British and German colonialists. The crop was brought to Kenya in the late 19th century by British East African Trading Company to be grown by the white settlers only in the white highlands (Durr and Lorenzl, 1980). Currently the potato production is practiced by many farmers in the country.

## 2.2 Botanical traits of potatoes

Potato is a member of the *Solanaceae* family and genus *Solanum* (Bradeen et al., 2011). It can be produced from seed potato tubers, true potato seed, apical and root cuttings processed through tissue culture techniques. Similarly, its roots can also grow from stolon's (Muthoni and Kabira, 2015) and develop into a full plant. Potato roots are best obtained from seed potato tubers. Potato plant has a stem system consisting of stem, stolon and tubers (Sadik, 2018). The stem is usually round to angular in cross-section supporting branches with green leaves which form a rosette or semi-rosette pattern (Sadik, 2018). Potato is known to be a short-day and cool-season crop, but can also be grown in wormer regions with provision of adequate water that is uniformly supplied to mitigate the transpiration demands (Salgado de Oliveira, 2015). Normally potato tuber seeds are preferred when compared with other forms of seed. The tuber seed is sown to a depth of 5 to 10 cm deep after a short while it develops root system.

The tuber seeds of high quality should be disease-free, well-sprouted and weigh between 30 to 40 grams per seed. After the plant has emerged, the photosynthetic process takes up the plant nutritional need and roots start absorbing water and mineral salts (Sterrett, 2015). Tuber setting occurs at the tips of the stolons and lasts for about two weeks followed by tuber bulking, accumulation of water, nutrients and sugars. The tubers finally mature and then the photosynthetic tissue loses function (Patil et al., 2017).

**2.3 Potato genetics**

The commonly cultivated potato genotypes include; tetraploid (2n = 4x = 48) with a basic chromosome number of 12, diploid (2n = 2x = 24) and pentaploid (2n = 5x = 60) levels (Machida-Hirano, 2015). Both cultivated and wild types are sources of genes that can be used for potato improvement (Watanabe, 2015). The diploid potato species are mostly grown in South America while tetraploids are distributed world-wide (Watanabe, 2015). The origin of potato tetraploid species is not clear. The available information points towards diploid chromosome doubling and because of this, the number of potato species differs greatly among the taxonomic levels (Machida-Hirano, 2015).

The existence of many species within a taxonomic level is advantageous because it provides a broad natural resource pool necessary for improvement. Increment of the ploidy levels is enhanced by the 2n nature and instances where of gamete reduction fails to take place (Carputo et al., 2003). Tuber seeds are the main potato propagation materials. The use of apical and rooted cuttings processed through biotechnological techniques is also gaining popularity. Most farmers prefer tuber seed as the convenient method of propagation (Gebreselassie, 2017).

Gene-flow is low among the *Solanum* species due to internal hybridization obstacles such as genomic structural differences and ploidy levels. This limits variation which is a major attribute to crop improvement. To enhance variation deliberate approaches have been made to transfer genes of interest from wild relatives to cultivated potato. This interspecies crossing requires a series of backcrossing to ensure the required qualities are present in the final progeny (Ramsay and Bryan, 2011). The other approach involves expanding the genetic base by having many genotype (Bradshaw, 2007). This method introduces new alleles and new genes enhancing heterozygosity. This process results in improved genotypes that can be used as parents in breeding programs (Bradshaw, 2007).

A low number of potato species have been explored for possibility of their use in potato improvement programs (Bradshaw, 2007a). These few that have been tried provide other traits that are not well understood by the research community. The use of wild relatives hosts a great potential for potato improvement however, it requires one to understand them in details before

using them (Gaiero, 2018). This a major limitation since there is limited information of the non-domesticated types. Modern genomic technologies can be of help in breaking the barriers of hybridization, to create room for crossing and predictable combinations (Gaiero, 2018).

The improvements achieved by hybridization procedure should have a commercial value and this is dependent on meeting the farmer, processor and consumer expectations. Many of the current varieties are highly susceptible pests, diseases and weather changes. This has led to heavy use of pesticides, an increase in the cost of production as well as poor yields that lead to food and environmental insecurity.

## 2.4 Potato production trends in Kenya

In Kenya, potato is cultivated in the short and long rainy seasons by a proximately 800,000 farmers. The annual production is about 3 million tons. The production of potato is mainly in the highlands (1500-3000 masl) where it is under rain-fed agricultural conditions in the Central, Eastern and Rift valley regions (Muthoni et al., 2017). Notwithstanding the contribution of potato to the economy of the country, its production has been unstable due to lack of high quality seeds, pests and diseases (Muthoni and Nyamongo, 2009). Unpredictable rainfall accompanied with elevated temperatures have contributed to poor yields (Muindi et al., 2013).

Potato production is practiced in the following in areas such as slopes of Mt. Kenya; Meru, Embu, Kirinyaga and parts of Laikipia, Aberdare Ranges, Nyeri, Muranga, Kiambu and Nyandarua. The crop is also grown in Mau-Narok, Narok and Molo and Tinderet, Nandi Escarpment and Cherangani hills. Small patches of potato farms are also found in Kericho, Kisii and Taita hills among others. The area under potato production in Kenya has been expanding (Janssens et al., 2013). Since the year 2006, both production and the economic benefits derived the potato values chain have been on increasing. The trend of production in has in the recent past been declining due to a number of constraints (Fig.2.1).
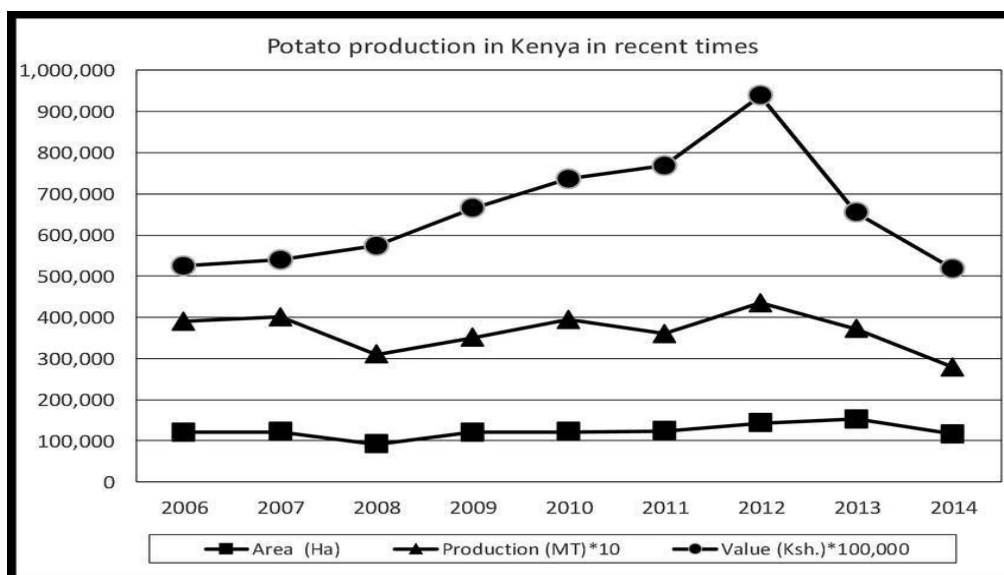
**Figure 2.1: Potato production trends in Kenya (Muthoni,2017)**

## 2.5 Potato production constraints

Potato farming is negatively affected by many production challenges such as limited access to quality seed, soil infertility, pest and diseases, poor seed packaging, lack of readily available market for potato and potato products (Muthoni and Nyamongo, 2009; Muthoni et al., 2013). Potato seed production in Kenya is below the demand from the farmers. The certified seed production is less than 1% of the domestic demand. The shortage has forced farmers to plant seeds from informal supply sources such as farm-saved seeds, seeds purchased from local markets and or from neighbors (Kyamanywa et al., 2011; Janssens et al., 2013). The informal seed supply system has led to a rise in diseases (late blight, bacterial wilt, viral diseases), pests (potato tuber moth) and nematodes resulting to low yields. (Schulte-Geldermann, 2013).

Increase in human population has resulted into increased land fragmentation which has led to increased mono-cropping hence depleting soil nutrients as well as accumulation of crop pests and diseases (Muthoni and Nyamongo, 2009). Continuous use of inorganic fertilizers has also resulted into increased soil acidity coupled with poor nutrient replenishment.
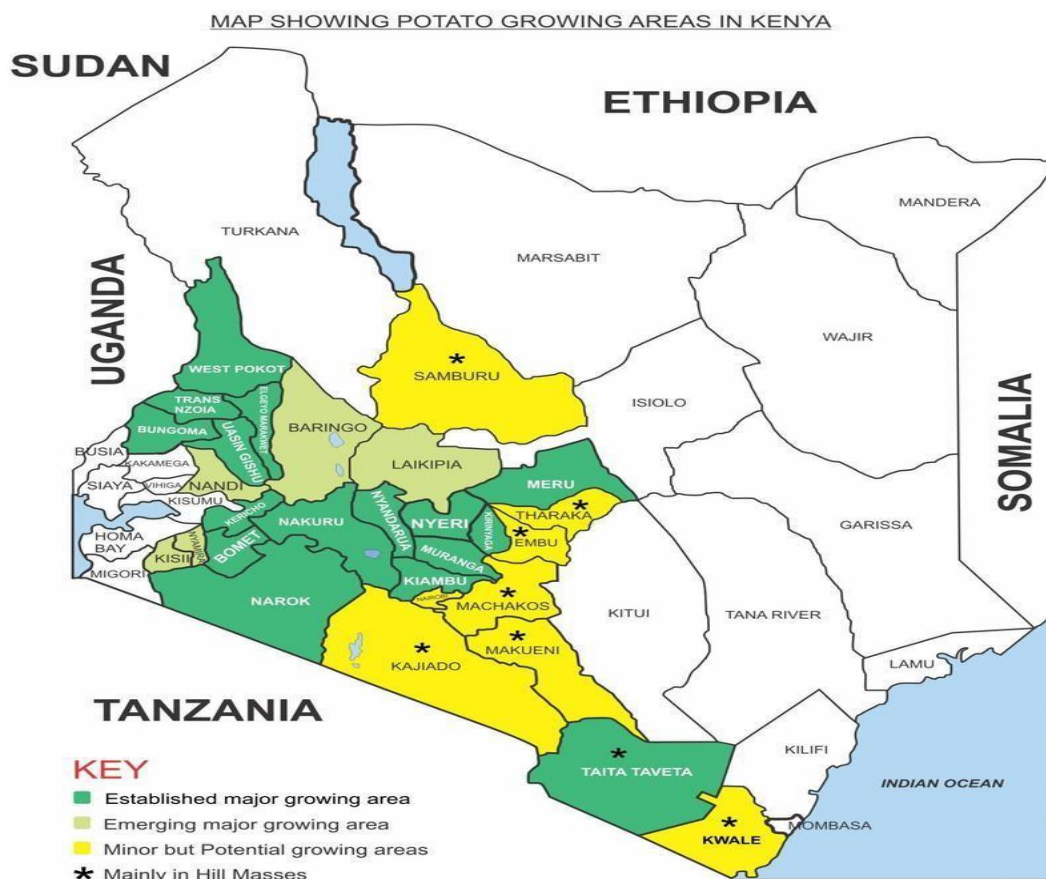
**Figure 2.2: Potato growing areas in Kenya (Muthoni,2016)**

## 2.6 Adaptability and Stability of Potato Genotype

Genotypes with high yielding ability and broad adaptation are most preferred (Obidiegwu et al., 2015). This is typical of genotypes with substantial genetic contribution to the observed yields and insignificant genotype environment interaction. The expression of genotypes provides information on how it relates with the environments. The individual genotype performance is the most critical aspect in establishing the genotype's value as a dependable variety to be released to farmers in a particular region or regions.

The variations in genotypes presentations in different environments delays the selection process (Demirel et al., 2017). This is because the process of identifying the genotypes that have desired traits and adapted in different environments is tedious and time consuming. Comprehensive information on how genotypes responds to environmental factors and the innate potential of genotypes is essential. The substantial variation among the genotypes over

environments is an indicator of major genetic differences between genotypes. These variances explain the diversity of genotypes that can be harnessed during selection and evaluation in different environments (Maharana et al., 2017).

Yield measurements are the most important parameters for consideration in variety development. Dependable recommendations require the deployment of reliable statistical methods that are discriminatory enough to establish the genotypes and environmental role in the expression of characteristics of interest especially yield (Hugh et al., 2016). These methods should account for adaptation and stability while sensitive enough to discriminately separate the environmental effects from the genotype and show the level of interaction. Yield is a quantitative trait that is obtained due to the interaction of various factors among them is the environmental factors (Dia et al., 2016). Establishing the nature and magnitude of the effects of these factors on genotype performance is important (Rukundo et al., 2013).

Analysis of genotype by environment interaction (G x E) guides the ranking of genotypes according to their performance in different environments. Understanding this interaction contributes to better measurements of the characteristics being improved such as yield in different environments. The genotype main effect (G) and genotype by environment interaction (GE) (GGE) provides an easy and effective evaluation method for analyzing and visualizing multi- environment data (Zulqarnain et al., 2017).

Plant improvement programs aim at creating superior varieties that are suitable to target locations, have desired qualities and with economic value (Brown et al., 1986). Achieving this is a major challenge due to the differential expression of genotypes from one location to another. The variation of the genotypes expression from one environment to the next is referred to as Genotype by Environment Interaction (G×E) (Ani et al., 2016). The inconsistence is due to environmental differences that affect the crop in growth and yield performance among other aspects (Crossa et al., 2004; Cabello et al., 2013, and Tamene., 2015). This differential expression is due to crossover interactions (COI) (Ani et al., 2016). These variations are responsible for the challenges in selection of candidates and matching them with their suitable

production environments. The ranking of genotypes on the basis of their performance across test locations helps in allocating genotypes their suitable production locations.

The genotype evaluation sites should have favorable conditions to minimize COI. Genotypes being evaluated are then ranked on the basis of their performance that can be linked to the genetic ability. Establishing the basis for this interactions can greatly enhance the matching of genotypes with the suitable locations (Ani et al., 2016). Determination of the factors influencing G×E is also important in determining the response of closely related genotypes to particular environments. These factors include soil characteristics, temperature, humidity and genetic composition of the genotypes (Ani et al., 2016).

Broadly adapted potato varieties are potent tools to tackle the impending threats of climate change and food insecurity (Zulqarnain et al., 2017). Use of the genetic resource is one of the approaches. Potato gene pool is a potential source of hereditary information that forms the foundation on which genotypes can be improved. It has also been reported that potato tuber productivity and quality in a given environment is genotype specific (Binod et al., 2016). This emphasizes the value seed quality has in improvement of potato productivity. Efforts are under way to breed and screen potato genotypes for adaptation to adverse agro-ecologies in a collaborative endeavor, unfortunately this gap is expected to grow bigger due to production challenges and climate change effects (Kivuva et al., 2015). To mitigate these challenges, efforts have to be directed towards increasing production areas (Fig. 2.2) and introduction of well adapted and stable varieties to new region that are suitable for potato production.

The environmental factors in different regions influence the way the genotypes express themselves phenotypically during multi-locational trials. This diversity in expression provides a foundation on which selection and crossing to generate new genotypes can be anchored. The significant genotype by environment interaction is a manifestation of broad genetic diversity among the genotypes however, it slows down the selection process (Gumu et al., 2017). Stability of a genotype is controlled by the homoeostatic potential that is due its genetic composition which enables the genotype to thrive in a given environment.

The relationship between the genes in different locus of the deoxyribonucleic acid (DNA) contributes to the phenotypic expression of the potato crop. Collectively heterozygosity and epistasis contribute to the manifestation of quantitative characteristics. It is not easy to identify the chromosomes responsible for any characteristic. The selection process helps in separation on the basis of observable phenotypic features (Watanabe, 2015). The different ploidy levels of potato present great diversity among the available genotypes. This is evident in the differences in alleles in the same locus, allelic interaction and segregation of both chromatids and chromosomes (Bradshaw, 1994). During random assortment several genetic combinations are expected which lead to phenotypic diversity (Watanabe, 2015).

The selection of high yielding and broadly adapted genotypes is the main objective of *Solanum tuberosme* improvement. This is a complex process because, the growth and development of crops is not only controlled by its genetic constitution but also the environmental factors (E) play a significant role (Xu et al., 2014). These interactions lead to a variety of phenotypic expressions depending on the different magnitudes of interaction (Muthoni et al., 2015). The outcome of G x E is a discrepancy in the genotypes performance across production environments. Such discrepancies arise from diverse gene expression due to the varying environmental factors (Muthoni et al., 2015). The differential expression can either be qualitative or quantitative (Mohammad et al., 2015). Therefore, reliable genotypes must be able to interact with the production conditions productively to meet both quality and high yield expectations. Stable and high yielding genotypes have low environmental interaction (Yan et al., 2006).

New improved genotypes should have superior characteristics than the existing ones for them to gain acceptability. Attributes such as adapted to diverse regions and high yielding with low production costs are important (Rodrigues, 2018). Multi-environments evaluations are used to establish the adaptability and stability of new lines while comparing them to locally adapted varieties (Ani et al., 2016). The genotypes' interaction with these heterogeneous environments provides information on stability and adaptability as either widely adapted or specifically adapted (Sholihin, 2017).

Genotypes with high yielding ability, broad adaptation and stable are most preferred. This is typical of genotypes with substantial genetic contribution and insignificant G x E interaction (Affleck et al., 2008). Therefore, the general reaction of tested genotypes gives an overview of the performance of genotypes in diverse environments. Comprehensive information on how a genotypes on evaluation responds to environmental factors and its innate potential is essential in decision making. The substantial variation among the genotypes across environments is an indicator of genetic richness of the genotypes (Maharana et al., 2017).

The most important parameters to be considered during variety development are yield quality and quantity as influenced by environment. Dependable recommendations then require deployment of reliable statistical methods that are discriminatory enough to establish the variety and environmental role in the expression of traits of interest (Hugh et al., 2016). Yield is a quantitative trait that is obtained due to the interaction of various factors both abiotic and biotic (Dia et al., 2016). Thus, understanding the type and the extent of these effects on genotypes' performance is important (Rukundo et al., 2013).

Genotype, Genotype-Environment (GGE) is one of the effective methods of evaluation and visualizing multi-environment data (Zulqarnain et al., 2017). Genotype by Genotype Environment Bi-plot have been used to conveniently analyze both mean of yields, stability and adaptability performance of genotypes across many environments (Zulqarnain et al., 2017). GGE can also be used to identify genotypes that have the similar sensitivity to the same environment by subdividing the environment into mega-environments (Zulqarnain et al., 2017). GGE Bi-plot has some limitations due to its lack of precision to measure with certainty aspects of mega–environments especially on genotypic performance (Xu et al., 2013).

The classification of genotypes as superior or inferior is determined by average yields as observed during multi-locational evaluation, which is due to G x E (Bai et al., 2014). On grouping test locations to one mega-environment GGE Bi-plot analysis provide an important approach for investigating this mega-region. The genotype stability is evaluated with the aid of the Average Environment Coordination (AEC) (Yan and Rajcan, 2002). Those genotypes that that have short distance from the AEC are considered stable and those far ways are highly

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influenced by environment. Reliable genotypes have high mean yield and high stability should be selected as the potential superior genotypes for advancement (Khamphas et al., 2015).

## 2.7 Methods of adaptability and stability analysis

Multi-environment trials data analysis can establish whether the selected genotypes are high yielding and stable under different production conditions or not. The analysis can be carried out on single season data from different environments or data collected from several seasons in a single environment (Ukalski and Marcin, 2016). The analysis helps to select the best environment for evaluating and genotype adaptability and stability. The results are then used to describe G x E interactions facilitating selection of genotypes for advancement for advancement and eventual cultivar release, that will help farmers get the desired yield as well as the consumer preferences (Gauch et al., 2008). This is possible if the adaptation patterns are stablished. Application of this approach is very important to variety developers (Zhao et al., 2016).

The ability of a cultivar to exhibit consistency in yield by achieving almost similar yields with low variations in different agro-ecological zones is termed as stable. Genotypes that exhibit this are very reliable because of the predictability of their performance. Variation in agro-climatic conditions among different potato production environments have an effect on cultivar yield (Arinaitwe et al., 2007). Varieties that show low $G \times E$ interaction are said to be stable and their performance is genetically controlled. This is why their yields are not much dependent on the environment but their genetic capabilities (Adjebeng-Danquah et al., 2017).

Yield performance data can be analyzed in several ways but not all methods can adjust it to give details of economic value (Gauch, 2008). The graphical presentations are the most popular, because they offer a wide range of explanations (Ukalski and Klisz, 2016). Biplot graphs have been identified as the ones with ability to give detailed information covering the genotypes, environments and genotypes by environments interaction (Sixto et al., 2015). Breeders now endeavor to manage the problems that arise due to genotype instability and utilize the gains that are associated with the instability in variety development (Gauch, 2008).

The expression of genotypes in different environments varies greatly and sometimes from season to season. These inconsistences in expressions provide a challenge selection of genotypes (Ani et al., 2016). More challenges arise when a genotype performance is greatly linked to a specific season. Analysis of this data requires use of appropriate methods. Several methods of analysis have been developed to help establish the adaptability and stability levels of genotypes in a more precise way (Mendes et al., 2014). These methods have been divided into two broad classes: parametric and non-parametric (Mendes et al., 2014). The parametric model also called univariate and multi-variate model employs statistical procedures to generate assumptions on data distribution just like linear regression while the non-parametric uses analytical ways to group the datasets to make generalized assumptions (Karimizadeh et al., 2012a). The univariate approach is inefficient in explaining the interaction aspects since they are made of many factors (Mendes et al., 2014). These methods require data to be displayed in a two-way table of means where the columns represent the environments and the rows represent the genotypes. The methods are based on three models described below,

a) $Mij = \bar{y}ij - \mu - cj = ri + rcij$

b) $Mij = \bar{y}ij - \mu - ri = cj + rcij$

c) $Mij = \bar{y}ij - \mu - ri - cj = rcij$ Where:

$Mij=$ Is the medium **M** with rows (genotypes), i = 1, …, k and l- tested environment = j = 1, ., l

$\bar{y}ij =$ the mean of $i$-th object in $j$-th environment $m=$ the overall mean $ri=$ the main effect of $i$-th object; $cj$ – the main effect of $j$-th environment;

$rcij$ – the interaction between $i$-th object and $j$-th environment

The first model ($Mij = \bar{y}ij - \mu - cj = ri + rcij$) generates its matrix by subtracting the grand mean and the main effects of the environment (columns) from the table of means values and factorizes it through Single Value Decomposition (SVD). Then the principal components are computed based on covariance or correlation matrix. The covariance matric is more reliable because it explains the variations (Yan, 2000). The principal component computation for the genotypes is divided by the root of the product genotype number and corresponding principal component eigen value and this results are similar to the use single value decomposition. This

can finally be presented graphically showing how genotypes interact with the environment and the genetic potential in each genotypes. The method is termed as Genotype, Genotype-Environment Interaction (GGE) by (Yan, 2000).

The findings from this method are similar to the one obtained by Site Regression (SREG) method proposed by Cornelius and Seyedsadr, (1997). GGE has more graphic explanations that particularly allow identification of any cross over interaction that arise from G x E interaction and facilitate pairwise comparisons (Ding et al., 2007). This presentation enables one to understand the interaction pattern between the genotype and environment, main effects and detailed dissection of the mega-environments and genotype genetic worthiness (Yan., 2007). The efficiency of GGE is highly dependent on analysis of variance output. When the interaction is significant GGE is the method of choice (Saxton, 2004). GGE is also efficient in analyzing observations where one of key factors under consideration is analyzed is randomly (Ukalski and Marcin, 2016). Employing GGE genotypes can effectively be categorized and ranked as well as environments (Yan, 2001). This method is more preferred to others because it is more specific to individual sites, genotypes and their interaction (Yan, 2001).

The second model (**Mij = ¯yij - μ - ri = cj + rcij***)* gives general view of the relationship between genotypes and the environment. This method only gives detailed information on environmental stability other than genotypes (Ukalski and Marcin, 2016). The results from this model are similar to those of genotype regression (GREG) methods developed by Finlay and Wilkinson, (1963) and Eberhart and Russell, (1966) who recommended the use genotype linear regression on environmental averages (Crossa, 2012). The reliability of description of the environment is only successful if principal component one and two are better than model (a) above (Ukalski and Marcin, 2014). In this model the overall mean is subtracted from the genotype main effect and the resultant matrix factorized by single value decomposition like (a) above (Cornelius and Seyedsadr, 1997). This is one of its main drawbacks because it fails to explain the genetic potential of a genotype.

In the third model, (**Mij = ¯yij - µ-ri − cj = rcij**) the matrix is arrived at from the interaction of the genotype and the environment. The results obtained through the use of this model are similar to that of Additive Main effects and Multiplicative Interaction (AMMI) (Gauch, 1992). This method is not efficient in identifying genotypes' genetic strength in different environments (Hugh et al., 2016) referred to as 'which-won-where'. This is because it removes genotypes' genetic effect, instead uses genotypes' sums of squares, interaction and residual. AMMI has a few graphical displays that limits the level of interpretation and hence low visualization of the results (Ding et al., 2007). The model can appropriately display with certainty general configuration of the way genotype(s) relates with the environment hence providing basis for analysis by a more sensitive model like GGE. The mega-environments that are generated by AMMI can only be explained if it is supported by some data like geographical information (Hugh et al., 2016). The AMMI method is a group of methods and thus requiring a keen scrutiny on which group is most appropriate to reveal the expected details (Gauch, 2013).

The most important aspects in multi-variate analysis is the genotype main effects and environment main effects and their interaction (Hugh et al., 2016). Both GGE and AMMI incorporate Principal Component Analysis (PCA) in their analyses and graphically display the results. AMMI integrates Analysis of Variance (ANOVA) and PCA to explain and quantify each genotype's contribution and environmental effects into interaction (Hugh et al., 2016). GGE is able to identify genotypes genetic potential, environmental effects, representative environments, stability of genotypes and discriminative environments (Hugh et al., 2016). For these reasons, in this study, GGE was used as the method of analysis to establish genotype environment interaction patterns.

# CHAPTER THREE:

# DETERMINATION OF ADAPTABILITY AND STABILITY OF POTATO GENOTYPES UNDER CONVENTIONAL MANAGEMENT

## 3.1 ABSTRACT

Tuber yield is the major characteristic that attracts both house hold utilization and commercial production of potato and utilization. Poor adaptation and stability are major constraint to potato production. Different potato production environments were used to evaluate Table and Processing genotypes during the long rainy season of 2015/2016. The study aimed at selecting potato genotypes that were well adapted with high and consistent tuber yield across selected agro-ecological zones in Kenya. Twenty-three (23) potato genotypes developed by Kenya Agricultural and Livestock Organization (KALRO) and International Potato Center (CIP) program were used in this study. The materials were evaluated alongside four commonly grown varieties as checks. Out of 23 genotypes, eleven (11) were Processing type and twelve (12) were of Table type. The experiments were conducted in the following regions; Molo, Burnt Forest, Cherengany and Narok, Timau and Kibirichia Kenya. The genotypes were evaluated in diverse regions using randomized complete block design (RCBD) with three replications. The experiments were managed based on conventional farmer practices in the target areas. Data on tuber yield was collected and was subjected to combined analysis of variance using R-Program. The stability and adaptability of the genotypes was determined using Genotype, Genotype-Environment (GGE) interaction model.

The findings showed that the environments, genotypes and the interactions of genotypes with the environments were highly significant (P<0.001). Table type genotypes had high yields compared to Processing type genotypes in all environments. The highest tuber yield was recorded in Narok where Table type genotypes yielded an average of 29.26 t ha$^{-1}$while Processing type genotypes produced 28.15 t ha$^{-1}$. Within this area, G13 was the high yielding genotype with 26.49 t ha$^{-1}$ among the Table type genotypes whereas G2 had the highest tuber yield among Processing type genotypes with 21.85 t ha$^{-1}$. G2 had yield 0.76 t ha$^{-1}$ yield advantage compared to the check whereas G13 had 1.84 t ha$^{-1}$ yield advantage compared to the best check among Table type genotypes.

G10 was the most stable genotype among the Processing type genotypes whereas G6 was the most stable among the Table types. Genotype adaptability and yield stability are very important aspects that determine cultivar's suitability to mitigation of food insecurity. Stability and adaptability are associated with the genotypic response to environmental factors.

**Key words**: **Adaptability, Environment, Genotype, Stability**

## 3.2 INTRODUCTION

Potato production in Kenya has been on a declining trend (Wang'ombe and Meine, 2014) due to invasion by insect pest and diseases both in field and in stores. The use of poor quality seeds, poor crop management practices, lack of well adapted and stable cultivars has greatly contributed to the declining trend. Among these factors, the quality of potato seed planted is important in determining the yield performance expected. Farmers need high yielding and stable cultivars to be able to meaningfully contribute to the enhancement of food security. Varieties with such characteristics can easily be adopted for long term production in contrasting environments. Such varieties are able to overcome the challenges of genotype environment interaction (G x E) (Gedif and Yigzaw, 2014)

Selecting genotypes that consistently give high yields is a challenge to potato variety development. The challenge is mainly due to the lack of full genetic expression of the progenies. This is becoming a major objective for variety developers (Affleck et al., 2008). Cultivar performance is determined by genotypic main effect (G), environmental influences (E) and the interaction between genotypes and environments (GE) (Yan et al., 2001). Hongyu et al., (2014) recommended that it is important to establish the behavior of the elite genotypes in different environments as part of the evaluation processes. This helps breeders to accurately determine the stability and adaptability of the genotypes. Stability of genotypes can be measured in all traits of interest to the farmer, processor and consumer (Affleck et al., 2017). Cotes et al., (2002) and Sabaghnia et al., (2012) classified stability into two categories, static stability which refers to the ability of a genotype to give the same or closely related yield across different environments and dynamic stability as the performance of a genotype compared to

the environmental average. This is why a high yielding genotype in one location may be the least performing in a different agro-ecological zone (Maharana et al., 2017).

Affleck et al., (2008) described a dependable genotype as one that has low value of interaction with the environment and high yield mean. Genotypes that show high stability in varying environments and high mean are preferred as opposed to the fluctuating ones. There is no environment that is ideal to all potato cultivars. The suitability of the environment will depend on how it enhances the expression of the genotypes. Therefore, is need to establish the appropriateness of the environments for potato production and match it with the its adapted genotypes (Ingleby et al., 2010). A stable cultivar should be able to produce high and consistent yields in different potato growing regions. Cultivars respond differently to environmental pressures thus there is need to understand the type and the magnitude of these pressures by measuring the interaction effects. Borges et al., (2010) suggested that the genetic potential of new lines to be released as a variety should be subjected to relevant pressures in order to establish its genotypic strength. This will help in developing recommendations based on their true genotypic values. Potato has many traits that can be of interest to breeders but it is the tuber yield that attracts most players in the potato value chain (Meenakshi et al., 2018 and Silva et al., 2018). Genotypes with large genotypic effect and a low variation across environments are considered more stable (Gauch, 2006) and can be released as varieties when they meet other important parameters.

## 3.3 MATERIALS AND METHODS

### 3.3.1 Description of the study area

The study was conducted in six locations namely Molo, Narok, Cherengangy, and Burnt Forest in Rift Valley, Timau in Meru and Kibirichia in Eastern Kenya during the long rainy seasons 2015 to 2016 (Table 3.2). The study locations were selected from areas that are known for potato production. The sites represent mid to high altitude regions with diverse agro-ecologies where potato farming is widely practiced. These locations receive different amounts of rainfall annually as well as varying temperatures with well-drained loamy soils and experience a bimodal rainfall pattern annually (Table .3.2 and Fig.3.1).
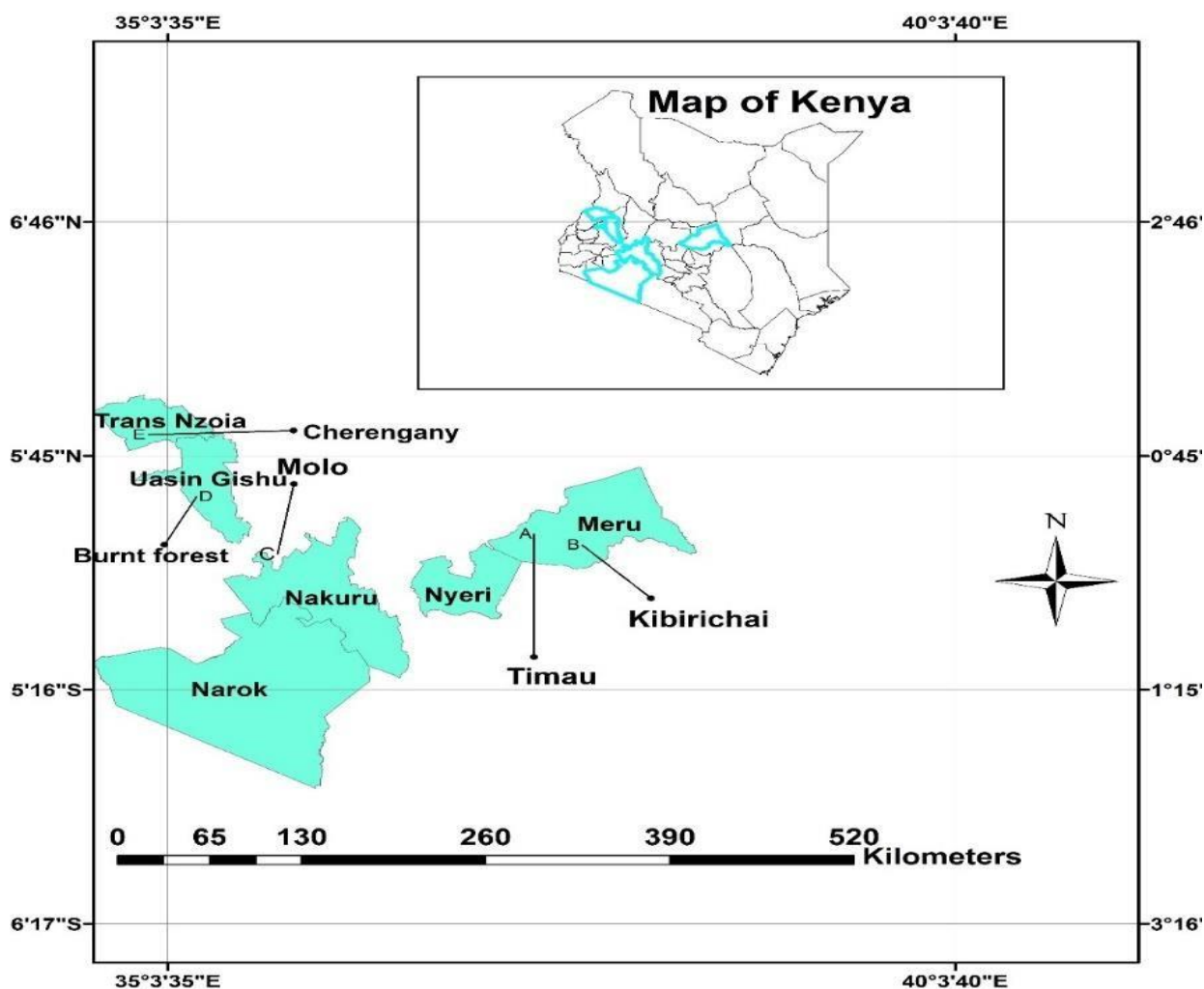
**Figure 3.1: Map of Kenya showing the evaluation environments**

### 3.3.2 Potato genotypes

The genotypes used were both the Table and Processing types and were obtained from Kenya Agricultural and Livestock Research Organization (KALRO) Tigoni and International Potato Center (CIP). Standard varieties were used as checks during the evaluation, twenty-three genotypes and four commercial checks were used. The commercial checks were G20 (Shangi), G11 (Kenya Karibu), G24 (Tigoni) for the Table type genotypes whereas G8 (Dutch Robjyin) was the check for Processing type genotypes (Table 3.1)

**Table 3.1: Potato genotypes that were evaluated for tuber yield under conventional management**

| Type | Genotypes | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Processing | G5 | G15 | G23 | G25 | G19 | G7 | G4 | G6 | G18 | G16 | G27 | G9 | G21 | G20 | G11 | G24 |
| Table | G2 | G22 | G13 | G10 | G26 | G3 | G17 | G1 | G12 | G14 | G8 | | | | | |

[1]The Table and processing genotypes that were evaluate under conventional management

### 3.3.3 Field experimental layout and design

In each of the selected sites, the experiments were managed using the subsistence potato farmer production routines from planting to harvesting. Di-ammonium Phosphate fertilizer was applied at a rate of 500kgs per $Ha^{-1}$(DAP), weeding was done ones. The experimental design was Randomized Complete Block Design (RCBD) with three replications measuring 35M by 11M with 1M spacing between blocks. Each block was further subdivided into 27 plots each measuring 3 M by 3 M, with spacing of 1M between each plot. The 27 genotypes were randomly allocated into each plot and planted. Furrows were made in each plot at a spacing of 75 cm from each other. Fifty seed tubers were planted at a distance of 30cm from each other 10 plants per row and 50 plants per plot and a population of 1,350 plants in each block. The stems were cut off at 90 days to enable tuber hardening and harvested 15 days later. Tuber yield data per treatment and site was collected and computed to tons per hectare.

### 3.3.4. Genotype, genotype-environment interaction model

The model for a GGE Biplot based on singular value decomposition (SVD) of the principal components was used involving application of the following three formulae

A) Yij- $\mu$ E j=O₁[ᵢ₁ηj1 O₂[ᵢ₂ηj2+Hij (1) Where:

Yij = the performance of genotype **i** in environment **j**, **μ** = the grand mean,

**βj**= the main effect of environment **j**,

O**₁**= singular values (SV) for the first principal component

O**₂**= singular values (SV) for the second principal component

[ᵢ₁ = eigenvector of genotype i for PC1

[$_{i2}$= eigenvector of genotype i for PC2

$\eta_{j1}$ = are eigenvectors of environment j for PCl $\eta_{j2}$ = are eigenvectors of environment j for

PC2 $\varepsilon ij$ = is the residual associated with genotype i in environment j.

Since PC1 and PC2 eigenvectors cannot be plotted directly to give a more detailed Biplot before the singular values are partitioned into the genotype and environment eigenvectors. Then singular value was partitioned into environment and genotype using the following formulae

b) gil=O1fi[i1 and eij=O11-fi$\eta$j1 (2)

c) To generate the GGE Biplot, the formulae was presented as

d) Yij- $\boldsymbol{\mu}$ E j=g$_{i1}$e$_{1j+}$ g$_{i2}$e$_{2j+}$ $\varepsilon ij$ (3)

Genotypes with the least interaction with the environment were considered the most stable. This was based on the tuber yield consistency of a genotype as visualized by the GGE software. The productivity of such genotypes is much dependent on their innate properties rather than on the environment. The stable ones with high yields across many environments are considered broadly adapted. Those that were high yielding in specific environments were considered as specifically adapted. The value of the interaction was obtained by getting the difference between the mean of each environment and the grand mean of the experiment. If the answer was negative the environment was considered unfavorable and a positive one was considered favorable environment.

### 3.3.5 Data analysis

Analysis of variance (ANOVA) for tuber yield data of the genotypes and environments was conducted using R statistical software. Least Significant Differences (LSD) at 5% was used to separate means of treatments. The multiplicative effects of G×E interactions were assessed using principal component analysis (PCA1 and PCA2) of the GGE Bi-plot software by adopting the following formula as recommended by (Yan, 2000).

$$Y_{ij} = \mu + \beta j = \lambda 1 \xi i 1 \eta i j 1 + \lambda 2 \xi i 2 \eta i j 2 + \varepsilon i j$$

Where: $Y_{ij}$ = the performance of genotypes **i** in environments **j**, $\boldsymbol{\mu}$ = the grand mean, $\boldsymbol{\beta j}$= the main effect of environments **j**, O$_1$= singular values (SV) for the first principal component, O$_2$=

singular values (SV) for the second principal component, [$_{i1}$ = eigenvector of genotypes i for PC1, [$_{i2}$= eigenvector of genotypes i for PC2, $\eta_{j1}$ = are eigenvectors of environments j for PCl, $\eta_{j2}$ = are eigenvectors of environment j for PC2 and **$\varepsilon_{ij}$** = is the residual associated with genotype i in environment.

## 3.4 RESULTS

### 3.4.1 Effect of different environments on yield of various genotypes

The analysis of variance for Processing type genotypes showed that genotypes, environments and their interactions were highly significant at ($P<0.05$) for the tuber yield (Table 3.3). There was significant difference in genotypic effect on tuber yield for Burnt Forest, Molo, Narok and Timau. Cherengany and Kibirichia recorded the lowest (Table 3.4).

**Table 3.2: Geographical and climatic description of the experimental areas**

| Location | Altitude (masl*) | AEZ | Annual rainfall | Mean Annual Temperature | |
|---|---|---|---|---|---|
| | | | | Minimum | Maximum |
| Molo | 2506 | Zone II | 1131 | 16 | 24 |
| Narok | 1827 | Zone III | 771 | 9.2 | 26 |
| Cherangany | 2,047 | Zone II | 1,200 | 14 | 30 |
| Burnt Forest | 2419 | Zone II | 1103 | 12 | 25 |
| Timau | 1767 | Zone II | 587 | 6.9 | 23.3 |
| Kibirichia [2] | 1827 | Zone III | 24 0 | 16 | 24 |
| Suera | 2300 | Zone II | 913 | 14 | 24 |

[i] Evaluation locations, their elevations, agro-ecological zones, average rainfall per year, minimum and maximum temperatures

\***masl** = meter above sea level.

**Source**: National Meteorological Agency.

**Table 3. 2: Analysis of variance for tuber yield among Processing potato type genotypes in six environments during the long rainy seasons of 2015 and 2016**

| Source of variation | D.F. | S.S. | M.S. | V.R. | F PR. |
|---|---|---|---|---|---|
| Rep | 2 | 142.52 | 71.26 | 2.62 | |
| Genotype | 10 | 1331.83 | 133.18 | 4.9 | <.001 |
| Site | 5 | 11747.83 | 2349.57 | 86.5 | <.001 |
| Genotype. Site | 50 | 2718.32 | 54.37 | 2 | <.001 |
| Residual | 328 | 8908.94 | 27.16 | | |
| Total | 395 | 24849.44 | | | |

[3] Variance between genotypes, environments and interaction

**DF- degrees of freedom, S.S-sums of square, M.S-mean sums of square, V.R-variance, FPR-probability**

**Table 3.3: Mean tuber yields in t ha$^{-1}$ of Processing type genotypes among test environments during the long rainy seasons of 2015 and 2016**

| YIELD T HA$^{-1}$ | | | | | | | |
|---|---|---|---|---|---|---|---|
| Genotype | B. Forest | Cherengany | Kibirichia | Molo | Narok | Timau | Mean |
| G2 | 29.07 | 15.75 | 11.88 | 19.67 | 30.43 | 24.32 | 21.85 |
| G22 | 20.08 | 14.73 | 13.58 | 18.5 | 30.76 | 27.54 | 20.87 |
| G13 | 13.91 | 11.93 | 17.14 | 20.52 | 32.62 | 24.31 | 20.07 |
| G10 | 16.67 | 15.00 | 15.15 | 19.75 | 30.91 | 22.43 | 19.99 |
| G26 | 16.56 | 17.52 | 12.66 | 22.3 | 24.93 | 24.37 | 19.72 |
| G3 | 18.27 | 11.01 | 11.47 | 19.51 | 27.43 | 27.37 | 19.18 |
| G17 | 21.38 | 10.76 | 12.78 | 18.51 | 23.23 | 26.4 | 18.84 |
| G1 | 12.3 | 14.85 | 13.21 | 21.01 | 25.74 | 23.56 | 18.45 |
| G12 | 15.12 | 14.73 | 11.22 | 15.8 | 25.63 | 20.81 | 17.22 |
| G14 | 8.88 | 9.66 | 12.17 | 12.19 | 26.33 | 21.16 | 15.07 |
| G8 | 11.54 | 15.14 | 17.72 | 22.07 | 31.61 | 29.04 | 21.19 |
| **MEAN** | **16.71** | **13.73** | **13.54** | **19.08** | **28.15** | **24.66** | **19.31** |
| LSD Genotype 2.417 | | | | | | | |
| LSD Environment 1.785 | | | | | | | |
| LSD Genotype x environment 5.919 | | | | | | | |

[4]Mean processing tuber yield across evaluation sites

Among the Processing type genotypes, G2 had highest average yield (21.9 t ha$^{-1}$) whereas G14 performed poorly across all the evaluation environments with a mean tuber yield of 15.07 t ha$^{-}$

[1]. The yield of G14 was 6.12 t ha$^{-1}$ less than that of the check variety (Table 3.4). Among the Table type genotypes, G5 (26.49 t ha$^{-1}$) and G15 (24 t ha$^{-1}$) were high yielding across the evaluation sites. The best check was G20 that had 23.65 t ha$^{-1}$ as the overall average tuber yield. Genotypes, G4 and G7 were high yielding than G20 and G24 the commonly grown varieties in Burnt Forest. The lowest yielding genotype was G21 with a yield range of between 12.86 t ha$^{-1}$ and 24.55 t ha$^{-1}$ (Table 3.4).

The two types of potato performed differently leading to different environmental means. All the Processing type genotypes showed significantly different environmental means except for Cherengany and Kibirichia which had near similar yield (Table 3.4). The Processing type genotypes, G2 (29.1 t ha$^{-1}$) and G22 (20.1 t ha$^{-1}$) produced higher yields in Burnt Forest than G8 (11. 54 t ha$^{-1}$) (Table 3.4). In Cherengany, G2 (15.75 t ha$^{-1}$) and G26 (17.52 t ha$^{-1}$) were the highest yielding genotypes. In Kibirichia the check varieties G13 and G8 had closely related yields in of 17.14 t ha$^{-1}$ and 17.72 t ha$^{-1}$ respectively. In Molo, G26 and G13 yielded 22.3 t ha$^{-1}$ and 32.62 t ha$^{-1}$ respectively. In Narok the yields of G26 and G13 were not significantly different from the check varieties (Table 3.4).

**Table 3.4: Analysis of variance for tuber yield among Table type genotypes during the long rainy seasons of 2015 and 2016**

| Source of variation | D.F. | S.S. | M.S. | V.R. | F PR. |
|---|---|---|---|---|---|
| Genotype | 15 | 2622.23 | 174.82 | 4.94 | <.001 |
| Site | 5 | 15050.32 | 3010.06 | 85.11 | <.001 |
| Genotype. Site | 75 | 9308.56 | 124.11 | 3.51 | <.001 |
| Residual | 478 | 16905.18 | 35.37 | | |
| Total | 575 | 44699.17 | | | |

[5] Analysis of variance for processing genotypes

**DF- degrees of freedom, S.S-sums of square, MS-mean sums of square, VR-variance, FPR-probability**

**Table 3.6: Average tuber yields of Table type genotypes among test environments during the long rainy seasons of 2015 and 2016**

| | yield t ha$^{-1}$ | | | | | | |
|---|---|---|---|---|---|---|---|
| Genotype | B.Forest | Cherengany | Kibirichia | Molo | Narok | Timau | Mean |
| G5 | 32.49 | 34.59 | 12.61 | 24.1 | 27.05 | 28.08 | 26.49 |
| G15 | 32.96 | 26.49 | 15.85 | 19.6 | 25.56 | 23.52 | 24.00 |
| G23 | 16.34 | 13.57 | 16.99 | 19.82 | 31.89 | 27.77 | 21.06 |
| G25 | 16.84 | 18.26 | 20.15 | 20.47 | 26.04 | 22.52 | 20.71 |
| G19 | 13.85 | 14.34 | 16.78 | 19.81 | 32.8 | 26.39 | 20.66 |
| G7 | 20.98 | 11.36 | 11.67 | 16.42 | 36.66 | 26.17 | 20.54 |
| G4 | 20.78 | 19.13 | 12.3 | 17.79 | 28.19 | 22.88 | 20.18 |
| G6 | 17.22 | 24.33 | 7.83 | 19.32 | 25.67 | 24.35 | 19.79 |
| G18 | 19.11 | 15.55 | 10.81 | 20.3 | 30.67 | 22 | 19.74 |
| G16 | 26.97 | 12.4 | 9.84 | 16.18 | 25.57 | 25.12 | 19.35 |
| G27 | 15.54 | 12.72 | 15.13 | 20.95 | 27.12 | 23.67 | 19.19 |
| G9 | 17.95 | 8.99 | 7.72 | 20.69 | 32.34 | 27.22 | 19.15 |
| G21 | 12.9 | 12.86 | 13.29 | 23.93 | 24.55 | 18.92 | 17.74 |
| **Check(S)** | | | | | | | |
| G20 | 18.34 | 27.76 | 13.15 | 21.05 | 32.82 | 28.75 | 23.65 |
| G11 | 24.48 | 22.98 | 9.72 | 16.97 | 33.19 | 28.22 | 22.59 |
| G24 | 14.35 | 26.61 | 10.77 | 24.56 | 27.98 | 22.41 | 21.11 |
| Mean | 20.07 | 18.87 | 12.79 | 20.12 | 29.26 | 24.87 | 21 |
| LSD Genotype 2.754 | | | | | | | |
| LSD environment 1.687 | | | | | | | |
| LSD genotype-environment 6.747 | | | | | | | |

[6] Mean yields of Table type genotype in different environments

The Table types genotypes displayed better performance in comparison to the Processing type across all evaluation environments. The analysis of variance showed significant differences between genotypes and also between the environments at (P<0.05) (Table 3.5). The highest yields were recorded in Narok (28.2 t ha$^{-1}$) for Processing and (29.3 t ha$^{-1}$) for Table type genotypes. Kibirichia was the lowest yielding location with 29.3 t ha$^{-1}$and 12 t ha$^{-1}$ for Processing and Table types respectively.

Table type genotypes had different yields across the evaluation locations. Genotypes, G5 and G15 consistently gave high yield in five out of six environments (Table 3.6). G5 (32.49 t ha$^{-1}$) and G15 (32.96t ha$^{-1}$) were the highest yielding genotypes compared to the check variety, G11 (24.48 t ha$^{-1}$) in Burnt Forest (Table 3.6). In Cherengany, G5 (34.59t ha$^{-1}$) out performed all the other genotypes. In Molo, G5 (24.1 t ha$^{-1}$) was the best genotype and its yield was closer to that of the best check variety G24 (24.56 t ha$^{-1}$). G7 (36.6 t ha$^{-1}$) was the out-standing genotype in Narok with a yield advantage of 3.47 t ha$^{-1}$ compared to G11 (33.19 t ha$^{-1}$) (Table 3.6). The performance of, G5 (28.08 t ha$^{-1}$) and G20 (28.75 t ha$^{-1}$) were not significantly different in Timau. G5 had a high yield of 26.49 t ha$^{-1}$and was outstanding in Burnt Forest, Molo, Cherengany and Timau. G20 was the best check variety with average yield of 23.65 t ha$^{-1}$ (Table 3.6). The highest tuber yield was observed in Narok at 29.26 t ha$^{-1}$ whereas was the lowest Kibirichia 12.79 t ha$^{-1}$ (Table 3.5 and 3.6).

**3.4.2 Adaptability and stability of the Processing and Table types genotypes**

Genotype, Genotype-Environment (GGE) Biplot analysis was used in establishing the relative performance of genotypes, environmental interaction and the similarity between the test environments based on genotypes mean yields. Genotype, Genotype- Environment biplot analysis revealed different levels of interaction in different environments Kibirichia was identified as a low yielding environment for all potato genotypes. Genotypes G13, G26 and G8 had higher compared to G1, G3, G10, G12 and G14 (Fig. 3.1). Burnt Forest and Timau had low interaction with the environment hence positive PC2 and PC1. Genotypes, G2 and G22 had positive PC2 and PC1 value meaning they had very low genotype environment interaction had specific adaptation (Fig. 3.2). Cherangany, Molo and Kibirichaia had a negative PC2 but a positive PC1 also the genotypes in the same quarter had a negative PC2 and a positive PC1

value. This implies that they had a significantly high genotype by environment interaction and with high yield (Fig. 3.2). Genotypes G1, G3, G10, G12 and G14 performed poorly. The GGE Bi-plot for Processing type showed that PC1 and PC2 accounted for 43.7% and 24.4% of GGE sum of squares respectively and collectively explaining a total of 68.1% variation.
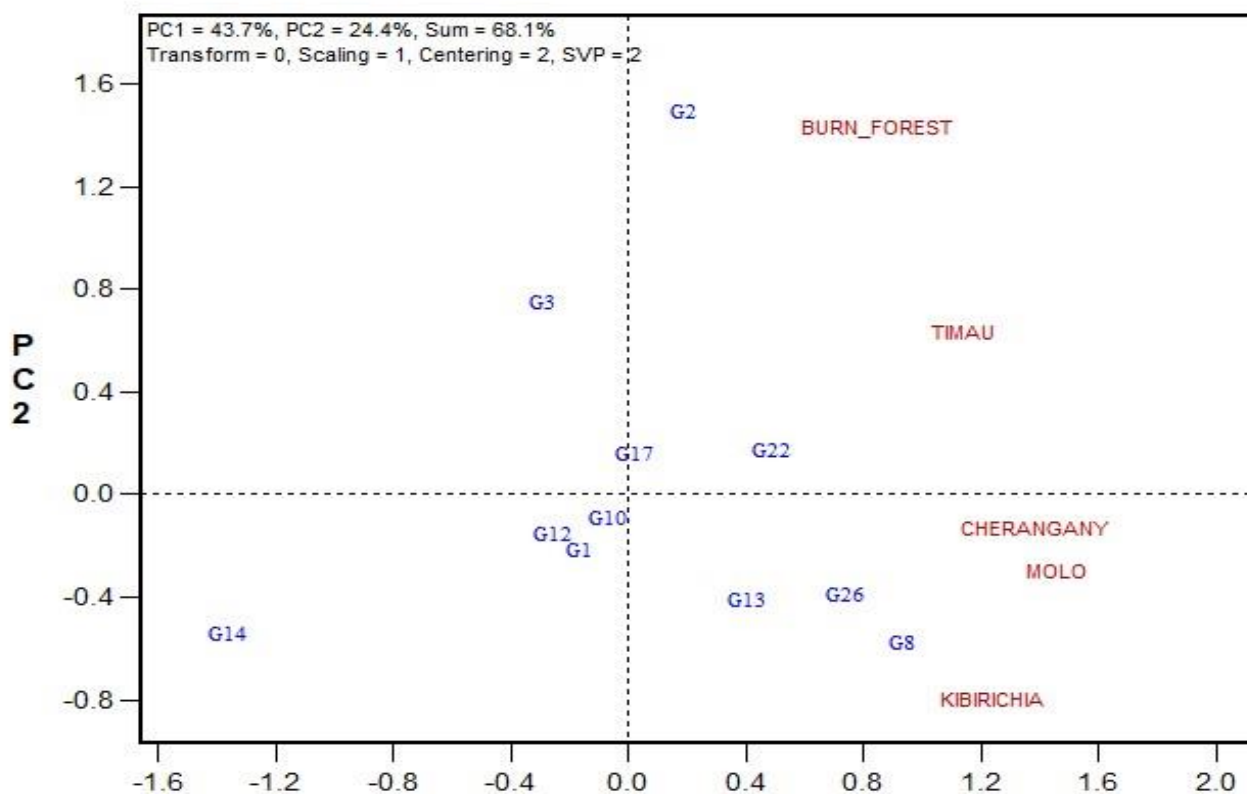
**Figure 3.2: GGE-biplot showing the relative performance of Processing potato genotypes in Burnt Forest, Timau, Cherangany, Molo and Kibirichia during the long rainy seasons of 2015 and 2016**

The bi-plot in Fig.3.2 indicates that Burnt Forest and Timau environments and genotype G2 and G22 had positive PC1 and PC2 values meaning that the genotypes had less interaction with the two environments. The remaining environments had negative PC2 and positive PC1 indicating that the genotypes in them had higher interaction with the environment. G2 was best suited in Burnt Forest whereas G8 was for Kibirichia. G14 was the weakest genotype. PC1 accounted for 43.7% and PC2 accounted 24.4% of the variations observed and cumulatively explained 66.1% of the observed variation (Fig.3.2).

The Table genotypes had different yield performances across environments (Fig.3.3). Genotypes, G15 and G5 were the specifically adapted to in Cherengany and Burnt Forest, the two environments had low interaction with the genotypes. G15 displayed better performance in Burnt Forest where it was specifically adapted whereas G5 performed best in Cherengany where it also had specific adaptation (Fig.3.3). Genotypes, G27, G23, G20, G25 and G24 performed better in Timau and Molo, however, they had a negative value of PC2 an indication that the G x E was significantly high in these environments. Genotypes G6, G19, G23, G23,

G25 and G27 had low yields. Genotypes that had PC1 scores of >0 were high in tuber yield and those that had PC1 scores of < 0 were the poor yielding genotypes. Genotypes, G5, G15, G19 and G24 with PC1 score > 0 had higher yields whereas G4, G6, G7, G9, G18, G11, G16, G18 and G21 had low performance (PC1 score < 0). (Fig.3.3).

Genotype, G24 and G25 were more adapted to Molo and Timau respectively and G20 adapted to Kibirichia. PC2 levels showed the yield potential and PC1 shows the consistence of a genotype in yield performance across sites. The GGE Bi-plot for Table type showed that PC1 and PC2 accounted for 39% and 28.4% of GGE sum of squares respectively and collectively explaining a total of 67.4% variation (Fig.3.3).
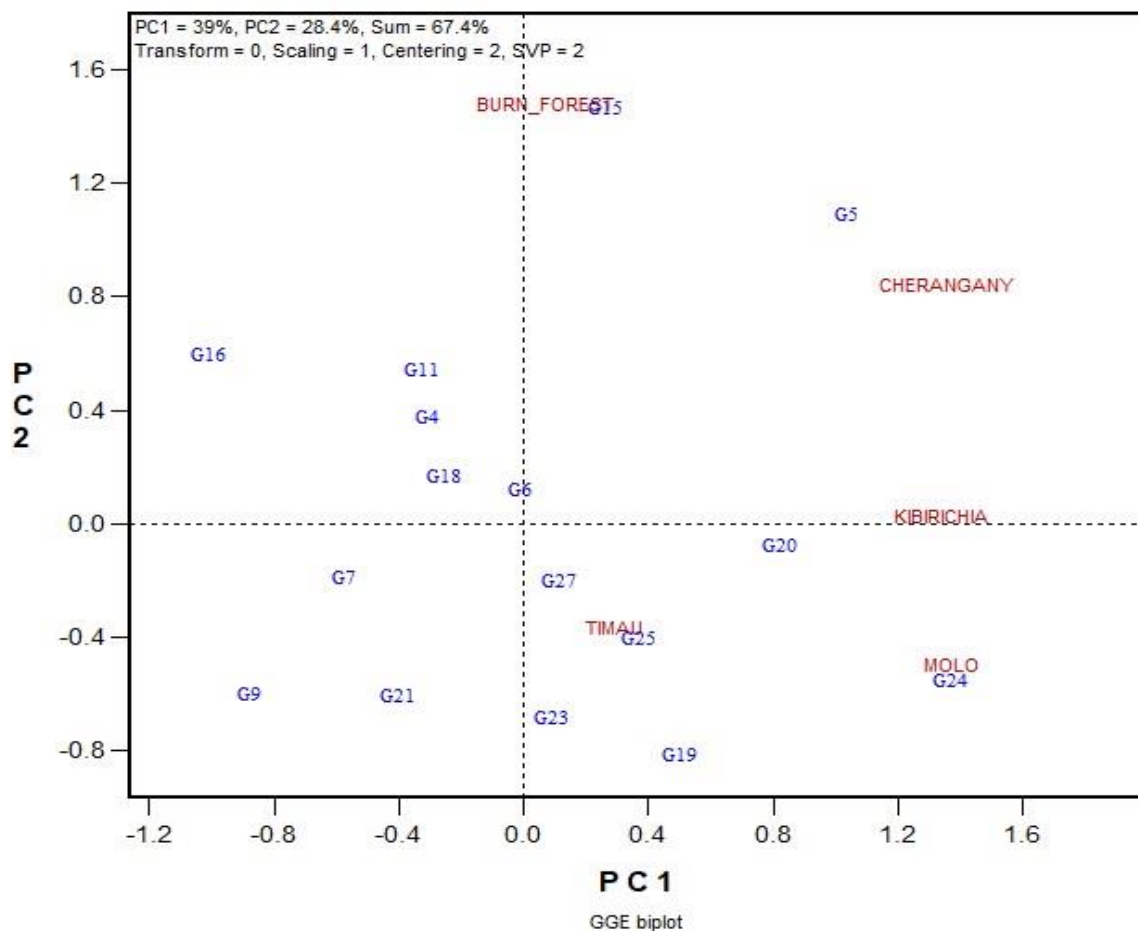


**Figure 3.3: GGE-bi-plot showing general Table type genotypes yield performance relative to the test environments in t ha$^{-1}$ during the long rainy seasons of 2015 and 2016**

Two mega-environments with different combinations of the evaluation locations were realized for the Processing types. The first one was Burnt Forest and Timau where G2 was the best performing genotype whereas G3, G22 and G17 had lower but dependable tuber yield (Fig.3.4). The second mega-environment consisted of Cherengany, Molo and Kibirichia in which G8 performed better followed closely by G26 and G13. Genotypes G1, G10, G12 and G14 had very low yields.



PC1 = 43.7%, PC2 = 24.4%, Sum = 68.1%
Transform = 0, Scaling = 1, Centering = 2, SVP = 2
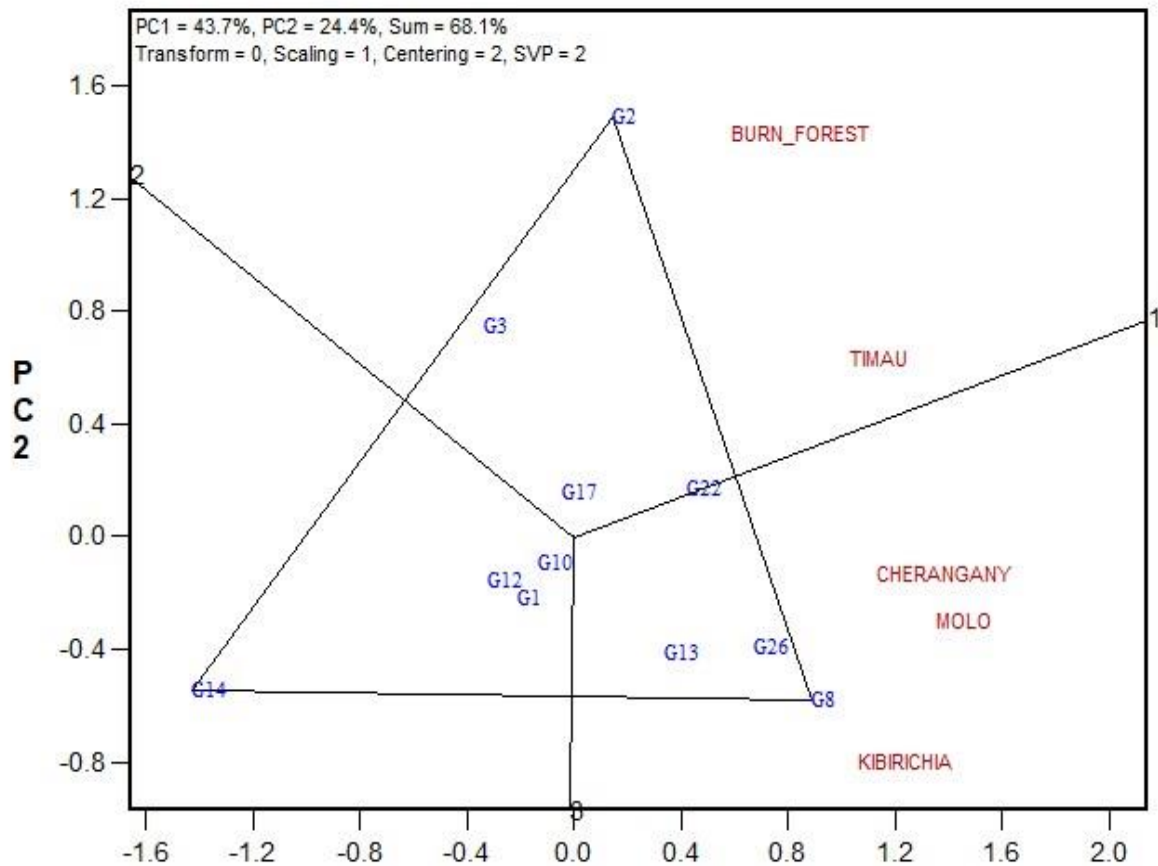
**Figure 3.4: GGE Bi-plot analyses showing the mega-environments and the winning Processing type genotypes during the long rainy seasons of 2015 and 2016**

In Fig.3.5, the midpoint of the concentric circles is the location for an ideal genotype that is one with high mean yield and is the most stable. High yielding and most stable genotypes have the longest horizontal vector and shortest vertical vector. Those genotypes located closer to the ideal genotype position were the best performing Processing type genotypes. Genotypes, G8 and G26 were closer to the ideal environment, whereas G14 was far from the ideal environment and hence performed poorly. Genotypes G8 and G2 displayed high yield performance in

specific environments thus have low general adaptability but high in specific environment adaptation.
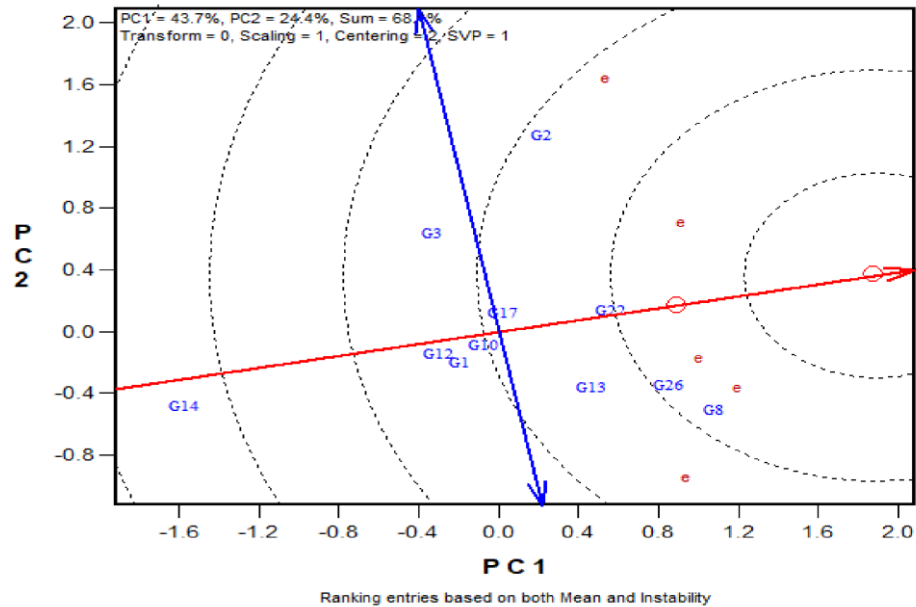


**Figure 3.5: Positioning Processing types genotypes relative to the ideal environment and their stability during the long rainy seasons of 2015 and 2016**

Genotype, G22 and G17 were the most stable genotypes better than the check variety. G8 the check variety was located closer to the ideal area with slightly lower stability because of high interaction with the environment. Genotypes, G2 and the check G8 were better adapted to environmental conditions in Burnt Forest and Timau whereas the check was also adapted to Molo, Kibirichia and Cherengany (Fig.3.5).

The bi-plots generated by GGE software established three mega-environments among the evaluation sites for Table type genotypes. The Table type genotypes had varied levels of interaction with the locations (Fig.3.6 and 3.7). The high yielding and adapted genotypes in a particular mega-environment occupied the corners of the polygon. Genotypes, G5, G9, G15, G16, G19 and G24 formed the corners because they had a high yield within the mega-environment where they formed corners (Fig. 3.6). Genotypes, G27, G25 and G20 were located to the center implying they were not the best in tuber yield in respective mega-environments.

The polygon formed three mega-environments, namely, Burnt Forest, Cherengany each forming a single mega-environment and the third one comprised of Kibirichia, Timau and Molo. On 'which won where' G15 won in Burnt Forest, G5 in Cherengany and G19 Timau,

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Molo and Kibirichia (Fig.3.6). Genotype G19 had similar yields as the check G24 whereas genotypes, G6 and G7 were stable but had low yields compared to G5, G20 and G24. This leaves G5 best performing genotype which was also close to the ideal environment (Fig.3.7). Genotype, G15 even though is one of the high yielding its was unstable but had specific adaptation in Burnt Forest (Fig.3.7). Genotypes, G6, G19, G25 and G27 yielded above the mean.
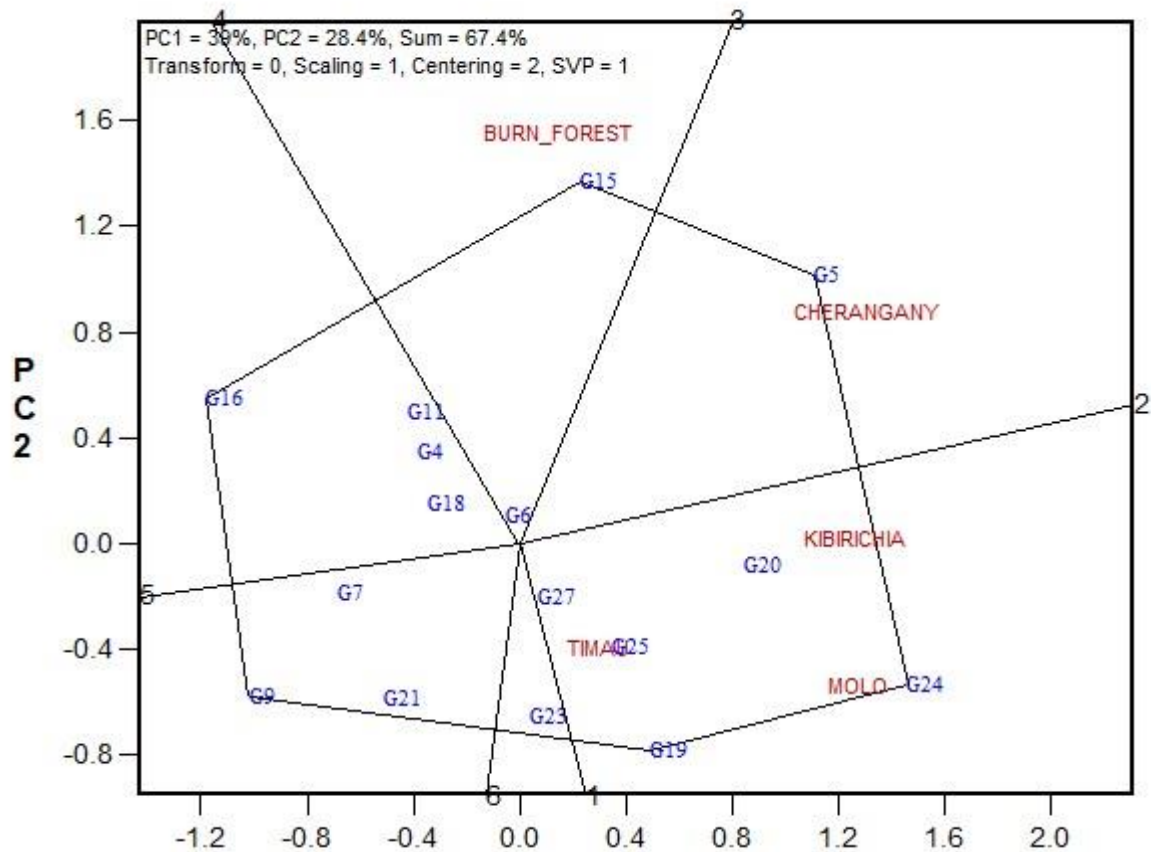


**Figure 3.6: GGE-Biplot showing Table type genotype yields and how they performed in different testing mega-environments during the long rainy seasons of 2015 and 2016**

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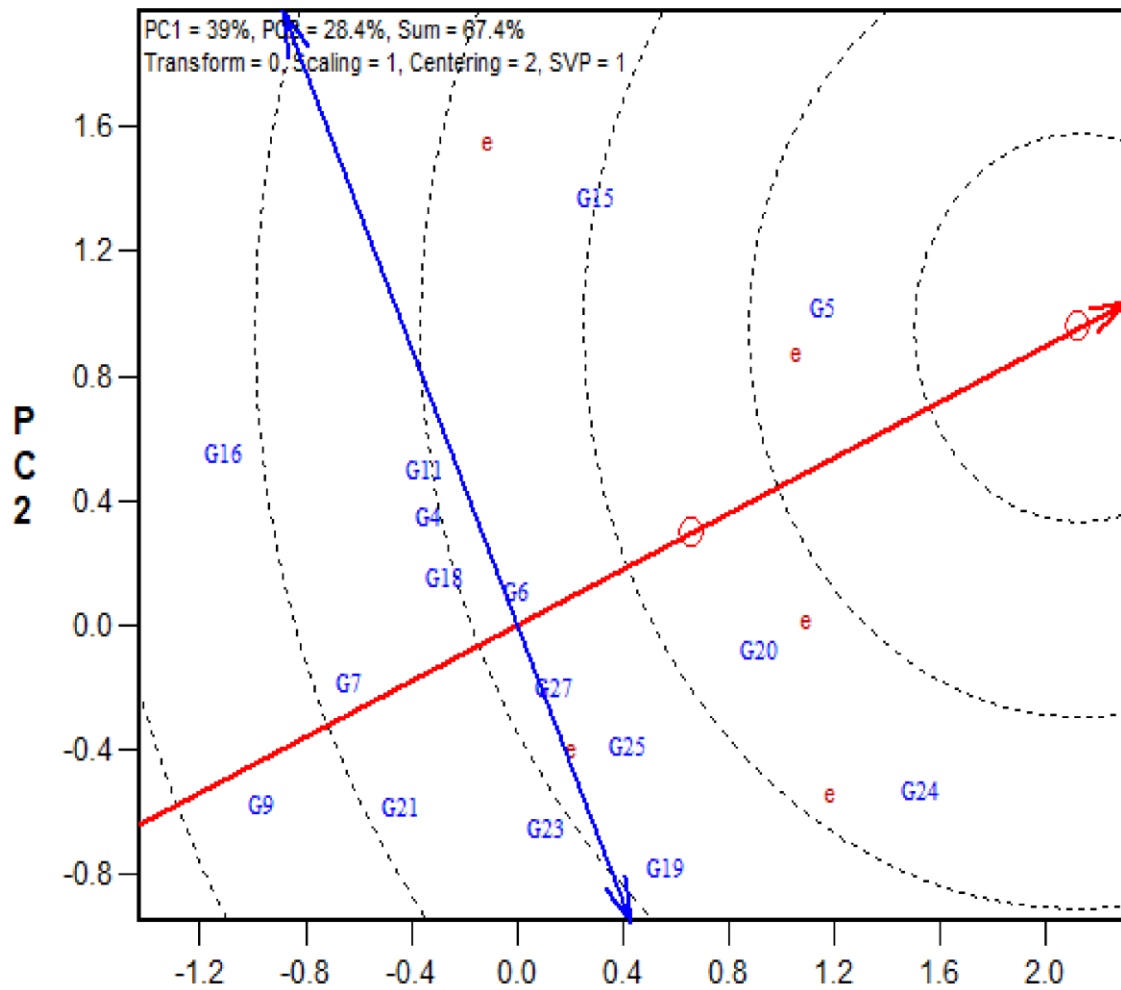
**Figure 3.7: Stability ranking of the Table type genotypes relative to the ideal environment during the long rainy seasons of 2015 and 2016**

### 3.4.3 Mean yield of Processing and Table potato genotypes in different sites

The mean yield performance of the Table and Processing genotypes varied greatly among the production sites. The yield variation ranged between 0.2 – 5.14 t ha$^{-1}$ between sites. Cherengany had the highest mean yield difference of 5.14 t ha$^{-1}$ between the Table and Processing whereas Timau was the lowest with 0.2 t ha$^{-1}$. The other environments had their mean differences as follows Burnt Forest, 3.36 t ha$^{-1}$, Kibirichia1.42 t ha$^{-1}$, Molo1.04 t ha-1and Narok1.11 t ha$^{-1}$(Fig.3.8). The Processing type genotypes were more sensitive to environmental factors than the Table type genotypes. This was most experienced in Cherengany and Burnt Forest as expressed by their yield differences.

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**Table 3.5*: Yield variations between Table and Processing type genotypes in environments in 2015/2016 season**

| Genotype | B. Forest | Cherangany | Kibirichia | Molo | Narok | Timau |
|----------|-----------|------------|------------|------|-------|-------|
| Processing | 16.71 | 13.73 | 13.54 | 19.08 | 28.15 | 24.66 |
| Table | 20.07 | 18.87 | 12.79 | 20.12 | 29.26 | 24.87 |

[7] Comparison between the Processing and Table type genotypes
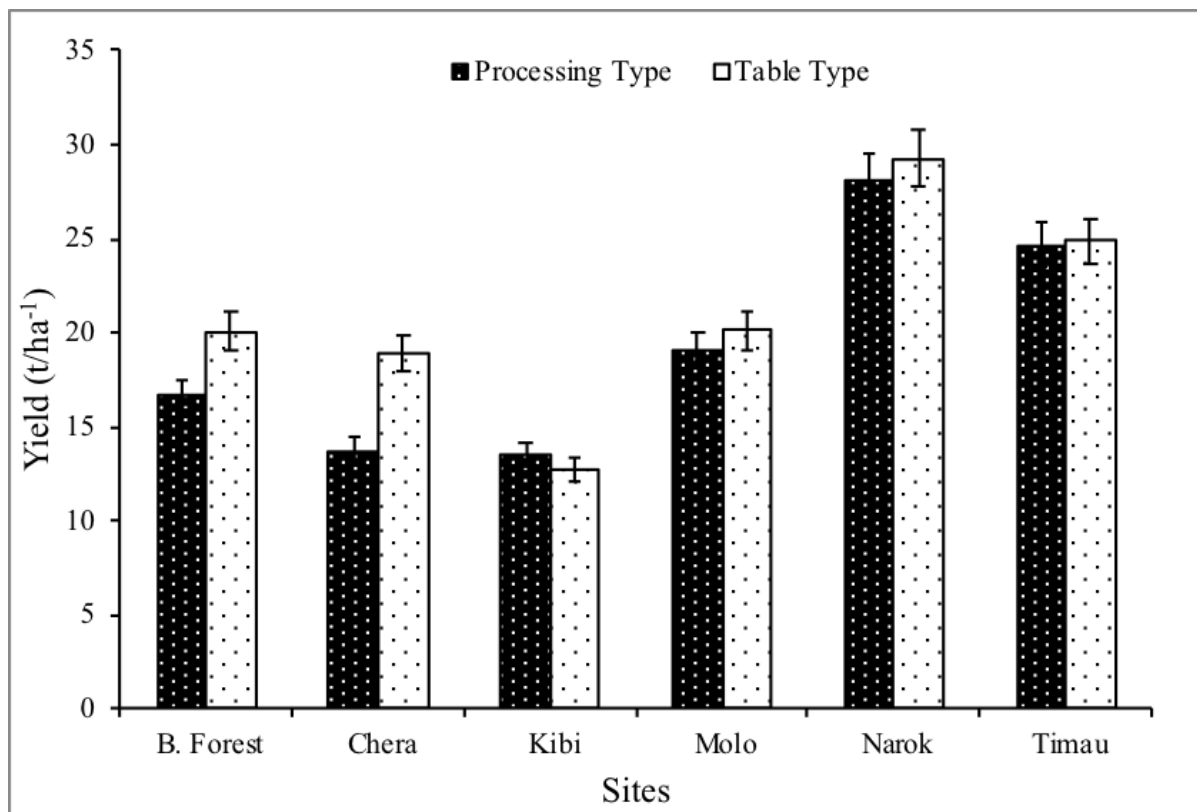


**Figure 3.8: Comparison between Table and Processing type genotypes based on means from each environment**

## 3.5 DISCUSSION

The analysis of variance for tuber yield revealed varied and highly significant G x E interaction between the genotypes and the environments for both the Table and Processing type genotypes. The significant G x E interaction is a reflection that tuber yield variation was due to the

genotypic diversity. This is an indication that they have different parental origins hence diverse responses to variations on exposure to environmental conditions. The variation in yield also showed that the factors responsible for yield had diverse responses to the different environmental factors that were in the evaluation sites.

Genotype, G15 of the Table type genotypes had the highest average tuber yield across environments than the checks means. The mean yield performance of genotypes across environments ranged between 12.79 t ha$^{-1}$ Kibirichia and 29.26 t ha$^{-1}$Narok. This was a reflection that the evaluation locations presented different factors that were either favoring tuber yield or stressing it.  The seasons were not significantly different implying that, the seasons did not present significantly different conditions that could have affected the yield of the genotypes.

The two types of potato had low mean yields in Kibirichia, signifying that this environment had more yield stressing factors. Some genotypes performed better in one environments but failed to maintain the same performance in different locations. This may be attributed to non-uniform and limited distribution of potato growth and development resources like nutrients and weather difference.  The genetic constitution of the genotypes that control the expression of tuber yield phenotype are also responsible for the variations. Narok recorded the highest yield for both the Table and Processing types whereas the lowest yields were recorded in Kibirichia for both. There were significant yield differences between environments, the variations were attributed to the differences in average daily temperature, humidity and soil moisture presented by the evaluation sites.

Two mega-environments for Processing type genotypes were identified and three for Table type genotypes by GGE bi-plot analysis. This is an indication that the Table and Processing genotypes responded differently to external factors in the environments. The existence of the mega-environments provides the guide on efficient utilization of resources without compromising the data quality. Timau, Molo, Kibirichia had similar conditions and any two could be left out and still reliable and representative information be obtained. Cherengany and Burnt Forest environments were similar and thus each formed an independent mega-environment and thus each should be evaluated independently for the Table types.

The Processing type genotypes formed two mega-environments. Similarly, some environments could be left out and still reliable information be obtained, for example Timau or Burnt Forest can be left out and any two of the remaining locations and still reliable data be obtained. This

also indicates that, the type of the genotype also determines the level of interaction with the environments as reflected by the different number mega-environments achieved by Processing and Table types.

Genotype, G22 was the most stable genotype whereas the most unstable genotype was G2 among the Processing type genotypes. G5 was the most stable and G19 and G15 were the most unstable for the Table types genotypes. The stable genotypes were characterized by constant yields across contrasting environments compared to unstable ones (Table 3.2 and 3.4). General and specific adaptation was observed in various locations among the evaluated genotypes. For the Table type genotypes, G15 and G5 expressed specific adaptation to Burnt Forest and Cherengany respectively by giving best yields in these environments whereas G19, G20, G24, G25 and G27 were adapted to more environments and because of this they passed as broadly adapted genotypes. However, within the Table type of genotypes there were those that had dismal performance across all locations such as G9 and G21 implying they lacked necessary factors to counter the environmental stress factors.

The evaluation of the Processing type genotypes revealed that, G2 was specifically adapted to Burnt Forest and G13, G26 and G8 were general adapted.  The Processing type genotypes such as G1, G12 and G14 were low yielding, due to the in ability to shield themselves from the environmental pressures. The findings from this study indicated that all genotype types were high yielding in Narok and Timau where the average yield of 29.26 t ha$^{-1}$and 24.87 t ha$^{-1}$ respectively for Table type genotypes and 28.15 t ha$^{-1}$and 24.80 t ha$^{-1}$for Processing type genotypes.

Across the evaluation environments the genotypes showed a lot of inconsistencies that are highly linked to environmental variations and the diversity in the genetic constitution of each genotype. Such varied performance best reflects specific genotypes adaptability and hence the basis for matching the genotypes with the suitable environment. The best adapted Table type genotype in Narok was G7 whereas the best check in the same environment was G11. The Processing genotypes had G13 (32.62 t ha$^{-1}$) as the best adapted slightly better than the check in the same location G8 (31.61 t ha$^{-1}$).  Genotypes G5 and G15 had high yields across many sites.

Five Processing type genotypes namely, G2, G20, G13, G10 and G26 displayed better yields above the grand mean yield. Genotype, G2 also doubled as the best performer in mega-

environment Burnt Forest-Timau. Even though G2 had exceptionally high yields and the most adapted genotype in these environment, it was quite unstable in other environments (Fig.3.4 and 3.5). This shows that this genotype has a genetic composition that is very sensitive to environmental factors leading to inconsistent tuber yield. In the second mega-environment, G8, the check had the best performance. G26 and G13 were reliable genotypes that can give high yields but had higher interaction. In both the Table and Processing type genotypes, stability was expressed in two forms; static stability where some genotypes performed in a similar way in many production sites and dynamic stability where there yields mean was comparable to the grand mean.

The Table type genotypes, namely, G6 and G7 showed static stability and had low yields. This shows that their genetic potential had been expressed to the maximum, and improvement of the production environment to achieve favorable conditions could not significantly alter their performance. G6 and G7 can be evaluated for other important traits that they have and that can be used to improve other genotypes. Dynamic performance was noted among genotypes, G5 and G15 showed potential of better performance if agronomic factors were improved with favorable weather conditions. This was noted by the way the yields varied from one evaluation location to the next. The Processing type genotypes, G22 and G17 showed static stability whereas G2, G13 and G26 showed dynamic stability and the standard variety G8 also expressed dynamic stability (Table 3.2).

These results are in agreement with the findings by Maharana et al. (2017) who reported that it is difficult to get a genotype that has same performance in many sites. Genotype phenotypic expression changes with change in external factors that influence genetic response which are responsible for the phenotype of interest. This accounts for the yield variation among and within genotypes in different environments. The highly significant yield variation from site to site is an indication that the expression of yield controlling factors is affected by the external factors as presented by the environment.

The mega-environments served as a reliable representation of all the environments used in the study since they provided reliable information about environments based on their similarity and differences (Yan, 2001). These mega-environments enhanced expression of primary and secondary effects and their measurement can be done with minimal costs. Therefore, the mega-environment data provides the basis for determination of the genotypic capabilities to aid

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successful selection. The findings, show that the genotypes sensitivity to environmental conditions varied among the Table and Processing genotypes.

Different environments had different genotypes doing better than others. The response to different factors in this environments for the two types of potato genotypes varied. In every environment the Table types performed better than the Processing types. This is demonstrating that genotype-environment interaction affects yield trait expression differently in different types of potato genotypes. These findings show that the environmental impacts influenced the type of genotypes differently and hence the varying degree of adaptability and stability. The Processing type genotypes were the most susceptible to the environmental pressures compared to the Table type genotypes. Jorge et al., (2015) observed similar findings and associated this expression to differential gene expression in response to different environmental conditions. The overall performance showed that Kibirichia is a low yielding site and lacks most of the potato production attributes.

All genotypes under evaluation were sensitive to the environmental conditions as reflected in the yield variations. Tumwegamire et al. (2016) suggested that stability and adaptability of genotypes should be established before they are recommended as varieties. This is because this information is helpful in understanding the true potential of the genotype in reproducing the characteristics of interest in target environments as early determined. This underscores the need to evaluated elite lines in the target environments for reliable information about their genetic potential. This study revealed that genotype had differences in their adaptability and stability in different test environments. Genotypes that could withstand environmental pressures were more stable compared to those that were sensitive to the environmental factors however, they were not necessarily the high yielding ones.

Relative humidity, temperature and soil moisture contents were the major external factors that were linked to the tuber yield variations observed. The tuber yields fluctuated across all the test environments. This indicated that the test genotypes interacted with the environmental factors of humidity and temperature differently. Gehan et al. (2013) associated potato yield variations across environments to genetic sensitivity of the genotypes to both weather and edaphic factors. This explains why a genotype will not maintain the same phenotypic expression in different environments, and across seasons. Cotes et al. (2002) also reported that genotypic performance over environments is meticulously connected to locations where the genotype is grown. Genotypes that are far from the origin of the polygon have better yields but are of low stability.

The further away the genotype is from the origin, the more it interacts with the environment (Yan et al., 2000).

## 3.6 CONCLUSION

Genotypes, G22 was the most stable among the Processing type genotypes whereas G5 was stable among Table type genotypes respectively. Genotypes G2, G8, G13, G17 and G26 had high yields but unstable, whereas genotypes G3, G10, G12 and G14 were unstable and had low yields. Kibirichia was the least favorable environment for potato production, Narok and Timau were the best production sites. The selection of the best genotypes requires careful considerations to ensure only superior genotypes move to the next level of evaluation.

# CHAPTER FOUR:

## ADAPTABILTY AND STABILITY OF POTATO GENOTYPES IN DIFFERENT POTATOP PRODUCTION REGIONS UNDER INTENSIVE MANAGEMENT

## 4.1 ABSTRACT

This study was aimed at determining the elite potato genotype adaptability and stability in different environments under high input management. The yield performance of test genotypes was measured. Potato stability and adaptability traits were evaluated for tuber yield across evaluation locations. Genotypes interaction with the environments was found to be responsible for the tuber yield variations observed in different environments. The analysis of variance revealed that the genotypes, environments and their interaction were significant for tuber yield.

Genotypes, G6 and G22 were the stable and high yielding ones for Table and Processing type genotypes respectively. Mean tuber yields for Table type genotypes varied between 33.6 t ha$^{-1}$ and 64.25 t ha$^{-1}$ whereas Processing type genotypes ranged between 15.9 t ha$^{-1}$ and 46 t ha$^{-1}$. Genotypes, G6 and G22 were more stable than the checks. The genotypes fitted in the following three categories a) Those with high and predictable yields, b) Those that had high stability and can be adopted across varied environment and c) Those that were unstable and low yielding. GGE biplot identified mega-environments giving room for elimination some of the evaluation sites for cost effectiveness. The genotypes of Table type and those of Processing type revealed different mega-environments. This shows that two types responded differently to the diverse environmental factors, an indication that there existed genetic diversity among the types. The mega-environments are made of locations that had more similarities than differences.

The results indicated that the analysis of genotype by environment interaction is important in determining the adaptability or stability of potato genotypes. This information is important selecting superior genotypes and eliminating the inferior ones. The Table type genotypes had higher yields than the processing types and were better adapted.

*Key words:* **Biplot analysis, Genotype by Environment interaction, Stability and Potato tuber yield**

**4.2 INTRODUCTION**

The diversity of the production environments present different factors that influence the phenotypic expressions of potato, especially the tuber yield. Even with the importance of potato at commercial and house hold levels, its productivity is experiencing a declining tendency due to inadequacy of improved cultivars with wide adaptation and stability in tuber yield (Lutaladio et al., 2009). In potato farming, seed tubers accounts for 40-50% of the total production cost compared to other crops such as cereals (Gildermacher et al., 2011). Kenyan small scale farmers are the largest potato producers, a majority of whom cannot afford certified seeds. This leads to the use own farm saved seed that is normally of low quality. The few large scale farmers that have enough capital base use certified seeds (FAO stat, 2010) but the yields from large scale farms cannot satisfy the ever rising potato demand. This scenario of the main producers who are the small scale farmers not accessing quality seed is a major impediment to potato production. The need to increase the availability and accessibility to quality seed potato to address the current potato seed deficit. This makes it necessary to evaluate genotypes across potential production environments to establish the levels of adaptability, stability under best management approaches. To achieve this goal breeder have increased their effort in developing better varieties which are high yielding to meet the increasing and dynamic demand of potato products.

Potato production is greatly influenced by the environmental and management factors such as temperature, solar radiation, soil moisture, relative humidity and fertilizer (Momirović, et al., 2016). Potato has inherent potential to do well in different agro-ecologies coupled with its short production cycle which has enabled it to become a food security crop (Worku et al., 2018). Interaction between different potato genotypes with various environments stimulates different responses in tuber yield of different genotypes (Byarugaba et al., 2018). Genotype by environment interaction is the major reason for varied adaptability and stability levels. Therefore, there is a need to carry out detailed studies that before the release of a new potato varieties. If the genotypes performances are dependent on environments, it should be considered weak, (Cotes et al., 2002). The stable and adaptable genotypes will give high yields consistently and has low environmental interactions effect.

During potato variety development, a numbers of factors such as days to flowering and days to maturity and tuber yield are put in consideration (Silva et al., 2018). The ability to successfully

combine the positive attributes like disease resistance, early maturity, high tuber yield among others in a cultivar is a complex activity. This slows down the rate of cultivar development leading to prolonged use of low quality seed that is responsible for low production.

Therefore, there is need to curry out multi-environmental evaluation to determine genotypes responses for informed decision making. The measurements of traits of interest from multi-environmental evaluation will give an indication of adaptability and stability of the genotypes being evaluated (Haynes et al., 2012). The information on these traits will provide the much needed guide in the recommendation of genotypes as broadly or specifically adapted and the stability characteristics under a specified management system (Sadeghi et al., 2011). Even though evaluation establishes genotypes stability and adaptability for the attributes of interest, the presence of genotype x environment interaction initiates variations that hinder faster selection and decision making.

Suitable techniques of analysis should be used to explain the existence, pattern and magnitude of the interaction between the genotypes and the environment (Gauch, 2008). Gumu et al., (2002) recommended that information from multi-environment trials be appropriately analyzed to establish the genotypes fitness and stability in a particular region. Yan et al., (2001) also recommended that a reliable evaluation should be based on genotypic main effects (G), environmental effect (E) and their interaction. Environmental conditions can significantly influence the adaptability and stability of genotypes (Silva et al., 2018).

Genotypes can express almost similar performance across environments of evaluation which is termed as static stability, or varied performance across different environments termed as dynamic stability. Dynamic stability can also be established by comparing the genotype performance with environmental mean. Some genotypes respond positively to optimized environments such as providing better agronomic practices such as fertilizer application (Kanguongo et al., 2008). Understanding the genotypes by environments interactions is important in correctly determining adaptability and stability of genotypes. Knowledge on stability and adaptability can improve the selection efficiency. According to Borges et al., (2010), dependable selection should be based on the true genetic value of the genotypes on evaluation for it to be released as cultivars. Breeding stable and adaptable potato varieties has gained more popularity than the focus than breeding for high yield (Cotes et al., 2002). Static

stability is recognized by similar genotypes performance in different environments whereas dynamic stability is characterized by the performance of genotypes compared to the environmental means (Cotes et al., 2002).

There is need to select quality seeds that can address the demand for high tuber yielding among other preferred attributes. Gehan and Hala, (2013) recommended the approach of establishing the stability and adaptation levels of the genotypes before deploying them as varieties. The emphasis on yield is because of it's the economic and nutritional value. Yield is a quantitatively controlled trait and therefore, it is challenging to effectively measure the genotypes' potential with precision (Panayotov and Dimova, 2014). The adaptability analysis of genotypes can be considered to be broad or specific environment adapted (Joshi, 2004).

## 4.3 MATERIALS AND METHODS
### 4.3.1 Description of the study area
The genotypes were evaluated in the following areas Cherengany, Marimba, Kamae, Mau Narok,Molo, Narok, suera, Thika and Timau as reflected in the site figure 4.1
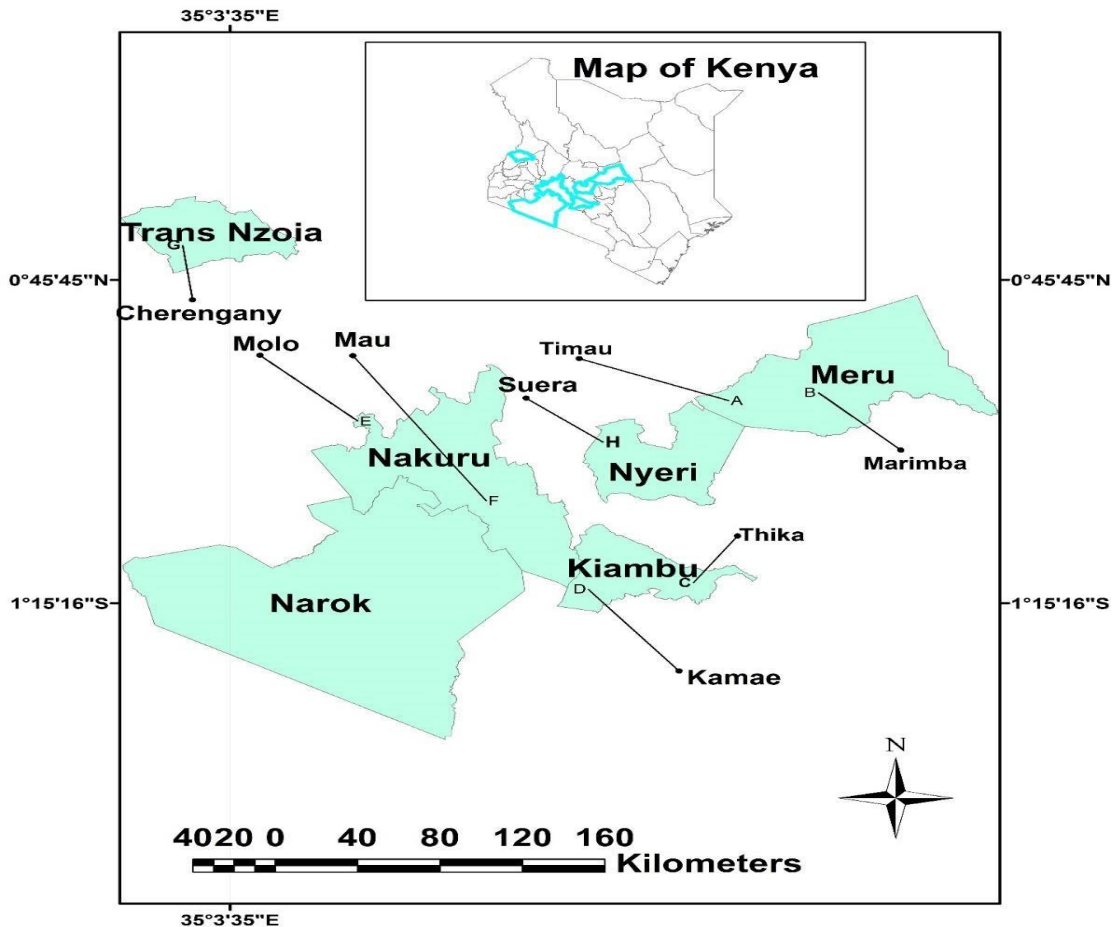
**Figure 4.1: Map of Kenya showing the evaluation environments**

### 4.3.2 Potato genotypes

The potato genotypes used in the intensive management evaluation were as shown in table 3.1 above. The genotypes were sourced from Kenya Agricultural and Livestock Research Organization (KALRO) Tigoni and International Potato Center (CIP). Commercial varieties were used as checks

### 4.3.3 Field experimental layout, design and management

The field experimental layout is as explained in Chapter 3, section, 3.3. The evaluation environments were provided with improved agronomical conditions. Diamonium Phosphate (DAP) fertilizer was applied at 500kgs per hectare and Calcium Ammonium Nitrate (CAN) at a rate 250kgs per hectare. Regular scouting for diseases and pests was done and neem based insecticide ACHOOK 0.15% EC and Ridomil fungicide were used to control insect pests and fungal diseases. Weeding and ridging was done four times to keep the field weed free and the tubers well covered.

### 4.3.4 Data collection

Tuber yield data was collected during harvesting per genotype in every evaluation sites in kilograms and computed to tons per hectare. The data was analyzed using R statistical software and visualized using genotype, genotype-environment.

### 4.3.5 Data analysis

Analysis of variance (ANOVA) for tuber yields for genotypes and locations was done using R statistical software. The Least Significant Differences (LSDs) was used to separate the means at 5% probability level. The effects that arise due to of G×E interactions were evaluated using the principal component analysis (PCA1 and PCA2) using the following formula;

$$Y_{ij} = \mu + \beta j = \lambda 1 \xi i1 \eta ij1 + \lambda 2 \xi i2 \eta ij2 + \varepsilon ij$$

Where: $Y_{ij}$ = the performance of genotype **i** in environment **j**, $\mu$ = the grand mean, $\beta j$ = the main effect of environment **j**, $O_1$ = singular values (SV) for the first principal component, $O_2$ = singular values (SV) for the second principal component, $\xi_{i1}$ = eigenvector of genotype i for PC1, $\xi_{i2}$ = eigenvector of genotype i for PC2, $\eta_{j1}$ = are eigenvectors of environment j for PCl, $\eta_{j2}$ = are eigenvectors of environment j for PC2 and $\varepsilon ij$ = is the residual associated with genotype i in environment j.

### 4.4 RESULTS

### 4.4.1 Adaptability and Stability of Table Genotypes in different environments under intensive management

The analyses of the genotypes performance across environments reflected the existence of significant differences between the genotypes, environments at (P≤0.05). The genotypes also interacted with the environment significantly (Table 4.1). Kenya Karibu and Sherehekea were outliers because of this they were excluded from the ANOVA. The performance of evaluated genotypes varied between the genotypes with a mean squares (MS) of 690 and seasonally with a mean of 244. Variance among of locations was 1035 mean square whereas that of interaction between genotypes and locations was 209 mean square (Table 4.1). Analysis of variance showed that the genotypes performances were significantly different in different environments. The outcome among the evaluated genotypes varied widely with mean square (MS=690.3). This performance was also significantly different in 2015 and 2016 seasons at (P≤0.05). The difference shows that the results for 2015 and 2016 seasons significantly varied with a mean

of 244.2. Therefore, environmental influence on the potato yields. Interaction between genotypes and the environment was significant with a wide variation of mean square (M=209.1). The interaction between the genotype, location and year was not significant.

**Table 4.1: Analysis of variance for Table type genotypes under intensive management during the long rainy seasons of 2015/2016**

| Source | DF | SS | MS | F | Prob |
|---|---|---|---|---|---|
| Genotype (G) | 9 | 6212.68 | 690.3 | 42.4 | 0.00001 |
| Year (Y) | 3 | 732.584 | 244.2 | 15 | 0.00001 |
| Location (L) | 6 | 6206.8 | 1034.5 | 63.6 | 0.00001 |
| L*Y | 6 | 3107.31 | 517.9 | 31.8 | 0.00001 |
| Block (L*Y) | 32 | 551.815 | 17.2 | 1.1 | 1 |
| G*Y | 21 | 4390.32 | 209.1 | 12.8 | 0.00001 |
| G*L | 54 | 13285.4 | 246 | 15.1 | 0.00001 |
| G*L*Y | 54 | 576.136 | 10.7 | 0.7 | 1 |
| Error | 276 | 4491.39 | 16.2731 | | |
| **TOTAL** | **461** | **39554.5** | | | |

[8] The of variation between Table type genotypes and interactions with environments

The yield performance among genotypes varied from one location to another. Some genotypes displayed significantly different yields whereas others had fairly similar yields (Table 4.2) Yields from genotypes; G6, Shangi, G4, Tigoni, G20, G11and G18 were not significantly different but differed significantly from those of genotypes, G10, G14 and Sherekea. Genotypes, G14 and G10 were not significantly different from Sherekea (Table 4.2). Kenya Karibu genotype, displayed the highest average yield (47 t ha$^{-1}$) however, Kenya Karibu and Sherekea were not planted in all evaluation environments. Genotype, Kenya Karibu had outstanding performance which was significantly different from the other genotypes. Highest yield performance was recorded at Suera with 64 t ha$^{-1}$while Molo had the least yield performance with 24 t ha$^{-1}$(Table 4.2).

**Table 4.2. Mean yield performance of Table type genotypes across evaluation environments in the long rainy season of 2015/2016**

| Genotypes | SITES | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | MAR | CHE | KAM | MAU | MOL | NAR | SUE | THI | TIM | MEAN |
| Kenya karibu | - | - | - | 48 | - | - | 51 | 43.06 | - | **47.35** |
| G6 | 3071 | 29.75 | 21.14 | 27.28 | 25.85 | 35.54 | 69.93 | 50.53 | 53.56 | **37.16** |
| Shangi | 35.85 | 26.82 | 26.68 | 33.22 | 29.29 | 42.86 | 51.72 | 34.03 | 42.93 | **35.96** |
| G4 | 28.68 | 25.55 | 33.06 | 30.19 | 24.83 | 39.2 | 71.35 | 38.4 | 31.73 | **38.32** |
| Tigoni | 31.89 | 26.11 | 30.72 | 24.72 | 23.91 | 49.89 | 74.87 | 22.32 | 42.14 | **35.13** |
| G20 | 21.85 | 27.52 | 12.53 | 34.66 | 13.97 | 36.18 | 73.09 | 51.38 | 21.29 | **32.71** |
| G11 | 33.33 | 35.68 | 36.55 | 18.58 | 30.77 | 29.32 | - | - | 44.03 | **32.61** |
| G18 | 33.27 | 38.65 | 37.84 | 24.7 | 24.28 | 28.37 | - | - | 34.14 | **31.61** |
| G24 | 22.69 | 20.31 | 29.5 | 27.75 | 15.17 | 27.77 | 74.35 | 32.95 | 29.51 | **30.77** |
| G14 | 25.28 | 23.51 | 23.81 | 20.34 | 22.93 | 22.66 | 74.93 | 45.67 | 21.66 | **30.11** |
| G10 | 24.93 | 31.69 | 25.95 | 32.85 | 25.04 | 37.65 | - | - | 29.54 | **29.66** |
| Sherehekea | - | - | - | 23.01 | - | - | 37.02 | 22.06 | - | **27.36** |
| **MEAN** | **28.85** | **28.56** | **28.08** | **28.6** | **23.6** | **34.94** | **64.25** | **37.82** | **35.05** | **33.54** |

[9] Mean yields for Table type genotypes under intensive management in different sites

The results from GGE biplot analysis revealed the existence of mega-environments, namely Mau-Narok, Suera, Thika and Narok formed one mega-environment each whereas Timau, Marimba, Molo, Kamae and Cherengany combined formed one mega-environment (Fig.4.3). The genotypes expressed preference for specific environments for example Tigoni, Shangi and Kenya Karibu were more adapted to Narok and Timau whereas, G4 and G6 were most suited

for Suera and G10, G11, G18 and Sherekea were broadly adapted in Thika and Mau. Kamae, Molo, Cherengany and Marimba (Fig. 4.2 and 4.3).

In Fig.4.2 the PC1 accounted for 7.8% of the variations whereas 63.91% of the variation was due to PC2 and only 8.8% of the variation was due to unknown factors. Genotypes, G4 and G6 had great interaction with the environment and also low yields. Genotypes, Shangi, Tigoni and Kenya Karibu had positive value for both PCI and PC2 an indication that they did not interact much with the environment. In Kamae, Cherenagany, Molo and Marimba and Mau-Narok, genotypes Sherekea, G11 and G18 had high yields but they were unstable (Fig.4.3). The performance of genotypes in each mega-environment was as follows: Kenya Karibu was yielded highest at Mau-Naok and Shangi at Narok. Sherekea was the highest yielding in the third mega-environment that was made up of Timau, Marimba, Molo, Kamae and Cherengany locations (Fig.4.3). The principal component 1 variance accounted for 64.4% whereas principal component 2 accounted 11.9% and collectively accounting for 76.3%. Therefore, only 23.7% of the variation could not be accounted for (Fig.4.3). Fig.4.3 below showed that Timau and Mau-Narok, were the environments in which most genotypes were stable for tuber yield. Suera environment had favorable conditions for high yield.
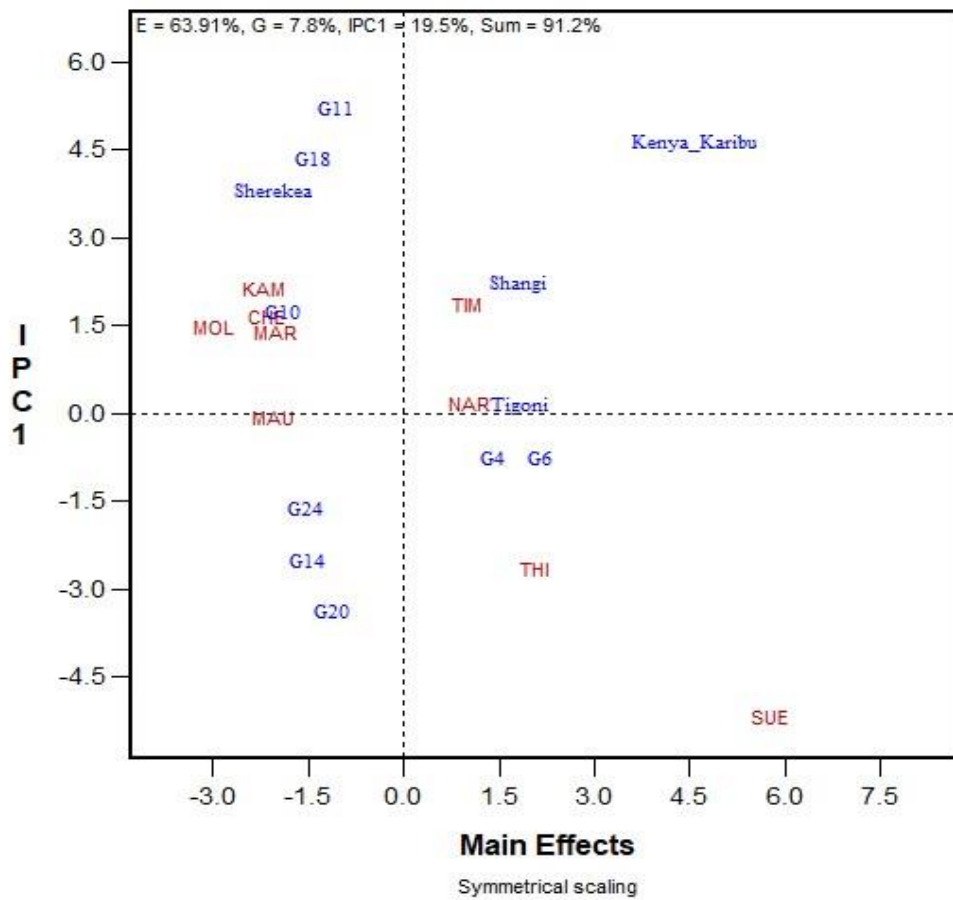
**Figure 4.2:Mega-environments obtained from intensive management of Table   type genotypes in the long rainy seasons of 2015/2016**

PC1 = 64.4%, PC2 = 11.9%, Sum = 76.3%
Transform = 0, Scaling = 1, Centering = 2, SVP = 2

Which wins where or which is best for what
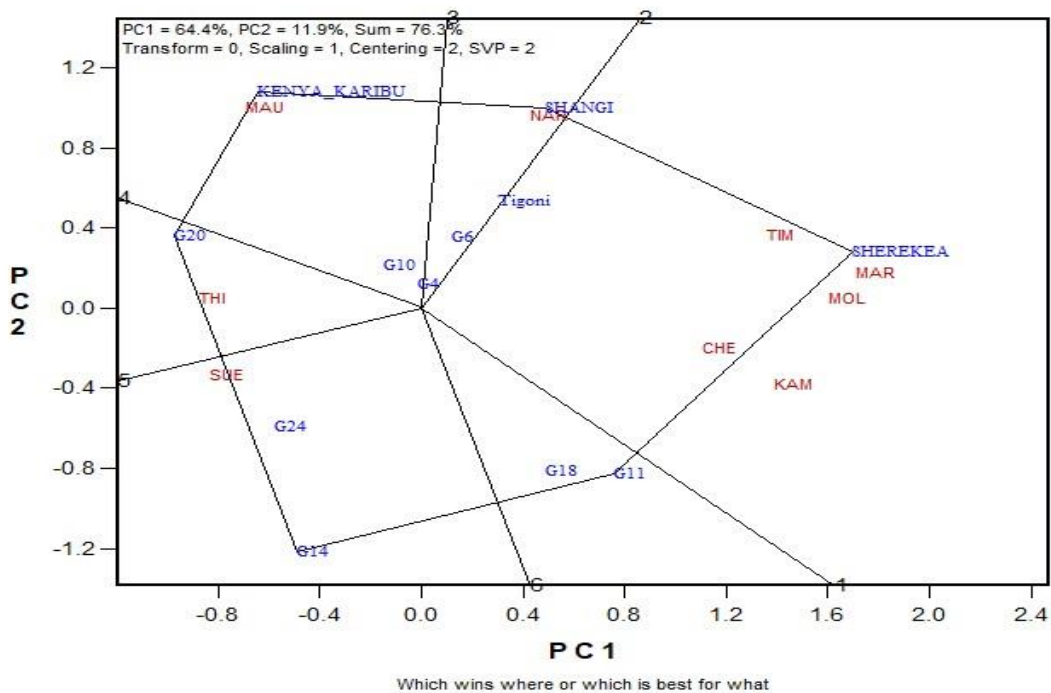
**Figure 4.3: Mega-environments obtained from intensive management of Table type genotypes in the long rainy seasons of 2015/2016**

The mega-environments were derived on the basis of their similarity in tuber yield of the genotypes in the environments. Mau-Narok, Narok, Suera and Thika, formed independent distinct environments whereas Timau, Cherengany, Kamae, Molo and Marimba fitted into one mega-environment. Sherehekea was more responsive to the conditions prevailing in these mega-environments whereas Genotypes G4 and G10 were less responsive (Fig.4.2). The genotypes that are located to the most exterior part of the polygon are those that had the highest yield in the mega-environment and most interactive with the environment. All the other genotypes contained within the polygon were less responsive in relation to yield trait within that sector.

Kenya Karibu was the highest yielding genotype in Mau-Narok, Shangi had the highest yield in Narok and Timau and whereas G11 had the highest yields in Cherengany, Kamae Molo and Marimba (Fig.4.2). G11 qualified for a broadly adapted category of genotypes for Cherengany, Kamae, Molo and Marimba. This evaluation showed that PC1 accounted for 64.4% and PC2 accounted for 11.9% hence 76.3% of the variation was accounted for and 23.7% was

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unexplained. Shangi, G11 and G20 had higher mean yields and interacted most with the environment. The ones that were on the inner part of the mega-environment had less interaction and had lower yield (Fig.4.2).

**4.4.2 Discriminative and representativeness of the test environment**

The test environments had diverse characteristics that were responsible for diverse genotypic expressions that are observed phenotypically in tuber yield. Tuber yield is one of the notable expressions by different potato genotypes. The environments used were varied, with both discriminatory and representative characteristic as observed from the data on obtained yields. The environments that were close to the ideal environment are considered to be the representative and less discriminative whereas those far from the ideal environment as the most discriminative. Timau and Marimba were the environments that provided on average favorable conditions for potato production hence they were considered representative sites whereas Suera, Mau-Narok, Thika and Kamae were the least representative test environments and considered discriminative environment.

Timau, Marimba and Cherengany came out as appropriate test environments for selecting broadly adapted genotypes. Suera, Mau-Narok were the best locations to select specifically adapted genotypes and elimination of poorly performing genotypes (Fig.4.5 and 4.6). The representative and discriminative environments can be arranged from the most representative to the least representative as Timau > Marimba > Molo > Cherengany > Kamae and Narok and the discriminative locations as Suera > Thika > Mau-Narok (Fig.4.4)

Ranking testers based on both discriminating ability and representativeness
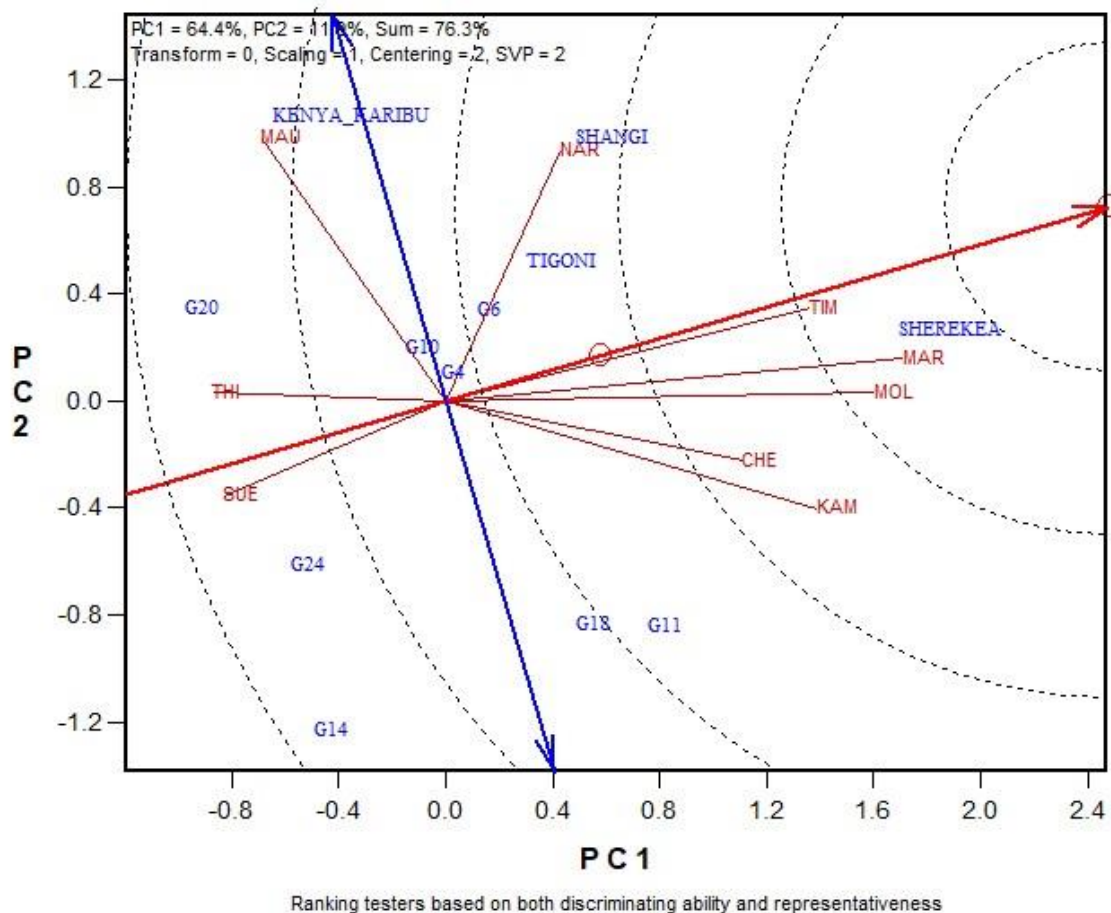
**Figure 4.4: Ranking of environments based on their representative and discriminative ability on Table type genotype production in the long rainy seasons of 2015/2016**

There was no much variation between the measured and the statistically predicted yield, however, there were major differences on the stability of genotypes (Table 4.4.). The most stable genotype was G6 whereas the most unstable was G11. The genotypes ranked from the most stable to the most unstable as follows, G6 > G4 > G24 > Tigoni > Shangi > G10 > G14 > G18 > G20 and G11 (Fig.4.5). The stability of the genotype is genetically controlled this is why different genotypes performed differently as shown in (Table 4.3). PC 1 accounted for 49.3% and 23.7% was accounted for by PC 2 and together 73% of the variation was explained. The genotypes that had their instability value greater than level + or – 4 in this case were considered unstable (Table 4.4.). The genotypes with consistent mean yield across the evaluation sites with minor variations were classified as stable and those with fluctuating yields were considered unstable. The stable ones had short vectors whereas the unstable genotypes had long vectors Fig. 4.5) The specifically adapted genotypes are recommended to locations

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where they are suited while the broadly adapted ones could be recommended to more than one location (Table 4.3)
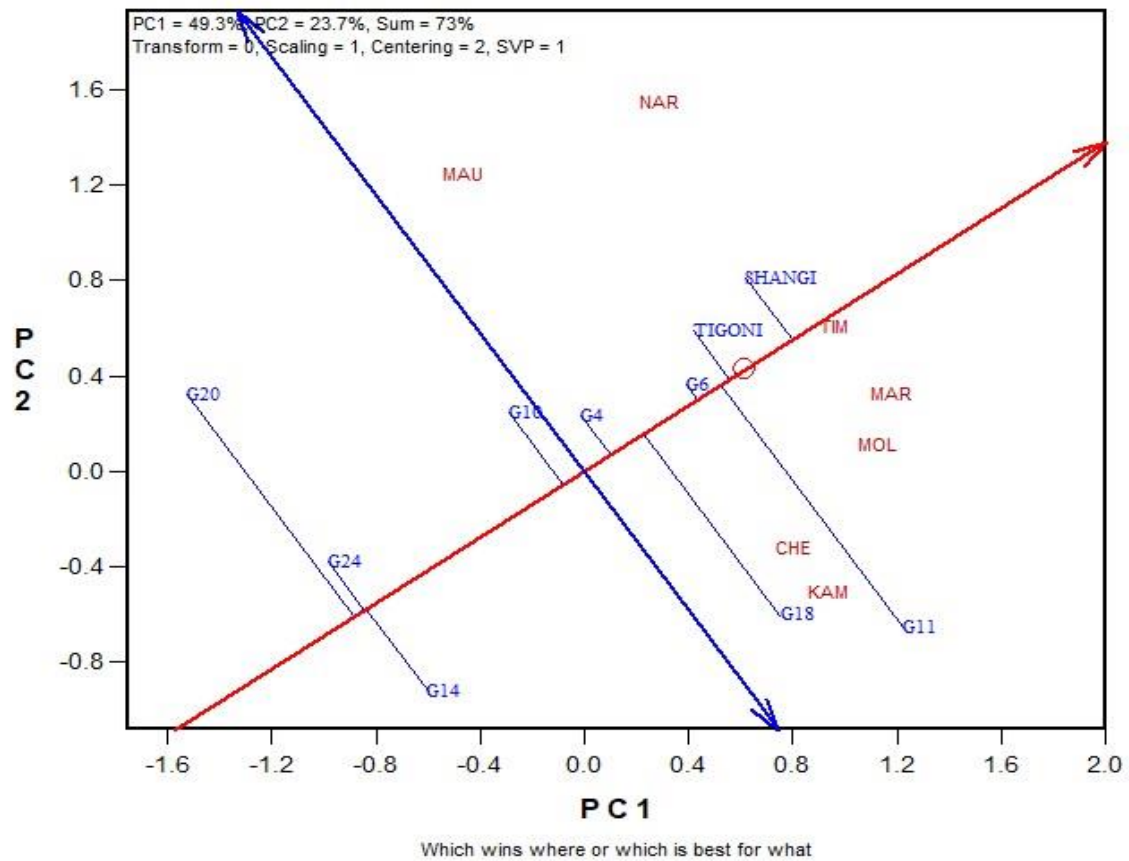


**Figure 4.5: Stability of performance of ten Table type genotypes in relation to the environment in the long rainy seasons of 2015/2016**

**Table 4. 3: Predicted mean performance of Table Genotypes in the long rainy seasons of 2015/2016**

| Measured and predicted Mean Performance for The Entries in Original Unit | | | | | |
|---|---|---|---|---|---|
| Grand Mean = 33.9; Average SD =8.3 | | | | | |
| Entries | Measured | Predicted | Instability | Integrated | |
| SHANGI | 40.1 | 42 | -2.6 | 40.7 | |
| TIGONI | 37 | 39.6 | -2.1 | 38.6 | |
| G11 | 37.7 | 39.2 | 10.2 | 34.1 | |
| G6 | 36.2 | 38.3 | -0.6 | 38 | |
| G18 | 37.2 | 36.3 | 7.7 | 32.4 | |
| G4 | 35.2 | 34.9 | -1.7 | 34.1 | |
| G10 | 34.6 | 33.1 | -3 | 34.6 | |
| G14 | 26.3 | 25.5 | 3.5 | 27.2 | |
| G24 | 27.4 | 25.4 | -2 | 26.5 | |
| G20 | 27.6 | 25 | -9.4 | 29.7 | |

[10] Stability prediction for Table type genotypes
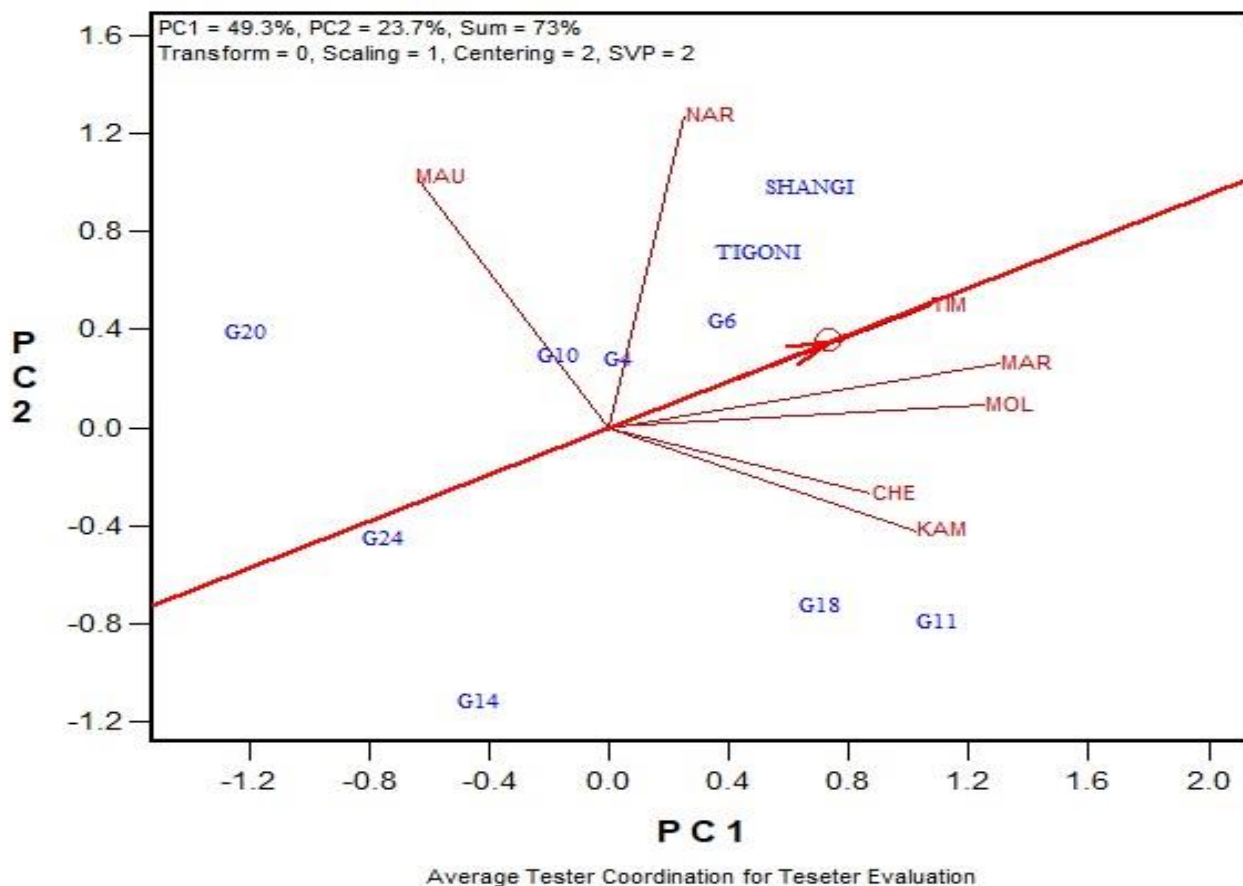
**Figure 4.6: GGE Biplot showing the relationship between environments and their representativeness as well as the discriminative abilities for the Table types in the long rainy seasons of 2015/2016**

To identify the best environment that could allow better screening discriminatively, average tester coordinate evaluation was done as described by (Yan and Kang, 2003). The circle on the AEC line with an arrow pointing to the ideal environment showed that Timau was close to the ideal environment (Fig.4.6). The ability of these environments to provide both discriminatory and representative evaluation was ranked as follows Timau>Mar>Molo>Cheranganyi>Kamae. Among the testers Timau was the ideal environment that could provide reasonably conducive conditions for evaluation of all genotypes. Other environments, with closely related potential were Marimba and Molo the test showed PC2 was low and high PC1 which is indicates the genotypes were genetically strong. The relationships between environments were also established where closely related genotypes had acute angles between them. The environments that are related had acute angles between them and those with obtuse angles were not related. The Mau Narok environment was related only to Narok whereas

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Kamae, Cherengany, Molo, Marimba and Timau are all related. Timau was identified as the most representative site for selecting general adapted genotypes while Mau-Narok and Narok environments, were suitable for selecting specifically adapted genotypes (Fig.4.6). To establish the interrelationship between genotypes, GGE biplots showed that some genotypes were different and others closely related. These means that the evaluated genotypes had different characteristics that led to diverse expressions in different environments. This shows that some genotypes shared some genetic characteristics and could have a common origin. Sherekea was the best performing but not closely related to any genotype (Fig.4.7). The very closely related genotypes were identified as Tigoni, G6, G4 and Shangi. This genotypes had acute angles between them, and those with obtuse angles between them were considered unrelated such us Kenya Karibu and G11 (Fig.4.7).
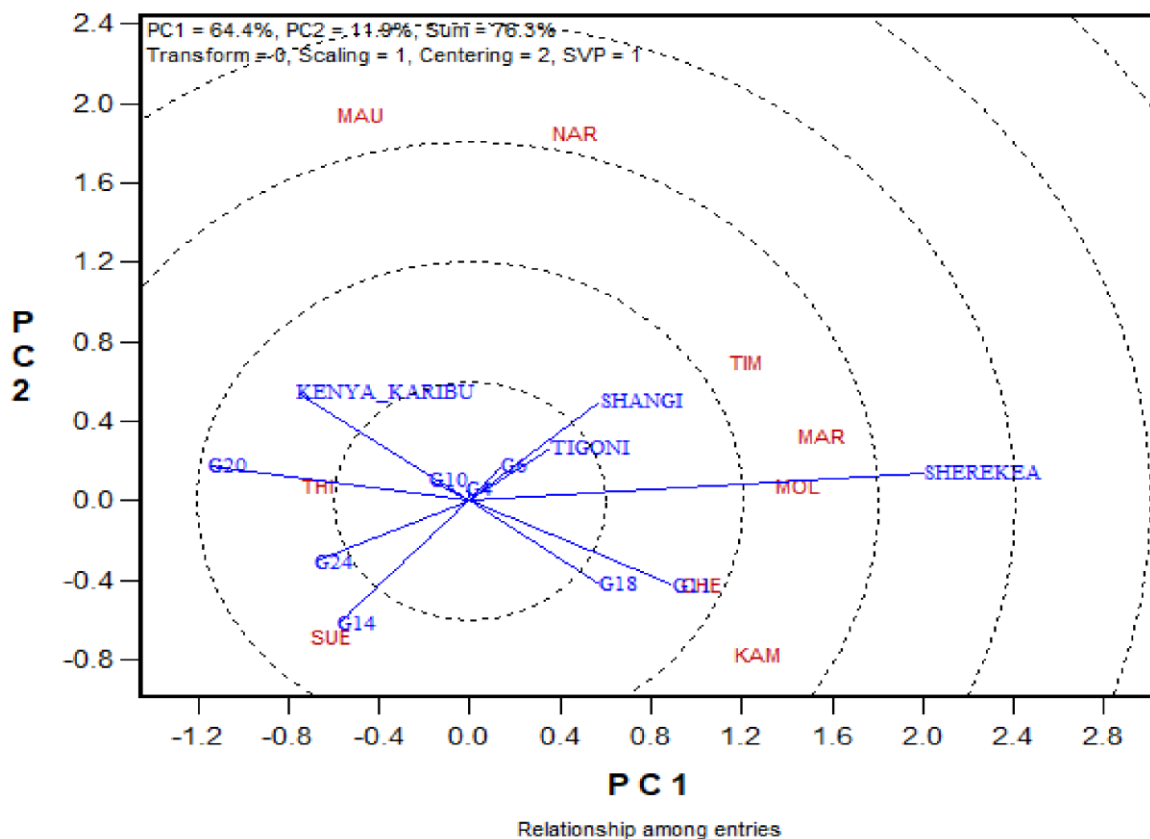


**Figure 4.7: The relationship between Table genotypes in the long rainy seasons of 2015/2016**

### 4.4.3 Yield performance of Processing genotypes in different production regions

The analysis of variance showed that genotypes, environments and their interaction were significantly different (Table 4.4). G2 on average was the best yielding genotype (38t/ha$^{-1}$) followed by genotypes, G8, G9 and G16 whereas the lowest performing genotypes were, G5, G15, G17 and G19 (Table 4.5). The check variety Dutch Robyjin had an average of 28 t ha$^{-1}$. The best environment for production of Processing type genotypes was Suera with (46t ha$^{-1}$) whereas Molo had lowest yield among the evaluation environment with (15.9 t ha$^{-1}$) followed by Thika, Kamae and Cherengany respectively (Table 4.5). Suera provided the environment with the best conditions where genotypes G3, G13, G16, G21 were best adapted. Environments such as Thika, Timau had more stress factors that led to poor yields (Table 4.5).

**Table 4.4: ANOVA for Processing genotypes under intensive management in the long rainy seasons of 2015/2016**

| Source | DF | SS | MS | F | Prob |
|--------|-----|----------|----------|-------|---------|
| GENO | 16 | 25835.36 | 1614.71 | 43.7 | 0.00001 |
| ENV | 8 | 48763.58 | 6095.447 | 165.1 | 0.00001 |
| GxE | 112 | 44235.4 | 394.9589 | 10.7 | 0.00001 |
| TOTAL | 887 | 146898.8 | | | |
| | | | | | |

[11] ANOVA for Processing genotypes under intensive management

**Table 4. 4 Mean yield performance of Processing type genotype across evaluation sites during the long rainy seasons of 2015/2016**

| Genotypes | Suera | Narok | Thika | Mauna | Timau | Chere | Marimba | Kamae | Molo | Mean |
|---|---|---|---|---|---|---|---|---|---|---|
| G2 | - | 34 | - | 28.4 | 46.87 | 33.8 | 45.8 | 32.8 | 42.9 | 37.8 |
| G8 | 36.2 | 43.5 | - | 29.6 | 42.1 | 36.2 | 30 | 28.4 | 35.7 | 35.1 |
| G16 | 61.2 | - | 21.9 | 18.9 | - | - | - | - | - | 34 |
| G9 | - | 39.7 | - | 37.3 | 37.91 | 32 | 26.1 | 31.5 | 30.8 | 33.6 |
| G1 | - | 36.3 | - | 23.5 | 38.3 | 28 | 27.5 | 35.5 | 28.7 | 31.1 |
| G12 | - | 33.8 | - | 22.9 | 32.4 | 23.9 | 25.2 | 25.5 | 23.3 | 26.7 |
| DR | 38.4 | 29.9 | 32.1 | 23.2 | 37.6 | 22.3 | 24.1 | 18.1 | 16.7 | 26.6 |
| G22 | 47.6 | 34.3 | 30 | 23.9 | 21.8 | 16.6 | 26.8 | 13.2 | 18.3 | 25.9 |
| G21 | 60.2 | 33.7 | 29.7 | 22.8 | 18.8 | 15.2 | 15.7 | 13.7 | 7.2 | 24 |
| G7 | 17.6 | 37.8 | 35 | 30.3 | 26.3 | 17.6 | 16.2 | 15.7 | 7.5 | 23.7 |
| G23 | 47.7 | 19.4 | 31.8 | 26.3 | 14.9 | 15.4 | 17.2 | 13.2 | 9 | 22.1 |
| G13 | 54.7 | 32.3 | 26.8 | 19.9 | 8.6 | 22.6 | 9.3 | 15.3 | 6.4 | 21.6 |
| G3 | 67 | 14.3 | 26.4 | 22.3 | 11.1 | 14.3 | 11.4 | 14.8 | 7.5 | 21.4 |
| G15 | 24.2 | 35.5 | 28.5 | 26.5 | 12.9 | 19.9 | 11.5 | 14.9 | 3.1 | 20.4 |
| G17 | 46.7 | 28.5 | 25.6 | 24.6 | 10.8 | 13.5 | 13.2 | 11.4 | 4 | 20.3 |
| G19 | 41.9 | 26.3 | 25.2 | 24.2 | 11 | 13.9 | 11.6 | 14.7 | 6.3 | 19.9 |
| G5 | 17.8 | 24.1 | 27.2 | 25.8 | 15.7 | 17.8 | 13.5 | 18.5 | 6.7 | 19.5 |
| Mean | 46 | 30.2 | 28.3 | 25 | 24.2 | 21.4 | 20.3 | 20 | 15.9 | 26.1 |
| - Represent genotypes that did not germinate or grow to maturity | | | | | | | | | | |

[12] Mean yield performance of Processing type genotype under intensive management
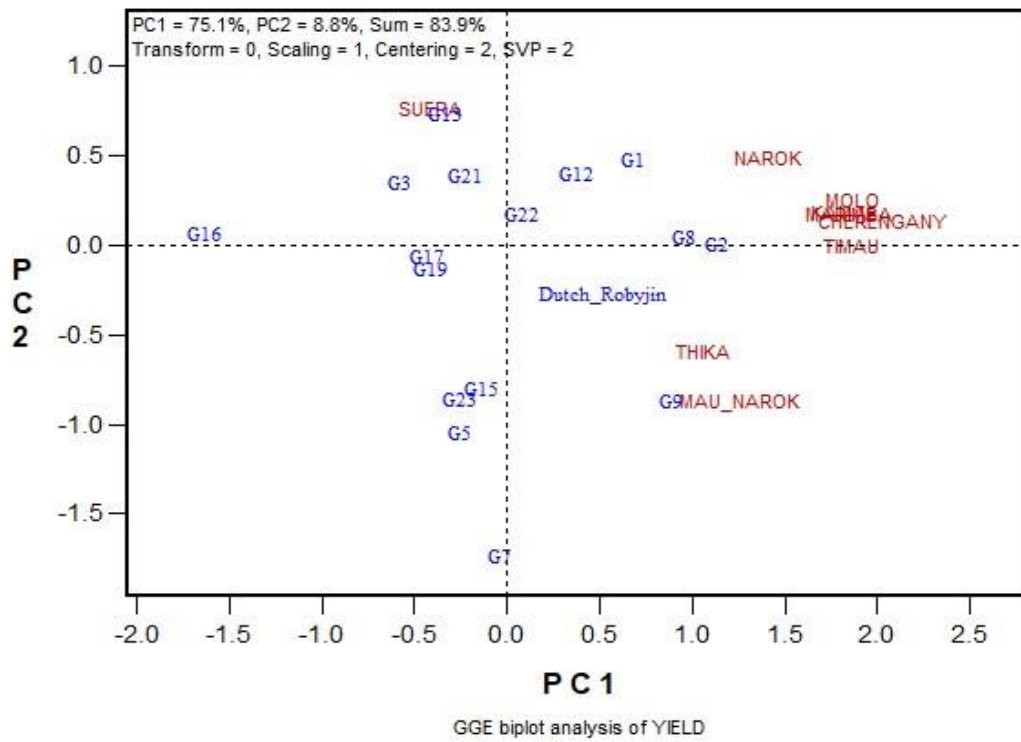
**Figure 4.8: The yield distribution of genotypes in various test environments during the long rainy seasons of 2015/2016**
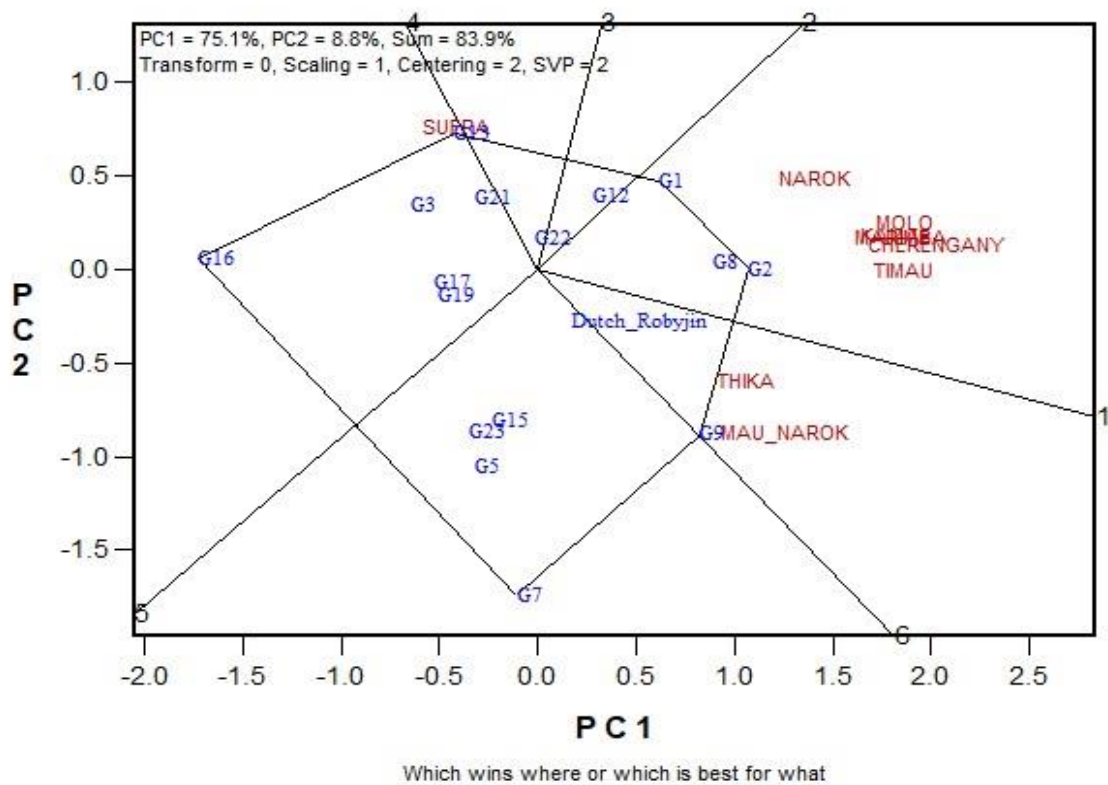
**Figure 4.9: The wining genotypes in different mega-environments in the long rainy seasons of 2015/2016**

The performance of Processing type genotypes tuber yield differed across environments leading to formation of three mega-environments namely Suera as one, Thika and Narok formed the second whereas Narok Molo Cherengany, Marimba, Timau and Kamae formed the third mega-environment (Fig.4.8). Narok Molo Cherengany, Marimba, Timau and Kamae environments had both PC1 and 2 in with positive value an indication that there was less environmental influence to the genotypes G1, G2, G8, G12 and G22 performance, Suera location had the best characteristics that favored excellent tuber yields for many genotypes where G13, G3, G21 and G16 had high yield performance. Thika and Mau-Narok Environments had a positive PC1 and negative PC2 implying this location had higher interaction with the genotypes (Fig.4.8). Three mega-environments that were formed were Suera, Narok Molo Cherengany, Marimba, Timau. Kamae formed the second mega-environments and Thika and Mau-Narok formed the third one. Dutch Robyjin and G9 were best suited genotypes in the third mega-environment comprising of Thika and Mau-Narok. G13 was the highest yielding genotype in Suera. G1 and G2 were superior in the second mega-

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environment and G9 in the third mega-environment that was made-up of Mau-Narok and Thika (Fig.4.9). The PC 1 accounted for 75.1% and PC2 accounted for 8.8% of the variation this is shows that 83.9% of the variation could be explained.
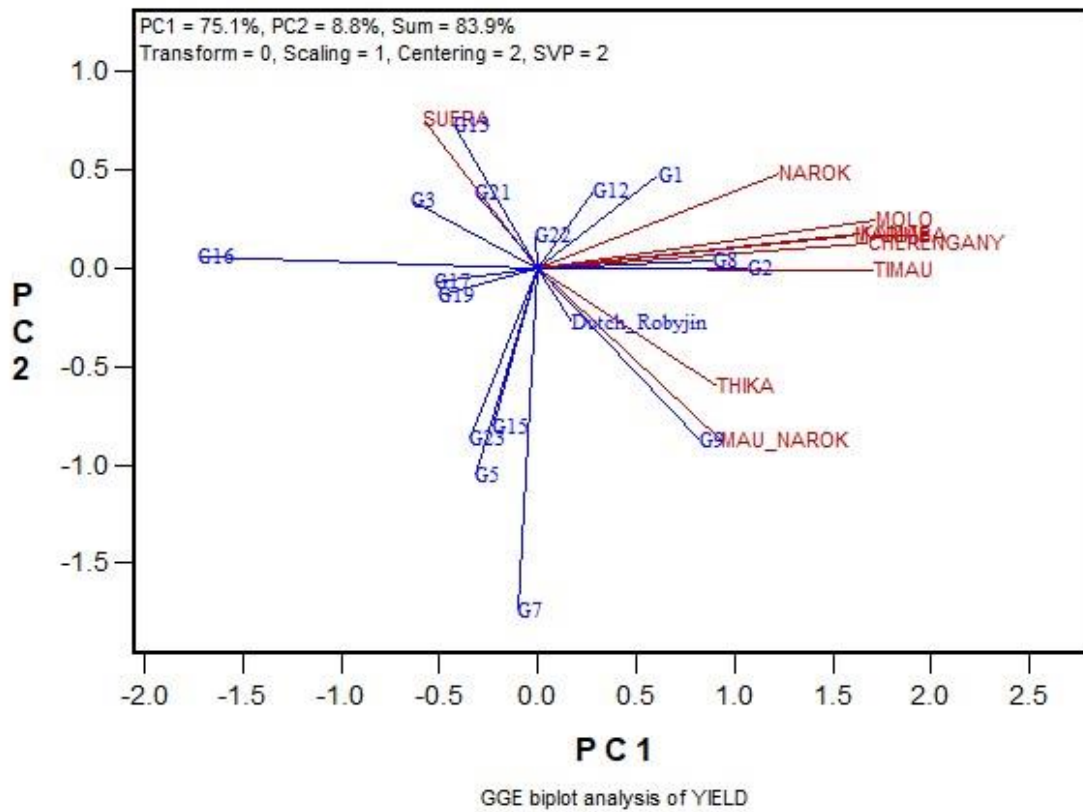


**Figure 4.10: The processing type genotype preference in the respective environment the long rainy seasons of 2015/2016**
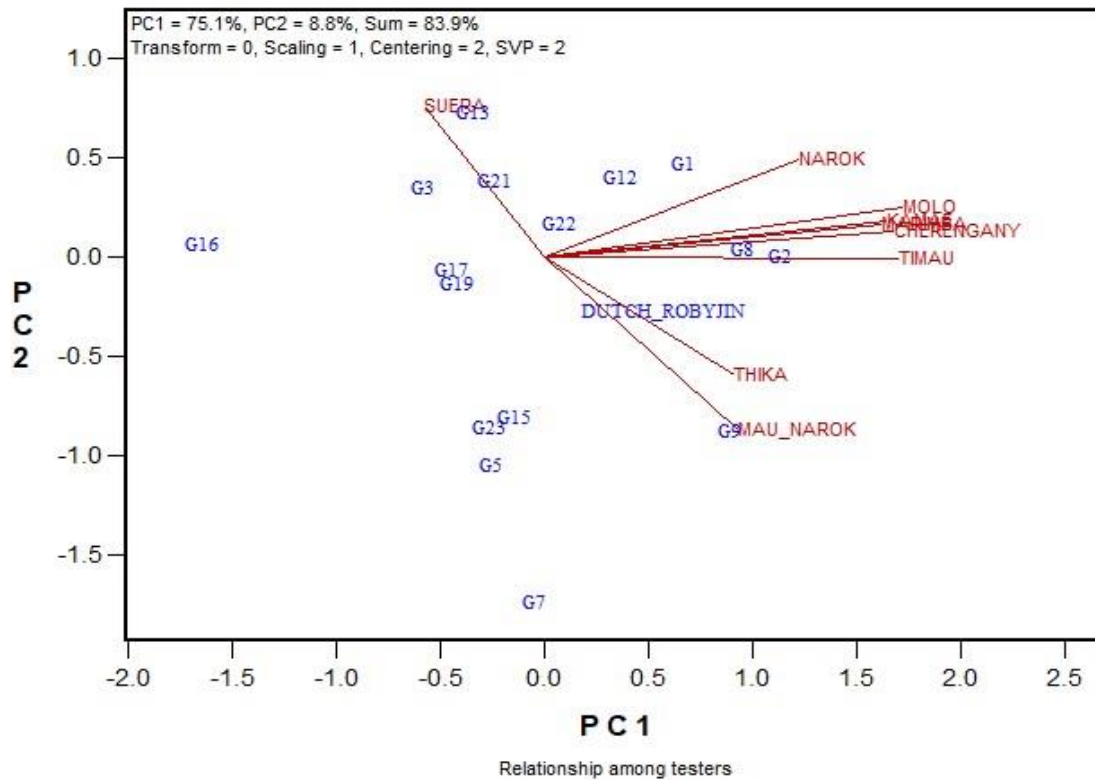
**Figure 4.11: The relationship between environments in the long rainy seasons of 2015/2016**

The discriminative ability and representativeness of the environment was established by the comparing the cosine of angle between vectors that represents the relationship between two environments, those environments with acute angels between them were considered to be positively correlated and those with obtuse angels are negatively correlated (Yan and Tinker 2006). The environmental vectors, which are the lines that connected each environment to the point of origin on the biplot were used to determine the angles between the environments (Fig.4.10 and 4.11). Among the test environments Narok, Molo, Kamae, Cherengany, Thika and Mau Narok had similar yields hence positively correlated. Suera yield was significantly different from other locations. Thika, Mau-Narok and Suera had different wider vector magnitudes providing varying test environments for expression genotypes yield trait. The relationship between genotypes was also determined and those genotypes that had acute angles between them were considered related and those with greater angles were considered unrelated as shown in figure 4.10.

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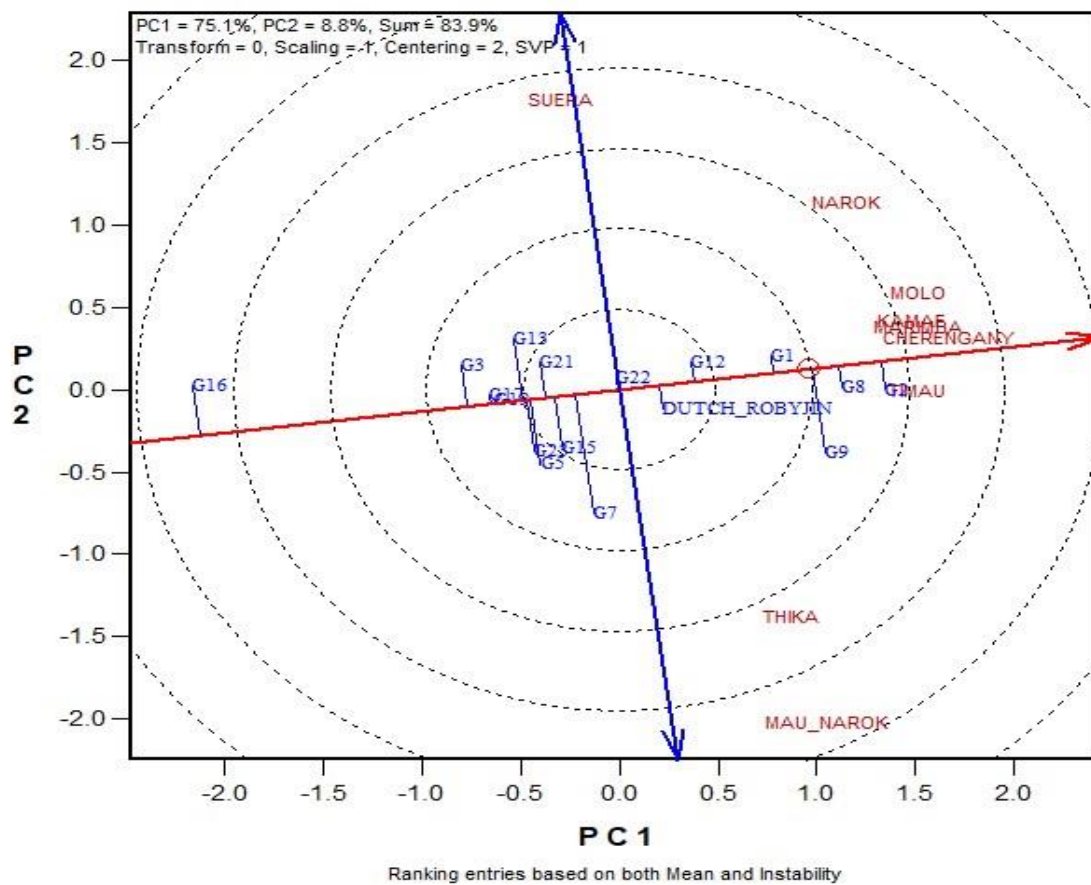
**Figure 4.12: The Processing genotypes stability in the long rainy seasons of 2015/2016**

Since all test environments were grouped into mega-environments, it was necessary to establish the genotypic stability. This was to provide information on the tuber yield consistence hence its predictability. Ascertaining the yields and stability of the genotypes based on average environment coordination (AEC) will inform selection (Fig. 4.12). The genotypes were categorized based on their average yields and stability performance (Fig. 4.12). The direction of the AEC points to the best yielding genotypes across test locations. The yield of G2 was the highest yielding genotype and G16 is the lowest yielding genotype among all the evaluated genotypes. The double arrowed line that passes the center of the biplot was used to establish the stability levels of the genotypes, the arrows point towards the most unstable direction. Those genotypes with shorter vectors from the origin are stable and the ones with the long vectors are the unstable ones. Genotypes G22, G17, G1 and G8 were the most stable ones whereas genotypes G7 and G9 were the most unstable.

To improve potato tuber yield, the genotypes with high yield mean, stable and are closer to the ideal environment are most preferred. The genotypes' vectors to the AEC abscissa determines their stability, the genotype is considered more stable and the environment has less influence on its yield performance when it has a shorter vector. For breeding purposes, the genotypes that are stable and have high average yield across environments are the potential ideal genotypes and should be close to the average environment (center of the small circle) in (Fig. 4.12). Although genotype G2 had the highest yield among all genotypes it was unstable when compared to genotypes G9, G1and G8 which are closer to the ideal environment. The poor stability of genotype G2 is associated with its high sensitivity to environmental factors (Fig. 4.12 and Table 2).

## 4.5 DISCUSSION

The Processing and Table type genotypes performed differently across different environments. The Table types had higher yield compared to the Processing types. Kenya Karibu, Shangi, G4 and G6 of the Table type genotypes performed better than their checks, G11, G20 and G24. The three checks (G11, G20 and G24) are commonly grown varieties but were sensitive to environmental pressures in the test locations. Based on the higher yields of Kenya Karibu, Shangi, G4 and G6, were less sensitive to environmental challenges thus, they provide better alternatives for the farmers.

Among the Processing types G2, G16, G9 and G1 were high yielding. G2 was the highest yielding among the test genotypes and outperformed G8 the check variety. The check variety is commonly grown for processed products such as crisp and French Fries. Based on the yields obtained in this study, it was found G8 the check variety was more sensitive to environmental pressures hence the lower yields than G2, G16, G9 and G1. Genotypes, G2, G16, G9 and G1 because of their high yields would be possible alternatives to the check for the farmers.

The significant differences in yield among the genotypes showed that genotypes have dissimilar genetic composition that were responsible to the diverse tuber yields. The diverse genetic composition observed among the test genotypes could be a culmination of the research activities from various programs. Among the major potato researching institutions are International Potato Center (CIP)and Kenya Agricultural and Livestock Research Organization (KALRO) in Kenya.

The Table type genotypes had highest yields in Thika, Timau and Narok environments but lowest in Molo. Thika, Timau and Narok had loam soils, optimum temperatures and adequate well spread rainfall during the growing period. These provided ample conditions for vegetative growth and tuber formation. Molo is located in a high altitude region with relatively low and varying temperatures and the rainfall was poorly distributed during growing period which impacted the genotypes yields negatively.

The Processing type genotypes had high yields in Narok, Thika and Mau-Narok but were low yielding in Molo. Mau-Narok had cold temperatures, loam soils and well distributed rain during the growing period that favored growth and tuber formation. This accounted for the realized high yields.

The GGE biplot distributed the Table type genotypes in mega-environments based on their adaptability. Genotype, Sherehekea was broadly adopted in Timau, Cherangany, Kamae, Molo and Marimba which could be attributed to its broad genetic base that enable it to withstand environmental challenges in these locations. Narok, Suera, Mau-Narok and Thika formed independent environments. Genotype, Shangi was adopted in Narok whereas genotype Kenya Karibu was adapted in Mau Narok, and genotype, G20 and G24 were adapted in Thika. The specific adaptation can be associated with the narrow genetic base which makes them sensitive to the conditions other production sites.

The Processing type genotypes were distributed in different mega-environments based on their adaptability using GGE biplots. Suera was identified to be a unique environment in which G4 was the most adapted. Thika and Mau-Narok formed the second mega-environment in which G9 was best adapted. G1, G2 and G8 showed wide adaptation in the third mega-environment that consisted Narok, Timau, Molo, Cherangany and Kamae. G1, G2 and G8 were able to show broad adaptation because of their wide genetic base.

The genetic diversity of genotypes in both the Processing and Table type genotypes was realized from the way they performed in different. The highest yield was 64 t ha$^{-1}$ for Table type genotypes and 46.0 t ha$^{-1}$ for the Processing type genotypes were recorded at Suera. Suera had the highest rainfall that was uniformly distrusted throughout the growing season and had optimum temperature. The cool temperature well distributed rainfall and loams soils were

responsible for the high yields in this location. The findings of this study were in agreement with those presented by (Mohammadi et al., 2012).

The classification of the evaluation locations intomega-environments reveals the significant differences in the growing conditions. The difference in the yields among the genotypes indicate the presence of genetic variation among the genotypes. The yield was as a result of the interaction between the genotype and the growing conditions across the test locations. These conditions led to the genotype expressing themselves as either specially or broadly adapted. During the study there were marginal gains due to intensive management. This is a reflection that intensive management does not have much effect on tuber yield, but the genetic base is most important in yield expression.

Genotype that were less adapted did not show appreciable improvement on tuber yield with intensive management. This means that they were either poor genotypes on tuber yield trait or require completely different environment to perform well. The adaptability of genotypes to particular environments was also established. The genotypes that were high yielding in the specificmega-environments were not necessarily the stable. The specially adapted Table type genotypes were Kenya Karibu, G20, G14 and Shangi whereas the Processing types were G4 and G9. Stability among genotypes was also diverse where G7 was most unstable among the Processing and G20 among the Table type genotypes. The most stable Table genotype was G6 while for the Processing G 22 was the most stable. This was associated to differential genetic expression as a response to production factors.

Based on stability measures, potato genotypes that were evaluated were classified into three categories. One, genotypes with highly yield, high stability and could be accepted across varied environment. This category includes G8, G2 and G1 among Processing and G6 among Table type genotype. In the second category were those genotypes which exhibited high yield but had low stability and adapted to specific locations such as genotypes G17 and G21 for Processing and G4 and G10 for the Table type genotypes. The third category made up of stable but low yielding genotypes consisted of genotypes such as G7 for Processing type genotypes and G18 and G11 for Table type genotypes. The inconsistency in tuber yield among the environments was attributed to soil physical and chemical characteristics. The observations were attributed

to recurring environmental factors that can be predicted and it is possible for breeders to develop environment specific varieties or broadly adapted varieties than when the factors are predictable. This was in line with the findings of Farshadfar, (2008) and Fikere et al., (2009).

The observed variations in genotypes yields underscore the effect of environments on genotypes phenotypic expression (Balakrishnan et al., 2016). The findings of this study were in agreement with those provided by Kumar et al., (2012), Tariku et al., (2013), Liang et al., (2015) and Katsura et al., (2016).

Test locations had different crop production conditions that were either favorable or unfavorable for expression of the yield trait. The yield outputs from the test environments was a factor of the genotypes interaction with both known and unknown environmental factors. The results in this study indicated genotype environment interaction was a major contributor to the tuber yield variations observed and agronomic improvement could have minimal effects.

## 4.6 CONCLUSION

The experiments revealed that there was a high degree of genetic variation among tested potato genotypes. The genotypes were variably sensitive to the evaluation environments hence the significant Genotype Environment Interaction (GEI). The GGE biplots revealed that under conventional management Table type genotypes could be grouped into two mega-environments. Timau Molo and Kibirichi were similar and formed one mega-environment whereas Cherengany and Burnt Forest formed the second mega-environment. The Processing type genotypes formed two mega-environments where Timau, Molo, Kibirichia were similar whereas Cherenagny and Burnt Forest formed the second mega-environment .

Under conventional management Narok was the best production site for Table type genotypes whereas Timau was the best for Processing type genotypes and kibirichia was the poor performing site for both. Suera was the best production site for both Table and Processing genotypes under intensive management whereas Molo was the least performing site.  GGE biplots identified Tigoni, Shangi and Sherehekea among Table type genotypes and G8, G2, G1, G12 and G2 as having similarities and a possibility of these genotypes having the same parental origin.

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The information about mega-environments and genotype similarities is necessary for planning and selection of the evaluation environments to avoiding duplication while maintaining quality data at a low cost. The process of improving potato is a complex undertaking that requires screening genotypes for G x E effects to understand the nature and extent of Genotype, Environment Interaction in order to determine the suitability of the test genotypes to certain environments. Intensive management has positive contributions to tuber yield but cost benefit analysis is necessary if it is to be adapted

# CHAPTER FIVE: GENERAL DISCUSSION, CONCLUSION AND RECOMMENDATION

## 5.1 General discussion

There were significant differences in performance of different genotypes in different environments for tuber yield and stability aspects. The Table type genotypes performed better on average when compared to Processing types genotypes across evaluation environments under both conventional and intensive management systems. The highest mean tuber yield on conventional management for Table type genotypes was 26.49 t ha$^{-1}$from G5 and the lowest performer was G21 at 17.74 t ha$^{-1}$. The Processing type genotypes equally had variations in their tuber yield and G2 had the best mean yield of 21.85 t ha$^{-1}$and G14 was the least performing genotype with 15.07 t ha$^{-1.}$ Narok was the best production environment with (32.82 t ha$^{-1}$and 28.14 t ha$^{-1}$) whereas Kibirichia was the lowest performing location with (13.15 t ha$^{-1}$and 13.54 t ha$^{-1}$) for Table and Processing types respectively.

The variations in yields were attributed to the diversity genetic compositions of the genotypes and environmental factors that prevailed in the various growing locations during the study. This interaction suggested the genotypes were not stable across all the environments. The differences in yield across environment show that yield trait can be improved by modification of the environment. Application of fertilizers, irrigation and proper pest and disease management as a form of environmental improvement can increase the yields.

The mega-environments identified by GGE bi-plot analysis for the two management systems served as a suitable representation of the environmental similarities and differences. They could be used to reduce the number of evaluation sites while maintaining the quality of the data obtained and reducing the cost of evaluation.

The results obtained show that different genotypes respond to environment factors differently. Table type genotypes had a better genetic buffer that reduced their sensitivity to environmental stress compared to the Processing type genotypes. These findings show that the environments influence on genotypes differently and hence the varying degree of adaptability and stability that was observed. This is because of the interactions between the genotypes and the environments that resulted in lack of consistency in tuber yield. The inconsistence hinders efficiency of selection of genotypes evaluated in diverse environments (Sorensen, 2010). The

interaction between environment and genotype reduces the association between the phenotypic and genotypic values and therefore this may lead to bias when estimating gene effect and combining ability of parameters sensitive to environmental conditions (Najafian, et al., 2010). Those genotypes with better genetic buffer will with stand the environmental influence and show stability in their performance.

The results revealed diversity in adaptability and stability among genotypes in different environments. The analysis of variance for tuber yield across the environments revealed that the major variations between genotypes were due to the way genotypes responded to the external pressures as presented by the evaluation environment. The genotype responses were attributed the genotype genetic constitution. Genotypes that were less sensitive to environmental effects were more stable compared to those that were sensitive to secondary effects. Genotype, G22 was found to be the most stable whereas G2 was identified as the genotype that was most unstable among the Processing type genotypes (Fig.3.4). G5 was the most stable and G15 as the most unstable for the Table type genotypes (Fig.3.6) for conventional production method. The intensive management system revealed that for Processing type genotype G22 was the most stable and G9 the most unstable (Fig.4.7) whereas for Table type genotypes the most stable one was G6 and the unstable one was G11 (Fig.4.14). This shows that the production systems determine the extent to which the genotypes' genetic potential is phenotypically expressed. Such varied performance reflects specific genotypes adaptability and this can be attributed to genetic control rather than external factors.

Adaptability and stability tests were found to be helpful in identification of genotypes whose yield is based the genetic ability and matching them with their suitable production sites, this was in agreement with the findings of Jorge et al., (2015). The yield performance that is based on genetic potential of the genotypes is important in determining the selection of the genotypes for advancement. These findings were similar to the findings of Hassanpanah (2010) and Byarugaba et al., (2018). A detailed knowledge of the way the elite lines could be affected by the environment in the expression of the characteristics of interest is important in increasing the efficiency of identifying and selecting potential lines to be released as varieties.

## 5.2 CONCLUSION

The study showed the value of establishing the level of interaction between the cultivars and the production location is crucial in determining adaptability and stability of the new genotypes before release as variety. When genotype environment interaction is due to the disparity that arise from foreseeable factors, potato breeders can develop varieties that are generally adapted to perform well under diverse environmental conditions. Potato variety developers are required to understand the conditions of the production locations and how the interact with the cultivars to aid selection of superior genotypes and their best environments. The findings show that the environment has an influence on the expression of tuber yield trait and multi-environment evaluations are necessary before a variety is released.

## 5.3 RECOMMENDATIONS

I. Newly developed potato candidate genotypes should be evaluated for adaptability and stability in multiple sites to establish their true genotypic significance and the suitable environment before release as variety

II. Narok and Suera environments should be considered ideal locations for potato tuber production for both Table and Processing type genotypes

III. G5, G15, G23 and G21 can be further evaluated for broad adaptation Table type genotypes

IV. G7 and G4 can be further evaluated for specific adaptability to Narok under conventional management

V. Before investing on intensive management the economic advantage to be obtained from the yield gap should well understood

VI. Genotype, genotype-environment analysis software should be adopted when analyzing mult-locational data

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