

**LINE BY TESTER ANALYSIS OF ELITE TROPICAL-TEMPERATE MAIZE LINES  
UNDER WATER-STRESS AND NON-STRESS ENVIRONMENTS**

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**A thesis submitted in partial fulfillment of the requirements for the award of  
the degree of Master of Science in Plant Breeding and Biotechnology**

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## **DEDICATION**

I dedicate this work to God who carried me through all the challenges and made everything possible; and to my loving and supportive family.

**DECLARATION**

This thesis is my original work and has not been presented for award of a degree in any other University.

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## ACRONYMS

AD	-	Days to anthesis
AMMI	-	Additive main effects and multiplicative interactions
ANOVA	-	Analysis of Variance
ASI	-	Anthesis silking interval
BIP	-	Bi-parental progenies
BLUE	-	Best linear unbiased estimates
CA	-	Combining ability
CAN	-	Calcium Ammonium Nitrate
CGIAR	-	Consultative Group on International Agricultural Research
CIMMYT	-	International Maize and Wheat Improvement Center
DTS	-	Days to silking
EH	-	Ear height
ET	-	Exserohilum Turcicum
FAO	-	Food and Agriculture Organization
GCA	-	General combining ability
GEI	-	Genotype by Environment interaction
GLS	-	Gray leaf spot
GY	-	Grain yield
L*T	-	Line by Tester
MLND	-	Maize lethal necrosis disease
MSV	-	<i>Maize streak virus</i>
NCD	-	North Carolina Design
PH	-	Plant height
SCA	-	Specific combining ability
SREG	-	Site regression
SSA	-	sub-Saharan Africa
TLB	-	<i>Turcicum</i> leaf blight

## ABSTRACT

Maize is the second most cultivated cereal crop in the world after wheat. In spite of its importance, the production challenges have continuously led to poor yields in sub-Saharan Africa. This has called for need to improve varieties that are adapted to the tropical ecosystem. The aims of this study were (i) to assess the combining ability of the tropical-temperate maize lines for grain yield, drought tolerance, disease resistance, and heritability of the traits, and (ii) to examine the yield and yield stability of the three-way cross hybrids in eight environments found in different agro-ecological environments and identify the genotypes, of wide or specific adaptation. The maize germplasm used in this study were obtained from various sources. These included seven elite tropical-temperate inbred lines (L), seven single cross testers (T) and six commercial hybrids that were used as checks during evaluation. The results indicated that inbred lines L5 and L3 gave high grain yield across well-watered environments and had a common single cross tester T6, with best linear unbiased estimates values of 8.5 t/ha and 8.4 t/ha, respectively. The two lowest hybrids across locations had a common single cross tester, T7, with two different pollen donors L6 and L7 yielding 6.0 t/ha and 5.5 t/ha, respectively. Forty eight hybrids had statistically better mean grain yield than the best check, Pioneer 3253. Under managed drought stress conditions, the top two performers in grain yield had different testers, namely T6 and T4 but shared the same pollen donor, L5, with values of 4.9 t/ha and 4.8 t/ha, respectively. DK8053 was the best check with value 3.7 t/ha. The results indicated that the inbred lines which produced the top yielding hybrids were related by pedigree and origin. To examine genotype  $\times$  environment interaction and yield stability, the three-way cross hybrids were planted in eight environments with two replications. Data was analyzed using REML, SAS and GGE biplot tools. The results revealed that Environment (E) contributed 67% of the total sum of squares for grain yield while GEI and genotypes (G) contributed a percentage of 12.5%



and 10.3%, respectively. The first two principal components (PCs) accounted for 67.9% total variation. The biplot figures demonstrated that across environments, entry 10 (L5 × T5), 14 (L5 × T3) and 28 (L3 × T3) were the highest yielding with stable genotypes. The additive or dominance gene action played a greater role in the inheritance of grain yield and the yield related agronomic traits. There were two mega-environments (ME) with ME1 represented by 3 locations and ME2 by 5 locations. The two testers included as checks in this study showed that tester 2 performed better under drought conditions and therefore it is a recommended hybrid for yield increase in water stress environments. Tester 5 should be utilized in Kirinyaga type moisture regimes, as it yielded higher than all experimental hybrids. L1, L3 and L6 could contribute to formation of hybrids with consistent earliness, while L5 contributes to stable high grain yield in both well-watered and water stress conditions. The heritability of most agronomic traits was noted implying that the traits characteristics can be passed to future generations. Tropical maize populations can be improved for these traits using these improved maize germplasm. The promising maize hybrids for yield and agronomic traits could be nominated for national performance trials for commercial release in various Eastern African countries.

## CHAPTER ONE

### 1 INTRODUCTION

#### 1.1 Background information

Maize (*Zea mays* L.) production dates back to about 7000 years ago when it was grown in form of a wild grass called *teosinte* in Central Mexico (Abbassian, 2006). The crop is widely adapted and is currently cultivated in varying ecologies ranging from sea level to about 3000 m above sea level (Kang'ethe, 2011). Although ranked third globally, maize demand is expected to surpass that of wheat and rice by 2020 (FAO, 2015; Mkumbwa, 2011) as it is increasingly becoming important in the livelihoods of many poor farmers in sub-Saharan Africa. Approximately 67% of the total maize production is from low and middle income countries with the global annual production being 13 times higher than that of Africa (Shiferaw *et al.*, 2011). Compared to the United States, Africa's production is averagely five times lower (Faostat, 2012b) as shown in Figure 1.1. This is probably due to the frequent onset of drought conditions, new diseases and insect pests. Africa's maize grain yield is low, averaging approximately 1.5 tons per hectare, in spite of being the backbone of food security in some of the poorest regions in Africa and the world (Shiferaw *et al.*, 2011). In Kenya, maize is ranked number one food crop in terms of area under production and consumption, with a per capita consumption of 98 kilograms translating to between 2.7 to 3.1 million metric tons of annual consumption (Kang'ethe, 2011). Yield penalties are mostly known to be stronger in the tropical and sub-tropical areas (Vermeulen, 2014) and are predicted to affect over 90% of productions for resource-poor maize farmers and consumers (AGRA, 2014; Wiggins and Sharda, 2013). Thus, there is need for practitioners to seek appropriate strategies of dealing with these challenges like drought, insect pests, disease

incidences, unavailability and untimely input supply and use of varieties with low production potentials (Lisuma *et al.*, 2006) that threaten grain yield.

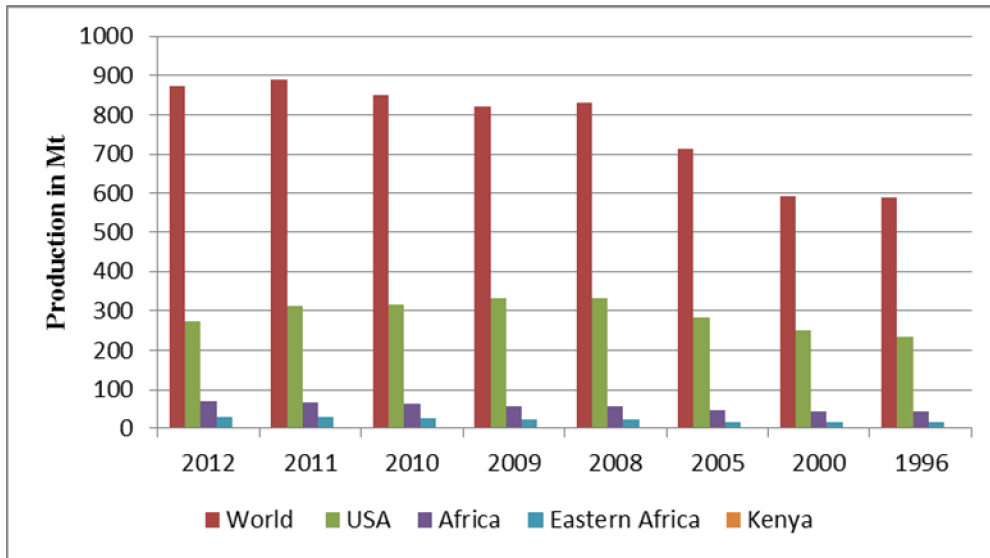


Figure 1.1 Annual world maize production (Adapted from FAOSTAT 2012)

## 1.2 Maize production constraints

While the world's population is increasing, the available arable land for maize production is declining (Jayne *et al.*, 2013) and thus maize demand is expected to double particularly in the developing world, leading to approximately 30% deficit (FAO, 2013). The deficit in grain yield in sub-Saharan Africa (SSA) is attributed to both biotic and abiotic factors (Lisuma *et al.*, 2006; Mombanyi *et al.*, 2010; Shiferaw *et al.*, 2011). Abiotic factors include extreme temperatures, low soil fertility, extremes of soil acidity and salinity, drought and flooding (Mombanyi *et al.*, 2010). On the other hand, diseases, weeds, field and storage insect pests are common biotic factors causing low maize yields. These concerted challenges will eventually lead to higher global prices, malnutrition, poverty and hunger. According to the Economic Review of Agriculture report (MoA, 2010), maize production has continued to decline hence necessitating imports.

Maize farmers on the other hand face challenges on poor storage, access to markets, availability of farm inputs like fertilizers, poor crop husbandry, poor mechanization and/or inadequate use of farm inputs. This in turn leads to depressed yields and food deficits (Keating *et al.*, 1992). The effects of climate change have and will continually be felt unevenly across the maize production areas thereby worsening the food security situation in these areas.

### **1.3 Problem Statement**

Drought stress affects production at any stage of crop development, but maximum damage is inflicted during flowering (Edmeades *et al.*, 1992). The stress during this period results in a significant reduction in grain yield which is associated with reduction in kernel size (Bolanos and Edmeades, 1993). In the developing world, Edmeades *et al.* (1992) estimated annual yield losses due to drought as 24 million tons, equivalent to 17% of a normal year's production. On the other hand, Fisher *et al.* (2015) estimated yield losses of 10-25%. This in turn leads to food shortages and food insecurity, which in turn give rise to famine and loss of human life (Fisher *et al.*, 2015). Due to the higher yield potential in temperate species, they are superior compared with tropical species (White *et al.*, 2012). For that reason, attention has been shifted to temperate introgressed tropicalized maize germplasm as a possible source of variation for drought. The introgression of temperate germplasm may widen the genetic base of tropical germplasm and allow greater flexibility in selection for improved yields as well as resistance to both biotic and abiotic stresses (CIMMYT and IITA, 2012).

### **1.4 Justification**

Drought is a common phenomenon in SSA countries with devastating effects on food security situation among small scale farmers in the region (Schlenker and Lobel, 2010; Rosegrant and

Team, 2012; Waithaka *et al.*, 2013; Vermeulen, 2014). Past maize breeding work has largely focused on improving yield levels, quality, early maturity, resistance to diseases and insect pests and resistance to drought stress among others (Edmeades, 2013b). Maize breeders have concentrated on tropically adapted germplasm as a viable source of variation for drought tolerance in maize (Araus *et al.*, 2012). In the recent past, maize breeders have shifted their attention to temperate introgressed tropicalized maize germplasm as a possible source of variation for drought. Temperate germplasm is known to exhibit high yield potential and stability, hence making them superior compared with tropical species. The introgression of temperate germplasm may allow greater flexibility in selection for improved yields as well as resistance to both biotic and abiotic stresses in tropical ecosystems (CIMMYT and IITA, 2012). Utilization of temperate maize germplasm requires backcrossing it with tropical adapted germplasm and conducting selection based on desirable traits. Contrary to tropical-adapted germplasm, there is limited literature on the heterotic patterns and the combining ability of this germplasm as well as how genotypes interact with the environment of growth. There is need to fully understand the genetic potential of introgressed germplasm in addressing the maize production constraints in SSA. There is also need to comprehend the combining ability of such inbred lines and hybrids as well as to gauge the magnitude of genotype by environment interaction of the resultant hybrids. Previous studies have been done to determine the combining ability for drought tolerance among temperate and tropical maize germplasm (de Souza *et al.*, 2009; Aminu *et al.*, 2014; Worrajinda *et al.*, 2013; Edmeades, 2013b). Literature shows that there has been many combining ability studies on temperate germplasm with small proportions of the tropical germplasm (Holland and Goodman, 1995; Reid and William, 2013; Whitehead, 2002; Cooper *et al.*, 2001). At present, there is little literature showing combining ability studies

with tropical-temperate germplasm in eastern Africa; thus the current study aims at increasing this information in the eastern African ecosystem.

### **1.5 Main objective of the study**

The general objective of this study was to assess the genetic potential and usefulness of temperate maize germplasm in tropical maize farming systems through targeted introgression into tropical adapted germplasm to improve maize productivity in Kenya

#### **1.5.1 Specific objectives**

1. To determine the combining ability of parental inbred lines, the heritability and correlation for grain yield performance under well-watered and water stressed conditions.
2. To assess the magnitude of genotype by environment (GE) interaction for grain yield of maize testcross hybrids in well-watered and water stressed conditions.

#### **1.5.2 Hypothesis**

1. Inbred lines derived from temperate germplasm have poor combining ability for grain yield performance, and low heritability and correlation of the agronomic traits compared to the tropical maize lines.
2. GEI is highly prominent among hybrids developed using tropicalized temperate germplasm for drought tolerance, grain yield performance and disease resistance.

## CHAPTER TWO

### 2 LITERATURE REVIEW

#### 2.1 Maize production and breeding trends in Kenya

Maize breeding program in Kenya began in 1955 in Kitale and the product was an open-pollinated maize variety- Kitale Synthetic II; which was in turn crossed with Ecuador 573, sampled germplasm from Latin America leading to release the first varietal hybrid, 611 (Hassan *et al.*, 1998). This hybrid had a yield advantage of over 40%, and became the basis of all subsequent hybrids developed by national breeding program. Currently, about 80% of maize is produced by small scale by farmers in Kenya, while a paltry 20% is by large scale farming systems (Anjichi *et al.*, 2005). Being a staple food, maize per capita consumption has been estimated to be about 100 kgs, translating to slightly below 3000 thousand metric tonnes per year (Nyoro *et al.*, 2004). Considerably the yield has fluctuated over the years (Onono *et al.*, 2013) despite the projected increase in demand estimated to be 45% by the year 2020 (Anami *et al.*, 2009). With these occasioned shortfalls in production, the Kenyan demands are met through imports from Tanzania, Uganda and among other countries (Onono *et al.*, 2013). It has been reported that the overall demand in the East African nations is rising (Mkumbwa, 2011) as shown in Table 2.1.

**Table 2.1 Projected domestic demand for maize in Eastern Africa**

Demand Projection (million metric tonnes)						
	Scenario 1: GDP growth is 5 %			Scenario 2: GDP growth is 6%		
Year	2010	2015	2020	2010	2015	2020
Maize demand	11.89	13.99	16.15	11.96	14.13	16.38

Compared to the developed nations, the Sub-Saharan Africa maize yields are lower, giving an average of about 1.5 tons per hectare (Shiferaw *et al.*, 2011; FAOSTAT, 2012a). Many reasons have been advanced to explain this including decreased agricultural areas due to overpopulation (Jayne *et al.*, 2013), coupled with salinity, acidity, low nitrogen (low N), insect pests in the field and storage, higher cost of fertilizer, extreme heat and inadequate water. Drought has caused a decline in genetic variance and heritability for grain yield (Blum, 1988) in the available germplasm. Thus, yield increases rather than area expansion becomes progressively more important as a means of increasing crop production (Jayne *et al.*, 2013).

To address these productions constrains, a lot of research has been conducted on tropical germplasm that are known to be drought and disease tolerant. However, literature shows that there is little information on the yield performance of tropical adapted temperate introgressed maize germplasm in eastern Africa, hence the study.



## **2.2 Drought stress in maize**

Drought results from insufficient moisture in the soil for adequate growth of a plant (Bänziger *et al.*, 2000). This could be due to shortage in rainfall, rough soil texture which retains little water in the root zone or drying winds. This stress is the most important abiotic constraint that destabilizes maize grain yields in arid and semi-arid regions (Bänziger *et al.*, 2000). Drought leads to physiological and biochemical changes like reduction of photosynthesis and changes in gene expression in maize (Lawlor and Cornic, 2002; Romo *et al.*, 2001). When maize plants grow under inadequate moisture environments, stomatal pores progressively close. This is regulated by leaf water potential but can be mediated by abscisic acid (ABA) (Tezara *et al.*, 1999; Lawlor and Cornic, 2002). Stomatal closure leads to low photosynthetic carbon dioxide (CO<sub>2</sub>) assimilation due to restricted diffusion of CO<sub>2</sub> into the leaf, therefore altered CO<sub>2</sub> metabolism. Because of the lower CO<sub>2</sub> availability, photosynthetic capacity is lost due to reduced stomatal conductance and direct damage to carbon metabolism (Colom and Vazzana, 2003). Drought affects all plant growth stages but is more serious on the events at flowering and therefore grain filling (Edmeades, 2013b). Ears that have been affected by drought have fewer kernels which remain poorly filled if the drought extends throughout grain filling (Blum, 2011; Edmeades *et al.*, 2000).

## **2.3 Drought tolerance mechanism in plants**

Drought tolerance is the ability of the plants to function at low tissue water potential (Blum, 2005). Drought stress tolerance mechanism involves maintenance of turgor and desiccation tolerance (Jones *et al.*, 1981). Desiccation tolerant plants are in a metabolically dominant or cryptobiotic state when dehydrated (VicrÉ *et al.*, 2004). This implies that they can recover from a fully air dried state. Drought stress can also be tolerated by osmotic adjustment where plant

tissues accumulate solutes or osmolytes making their water potentials more negative thus taking up water while avoiding reduction in turgor. During drought conditions, some solutes contribute towards stress-protective functions as free radicle scavengers and stabilization of macromolecules (Abebe *et al.*, 2003; Seki *et al.*, 2007).

#### **2.4 Breeding maize for drought tolerance**

Genetic variability in maize, especially of the tropical and subtropical germplasm, has been utilized through breeding efforts of CIMMYT; through various public regional and national breeding programs, and through private commercial maize breeding programs (Gracen, 1986). In the past about 30 years, CIMMYT has been selecting tropical maize for drought tolerance using rain free tropical locations and irrigation to create its managed drought stress environments. These studies have been widely described by (Bolanos and Edmeades, 1996; Edmeades, 2008; Edmeades *et al.*, 2000; Banziger *et al.*, 2006; Monneveux *et al.*, 2006). Recurrent selection using an index of traits was conducted for 2-9 cycles in six improved tropical populations, normally evaluated under well-watered and two distinct drought stress regimes (Edmeades, 2013b). Marker assisted selection has also been used for maize and it helps to reduce the volume of field testing. Gains in drought tolerance from selection under managed stress environments were significantly greater than those from selection of similar populations under well-watered environment.

Effective breeding for drought tolerance relies on elucidation of the heritable genetic variation for tolerance to drought and heat. Both field based and transgenic approaches have been used to improve the diverse and potentially additive component fundamental in breeding for drought tolerance maize (Banziger and Araus, 2007). Stress tolerant alleles are usually present at low frequencies in most elite breeding populations necessitating their evaluation (Blum, 1988). The

evaluation of the elite population has been enhanced through the use of marker assisted selection (MAS) due to the availability of high throughput and accurate phenotyping. The use of MAS has also made field testing more efficient through handling less number of populations (Prasanna *et al.*, 2012a; Prasanna *et al.*, 2012b; Cairns *et al.*, 2013).

## **2.5 Management of drought stress**

The symptoms of drought stress in maize are a change in leaf color from green to green-gray, rolling of lower leaves followed by the upper ones (Edmeades *et al.*, 2000). During drought stress, the stomata close, photosynthesis sharply reduces and growth slows, when stress coincides with the 7-10 day period prior to flowering. Ear growth slows more than tassel growth and there is a delay in silk emergence relative to pollen shed, giving rise to an interval between anther extrusion and silk exposure (Edmeades *et al.*, 2000). This anthesis-silking interval (ASI) has been used to predict drought-induced yield reduction (Edmeades, 2013a; Edmeades, 2008). Leaf senescence begins at the base of the plant and spreads upwards to the ear and severe stress at flowering may lead to the complete abortion of ears and the plant becomes barren. Drought-affected ears typically have fewer kernels that are poorly filled if drought extends throughout grain filling (Edmeades *et al.*, 2000). Genetic and management strategies that target improved grain yields in a water limited environment target three variables such as: (i) amount of water captured by the plant (W), (ii) the efficiency with which that water is converted to biomass and water use efficiency, (WUE) and (iii) the harvest index (HI) or the proportion of biomass forming grain (Passioura, 1977) each of which can be altered.

In addition, the widespread use and rapid analysis of remotely sensed environmental and phenotypic data has led to the steady increase in the volume of plots that can be evaluated for an

array of current and new traits in real time (Araus *et al.*, 2012; Berger *et al.*, 2010). There has been the establishment of networks of managed stress testing sites at carefully chosen locations in the target population environments (TPE) (Rebetzke *et al.*, 2012).

## **2.6 Potential of introgression of exotic germplasm in addressing the drought problem in maize**

Most of the available tropical germplasm in the Sub-Saharan African countries is adapted to the tropical conditions. The tropical maize germplasm contains many ecotypes with good adaptation traits but sometimes shows poor husk cover, low yield potential, low harvest index, excessive plant or ear height and lateness (Abadassi and Hervé, 2000). Previous studies involving the identification of drought, heat, and combined drought and heat tolerant donors in maize has revealed that many current lines are susceptible to drought stress at elevated temperatures (Cairns *et al.*, 2013). On the other hand, temperate germplasm show stability, high yield potential, and high harvest index among other desirable characteristics, but are known to be susceptible to tropical diseases (Goodman, 1999). The introgression of the temperate germplasm into tropical germplasm can broaden the genetic base of tropical germplasm. This could also improve the adaptability of new hybrids and help to establish new heterotic patterns (Goodman, 1999). Research has been carried out on the introgression of exotic germplasm to improve adapted tropical maize populations (Abadassi, 2014; Xu and Crouch, 2008; Nelson and Goodman, 2008; Nastasic *et al.*, 2011).

Abadassi and Herve (2000) summarized the history of research on introgression of exotic germplasm as: Avila (1985), Efron (1985) and Sauvaire and Sanou (1989) for tropical populations. Various author attempted the introgression of exotic germplasm to improve adapted temperate maize populations (Griffing and Lindstrom, 1954; Kramer and Ullstrup, 1959;

Oyervides-Garcia *et al.*, 1985; Gutierrez-Gaitan *et al.*, 1986; Albrecht and Dudley, 1987; Crossa and Gardner, 1987; Crossa *et al.*, 1987; Mungoma and Pollak, 1988; Eagles *et al.*, 1989; Eagles and Hardacre, 1990; Tracy, 1990; Beck *et al.*, 1991). The results obtained varied with materials and traits (Abadassi and Hervé, 2000). Genotype by environment interaction has been reported as key component in the management of drought tolerance. Heat effects on final kernel weight at different growth stages affects kernel growth, water relations and assimilate availability for grain yield (Edreira *et al.*, 2014). New tropicalótemperate hybrids need to be evaluated for yield performance and stability across environments and also tested for resistance to tropical diseases. This should also be coupled with establishing the combining ability for the different traits to enable the efficient utilization of the new hybrids.

## **2.7 Combining ability**

Combining ability is the ability of a parent to transmit desirable performance to the resultant hybrid after crossing (Sprague and Tautum, 1942). It involves two components namely the general combining ability (GCA) and the specific combining ability (SCA). The GCA refers to the relative performance of individuals, in a similar group of organisms, when crossed with a heterogeneous tester. The SCA refers to the progeny performance resulting from a particular cross as related to the performance of other particular crosses of a similar nature (Sprague and Tautum, 1942).

### **2.7.1 Determination of the combining ability for drought tolerance in maize**

Different genetic methods or mating designs have been used to study the combining ability in maize. This includes diallel, North Carolina Designs (NCD) and Line x Tester among others.

### **2.7.1.1 Diallel**

Diallel analysis (Griffing, 1956a) is a mating design that entails making all possible crosses among a set of inbred parents and has been utilized in estimation of combining ability in many crops. Diallel analysis helps in explaining the genetic control of important plant traits performance while enhancing breeding and selection of promising parents (Bello and Olaoye, 2009). The diallel crosses enable breeders to predict progeny performance from parental performance (Iken and Olakojo, 2002). The analysis of diallel cross by the method proposed by Griffing (1956) which partition the total genetic variation into general combining ability (GCA) of the parents and specific combining ability (SCA) (Griffing, 1956a) of the crosses have been widely used in breeding. Griffing's experimental method II, Model II is a new method that gives a step-by-step approach in statistical and genetic analysis (Griffing, 1956b; Bolboaca *et al.*, 2011). Tabassum *et al.* (2007) did a combining ability (CA) study in maize under normal and water stress conditions using diallel design and found some good general combiners for plant height, number of grains per ear and grain yield per plant (Tabassum *et al.*, 2007). In another study under drought stress done by Souza *et al.* (2009) tropical maize germplasm were studied and using grain yield, environments were classified as favorable, low stress, high stress and intense stress. A diallel experiment in the tropical lowlands of West Africa for one season under high and low nitrogen conditions were reported by Kling *et al.* (1997). The GCA for grain yield was significant under both N treatments while SCA was only significant under high-N (Kling *et al.*, 1997). For ears per plant, GCA was significant only under low-N while SCA was significant under high-N.

### **2.7.1.2 North Carolina Designs (NCD)**

NCD are three mating designs initially introduced by Comstock and Robinson (1948 and 1952) (Singh and Chaudhary, 1979). NCD I is appropriate only for estimating genetic components of

variance for a reference population (Hallauer and Miranda, 1988b). NCD II uses two reference populations and therefore provides GCA information for males and females. NCD III estimates the average level of dominance of genes affecting the traits evaluated (Hallauer and Miranda, 1988b). It is the most powerful since its modifications made by Kearsley and Jinks that adds a third tester apart from the two inbreds (Acquaah, 2012). Adebayo and Menkir (2015) using NCD II studied the CA of adapted and exotic drought-tolerant maize inbred lines. They observed high significance for all agronomic traits and leaf blight (Adebayo and Menkir, 2015). Other studies using these designs were done by (Mhike *et al.*, 2011; Kumar *et al.*, 2013).

### **2.7.1.3 Line x Tester design**

Line by tester ( $L \times T$ ) design, proposed by Kempthorne (1957), is an extension of top cross design (Sharma, 2006) in that instead of using one tester as in top cross, more than one tester is used.  $L \times T$  design provides both full-sibs and half-sibs simultaneously. The design provides SCA of each cross and GCA of both the lines and of the testers. Both the lines and testers have different sets of genotypes (Farhan *et al.*, 2012). A significant  $L \times T$  interaction provides evidence that the ranking of experimental lines differs depending on the tester used (Packer, 2007), hence an appropriate tester must be selected to evaluate new germplasm lines (Ali *et al.*, 2011). The testers that can be used in a breeding program may either be genetically narrow or broad-based, related or unrelated to the lines being evaluated or may have high or low frequency of favorable alleles and high or low yielding (Ali *et al.*, 2011; Packer, 2007). In general the combining ability between the line and the tester determines the performance of hybrids. Packer (2007) pointed out that an effective tester should correctly rank inbred lines for performance in hybrid combination, and that it should maximize the variance between testcross progeny to allow for efficient discrimination of new inbred lines. Consequently, lines with poor combining

abilities are discarded and only good performing lines are advanced in the program (Shahab *et al.*, 2011). Line by tester studies conducted by several researchers (Shushay *et al.*, 2013; Udaykumar *et al.*, 2014; Gouda *et al.*, 2013) with different findings on general and specific combining abilities for grain yield and other agronomic traits. Shushay *et al.* (2013) working on line by tester analysis of maize inbred lines for grain yield and yield related traits reported highly significant SCA for grain yield. Udaykumar *et al.* (2014) also worked on maize using line by tester analysis.

## **2.8 Genotype x Environment interaction (GEI)**

Sub-Saharan Africa experiences fluctuation in environmental conditions, drought, low soil fertility, non-uniform management practices and occurrence of diseases and pests (Martin, 2004). Increasing maize grain yield and yield stability under these changing environmental pressures and drought calls for focused field testing breeding approaches. However, plant breeding efforts should be augmented with proper and precise phenotyping under different environmental conditions. GXE delineates the change in relative performance of a character of two or more genotypes measured in two or more environments (Bowman, 1972; Vargas *et al.*, 2001). GEI also involves changes in the relative behavior of genotypes in different environments. Interactions may involve changes in rank order for genotypes between environments and changes in the absolute and relative magnitude of the genetic, environmental and phenotypic variances between environments (Bowman, 1972). The phenotypic expression of maize genotypes is determined by the genotype, environment and the interaction between genotype and environment (Martin, 2004). The GEI complicates the process of hybrids selection for wider adaptation (Abdurahman, 2009). Thus role of GEI must be quantified in order to devise an efficient breeding strategy and to enable the classification of genotypes by their behavior in different situations. Thus, the GEI should be quantified by conducting multi-environment testing to



identify genotypes with broad adaptation (genotype is widely adapted for the whole range of environmental conditions) or specific adaptation (genotype adapted to separate genotypes and which must be selected for different sub-environments) (Yan *et al.*, 2011).

Studies by Banziger *et al.* (1999) showed that gains transferred well to environments with moderately low nitrogen and showed only moderate levels of GEI. This suggested that selection resulted in a constitutive change in floral behavior and reproductive efficiency through changes in biomass partitioning to and within the ear (Edmeades, 2008). Different methods which differ in their approach towards analysis of multi-environment trials have been developed and used to study the nature of GEI (Eberhart and Russel, 1966).

Diverse statistical approaches have been published for the analysis of the GEI. The methods include analysis of variance, regression (Finlay and Wilkinson, 1963), nonparametric methods (Kang, 1988; Fox *et al.*, 1990) and pattern analysis of multivariate analytical methods like the additive main effects and multiplicative interaction (AMMI) model (Zobel *et al.*, 1988) and genotype plus genotype  $\times$  environment interaction (GGE) biplots (Yan *et al.*, 2000). However, not all methods are effective enough in analyzing the multi-environment data structure in breeding programs (Zobel *et al.*, 1988; Navabi *et al.*, 2006). The most widely used methods of statistical analyses are AMMI, the site regression (SREG) and GGE biplot models as they are relatively powerful for effective analysis and interpretation of multi-environment data structure (Ezatollah *et al.*, 2013; Zobel *et al.*, 1988; Yan *et al.*, 2000). In the case of balanced data, mixed models can be fitted by standard least squares procedures but a more general method of inference to fit mixed models is by residual maximum likelihood, or REML (Patterson and Thompson, 1971). Results of REML analyses are presented in another way than the familiar ANOVA tables. In REML the likelihood is partitioned into two components. The first component is a likelihood

of one or more statistics and involves all fixed parameters and may involve variance parameters as well (Neill, 2010). The second component is a residual likelihood and involves only the variance parameters of the random effects. Each component is then maximized separately. The estimates of these variance parameters are known as REML estimates (Neill, 2010).

### **2.8.1 Additive main effect and multiplicative interaction**

Additive main effect and multiplicative interaction (AMMI) model combines the additive main effect and multiplicative interaction principal components (IPC) of two-way data structure (Reza *et al.*, 2007). It clearly gives the difference between the main and the interaction effects (Gauch, 1992). Recent papers compare AMMI and GGE like (Gauch *et al.*, 2008) where GGE biplot analysis is based on environment-centred PCA, whereas AMMI analysis refers to double-centred PCA. For distinguishing mega-environments, both AMMI and GGE are suitable and comparisons indicate similar results (Gauch *et al.*, 2008). The AMMI biplots help to visualize relationships among genotypes and environments and show both main and interaction effects. AMMI enables the identification of target breeding environments and the choice of representative testing sites in those environments. It also enables the selection of varieties with good adaptation to target environments.

### **2.8.2 SREG and/or GGE Model**

Site regression (SREG) GGE model is a multiplicative model which combines the main effect of the genotypes (G) and the  $G \times E$  interaction (abbreviated as G+GE or GGE) (Yan *et al.*, 2000; Yan and Tinker, 2006a). Plant breeders are interested in the total genetic variation and not exclusively in the GEI part. Because genotypic scores describe genotypic main effects, genotype and GEI together, this type of model is also known as the "Genotype main effects and GEI model," or "GGE model" and the biplots are called "GGE biplots" (Yan *et al.*, 2000). GGE biplots approximate overall performance (G + GEI). This is in contrast to AMMI biplots that

approximates only the GEI part of the phenotype. GGE biplot is a data visualization tool, which graphically displays a G x E interaction in a two way table (Yan *et al.*, 2000). GGE is an effective tool for: 1) mega-environment analysis (‘‘which-won-where’’ pattern), whereby specific genotypes can be recommended to specific mega-environments (Yan and Kang, 2003; Yan and Tinker, 2006a) genotype evaluation (the mean performance and stability), and 3) environmental evaluation (the power to discriminate among genotypes in target environments).

### **2.8.3 PLS – Partial Regression Squares**

Partial least squares regression is a bilinear model that can utilize information about environmental factors (covariables e.g. rainfall, temperature and soil type). It can also accommodate additional data like disease reaction and molecular marker scores. Analysis of PLS indicates which environmental factors are genotypic traits can be used to predict GEI for grain yield.

### **2.8.4 Factorial regression**

This model assumes that there is no explicit information about the environments, as it is a fixed effect linear model. This model can be useful to explain GEI, though the biological interpretation of their results is not always obvious. A straightforward approach is to correlate environmental scores with environmental covariables. However, if there is explicit information about the environment, the information can be used directly in the model by including it in the form of explanatory variables. GEI is then described as differential genotypic sensitivity to explicit environmental factors such as temperature, precipitation, water availability etc. Such models are known as factorial regression models (Denis, 1988; van Eeuwijk *et al.*, 1995). Two examples of factorial regression models are: single environmental covariable and multiple environmental covariables. Factorial regression is easier to interpret than PLS, but may give misleading results when there are correlations among the explanatory variables in the model.

GGE biplot model was used in this study as it helps to visualize relationships among genotypes and environments and uses a classification procedure to identify environments which show similar discrimination among the genotypes. Additionally, it enables the selection of varieties with good adaptation to target breeding environments. It can be used to identify key agro climatic factors, disease and insect pests, and physiological traits that determine adaptation to environments. It may also be used to evaluate test environments (Yan and Holland, 2010). There have been several GEI studies using AMMI and SREG analysis and GGE biplot models. Using biplot analysis, Stojakovic *et al.* (2012) in their experiment reported that the new maize hybrids showed higher grain yield than the standard by 0.883 to 1.720 t/ha using the biplot analysis (Stojakovic *et al.*, 2012).

## **2.9 Genotypic variability and phenotypic correlation of yield related traits**

Yield related traits (days to anthesis, anthesis silking interval, ear and plant height, stem and root lodging, plant diseases) can be used to improve selection efficiency when grain yield has been reduced (Banziger and Lafitte, 1997; Bolanos and Edmeades, 1996). These have been revealed through studying the genetic correlations with grain yield and other traits. This has involved estimating the correlated response after selecting for grain yield (Edmeades *et al.*, 1997) or applying divergent selection for the particular trait. The phenotypic and genetic correlations of secondary traits with grain yield have been studied in the past (Bolanos *et al.*, 1993; Bolanos and Edmeades, 1996; Chapman and Edmeades, 1999; Edmeades *et al.*, 1993; Edmeades *et al.*, 1999; Westgate, 1997). Other traits such as days to anthesis, ear and plant height, stem and root lodging, leaf senescence and diseases are associated with stress tolerance. They are recommended for improving crop yields in water stressed environments include dense and deep

roots, osmotic adjustment and ability to remobilize stem reserves (Blum, 1988). Photosynthesis seems to highly support the formation of developing ear under drought (Westgate, 1997). A decrease in demand from other organs developing during flowering, such as stems, tassels, and roots, could also favor the developing ear. Reduced tassel size and plant height have been associated with improved drought tolerance (Bolanos *et al.*, 1993). Delayed leaf senescence, erect upper leaves, and reduced leaf rolling under drought have been suggested as stress-adaptive traits in maize (Blum, 1988; Chapman and Edmeades, 1999). Yield components and physiological components that contribute to the formation of yield under drought stress can allow breeders to address key weaknesses in selection and progress yield (Edmeades, 2013b).

Ceccarelli *et al.* (1992) reported variable genetic correlations between grain yield in low-yielding sites and grain yield in high yielding sites. Bänziger *et al.* (2000) evaluated maize populations improved for tolerance to drought under both well-fertilized and N stress. Bänziger *et al.* (2000) found out that selection for tolerance to midseason drought stress led to an increase in grain yield of 86 kg ha<sup>-1</sup> yr<sup>-1</sup> across populations. Heritability studies were done by Badu-Apraku *et al.* (2004) where 270 full-sib families derived from drought-tolerant-population pool 16DT estimated for drought adaptive traits and genetic correlations among them (Badu-Apraku *et al.*, 2004). In their study, narrow sense heritability for ASI was 23% in non-stress and ranged between 22 to 51% in stress environments, respectively, while heritability for days to anthesis (AD) was 30% in non-stress environments and ranged between 34 to 52% in stress environments. Genetic correlation between grain yield (GY) and AD was negative in each site and across sites, while that between GY and ASI was positive across sites. Dow *et al.* (1984) reported that AD and ASI were highly correlated to drought resistance (-0.61 and -0.71

respectively) (Dow *et al.*, 1984). Ud-Din *et al.* (1992) estimated genetic parameters for grain production in drought stress and irrigated environments in a winter wheat population. They found that genetic variance for grain yield was greater in the irrigated environments than in the stress environments. They reported higher error variances than genetic variances in drought-stressed and irrigated environments. Ud-Din *et al.* (1992) also reported low genetic correlation between grain yields in drought-stresses and irrigated environments (Ud-Din *et al.*, 1992). F3 families of barley in two environments with differing rainfall amounts were evaluated by Ceccarelli (1987) (Ceccarelli *et al.*, 1992). A high and negative correlation was found between the drought susceptibility index and GY at the water stressed site, indicating that larger yields are associated with higher levels of drought tolerance or with higher stability. The highest yielding families under moisture stress had grain yield below average under well-watered conditions (Ceccarelli *et al.*, 1992). There was significant reduction in yield of wheat cultivars subjected to drought stress as reported by (Fischer and Maurer, 1978). Mild drought stress led to a greater reduction in kernel weight than in grain number, but number of grains was reduced more as drought severity increased.

## CHAPTER THREE

### 3 Combining ability of parental maize inbred lines for grain yield performance and disease resistance under well-watered and water stress conditions

#### 3.1 Introduction

Maize plays a major role in many diets more so in the East Africa (EA), it accounts for the more than 35% of the total caloric intake (Speca, 2013). Its importance in the livelihoods of the people in EA can therefore not be underestimated. Challenges including attacks by insects, pests, diseases, high temperatures, low soil fertility, flooding, drought stress, extremes of soil acidity and salinity, have seen the decline of the yields in the recent past (Lisuma *et al.*, 2006; Mømboyi *et al.*, 2010). The challenges affect crop yield by wilting, low grain filling, susceptibility to diseases outcompeted with weeds among others. A number of strategies are being put in place to avert the declining yield including breeding for tolerance to drought stress, heat stress, pests and diseases. As these strategies have offered some success, the stress challenges have compounded and are multifactorial overstressing the conventional tropical hybrids most of which are drought tolerant. Other alternatives involving use of temperate maize hybrids in the tropical breeding systems have been proposed. This method entails backcrossing tropical with temperate maize that offers yield advantage. Efforts by CIMMYT breeding programs resulted in the generation of the tropical-temperate hybrids which so far have not been well exploited.

A successful breeding requires battery of tests for determination of stability, combining ability, heritability and correlation of the agronomic traits. This would be able to enhance the efficacy of hybrid selection for yield improvement. Furthermore, it is well established that temperate and tropical varieties differ in yield performance and this can be utilized to increase hybrid vigor. For example, Abadassi (2015) successfully crossed some tropical maize populations bred by IITA

and CIMMYT with a single hybrid widely cultivated in France and noted that the populations could be improved for earliness and grain yield. In this respect, crossing CIMMYT tropical line with off patent varietal lines that are temperate in nature could offer stable hybrids with high genetic potential for yield, therefore useful in the tropical maize farming systems.

Water stress has been documented as a major influence to grain yield. This is because it affects flowering, ear development and grain filling and causes leaf senescence (Edmeades, 2008; Edmeades *et al.*, 2000). These traits are very important for efficient selection of better yielding hybrids when grain yield has been reduced (Banziger and Lafitte, 1997; Edmeades, 2013a). The importance of yield related traits in breeding for drought tolerance has been explained by studying genetic correlations with grain yield. This is achieved by obtaining the hybrids and estimating the correlated response after selecting for grain yield or applying divergent selection for the particular trait (Abadassi, 2015; Edmeades *et al.*, 1997). As such the effects of these traits on grain yield of tropical-temperate material under water-stress needs more investigation. A number of research have documented the effective use of line  $\times$  tester analysis to determine combining ability and correlation between key agronomic traits in maize hybrids (Nzuve *et al.*, 2014; Abadassi, 2014; Abadassi, 2015; Udaykumar *et al.*, 2014; Shushay *et al.*, 2013; Gouda *et al.*, 2013). The Line  $\times$  tester design involves hybridization between lines and wide based testers in one to one fashion generating hybrids (e.g.  $f \times m = fm$  hybrids) (Sharma, 2006; Nduwumuremyi *et al.*, 2013). This design generates important information on the germplasm such as general combining ability (GCA) of both the lines and testers and specific combining ability (SCA) of each cross. GCA is the relative performance of individuals in a similar group of organisms when crossed with a heterogeneous tester, while SCA is the progeny performance resulting from a particular cross as related to the performance of other particular crosses of



similar nature (Hallauer and Miranda, 1988a). Information on heritability and correlation of the agronomic traits is also provided. The objective of this work was, therefore, to determine the combining ability, heritability and correlation of seven tropical-temperate maize lines for yield performance and potential use in breeding programs in Kenya.

## **3.2 Materials and methods**

### **3.2.1 Germplasm**

The maize germplasm that was used in this study were obtained from various sources. These included seven elite tropical-temperate inbred lines, seven single cross testers and six commercial hybrids that were used as checks during evaluation. The seven maize inbred lines used in the study were selections from a pool of 380 tropicalized temperate backcross lines obtained from the International Maize and Wheat Improvement Centre (CIMMYT) breeding programs in Kenya and Zimbabwe (Table 3.1) in 2012. These 380 lines were developed by crossing several CIMMYT tropical lines to 8 off-patent varietal lines (OFP) which were temperate in nature and backcrossing them for five generations to recover the tropical parent genome. The 380 lines were subsequently testcrossed to 10 tropical single cross testers (DH x DH, DH x CML and CML x DH) from divergent heterotic groups in KARLO Kiboko. Evaluation was done across locations under water stress and non-stress conditions and top performing lines for yield selected. A seed increase nursery was grown in Kiboko in 2013. The seven lines, therefore, are derivatives of 4 CMLs (CML312, CML495, CML537 and CML539) with known good yield performance under water stress and no-stress regimes. Four commercial checks widely grown by farmers in the mid-altitude growing ecology were included in this study. Two single cross testers representative of the 7 testers were also included in the study.

Table 3.1 Tropical-temperate lines, testers and checks used in the study

Line(L) / Tester(T)	Genotype	Sources	Type
L1	CKLTI0344	Temperate*Tropical	Inbred line ( )
L2	CKLTI0368	Temperate*Tropical	Inbred line ( )
L3	CKLTI0200	Temperate*Tropical	Inbred line ( )
L4	CKLTI0147	Temperate*Tropical	Inbred line ( )
L5	CKLTI0152	Temperate*Tropical	Inbred line ( )
L6	CKLTI0272	Temperate*Tropical	Inbred line ( )
L7	CKLTI0036	Temperate*Tropical	Inbred line ( )
T1	CML489/CML444	Tropical	Tester ( )
T2	CKDHL0159/CKDHL0295	Tropical	Tester ( )
T3	CKDHL0089/CKDHL033	Tropical	Tester ( )
T4	CML395/CML444	Tropical	Tester ( )
T5	CKDHL0089/CKDHL0295	Tropical	Tester ( )
T6	CKDHL0089/CML395	Tropical	Tester ( )
T7	CML312/CML395	Tropical	Tester ( )
Tester	CKDHL0089/CKDHL0295	Tropical	Check
Tester	CKDHL0159/CKDHL0295	Tropical	Check
	DH04	Tropical	Check
	DK8053	Tropical	Check
	DK8031	Tropical	Check
	Pioneer 3253	Tropical	Check

NB: CKLTI ó CIMMYT Kenya Line Temperate Introgression; CML - CIMMYT Maize Line; CKDHL - CIMMYT Kenya Doubled Haploid Line; All testers are single crosses.

### 3.2.2 Experimental sites

In the present study the yield performance of the three-way cross maize hybrids and commercial checks were tested in eight different environments (Table 3.2).

Table 3.2 Agro-climatic description of the experimental study sites

Site	Elevation (masl)	Rainfall (mm)	Soil type	Latitude	Longitude	characteristics
Embu	1,480	1,200- 1,500	Clay loam	0.54° S	37.45° E	Temperate vegetable zone.
Homabay	1,165	1,100	Sandy loam	0.53° S	34.46° E	Inadequate soil moisture content.
Kaguru	1,450	600- 1,200	Sandy loam	0°04'S	37°40'E	Fertile volcanic soil; reliable water.
KARLO Kakamega	1,521	1,995	Sandy loam	00°16.849 <sup>1</sup> N	034° 46.313 <sup>1</sup> E	Mid-altitude zone; drought prone. A natural disease pressure region.
Kiboko (2)	940	545-629	Sandy clay	02°13.186 <sup>1</sup> S	037°43. 454 <sup>1</sup> E	Drought tolerance screening site with reliable irrigation facilities.
Kirinyaga	1,464	1,000- 1,500	Clay loam	0°30 <sup>1</sup> (0.5°) S	37°20 <sup>1</sup> 37.283° E	Soil type is nitisol which is favorable for maize crop production.
Shikusa	1,577	1735	Sandy loam	0°19 <sup>1</sup> N	34°49 <sup>1</sup> E	A natural disease pressure region; windy/stormy rains.
Mtwapa	23	1,200	Deep loamy and sandy soil	4° 347 S	39° 219 E	Drought prone environment because of low and unreliable rainfall. Prone to a diversity of diseases and pests

### **3.2.3 Development of the hybrids**

A line x tester mating design with seven lines and seven testers was used to form 49 three-way cross hybrids in a non-replicated nursery in Kiboko, Kenya during the short rain season (October 2013 ó February 2014). Single cross testers were used as females and tropical-temperate inbred lines as males. The males were sown in two rows at two different times; five days before and same day of planting the females to effect nicking at pollination to synchronize flowering. The females were planted in five rows of five-metre lengths. For both male and female plots, two seeds were planted per hill and later thinned to one seed per hill with a spacing of 0.75 m (inter-row) and 0.25 m (intra-row). Supplementary irrigation was applied when needed. Before silk emergence, ears of female plants were covered with shoot bags, and the pollen collected and bulked from the male plants when 20% of the males started to shed pollen. The female plants that were free from any defects were pollinated to make maximum number of crosses within a plot. Self-pollination was carried out simultaneously in the male plots. Harvesting was done in March 2014.

### **3.2.4 Evaluation of the parents and the single cross hybrids**

A 55 entry hybrid trial was constituted by adding 4 commercial checks and 2 single cross testers to the 49 experimental three-way cross hybrids. The germplasm was evaluated across eight locations in Kenya described in Table 3.2. An 11×5 alpha-lattice experimental design with 2 replications was used to evaluate the hybrids under two moisture regimes during the long rains season of 2014. Each plot comprised two rows of five metres length with an inter-row distance of 0.75 cm and intra-hill distance of 0.25 cm, ensuring a plant population density of 53,333 plants per hectare. Across locations, a

minimum of two border rows round the trial was planted. In Kiboko, the experiment was grown under two moisture regimes; well-watered conditions during April ó August and water-stress conditions during June ó October 2014 season. During water-stress conditions treatments were irrigated till two weeks to flowering. An additional irrigation was applied about 14 days after the end of male flowering to ensure that the small amount of grain formed filled adequately.

### **3.2.5 Agronomic management**

Three weeks after germination, weeds were removed and stem borer controlled using Bulldock (beta-cyfluthrin 25 g/L). Topdressing with Calcium Ammonium Nitrate (CAN) at the rate of 60 kg N/ha was applied as a split, with half applied at planting and the rest at about the 10<sup>th</sup> leaf. Supplementary irrigation was applied whenever needed.

### **3.2.6 Data collection**

During the growing season, various data parameters were recorded as follows;

- 1. Anthesis date (AD)** was calculated as the number of days after planting when 50% of the plants in a plot shed pollen.
- 2. Silking date (SD)** was calculated as the number of days after planting when 50% of the plants produced silks.
- 3. Anthesis-silking intervals (ASI)**; Calculated as the difference in days between SD and AD.
- 4. Ear height (EH)** was measured as height from ground level up to the base of the upper most cobs bearing internode in metres for the 21 plants per plot.
- 5. Plant height (PH)** was measured as the distance between the base of the plant to the insertion point of the top ear in centimeters. It was measured when all the plants have flowered, since plants reach their maximum height at flowering.

6. **Ear position (EPO)** was calculated as the ratio of ear height to plant height.
7. **Number of ears per plant (EPP)**; the number of ears per plot were counted and divided by the total number of plants in the respective plot.
8. **Stem lodging (SL)**; the number of plants with breakage of stalk below the ear was counted and expressed as a percentage of total plants per plot.
9. **Root lodging (RL)**; the number of plants leaning from the vertical axis at an angle approximately 30° or greater was counted before harvest and converted as a percentage of total number of plants per plot.

**10. Foliar disease**

- i) Gray leaf spot, caused by *Cercospora zea-maydis*: - a visual score on a 1-5 scale (1 = healthy plants, 2 = about 2% ó 44% infection, 3 = 45 - 55% infection, 4 = 56% ó 89% infection, 5 = over 90% of plants within a plot showing severe symptoms) was conducted by assessing the plant leaves for presence of GLS disease, considering all the plants in the plot and done once after flowering.
- ii) Northern leaf blight caused by *Exserohilum turcicum* (1 = no symptom, 2 = moderate lesion below leaves subtending the ear, 3 = heavy lesion development on and below the leaf subtending the ear with few lesions above, 4 = severe lesion development on all but upper leaves may have few lesions and 5 = all leaves dead).
- iii) Maize streak disease, caused by the *maize streak gemminivirus* (MSV) (1 = no symptom, 2 = moderate lesion below leaves subtending the ear, 3 = heavy lesion development on and below the leaf subtending the ear with few lesions above, 4 = severe lesion development on all but upper leaves may have few lesions and 5 = all leaves dead).

- iv) Common leaf rust, caused by *Puccinia sorghi* (1 = healthy plants, 2 = about 1% ó 44% infection, 3 = 45 - 54% infection, 4 = 55% ó 89% infection, 5 = over 90% of plants within a plot showing severe symptoms).
- v) Leaf senescence scores were recorded on each of the plots on scale of 1 to 9 (1 no senescence, 2; 2% - 29% senescence, 3; 30% - 39% senescence, 4; 40% - 49% senescence, 5; 50% - 59% senescence, 6; 60% - 69% senescence; 7; 70% - 79% senescence; 8; 80% - 89% senescence, 9; 90% of the plants showing senescence).

11. Field weight of unshelled ears (t/ha) was recorded by weighing all the ears harvested from the two row plots.

12. Grain yield (t/ha) was calculated after harvesting the ears from every two row plot, taking field weight and adjusting the weight to moisture content recorded for each plot. These parameters were used to compute grain yield per plot in tons ha<sup>-1</sup> using formula below:

$$GY = [(FW/1000)*((100 - MOI)/(100 - 12.5))*(10/A)]*P$$

Where:

*GW* refers to grain weight (in Kg) recorded after threshing all cobs in a plot,

*MOI* refers to the moisture content (in percentage) recorded immediately after threshing,

*A* refers to net plot area, computed as follows: [(no. of hills ó discarded border plants) x spacing between hills (cm) x spacing between rows (cm) x 2 rows per plot], and

$P$  refers to shelled percentage; 0.8 if field weight was used to compute grain yield and 1 if plots were shelled.

**13. Grain moisture (MOI)** was measured as a percentage of water content of grain at harvest using Dickey Johns moisture meter.

### 3.2.7 Data analysis

#### 3.2.7.1 Analysis of variance

The data were subjected to analysis of variance (ANOVA) using the General Linear Model of SAS for each of the sites and across similar sites considering genotypes as fixed effects and environments as random effects. Mean squares due to replication, location, genotype, lines, testers and various interactions for the grain yield and other traits of both individual and combined locations were calculated to explain the observed variation using the following model:

#### Equation 1: Model ANOVA equation

$$Y_{ijkl} = \mu + r_i + L_j + T_k + EI + L \times T_{jk} + L \times E_{jl} + T \times E_{kl} + L \times T \times E_{jkl} + e_{ijkl}$$

Where,  $y_{ijkl}$  = observed hybrid response

$\mu$  = overall trial mean

$r_i$  = replication

$T_k$  = effect of the  $K^{\text{th}}$  tester

$L_j$  = effect of the  $J^{\text{th}}$  line

$L \times T_{jk}$  = effect of the interaction of  $j^{\text{th}}$  line and  $k^{\text{th}}$  testers



$L \times E_{jl}$  = effect of the interaction of  $j^{\text{th}}$  line and  $l^{\text{th}}$  environments

$T \times E_{ki}$  = effect of the interaction of  $k^{\text{th}}$  tester and  $l^{\text{th}}$  environments

$L \times T \times E_{jki}$  = effect of the interaction of  $j^{\text{th}}$  line,  $k^{\text{th}}$  tester and  $l^{\text{th}}$  environments

$eijkl$  = random experimental error

### 3.2.7.2 Estimation of the general combining ability (GCA) and specific combining ability (SCA)

The estimates of the GCA and SCA effects were obtained using PROC GML model of SAS. The GCA effects for each line and tester were estimated (Hallauer and Miranda, 1988b).

Equation 2: GCA effect of the testers

$$\text{Tester} = \frac{x_i}{mr} + \frac{x \dots \dots}{mfr}$$

Where;

$x_i$  .. = total of  $i^{\text{th}}$  female parent over all male (m) parents and replications (r).

$x_i$  = Grand total of all the hybrids over all male parents (m), female parents (f) and replications (r).

$$\text{Tester} = \frac{x_j}{fr} + \frac{x \dots \dots}{mfr}$$

Where,

$x_j$  = Grand total of the  $j^{\text{th}}$  male parent over all female parents (f) and replication (r).

The standard error (SE) for line and tester GCA effects was estimated following the Dobholkar (1999) as cited by Makanda (2009):

Equation 3: standard error (SE) for line

$$SE_{Line} = \frac{\sqrt{MSE}}{S \times T}$$

Equation 4: Standard error (SE) for the tester

$$SE_{Tester} = \frac{\sqrt{MSE}}{S \times L}$$

Where:

MSE = mean square error; S = number of sites; L and T = number of lines and testers, respectively.

The t-tests were calculated to determine the significance of lines and testers as follows:

$$t_x = \frac{GCA_x}{SE_x}$$

Where:  $t_x$  = t-statistic of either line or tester

$GCA_x$  = general combining ability for either line or tester

$SE_x$  = standard error of line or tester;

The SCA effects for each line and tester were estimated following Shashidhara (2008) method

Equation 5: SCA effects for each line and tester

$$SCA = \frac{x_{ij}}{r} - \frac{x_{i...}}{mr} - \frac{x_{.j}}{fr} + \frac{x_{...}}{mfr}$$

Where:

$x_{ij}$  =  $j^{\text{th}}$  combination total over all replications (r).

The standard error (SE) for line by tester SCA effects was estimated following the method of Dobholkar (1999) as cited by Makanda (2009):

Equation 6: Standard error (SE) for line by tester SCA effects

$$SE = \frac{\sqrt{MSE}}{\sqrt{S}}$$

The t-tests were calculated to determine the significance of line by tester interaction as follows:

Equation 7: Significance of line by tester interaction

$$t_x = \frac{SCA_x}{SE_x}$$

### 3.2.8 Estimation of Heritability ( $H^2$ )

Heritability in a broad sense was estimated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage following the Darbeshwar (2000) method.

Equation 8: Heritability across environments

$$H^2 = \frac{\sigma^2_g}{\sigma^2 + \sigma e^2/rs} \times 100$$

Equation 9: Heritability within environments

$$H^2 = \frac{\sigma^2_g}{\sigma^2 + \sigma e^2/r} \times 100$$

Where,  $\sigma^2_g$  = Genotypic variance,  $\sigma^2_e$  = environmental variance, r= replication and s = site

The simple linear phenotypic and genotypic correlations were estimated following the procedure indicated by Gomez and Gomez as:

Equation 10 Phenotypic correlation coefficient

$$r = \frac{\text{Cov}(X, Y)}{\sqrt{V(X)V(Y)}}$$

Where:

$r$  = phenotypic correlation coefficient; Cov (X,Y) = phenotypic covariance of X and Y; V (X) = phenotypic variance of X; V (Y) = phenotypic variance of Y (Gomez and Gomez, 1984).

### **3.3 Results**

#### **3.3.1 Analysis of Variance**

In maize grown under well-watered conditions, highly significant differences ( $P < 0.001$ ) were recorded for all traits except Turcicum blight across locations (Table 3.3). Highly significant ( $P < 0.001$ ) differences for grain yield were recorded due to lines, testers and the interaction of line and tester. Lines and testers mean squares were significant at various levels for all traits except root lodging. There were significant differences ( $P < 0.05$ ) for shoot lodging due to line, tester and site interaction.

Under managed drought, there were highly significant differences ( $P < 0.001$ ) for grain yield, plant and ear heights due to replication and location (Table 3.4). Sources of variation due to lines, testers and the interaction of lines  $\times$  testers showed significant differences ( $p < 0.05$ ) for ear aspect. Significant differences ( $p < 0.05$ ) were also observed due to lines and testers for anthesis-silking interval. Line mean squares were significant at various levels for all traits except root lodging. Tester mean squares were significant for days to anthesis, anthesis-silking interval, plant and ear height while the mean square of the sites were highly significant ( $p < 0.001$ ) for all traits except ear aspect.

Table 3.3 Analysis of variance for hybrids evaluated under well-watered conditions during 2014

Source	DF	GY (t/ha)	AD (days)	ASI (days)	PH (cm)	EH (cm)	Root lodging (cm)	Stem lodging (cm)	GLS (1-5)	ET (1-5)	MSV (1-5)
REP	1	0.4	0.8	2.6*	3142.0***	9.5	7.8	45.9*	2.0*	0.3	0.0
Site (S)	5	254.5***	6404.3***	37.0***	238244.6***	97474.5***	35.7***	1960.5***	2.2***	0.1	1.6**
Line (L)	6	8.8***	64.5***	7.6***	7225.3***	6757.5***	4.9	40.0**	0.5	0.4**	0.3
Tester (T)	6	10.0***	8.7***	2.1*	1305.1***	1472.1***	6.5	44.1**	0.7*	0.3*	1.0*
S*L	30	4.8***	3.7***	1.7**	131.6	104.1*	5.4*	35.4***	0.9**	0.1	0.4
S*T	30	1.4	2.1	1.0	107.6	118.7**	5.7*	51.7***	0.4	0.1	0.4
L*T	36	2.6***	2.1	0.5	322.2***	197.5***	3.0	17.8	0.2	0.1	0.3
S*L*T	180	1.1	1.54	1.0	103.7	54.0	3.8	17.8*	0.2	0.1	0.4
Error	293	1.1	1.6	1.0	113.7	62.4	3.9	13.3	0.3	0.1	0.4

Key: Well-watered sites: Kiboko, KARLO Kakamega, Shikusa, Mtwapa, Kirinyaga University College and Kaguru; ASI-anthesis silking interval; GLS-gray leaf spot; \* Significance at  $P < 0.05$ ; \*\*Significance at  $P < 0.01$ ; \*\*\*Significance at  $P < 0.001$  DF-degree of freedom, GY-grain yield, AD-days to anthesis, MSV-*Maize streak virus*, ET-*Turcicum* leaf blight, PH-plant height, EH-ear height

Table 3.4 Analysis of variance for hybrids evaluated under water stress/drought conditions during 2014

Source	DF	GY (t/ha)	AD (days)	ASI (days)	PH (cm)	EH (cm)	Root lodging (cm)	Stem lodging (cm)	GLS (1- 5)	ET (1-5)	MSV (1-5)
REP	1	41.5***	17.8**	0.0	14425.7***	3848.4***	233.2	18154.4***	78.4*	78.4*	33.2**
Site (S)	1	275.0***	1084.3***	4	10021.4***	5107.1***	14480.2***	58880.5***	651.0***	651.0***	4762.4***
Line (L)	6	3.4*	48.3***	4.1*	955.0***	1785.3***	101.3	1035.6*	24.1*	24.1*	6.4*
Tester (T)	6	0.8	4.6*	3.3*	421.2	323.9**	31.0	502.2	16.4	16.4	3.6
S*L	6	1.8	7.6**	7.0**	529.6*	136.3	101.3	981.2*	24.1*	24.1*	5.6
S*T	6	1.3	0.9	2.3	383.8	154.1	31.0	285.4	16.4	16.4	7.1*
L*T	36	1.0	2.7	1.7	283.9	109.3	80.5	275.6	8.5	8.5	2.8
S*L*T	36	1.0	2.1	1.3	203.3	78.3	80.5	244.4	8.5	8.5	1.7
Error	97	1.2	2.1	1.7	229.2	98.4	116.7	472.6	11.7	11.7	3.3

Key: Water stressed condition sites: Homabay and Kiboko. \* Significance at  $p < 0.05$ ; \*\* significance at  $p < 0.01$ ; \*\*\* significance at  $p < 0.001$ ; GLS-gray leaf spot; ET-*E turcicum*, DF-degree of freedom, GY-grain yield, AD-days to anthesis, MSV-*Maize streak virus*, ET-*Turcicum* leaf blight, PH-plant height, EH-ear height

### **3.3.2 Mean performance of the 55 three way cross hybrids across locations**

#### **3.3.2.1 Well-watered conditions**

The top two hybrids in yield performance across well-watered environments, though not statistically different (LSD 0.5), had a common single cross tester (CKDHL0089/CML395) but different pollen donors, with best linear unbiased estimates (BLUE) of 8.5t/ha and 8.4 t/ha for parents CKLTI0152 and CKLTI0200, respectively (**Table 3.5**). The results showed the best five hybrids in yield performance were statistically similar, and had CKDHL0089 as a common tester parent, showing its superiority in yield performance (**Table 3.5**). On the other hand, the two lowest hybrids across locations had a common single cross tester, CML312/CML395, with two different pollen donors CKLTI0272 and CKLTI0036 yielding BLUE values of 6.0 t/ha and 5.5 t/ha, respectively. 48 hybrids had better mean grain yield than the best check, Pioneer 3253 (5.4 t/ha) (**Table 3.6**). There was no significant difference in flowering time among the hybrids. Most of the top performing hybrids were more or equally resistant to diseases compared with the best yielding commercial check, Pioneer 3253.

#### **3.3.2.2 Water stress conditions**

Under managed drought conditions, the top two performers in grain yield had different testers (CML395/CML444 and CKDHL0159/CKDHL0295) but shared the same pollen donor, CKLTI0152, with BLUE values of 4.9 t/ha and 4.8 t/ha, respectively. (CML489/CML444)/(CKLTI0272) and (CKDHL0089/CKDHL0295)/(CKLTI0368) were the poorest with 2.8 t/ha and 2.6 t/ha respectively. DK8053 was the best check with a mean yield of 3.7 t/ha (**Table 3.6**)



Table 3.5 Means of top and bottom five tropical-temperate maize hybrids evaluated under well-watered conditions during 2014

	Entry	Cross	Pedigree	BLUE Yield	AD (days)	ASI (days)	Ear Height (cm)	Plant Height (cm)	GY (GWT) (t/ha)	RL (%)	SL (%)	<i>Turc.</i> Blight (1-5)	GLS (1-5)	MSV (1-5)
Top	14	L5×T3	CKDHL0089/CML395//CKLTI0152	8.5	67.9	0.7	115.0	245.9	8.1	0.4	3.3	2.0	1.0	0.1
	28	L3×T3	CKDHL0089/CML395//CKLTI0200	8.4	66.0	0.6	108.0	241.4	8.0	1.4	1.8	2.1	1.1	0.0
	11	L5×T2	CKDHL0089/CKDHL0333//CKLTI0152	8.3	68.1	0.9	116.6	245.5	8.5	0.1	1.5	2.0	1.1	0.4
	12	L5×T1	CKDHL0089/CKDHL0295//CKLTI0152	8.1	67.9	0.9	112.7	240.9	9.1	0.7	2.6	2.0	1.1	0.0
	7	L2×T3	CKDHL0089/CML395//CKLTI0368	8.1	68.7	0.5	108.8	219.7	8.2	0.9	2.1	2.0	1.0	0.0
Bottom	10	L5×T5	CML312/CML395//CKLTI0152	8.0	67.3	1.1	110.6	248.2	9.2	0.1	1.6	2.0	1.6	0.0
	23	L3×T7	CML489/CML444//CKLTI0200	6.6	65.3	0.2	106.6	231.0	7.3	0.5	2.2	2.1	1.3	0.0
	19	L7×T1	CKDHL0089/CKDHL0295//CKLTI0036	6.6	67.7	1.1	131.7	247.1	7.6	0.0	8.6	2.1	1.5	0.0
	45	L1×T5	CML312/CML395//CKLTI0344	6.5	66.0	0.6	118.7	241.9	7.4	0.0	1.1	2.0	1.1	0.0
	31	L6×T5	CML312/CML395//CKLTI0272	6.0	66.6	1.4	109.9	242.2	6.7	0.8	0.4	2.2	1.5	0.0
Checks	17	L7×T5	CML312/CML395//CKLTI0036	5.5	67.7	1.1	116.4	234.7	7.3	1.2	1.5	2.2	1.5	0.0
	54		Pioneer 3253	5.4	67.0	1.6	121.3	245.4	5.6	0.6	7.1	2.5	1.5	0.4
	52		DK8053	4.7	66.4	1.1	116.3	232.5	6.8	0.8	3.1	3.8	2.0	0.0
	55		DH04	4.7	65.8	1.1	114.5	234.2	6.8	1.9	2.3	3.5	1.4	0.1
	53		DK8031	3.6	65.4	4.2	111.9	232.3	4.2	2.7	3.5	2.3	1.5	0.0
Grand_Mean				7.3	66.9	0.8	118.1	241.0	8.0	0.6	2.7	2.2	1.3	0.1
LSD				1.1	1.1	0.9	6.7	7.9	1.5	1.8	4.0	0.5	0.7	0.6
CV				7.5	0.8	60.1	2.9	1.7	9.6	142.6	75.8	12.3	28.9	267.5
Heritability				0.8	0.9	0.7	0.9	0.9	0.7	0.1	0.1	0.7	0.0	0.1

Key: AD days to 50 % anthesis; ASI anthesis silking interval; EPP ears per plant; GY grain yield; RL root lodging; SL stem lodging; GLS Gray leaf spot; LSD Least significant difference; CV Coefficient of variation.

Table 3.6 Means of top and bottom five tropical-temperate maize hybrids evaluated under water stress/managed drought conditions during 2014

	Entry	Cross	Pedigree	BLUE Yield	AD (days)	ASI (days)	Ear Height (cm)	GY (GWT) (t/ha)	Leaf Sen (1-9)	Plant Height (cm)	Root Lodg. (%)	Plant Stand (#)	Stem Lodg. (%)
Top	8	L5×T6	CML395/CML444//CKLTI0152	4.9	65.6	1.6	114.2	4.8	5.7	221.9	10.1	38.3	13.2
	13	L5×T4	CKDHL0159/CKDHL0295//CKLTI0152	4.8	64.6	1.0	112.1	4.7	5.6	217.9	7.7	40.0	31.7
	39	L4*T2	CKDHL0089/CKDHL0333//CKLTI0147	4.7	64.5	1.0	116.6	4.5	5.1	236.1	2.2	38.5	38.1
	1	L2*T6	CML395/CML444//CKLTI0368	4.7	64.9	1.0	119.3	4.5	5.0	221.8	5.9	37.6	30.0
	42	L4*T3	CKDHL0089/CML395//CKLTI0147	4.6	63.5	2.2	117.9	4.5	5.4	233.7	9.2	35.4	30.6
	20	L7*T4	CKDHL0159/CKDHL0295//CKLTI0036	4.6	63.5	0.5	132.4	4.6	8.1	232.4	4.6	37.9	27.9
Bottom	28	L3*T3	CKDHL0089/CML395//CKLTI0200	4.1	62.1	2.1	106.2	4.1	6.3	225.8	3.8	39.4	27.4
	18	L7*T2	CKDHL0089/CKDHL0333//CKLTI0036	4.1	64.0	1.5	127.1	4.0	7.6	227.3	10.0	36.4	36.4
	22	L3*T6	CML395/CML444//CKLTI0200	4.0	61.8	2.5	110.1	4.0	6.3	225.6	10.6	39.7	23.1
	41	L4*T4	CKDHL0159/CKDHL0295//CKLTI0147	4.0	66.1	0.6	113.3	3.8	5.9	225.0	6.6	37.3	34.4
	44	L1*T7	CML489/CML444//CKLTI0344	3.9	62.8	0.5	124.4	4.1	6.4	225.8	7.3	37.2	21.3
Checks	51		CKDHL0159/CKDHL0295	3.9	64.2	1.0	125.5	3.8	5.8	216.4	12.0	38.7	44.4
	50		CKDHL0089/CKDHL0295	3.4	62.6	4.5	110.4	3.6	8.0	219.3	5.2	34.8	1.1
	52		DK8053	3.7	66.2	3.1	122.1	3.4	7.0	224.6	6.7	39.7	22.8
	55		DH04	2.6	58.8	0.3	97.7	3.0	8.9	199.7	5.4	35.0	45.1
	54		Pioneer 3253	2.6	64.5	4.9	135.2	2.6	7.8	233.9	14.6	40.2	9.2
	53		DK8031	2.2	61.2	4.4	118.2	2.4	7.6	219.2	7.6	35.2	20.2
Grand_Mean				3.8	63.6	1.8	116.0	3.8	6.5	224.4	8.5	37.8	28.0
LSD				1.3	3.4	2.2	10.8	1.3	1.3	16.3	12.8	4.7	26.0
CV				17.7	2.7	62.6	4.6	16.8	9.8	3.6	75.6	6.2	46.3
Heritability				0.4	0.4	0.4	0.9	0.4	0.7	0.6	0.0	0.3	0.2

ASI-anthesis silking interval; LSD-least significant difference; CV-coefficient of variation; AD - days to anthesis; GY grain weight; BLUE Best linear unbiased estimate; RL root lodging; SL stem lodging.

### **3.3.3 Mean performance of the two single cross testers**

Single cross tester CKDHL0159/CKDHL0295 (entry 51) had high best linear unbiased estimates (BLUE) in kiboko drought, Homabay and Kaguru; but performed almost similarly with entry 50 in the latter two sites (Table 3.5, Table 3.6). Tester CKDHL0089/CKDHL0295 (entry 50) out yielded even the best performing tropical/temperate maize hybrid in Kirinyaga University College. In KARLO Kakamega, BLUE yield of entry 51 was higher (LSD 0.5) than entry 50 which performed slightly below the check Pioneer 3253. KALRO Kiboko well-watered mean results showed that entry 50 yielded better than entry 51 and likewise Mtwapa. However, the mean BLUE yield of entry 51 was better than that of entry 50 in Shikusa.

### **3.3.4 General combining ability of the seven inbred lines**

Under well-watered conditions, four of the seven inbred lines had positive GCA for grain yield, with CKLTI0152 emerging as the best general combiner for grain yield with a positive and significant GCA of 0.54 (Table 3.7). Among the insignificant three, CKLTI0036 was the poorest general combiner with a significant GCA of -0.41. Three out of the seven lines had negative and significant GCA for days to anthesis (AD) (Table 3.7), line CKLTI0200 being the earliest flowering with a significant GCA of -1.04. Line CKLTI0368 was late to flower out of all the positive and significant lines with a GCA of 1.35. Line CKLTI0036 was the least for anthesis silking interval (ASI) a highly significant positive GCA of 0.52. Six of the seven lines were significant for plant height (PH) with line CKLTI0200 having a negative and significant GCA of 2.25. Line CKLTI0368 was best for ear height (EH) with a significant GCA of -10.05 while line CKLTI0344 had a positive GCA of 7.54 (Table 3.7). Lines CKLTI0147 and CKLTI0036 had positive and significant GCA for root and stem lodging (SL), respectively and therefore non

desirable. Two of the seven lines were negative and significant for *Turcicum* leaf blight, therefore preferable since they are more resistant compared to the other two positive and significant lines. Out of the three lines with positive GCA effects for *Maize streak virus* (MSV), CKLTI0272 was the least desired with a significant GCA of 0.13 (Table 3.7).

Though line CKLTI0152 had good GCA for grain yield, it was significantly poor ( $P < 0.001$ ) for AD and PH, while line CKLTI0368 with a negative GCA for yield combined well for ASI, PH, EH, and all the diseases. Though not significant line CKLTI0200 was positive for grain yield and combined well for all other traits except root lodging. On the contrary, there was no consistency in performance of the lines in well-watered and managed drought conditions. Line CKLTI0344 was positive and significant for grain yield under managed drought conditions with a positive GCA of 0.44; while line CKLTI0368 was negative and significant with a GCA of 0.46 (Table 3.8). Six of the seven lines were significant for AD. Line CKLTI0344 was early with regard to AD with the most negative and significant GCA of 1.40 while line CKLTI0368 was late flowering with a positive and significant GCA of 1.74. Though line CKLTI0344 was good for grain yield, it was undesirable for ASI, PH, EH and RL while line CKLTI0368 was desirable for these similar traits except RL and SL though poor for grain yield (Table 3.8).

Table 3.7 General combining ability of lines of tropical-temperate maize hybrids evaluated under well-watered conditions during 2014

Line (L)	Line Pedigree	Grain Yield (t/ha)	Days to anthesis (days)	Anthesis silking interval (days)	Plant height (cm)	Ear height (cm)	Root lodging (cm)	Stem lodging (cm)	GLS (1-5)	ET (1-5)	MSV (1-5)
L1	CKLTI0344	0.07	0.94***	0.25*	4.42***	7.54***	-0.17	-0.56	-0.11	0.12*	-0.08
L2	CKLTI0368	-0.09	1.35***	0.32*	-20.18	10.05***	0.06	0.34	-0.06	-0.05	-0.01
L3	CKLTI0200	0.17	1.04***	-0.17	2.25*	9.10***	0.13	-0.53	-0.13	0.12*	-0.05
L4	CKLTI0147	0.07	0.25	-0.11	5.77***	-0.09	0.45*	0.03	0.04	0.02	0.04
L5	CKLTI0152	0.54*	0.75***	0.12	3.31**	2.64*	-0.22	-0.40	-0.07	-0.05	0.01
L6	CKLTI0272	-0.35	0.45*	0.22*	4.11***	-0.97	-0.21	-0.27	0.14	0.16**	0.13*
L7	CKLTI0036	0.41*	0.08	0.52***	4.82***	15.30	-0.04	1.39*	0.16	0.16**	-0.03

Least significant difference (LSD) of 0.05; \*-Significance at P<0.05; \*\*-Significance at P<0.01; \*\*\*-Significance at P<0.001; GLS-gray leaf spot; ET- *E turcicum*/ Turcicum leaf blight

Table 3.8 General combining ability of lines of tropical-temperate maize hybrids evaluated under water stress/managed drought conditions during 2014

Line (L)	Line Pedigree	Grain Yield (t/ha)	Days to anthesis (days)	Anthesis silking interval (days)	Plant height (cm)	Ear height (cm)	Root lodging (cm)	Stem lodging (cm)	GLS (1-5)	ET (1-5)	MSV (1-5)
L1	CKLTI0344	0.44*	1.40*	0.01	9.51*	11.14***	0.80	-2.06			
L2	CKLTI0368	0.46*	1.74**	-0.24	10.24*	4.63*	1.66	10.91*			
L3	CKLTI0200	-0.01	1.22*	0.33	-1.53	8.45**	-1.96	-5.35			
L4	CKLTI0147	0.16	0.99*	-0.45	1.61	-3.46	-1.94	0.72			
L5	CKLTI0152	0.39	1.13*	0.15	0.27	-3.38	2.70	-5.86			
L6	CKLTI0272	-0.35	1.26*	0.58	1.65	-2.82	0.52	-3.29			
L7	CKLTI0036	-0.16	0.03	-0.38	-1.26	11.59***	-1.78	4.93			

Least significant difference (LSD) of 0.05; \*-Significance at P<0.05; \*\*-Significance at P<0.01; \*\*\*-Significance at P<0.001; GLS-gray leaf spot; ET- *E turcicum*/ Turcicum leaf blight

### 3.3.5 Specific Combining Ability (SCA)

#### 3.3.5.1 Well-watered conditions

Well-watered conditions revealed that the most desirable crosses with regard to high SCA effects for grain yield were L5 × T5 (0.86), followed by L4 × T5 (0.75), L7 × T4 (0.58), L2 × T7 (0.54), L2 × T5 (0.52) then L7 × T6 (0.46). Crosses L7 × T4 (-0.90) and L2 × T5 (-0.88) showed significant earliness with regard to anthesis, while L7 × T5 (0.88) showed lateness. As regards flowering, crosses L1 × T3 and L4 × T6 showed significant lateness (0.43) (Table 3.9). For plant and ear height, the estimates of SCA effects were each significant in 14 of the 49 crosses. The cross, L7 × T5 was the best specific combiner as it showed tendency to reduce both plant and ear height. Root, shoot lodging and ear aspect SCA effects were significant in 3, 4 and 17 of the 49 crosses respectively. The significant estimates of SCA effects on GLS showed that crosses, L1 × T3 (0.36) and L5 × T5 (0.27) were susceptible, while L5 × T7 (-0.33) was resistant to GLS. Crosses L6 × T2 (0.30) and L7 × T2 (0.30) were significantly susceptible to *E. Turcicum*, and crosses, L4 × T2 (-0.31) and L6 × T4 (-0.27) were significantly resistant. For MSV, the SCA effects showed high significant ( $p < 0.001$ ) susceptibility of the cross L6 × T2, while two of the 49 crosses were significantly resistant (Table 3.9).

#### 3.3.5.2 Water stress conditions

Significant estimates of SCA effects for grain yield were recorded (Table 3.10) Crosses L2 × T6 (1.15) and L7 × T4 (1.04) were good specific combiners while crosses L2 × T1 (-0.99) and L7 × T3 (-0.78) were poor specific combiners for grain yield (Table 3.11). With respect to number of days to anthesis, cross, L2 × T1 was the latest while cross L7 × T1 was the earliest. For days to silking, crosses L3 × T1 and L3 × T2 SCA effects of -1.15 were best for earliness, whereas cross L3 × T7 showed significant lateness. SCA effects on plant height were significantly positive

( $P < 0.05$ ) in 4 of the crosses and significantly negative on 2 of the crosses. For ear aspect, crosses,  $L2 \times T1$  (-8.77),  $L7 \times T5$  (-8.18),  $L3 \times T7$  (-7.46),  $L5 \times T3$  (-6.46) were best specific combiners because they showed a tendency to reduce ear height. Crosses,  $L2 \times T7$  (9.09),  $L1 \times T1$  (7.59),  $L2 \times T6$  (7.18),  $L3 \times T5$  (7.11),  $L4 \times T3$  (7),  $L3 \times T2$  (6.95),  $L7 \times T4$  (6.59) and  $L5 \times T7$  (6.46) showed tendency to increase ear height therefore poorest specific combiners (Table 3.10). SCA effects on three root lodgings and five shoot lodgings of the 49 crosses were significant.

Table 3.9 Specific combining ability of tropical-temperate hybrids evaluated during 2014 under well-watered conditions

No	Cross	Grain Yield (t/ha)	Days to anthesis (days)	ASI (days)	Plant height (cm)	Ear height (cm)	Root lodging (cm)	Stem lodging (cm)	GLS (1-5)	ET (1-5)	MSV (1-5)
1	L1XT1	0.18	-0.18	-0.07	7.09**	8.39***	0.15	-1.41	-0.07	0.09	0.19
2	L1XT2	0.13	0.29	0.15	-0.94	-2.83	0.21	-0.29	0.08	-0.16	0.31*
3	L1XT3	-0.22	-0.05	0.43*	6.75**	6.49***	-0.28	1.4	0.36*	0.05	0.07
4	L1XT4	0.38	0.29	-0.35	4.36*	4.19*	-0.19	-0.11	-0.11	0.02	-0.01
5	L1XT5	-0.43	0.07	-0.07	4.35*	0.47	-0.27	0.11	-0.18	-0.02	0.03
6	L1XT6	0	0.60*	-0.01	-0.08	-2.68	0.1	0.81	-0.18	0.09	-0.02
7	L1XT7	-0.03	0.18	-0.08	0.66	-1.05	0.29	0.52	0.12	-0.06	0.05
8	L2XT1	-0.19	0.29	0.09	-1	-1.15	-0.4	-0.38	-0.12	0	2
9	L2XT2	0.60*	0.42	-0.2	10.90***	6.64***	0.21	-0.12	0.03	0.27	0.38*
10	L2XT3	0.27	0.58*	0.09	-0.91	2.11	0.42	-1.2	-0.03	-0.02	-0.01
11	L2XT4	0.51*	-0.08	0.13	6.08*	-2.2	-0.07	2.33*	-0.17	-0.06	0.17
12	L2XT5	0.52*	0.88**	0		12.07***	5.00**	-0.51	0.36**	0.27	-0.09
13	L2XT6	-0.02	-0.38	-0.19	3.36	1.03	0.33	0.77	-0.23	0.02	-0.09
14	L2XT7	0.54*	0.06	0.16	3.45	1.85	0.01	-1.25	0.17	-0.13	0.1
15	L3XT1	-0.06	-0.08	0.35	-2.45	-0.36	-0.46	-0.12	0.2	0.09	
16	L3XT2	0.26	0.62*	0.06	2.71	2.54	-0.54	0.21	0.1	-0.16	-0.22
17	L3XT3	0.4	0.3	-0.07	-0.46	-0.45	0.76	-0.85	0.04	0.05	0.03
18	L3XT4	-0.12	0.05	-0.19	-1.81	-1.12	1.30**	-0.92	-0.1	0.02	-0.04
19	L3XT5	0.04	-0.08	0.02	0.93	-0.03	-0.36	1.05	-0.17	0.23	0.12
20	L3XT6	0.2	0.5	-0.09	1.11	1.75	-0.2	0.78	0.08	-0.16	0.07
21	L3XT7	0.73**	-0.06	-0.08	-0.02	-2.33	-0.5	-0.15	-0.07	-0.06	0.01
22	L4XT1	0.12	0.13	-0.21	-2.32	-1.22	-0.31	0.36	0.03	-0.06	-0.06
23	L4XT2	0.05		0.07	-0.08	2.47	0.48	0.23	0	-0.07	0.31*

Table 3.9 Specific combining ability of tropical-temperate hybrids evaluated during 2014 under well-watered conditions

No	Cross	Grain Yield (t/ha)	Days to anthesis (days)	ASI (days)	Plant height (cm)	Ear height (cm)	Root lodging (cm)	Stem lodging (cm)	GLS (1-5)	ET (1-5)	MSV (1-5)
24	L4XT3	0.75**	-0.15	-0.21	-1.97	-2.26	-0.68	0.62	-0.13	-0.09	-0.06
25	L4XT4	-0.12	0.1	-0.08	2.6	2.46	0.7	0.45	-0.07	0.12	-0.13
26	L4XT5	0.75**	-0.37	.12	3.2	4.64*	0.03	-0.21	0	7	0.09
27	L4XT6	-0.22	0.05	0.43*	-2.72	3.64*	-0.29	-0.66	0.26	0.19	0.1
28	L4XT7	0.17	0.32	0.03	-1.26	-0.46	0.76	0.48	0.17	0.05	0.05
29	L5XT1	0.2	-0.2	0.06	-2.84	-1.81	0.56	-0.27	-0.11	0.02	-0.02
30	L5XT2	-0.06	0.01	0.28	1.74	1.1	0		0.06	0.04	-0.23
31	L5XT3	0.24	-0.07	-0.19	3.36	2.11	0.22	0.75	-0.02	-0.02	0.1
32	L5XT4	-0.23	0.43	0.11	-1.67	3.71*	-0.35	-0.79	0.24	0.19	0.16
33	L5XT5	0.86**	0.05	0.06	4.05	2.39	-0.22	0.5	0.27*	-0.09	-0.06
34	L5XT6	0.58*	0.13	-0.29	4.19*	-1.62	-0.06	-0.92	-0.03	0.27	-0.11
35	L5XT7	-0.42	-0.26	-0.03	-0.46	1.54	-0.15	0.65	0.33*	-0.13	-0.04
36	L6XT1	0.21	-0.33	-0.13	-1.02	-2.95	0.75	2.14*	-0.12	0.05	-0.15
37	L6XT2	-0.02	0.3	-0.16	5.41*	4.43*	0.25	1.19	-0.1		0.30*
38	L6XT3	-0.1	0.54*	-0.04	4.08	1.86	-0.25	0.34	-0.23	0.02	-0.15
39	L6XT4	0.02	0.13	0	-3.29	4.69*	0.83*	-0.71	0.03	0.27*	-0.22
40	L6XT5	0.64*	0.33	0.29	-3.57	-0.82	0.52	-0.14	0.06	-0.06	-0.18
41	L6XT6	0.16	0.25	0.1	24.72	-0.11	-0.08	-0.54	0.23	-0.2	0.01
42	L6XT7	0.36	-0.14	-0.06	3.11	2.28	-0.36	2.00*	0.13	0.16	-0.17
43	L7XT1	0.47*	0.46	-0.09	2.54	-0.9	-0.29	3.96***	0.15	-0.2	0.01
44	L7XT2	0.26	-0.32	-0.04	-0.49	0.92	-0.37	-0.04	0.05	0.30*	-0.11
45	L7XT3	0.16	-0.07	-0.01	2.65	3.12*	-0.19	-1.06	-0.05	0.02	
46	L7XT4	0.58*	0.90**	0.37	5.89*	5.07**	-0.12	-0.25	0.21	-0.02	0.07
47	L7XT5	1.10***	0.88**	0.34	12.33***	11.65***	0.81*	-1.17	-0.06	-0.06	-0.02
48	L7XT6	0.46*	0.05	0.05	7	24**	5.27**	0.21	0.36*	-0.06	-0.2
49	L7XT7	0.11	-0.1	0.06	5.48*	-1.84	-0.04	-1.2	-0.22	0.16	-0.01

ASI Anthesis silking interval; GLS- gray leaf spot; MSV ó maize streak virus; ET- Turcicum leaf blight;

Table 3.10 Specific combining ability of tropical-temperate maize hybrids evaluated during 2014 under water stress/Drought conditions

No	Cross	GY (t/ha)	AD (days)	ASI (days)	PH (cm)	EH (cm)	Root lodging (cm)	Stem lodging (cm)	Leaf Senescence (1-5)	MSV (1-5)
1	L1XT1	0.16	-0.88	0.56	3.6	7.59*	-1.19	-0.9	0.94	0.94
2	L1XT2	-0.23	0.08	0.92*	-4.17	-4.02	-5.87	19.76**	-0.85	-0.9
3	L1XT3	0.43	0.37	0.94*	5.96	2.77	-1.55	-0.67	0.51	0.51



Table 3.10 Specific combining ability of tropical-temperate maize hybrids evaluated during 2014 under water stress/Drought conditions

No	Cross	GY (t/ha)	AD (days)	ASI (days)	PH (cm)	EH (cm)	Root lodging (cm)	Stem lodging (cm)	Leaf Senescence (1-5)	MSV (1-5)
4	L1XT4	-0.56	0.51	0.1	-3.9	-2.71	4.87	11.23*	-0.42	-0.4
5	L1XT5	0.04	-0.1	0.35	-2.2	-0.98	3.12	7.48	-0.2	-0.2
6	L1XT6	0.03	-0.78	-0.12	0.1	-0.71	4.4	10.84	0.22	0.22
7	L1XT7	0.13	0.8	0.87*	0.6	-1.93	-3.76	-8.23	-0.2	-0.2
8	L2XT1	0.99*	1.72**	-0.19	16.02*	8.77*	2.57	-0.91	0.51	0.51
9	L2XT2	-0.34	0.19	0.17	-3.92	-3.88	0.18	-3.9	0.22	0.22
10	L2XT3	0.09	-0.03	-0.44	1.96	1.54	0.06	12.62*	0.58	0.58
11	L2XT4	-0.19	0.12	0.35	-5.9	-1.95	9.59*	2.83	0.15	0.15
12	L2XT5	-0.12	-0.99	0.85*	0.42	-3.21	8.67*	-10.53	-0.13	-0.1
13	L2XT6	1.15**	-0.92	-0.62	8.35	7.18*	-2.79	-5.7	-0.7	-0.7
14	L2XT7	0.39	-0.1	-0.12	15.10*	9.09*	-0.95	5.59	-0.63	-0.6
15	L3XT1	-0.18	0.94	1.51**	-0.11	2.8	-1.09	-2.57	-1.35	-1.4
16	L3XT2	0.58	0.4	1.15*	9.87	6.95*	7.64*	5.07	-0.13	-0.1
17	L3XT3	0.13	-0.06	0.24	-5.51	-4.27	-2.12	4.67	0.22	0.22
18	L3XT4	-0.1	-0.17	0.78	-2.86	-2	-4.48	-7.44	-0.2	-0.2
19	L3XT5	0	0.47	0.03	13.71*	7.11*	2.06	-8.73	0.01	0.01
20	L3XT6	-0.21	-0.45	0.56	-4.99	-3.13	2.12	6.43	0.44	0.44
21	L3XT7	-0.23	1.13*	1.06*	-10.11	7.46*	-4.12	2.56	1.01	1.01
22	L4XT1	0.23	0.22	0.53	-3.13	-4.55	-2.97	-8.36	-0.49	-0.5
23	L4XT2	0.52	-0.56	-0.37	6.73	5.46	-3.77	9.75	-0.28	-0.3
24	L4XT3	0.63	1.28*	1.03*	5.6	7*	4.13	7.63	-0.42	-0.4
25	L4XT4	-0.4	1.12*	-0.19	-1.63	-1.36	-0.47	-4.38	-0.35	-0.4
26	L4XT5	-0.29	0.76	0.06	-2.06	1.13	6.1	2.12	0.37	0.37
27	L4XT6	-0.37	0.08	-0.4	1.49	-4.36	-4.74	-3.26	0.8	0.8
28	L4XT7	-0.32	-0.35	-0.65	-7.01	-3.32	1.73	-3.5	0.37	0.37
29	L5XT1	0.12	-0.67	-0.08	3.08	-0.02	-0.46	7.5	0.22	0.22
30	L5XT2	-0.69	0.05	0.53	-6.43	-2.75	-4.54	1.23	-0.06	-0.1
31	L5XT3	-0.45	0.83	0.17	-4.68	6.46*	-0.83	-5.28	-0.2	-0.2
32	L5XT4	0.31	-0.53	-0.3	-5.29	0.43	-4.41	6.1	-0.13	-0.1
33	L5XT5	0.29	-0.88	-0.55	4.28	3.41	5.75	7.49	0.08	0.08
34	L5XT6	0.1	1.19*	-0.26	-1.17	-1.07	-0.2	-9.9	0.01	0.01
35	L5XT7	0.32	0.01	0.49	10.21*	6.46*	4.69	-7.12	0.08	0.08
36	L6XT1	0.68	0.22	0.24	6.08	-0.07	-1.64	2.51	0.22	0.22
37	L6XT2	-0.27	0.44	-0.15	-8.81	-4.3	2.96	7.08	0.44	0.44
38	L6XT3	-0.05	-0.03	-0.26	3.32	1.73	1.37	13.48*	-0.2	-0.2
39	L6XT4	-0.1	-0.38	-0.47	1.83	1	-2.41	-1.04	0.37	0.37
40	L6XT5	0.17	0.01	0.28	3.91	0.73	-4.53	-4.47	0.08	0.08

Table 3.10 Specific combining ability of tropical-temperate maize hybrids evaluated during 2014 under water stress/Drought conditions

No	Cross	GY (t/ha)	AD (days)	ASI (days)	PH (cm)	EH (cm)	Root lodging (cm)	Stem lodging (cm)	Leaf Senescence (1-5)	MSV (1-5)
41	L6XT6	-0.08	-0.42	0.56	2.46	5.38	4.14	-1.74	-0.49	-0.5
42	L6XT7	-0.35	0.15	-0.19	-8.79	-4.46	0.11	11.15*	-0.42	-0.4
43	L7XT1	-0.03	1.56*	0.45	6.49	3.02	4.79	2.73	-0.06	-0.1
44	L7XT2	0.44	-0.6	0.06	6.73	2.54	3.4	0.54	0.65	0.65
45	L7XT3	0.78*	0.19	0.2	-6.65	-2.3	-1.05	-5.49	-0.49	-0.5
46	L7XT4	1.04*	-0.67	-0.26	17.74**	6.59*	-2.68	-7.3	0.58	0.58
47	L7XT5	-0.09	0.72	1.01*	18.06*	8.18*	-3.82	6.65	-0.2	-0.2
					*					
48	L7XT6	-0.63	1.30*	0.28	-6.26	-3.29	-2.94	3.33	-0.28	-0.3
49	L7XT7	0.05	0.62	0.28	-0.01	1.63	2.31	-0.46	-0.2	-0.2

GLS Gray leaf spot; MSV Maize streak virus, ET *Turcicum* leaf blight; GY grain yield; AD days to anthesis; ASI anthesis silking interval; PH plant height, EH ear height

### 3.3.6 Heritability and correlation

The heritability percentage was categorized as: Low, 0 - 30%; Moderate, 30 - 60%; and High >60% (Robinson *et al.*, 1949). It ranged between 0 - 90% in both optimum and drought conditions, for yield and the measured traits in this study. Higher heritability was observed under optimum conditions. There was high heritability of above 80% in well-watered conditions and moderate (slightly above 40%) in water stress conditions. In the individual sites, heritability was low to high, ranging from 10% to 70% under water stress conditions (KARLO Kiboko and Homabay), while it ranged from 0% to 80% in the well-watered conditions (KARLO Kiboko, Kirinyaga University College, Kaguru, KARLO Kakamega, Shikusa and Mtwapa) (APPENDIX 11-18).

Heritability for grain yield under water-stress was moderate (Table 3.11) as it was noted to be slightly above 40%. This was similar to flowering. However, ear height, plant height and leaf senescence were highly heritable (> 60%) (Table 3.11), hence could be passed to subsequent

generations. The ANOVA table revealed no significant differences for all the agronomic traits in drought stress conditions. The negative GCA for yield of line CKLTI0368 must have been influenced by significant lateness in flowering and significant stem lodging susceptibility, because the ear and plant heights were significantly low. The highest yielding line in water stress was early flowering and had a short flowering interval; however, both the plant and ear heights were high.

For specific combining ability, most of the top yielders were early flowering and showed resistance to root and stem lodging. The top yielder (1.15) with regard to SCA had a negative value for leaf senescence (-0.7). A negative SCA value for leaf senescence per se does not influence grain yield. Earliness was observed to have more influence on yield performance.

Correlation is significant if it is above 0.5 (Table 3.12). The correlation for yield in my trial was positive and significant for Shikusa and Kakamega as it was 0.72 (Table 3.12). Kaguru and KYUC were significantly similar with correlation of 0.51. The yields of Kiboko\_Opt, Mtwapa, Homabay and Kiboko\_DT, though not significant, were positively correlated.

Table 3.11 Heritability of tropical-temperate maize hybrids evaluated during 2014

Trait	Managed Drought	Well-watered
Grain yield	0.449	0.748
Days to anthesis	0.448	0.8635
Anthesis silking interval	0.383	0.729
Plant height	0.631	0.927
Ear height	0.858	0.938
Leaf senescence	0.665	-
Grain moisture	0.068	0.730
Root lodging	0	0.085
Stem lodging	0.228	0.102
Ear aspect	0.499	0.777
<i>Turcicum</i> leaf blight	-	0.706
<i>Gray leaf spot</i>	-	0.041
<i>Maize streak virus</i>	-	0.114

Table 3.12 Phenotypic correlation for grain yield among locations

Site	Homabay	KYUC	Kaguru	Kakamega	Kiboko_DR	Kiboko_Opt	Mtwapa	Shikutsa
Homabay	1.00	0.23	0.23	0.27	0.23	0.10	0.16	0.33
KYUC	0.23	1.00	0.51	0.41	0.48	0.61	0.33	0.50
Kaguru	0.23	0.51	1.00	0.62	0.54	0.39	0.30	0.57
Kakamega	0.27	0.41	0.62	1.00	0.56	0.36	0.30	0.72
Kiboko_DT	0.23	0.48	0.54	0.56	1.00	0.43	0.33	0.52
Kiboko_Opt	0.10	0.61	0.39	0.36	0.43	1.00	0.38	0.32
Mtwapa	0.16	0.33	0.30	0.30	0.33	0.38	1.00	0.33
Shikutsa	0.33	0.50	0.57	0.72	0.52	0.32	0.33	1.00

KYUC Kirinyaga University College; DT drought trial; Opt optimum conditions

### 3.4 Discussion

The experimental hybrids performed better than the checks in grain yield and the other agronomic traits measured. The results clearly showed that parent L1 (CKLTI0344), L3 (CKLTI0200) and L6 (CKLTI0272) contributed more to early maturity compared to the other inbred lines and could therefore be important sources of early maturity in breeding programs for yield increase and drought escape. Significant differences for resistance to GLS, ET and MSV among the hybrids showed an existence of possibility to select for these traits in the hybrids. Site by line by tester interaction showed a significant ( $P < 0.05$ ) difference for stem lodging under well-watered conditions, indicating that genotypes responded differently for this trait in this environment. There were highly significant interactions for site  $\times$  line and line  $\times$  tester for grain yield signifying differential responses for lines and testers across sites and that the potential of a line in a cross was different depending on the tester used. These findings are in agreement with (Betran *et al.*, 2003; Narro *et al.*, 2003; Ndhlela, 2007). The highly significant line  $\times$  tester interaction for grain yield, plant height, ear height and ear aspect in well-watered conditions is an indication that each specific cross was unique from the other. This result also shows that the

testers and lines had markedly different combining ability effects and that there is a positive measure of yield performance under optimum conditions. A significant,  $L \times T$  interaction provided evidence that the ranking of experimental lines differed depending on the tester used (Packer, 2007), hence an appropriate tester may be selected to evaluate new germplasm lines (Ali *et al.*, 2011). The insignificance of interaction of lines by testers in the study under water stress showed there was poor yield performance.

Site  $\times$  line interaction was highly significant ( $p < 0.01$ ) for grain yield in optimum conditions indicating that the inbred lines performed differently in their respective environments. The significant site  $\times$  line interactions make it possible to select the best specific combiners under the different environments. On the other hand, the lack of significant differences for Testers  $\times$  Site interaction for yield in both optimum and drought conditions suggested that testers performed similarly in different environments. The interaction between, line  $\times$  tester  $\times$  site was not significant indicating hybrids performed similarly in all environments. Genetic diversity is highly advantageous in sourcing for genetic gain through creating hybrids (Khoza, 2012). Most of the traits studied in all well-watered sites were highly significant except for *E. turcicum*.

The lines and testers differed significantly for days to anthesis (AD) under different environments. Similar findings were also observed by (Betran *et al.*, 2003; Ndhlela, 2007). The mean AD was less under water stress due to the stress effect on growth of the maize crop. Vasal *et al.* (1992) recorded a mean AD of 71 under temperate environments and 54 under subtropical environments. This shows that selection for AD has to be done under optimum conditions to cater for grain filling, therefor proper seed production. The number of AD also differed within specific combinations, with the earliest being 53 days and the latest 80 days in different sites (APPENDIX 11-18). Entry 27 and 44 and 48 were early flowering while entry 50 was late

flowering. Therefore, good specific combiners for earliness can be identified and selected for using the results from this study.

From the mean yields, it was noted that the distribution of grain yield and yield related traits slightly varied in the different environments due to environmental effect on the genotypes. Some genotypes were high yielding and some were low yielding. Environments with high rainfall were more favorable for yield increase. In managed drought conditions, many genotypes produced pollen late and this could be due to the sensitivity of the flowering stage to drought. Under both optimum and managed drought conditions, the means of the hybrids revealed the involvement of additive and non-additive gene effects towards yield production.

In well-watered conditions, line 5 had the highest GCA for grain yield of 0.54; line 7 had the least GCA for grain yield of -0.41. Line 5 was positively significant for grain yield therefore desired as good general combiner for grain yield under optimum conditions. Line 7 was negatively significant, therefore not desirable. Most of the top performing hybrids in well-watered conditions were more or equally resistant to diseases (a score of 0 - 2.5) compared with the best yielding commercial check (Pioneer 3253) as shown in Table 3.6. The means of the hybrids revealed the breeding potential of the germplasm involved in the study and these could be more favored than poor lines in breeding programs. In this study, the single cross testers made good crosses with the inbreds therefore resulted to high yields which are disease resistant. The highest yielding hybrid showed a high mean of root lodging and a bit low mean of stem lodging while the mean of leaf senescence was rated moderate to high ranging from 4.9 - 8.1 for the hybrids. The best check was rated 7.0 and poorest 8.9.

The significant differences among the lines, testers and their interaction on grain yield implied that the GCA due to lines, GCA due to testers and SCA effects were important in explaining differences between hybrids. In traits like grain yield and number of ears per plant, a positive GCA is preferred. In the case of days to anthesis, anthesis silking interval, ear aspect and silking dates, a negative GCA could imply good performance of the lines across testers. Lines 1 and 5 were positively significant for grain yield under drought and optimum conditions respectively therefore desired as a good general combiners for grain yield under their respective environments. Lines 2 and 7 were negatively significant, therefore did not combine high yields. Lines 6 and 7 were negative for grain yield (Table 3.7, Table 3.8) with line7 being negatively significant in well-watered conditions therefore low yield production. They were also significant for ASI and plant height; but were most susceptible inbred lines to *E. Turcicum* while line 6 was more susceptible to *Maize streak virus*.

The negative, positive and significant estimates of SCA effects on grain yield were recorded among the crosses (Table 3.9, Table 3.10). The most desirable cross combination for grain yield SCA effects were L5 × T5 with 0.86, followed by L4 × T5 with 0.75, L7 × T4 with 0.58, L2 × T7 with 0.54, L2 × T5 with 0.52 then L7 × T6 with 0.46. This implies that the additive gene action in the inbred lines for grain yield and the non-additive gene action in the testers for disease resistance and grain yield complement each other in the crosses. The crosses with significant estimates of SCA effects could be selected for their specific combining ability to use in maize improvement program. Motamedi *et al.* (2014), Shushay *et al.* (2013) in their study on grain yield in maize, reported significant to highly significant level of SCA effects in most of the crosses they studied (Motamedi *et al.*, 2014; Shams *et al.*, 2010; Shushay *et al.*, 2013).

New varieties from the evaluated germplasm can be developed through recurrent selection strategies which take advantage of additive gene actions. Grain yield shown to be conditioned by additive gene action could be selected. Beyene *et al.* (2011) stated that non-additive gene action has been found to condition grain yield among hybrids developed from insect resistant hybrids, and therefore the nature of gene action conditioning grain yield cannot be generalized. Different hybrids should more often be evaluated across environments with differing ecological conditions and disease intensities. The mean squares due to environment were significant for all traits all the locations were distinct, thus suggesting that different hybrids should be developed for different environments.

From the mean performance results it can be clearly noted that Tester entry 51 performed better under water stress conditions. It is therefore recommended for yield increase in water stress environments. Tester entry 50 on the other hand should be well utilized particularly in Kirinyaga type moisture regimes as its BLUE yield was higher than all the hybrids. In well-watered environments, the two single cross testers yielded almost similarly, though in a combination, tester 51 should be recommended for testing in all locations. However, the high yielding hybrids under drought conditions were observed to have a combination of tester CKDHL0159/CKDHL0295 while some that yielded high in well-watered conditions were crosses with tester CKDHL0089/CKDHL0295.



### 3.4.1 Heritability of agronomic traits and correlation for grain yield among locations

The heritability percentage was categorized as: Low, 0 - 30%; Moderate, 30 - 60%; and High >60% (Robinson *et al.*, 1949). It ranged between 0 - 90% in both optimum and drought conditions, for yield and the measured traits in this study. Higher heritability was observed under well-watered conditions. There was high heritability of above 80% in well-watered conditions and moderate (slightly above 40%) in water stress conditions (Table 3.11). In the individual sites, heritability was low to high, ranging from 10% to 70% under water stress conditions (KARLO Kiboko and Homabay), while it ranged from 0% to 80% in the well-watered conditions (KARLO Kiboko, Kirinyaga University College, Kaguru, KARLO Kakamega, Shikusa and Mtwapa) (APENDIX 16-24).

In well-watered environments, grain yield, days to anthesis, anthesis silking interval, ear and plant height and Turicum leaf blight were highly heritable (above 80%) hence these traits could be passed on to the next generations (Table 3.11). MSV, root and stem lodging were less heritable hence subsequent generations may not experience their effects. In managed drought conditions, heritabilities for yield and other agronomic traits were slightly above 40% therefore moderate. These results in the present study are in accordance with earlier findings by Iqbal (2009); who reported the heritability of between 44% - 82% for grain yield. Ali and others reported a high heritability of 67% for grain (Ali *et al.*, 2011). Unlike these results, Asghar and Mehdi (2010) reported a heritability of 38%. This tells that the germplasm can be directly selected.

Heritability for earliness traits was low under drought (Table 3.11). Since maize is a water demanding plant, under drought stress, susceptible maize plants show prolonged anthesis-silking interval, smaller leaf area, thinner stalk, shorter and smaller ears, a decline in plant height and ear

position, reduced grain number per ear and grain weight which leads to yield losses (Zhang *et al.*, 2008). Maize is very sensitive to moisture stress during flowering (IITA, 1982). Yield losses of up to 75% have been reported (Bolanos *et al.*, 1993). Drought tolerant varieties are therefore important for crop production, yield improvement and yield stability under drought stress conditions (Khodarahmpour and Hamidi, 2011). Heritabilities for plant height, ear height, leaf senescence were high (>60%) under water stress and well-watered conditions. Aminu and Izge (2012) estimated broad sense heritability of ASI, PH, weight of cobs and GY affected by drought, under drought conditions, and found they were high (60.61% to 67.44%). Leaf senescence begins at the base of the plant and spreads upwards to the ear and severe stress at flowering may lead to the complete abortion of ears and the plant becomes barren. Drought-affected ears typically have fewer kernels that will be poorly filled if drought extends throughout grain filling (Edmeades *et al.*, 2000). The correlation for grain yield among locations revealed that Kaguru and KYUC were significantly similar, the highest correlation being for Shikutsa and Kakamega. This implies that the two locations can be used interchangeably for yield trial experiments. This however depends on the mean yields of each site as the site with the highest mean yield is most preferred (Table 3.12 and Table 3.13). For the other locations, yield trials could be done differently.

Table 3.13 Locations statistics on the mean grain yields of the 55 entries

Location	Geno	Rep	Mean	Max	SE	LSD5%	SD	Heritability	N_H75	CV%
Kakamega	55	2	7.7	10.0	1.1	2.2	1.7	0.8	1.4	13.7
KYUC	55	2	6.5	8.5	0.7	1.4	1.1	0.8	1.3	10.4
Hbay	55	2	5.0	7.0	1.2	2.5	1.0	0.3	14.6	24.4
Kib_Opt	55	2	8.0	11.1	0.9	1.8	1.1	0.7	2.6	10.9
Shikusa	55	2	8.3	11.2	1.1	2.3	1.4	0.7	3.0	13.7
Mtwapa	55	2	4.5	6.4	1.2	2.5	1.0	0.3	17.5	27.5
Kaguru	55	2	8.6	11.0	1.1	2.3	1.3	0.6	3.8	12.9
Kib_DT	55	2	2.6	3.7	0.6	1.1	0.5	0.4	10.2	21.2

KYUC Kirinyaga University College; Rep Replications; Geno Genotypes; SE standard error; LSD Least significant difference; SD Standard deviation; CV Coefficient of variation

### **3.5 Conclusion**

The tropical/temperate maize inbred lines showed the capability of expressing dominance gene action and high heritability levels in hybrid combinations. Most of the top performing hybrids had a combination with line CKLTI0152. For instance, inbred lines (CKLTI0152) and (CKLTI0147) can be successfully utilized in well-watered and drought conditions, to develop hybrids with better combinations for yield increase. The best performing hybrids (entry 14, 10 and 28) for specific combining ability in this study should be availed in breeding to exploit hybrid vigor.

## CHAPTER FOUR

### 4 Genotype by Environment interaction for grain yield of maize testcross hybrids in optimum and water-stress conditions

#### 4.1 Introduction

Maize is an important food crop globally as it provides over 15% of the total protein while accounting to about 20% of the total calories in the developing countries (Shakoor *et al.*, 2007; Nzuve *et al.*, 2014). With the increasing climatic change, several abiotic stress factors have resulted into the declining yields in Africa and particularly in eastern and southern Africa. It has been reported that factors of drought and low soil fertility are major contributors to this decline (Bänziger and Diallo, 2004). Unfortunately, maize production in the Sub-Saharan Africa is rain fed and therefore overcoming the challenge of drought is not foreseeable at present. Physiologically, drought affects production at all stages of crop development, but near irreversible effect occur at the flowering stage when the crop needs water the most (Edmeades *et al.*, 1992). It has been estimated that in developing countries, the loss due to inadequate soil moisture contributes to about 20% annual production losses. A number of multiple factors have led to the increasing drought including climate change, declines in soil organic matter, reducing soil fertility and water holding capacity (Banziger *et al.*, 2000; Makumbi, 2005).

Given drought challenge, breeding efforts on drought tolerance in the sub-Saharan Africa began with improved tropical maize for stress tolerance under both drought and low nitrogen conditions (Edmeades *et al.*, 1992). These programs approached breeding for stress tolerance by simulating abiotic stress factors that are important in the target environment. Breeding experiments were then exposed to a clearly defined abiotic factor in environments termed -managed stress

environments (Bänziger and Cooper, 2001). Spatially, maize is produced in a wide range of environments in Sub-Saharan Africa, ranging from lowland tropical zones (0-1,000 meters above sea level (masl)), wet subtropical zones (900-1500 masl), dry subtropical zones (900-1500 masl), and highland zones (>1800 masl), with varying amounts of rainfall (Hassan *et al.*, 2001).

Different environmental conditions influence the interaction of several genes that determine maize yields (Bocanski *et al.*, 2009). The yield therefore is as a result of many factors referred to as yield components, which have a multiplicative effect on the end product (Zeeshan *et al.*, 2013). These yield components are simply inherited with minimal environmental deviations (Nzuve *et al.*, 2014). Large genotype  $\times$  environment interaction GEI variation decreases the accuracy of yield estimation and reduces the relationship between genotypic and phenotypic values (Nachit *et al.*, 1992; Beyene *et al.*, 2012). When GEI is present, breeders opt to use stability analyses to identify the most high-yielding and stable cultivar (Beyene *et al.*, 2012). The genotype plus genotype  $\times$  environment interaction (GGE) biplot (Yan and Tinker, 2006b) has been suggested as the appropriate model for analyzing multi-environment trials when large yield variation is due to different environments (Yan *et al.*, 2000). The GGE (Yan *et al.*, 2000) is an effective tool for: (1) mega-environment analysis (‘‘which-won-where’’ pattern), whereby specific genotypes can be recommended to specific mega-environments (Yan and Kang, 2003; Yan and Tinker, 2006a) (2) genotype evaluation (the mean performance and stability), and (3) environmental evaluation (the power to discriminate among genotypes in target environments). This therefore is an effective tool for determining the stable environments for the best tropical-temperate genotypes. The objective was therefore to determine the yield stability of the tropical-temperate maize hybrids, their agronomic performance and their reaction to foliar diseases evaluated across eight locations in Kenya.

## 4.2 Materials and Methods

### 4.2.1 Germplasm and experimental sites

The maize germplasm that was used in this study were from various sources as shown in Table 4.1. The hybrids were planted in eight sites during the planting season 2014 (Table 3.2). Water stress sites were: Kiboko and Homabay; well-watered sites were: Kenya Agricultural Research and Livestock Organization (KALRO) Kakamega, Shikusa, Kiboko, Mtwapa, Kaguru and Kirinyaga University College (KYUC).

### 4.2.2 Development of crosses

The crosses were developed as described in Section 3.2.3 and Table 4.1.

Table 4.1 Table of the hybrids used in this study

Entry	Hybrid (inbred lines names coded)	Cross
1	CML395/CML444//CKLTI0368	L2 × T4
2	CML489/CML444//CKLTI0368	L2 × T1
3	CML312/CML395//CKLTI0368	L2 × T7
4	CKDHL0089/CKDHL0333//CKLTI0368	L2 × T3
5	CKDHL0089/CKDHL0295//CKLTI0368	L2 × T5
6	CKDHL0159/CKDHL0295//CKLTI0368	L2 × T2
7	CKDHL0089/CML395//CKLTI0368	L2 × T6
8	CML395/CML444//CKLTI0152	L5 × T4
9	CML489/CML444//CKLTI0152	L5 × T1
10	CML312/CML395//CKLTI0152	L5 × T7
11	CKDHL0089/CKDHL0333//CKLTI0152	L5 × T3
12	CKDHL0089/CKDHL0295//CKLTI0152	L5 × T5
13	CKDHL0159/CKDHL0295//CKLTI0152	L5 × T2
14	CKDHL0089/CML395//CKLTI0152	L5 × T6
15	CML395/CML444//CKLTI0036	L7 × T4
16	CML489/CML444//CKLTI0036	L7 × T1
17	CML312/CML395//CKLTI0036	L7 × T7
18	CKDHL0089/CKDHL0333//CKLTI0036	L7 × T3
19	CKDHL0089/CKDHL0295//CKLTI0036	L7 × T5
20	CKDHL0159/CKDHL0295//CKLTI0036	L7 × T2
21	CKDHL0089/CML395//CKLTI0036	L7 × T6
22	CML395/CML444//CKLTI0200	L3 × T4
23	CML489/CML444//CKLTI0200	L3 × T1
24	CML312/CML395//CKLTI0200	L3 × T7

<b>Entry</b>	<b>Hybrid (inbred lines names coded)</b>	<b>Cross</b>
25	CKDHL0089/CKDHL0333//CKLTI0200	L3 × T3
26	CKDHL0089/CKDHL0295//CKLTI0200	L3 × T5
27	CKDHL0159/CKDHL0295//CKLTI0200	L3 × T2
28	CKDHL0089/CML395//CKLTI0200	L3 × T6
29	CML395/CML444//CKLTI0272	L6 × T4
30	CML489/CML444//CKLTI0272	L6 × T1
31	CML312/CML395//CKLTI0272	L6 × T7
32	CKDHL0089/CKDHL0333//CKLTI0272	L6 × T3
33	CKDHL0089/CKDHL0295//CKLTI0272	L6 × T5
34	CKDHL0159/CKDHL0295//CKLTI0272	L6 × T2
35	CKDHL0089/CML395//CKLTI0272	L6 × T6
36	CML395/CML444//CKLTI0147	L4 × T4
37	CML489/CML444//CKLTI0147	L4 × T1
38	CML312/CML395//CKLTI0147	L4 × T7
39	CKDHL0089/CKDHL0333//CKLTI0147	L4 × T3
40	CKDHL0089/CKDHL0295//CKLTI0147	L4 × T5
41	CKDHL0159/CKDHL0295//CKLTI0147	L4 × T2
42	CKDHL0089/CML395//CKLTI0147	L4 × T6
43	CML395/CML444//CKLTI0344	L1 × T4
44	CML489/CML444//CKLTI0344	L1 × T1
45	CML312/CML395//CKLTI0344	L1 × T7
46	CKDHL0089/CKDHL0333//CKLTI0344	L1 × T3
47	CKDHL0089/CKDHL0295//CKLTI0344	L1 × T5
48	CKDHL0159/CKDHL0295//CKLTI0344	L1 × T2
49	CKDHL0089/CML395//CKLTI0344	L1 × T6
50	CKDHL0089/CKDHL0295	Check
51	CKDHL0159/CKDHL0295	Check
52	DK8053	Check
53	DK8031	Check
54	Pioneer 3253	Check
55	DH04	Check

#### 4.2.3 Evaluation of the hybrids

Hybrid evaluation was done as described in Section 3.2.4. Agronomic management and data collection were done as described in Sections 3.2.5 and 3.2.6, respectively.

## 4.2.4 Data analysis

### 4.2.4.1 Analyses of variances

The data collected was subjected to PROC GML of SAS to obtain means of all the data collected. The ANOVA equation below was followed based on the model by (Yan and Tinker, 2006b)

Equation 4.11 The ANOVA equation of genotype by environment interaction

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij}$$

Where,

$Y_{ij}$  is the observed mean yield of the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment,

$\mu$  is the general mean,

$G_i$  and  $E_j$  represent the effects of the genotype and environment, respectively,

$\lambda_k$  is the singular value of the  $k^{\text{th}}$  axis in the principal component analysis,

$\alpha_{ik}$  is the eigenvector of the  $i^{\text{th}}$  genotype for the  $k^{\text{th}}$  axis,

$\gamma_{jk}$  is the eigenvector of the  $j^{\text{th}}$  environment for the  $k^{\text{th}}$  axis,

$n$  is the number of principal components in the model, and

$e_{ij}$  is the average of the corresponding random errors.

### 4.2.5 GGE biplot analysis

The data obtained was subjected to GGE biplot analysis software. The effects of environment and their interactions were analyzed for all traits by analysis of variance on each site.



Experimental error and the effects of  $G \times E$  interaction were the standardized residuals, which represented the principal component analysis.

#### **4.2.6 Genotype and Genotype by Environment interaction (GGE) biplot**

The Genotype and Genotype by Environment interaction (GGE) biplot (Yan and Tinker, 2006a) was used to explore patterns produced by the  $G \times E$  interaction in order to discover which genotypes obtained the highest and the lowest yields in each environment and to distinguish mega-environments. Furthermore, in order to determine a mega-environment in a graphical set up, the extreme genotypes of the biplot were joined to form a polygon, and perpendicular lines were drawn on each side of the polygon through the origin. GGE biplot models, including biplot graphics and discrimination of mega-environments were obtained automatically with GGE biplot software (Yan and Tinker, 2006a). The least significant differences for the means were tested at significance level of 5%.

### **4.3 Results**

#### **4.3.1 Analysis of Variance and mean yields**

Combined ANOVA for grain yield and the other measured traits showed significant differences among the genotype (G), environment (E) and genotype  $\times$  environment interaction (GEI) at  $p < 0.001$  (Table 4.2). The mean of sum of squares (SS) showed genotypic differences for the environments were large (about 66.95% of the total SS mean). Sum of squares of genotype  $\times$  environment interaction was a bit higher than that of genotypes indicating the importance of this source of variation.

Table 4.2: Combined ANOVA for grain yield in maize genotypes across environments

Source	Df	SS	MS	F	Total variation (%)
Genotypes	54	554.3	10.3	10.1***	10.3
Environments	7	3610.3	515.8	505.9***	66.9
GxE interactions	378	674.6	1.8	1.8***	12.5
Block (Env)	8	113.2	14.1	13.9***	2.1
Error	432	440.4	1.0		
Grand Mean	6.4				
CV%	15.8				
LSD5%	2.0				
G/GGE	0.5				
Total	879	5392.7			

\*\*\* denotes significance level at  $p < 0.001$ ; LSD- least significant difference; CV- coefficient of variation; G/GGE Genotype and Genotype by environment interaction

#### 4.3.2 General performance across environments and adaptability

The comparison of mean performance across locations showed that the highest yielding entries were 14 and 28 while the lowest yielding were from entries 17, 31 and from all the checks (**Error! Reference source not found.**). Among the locations, Kaguru had the highest mean grain yield of 8.57 kg/ha while Kiboko\_DT had the lowest mean grain yield of 2.61 kg/ha (Table 4.4). There were significant differences among the hybrids for grain yield and yield related traits (Table 4.3) Thirty two hybrids showed average and above grain yield performance (LSD 0.9) while 23 yielded below average. In terms of anthesis silking interval and reaction to leaf diseases, the hybrids and commercial checks were almost similar.

**Error! Reference source not found.** Grand\_M grand mean; LSD- least significant difference; CV- coefficient of variation; Her Herirability; GY grain yield; FWT field weight AD days to 50% anthesis; ASI anthesis silking interval; EH ear height; PH plant height; RL root lodging; SL stem lodging; ET *Turicum leaf blight*; GLS *Gray leaf spot*; MSV *Maize streak virus*; Leaf Sen leaf senescence

**Error! Reference source not found.** The first two principal components explained a total GGE variation of 67% (PC1 55 % and PC2 12.9 %). The biplot of Figure 4.1 explained 67.9% of the environment-centered G by E table. In this study, the angle between Kakamega, Shikusa and Kaguru were positively correlated with regard to well-watered conditions, while Homabay and

Kiboko\_DT were positively correlated under drought, therefore similar in their discrimination of genotypes. Mtwapa, KYUC and Kiboko\_Opt (well-watered sites) explained the variability of the data in terms of principle component 2 (PC2).

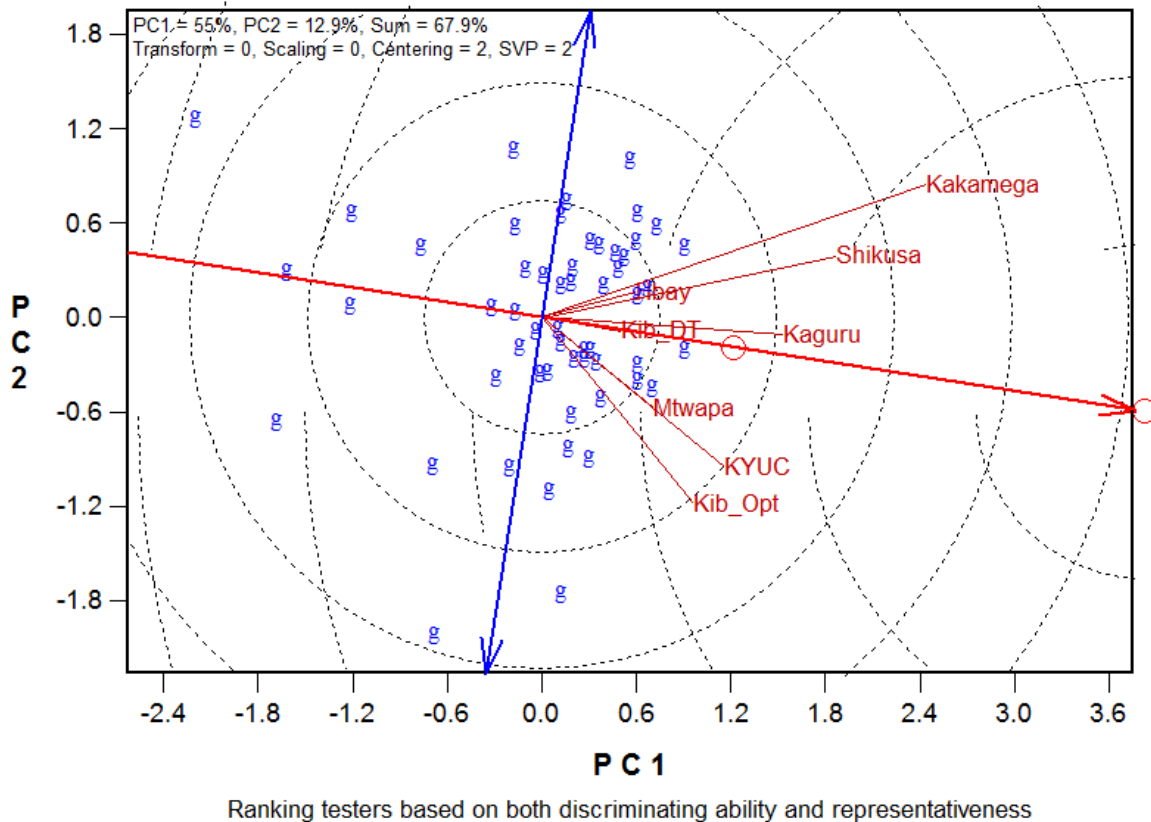


Figure 4.1 Vector view of GGE biplot for relationships of genotypes across study environments

### 4.3.3 Mean performance and stability of genotypes

Entries 14, 28, 46, 15, 21, 20 showed above average yield as revealed in figure 4.2. Genotypes located on the left Figure 4.2 of the perpendicular line showed lower than average yield and they included entries 19, 45, 34, 17, 6 and 23. Entry 16 showed nearly average yield while entry 14 and 28 had the highest mean yields. Entry 53 which was a commercial check had the poorest mean yield.

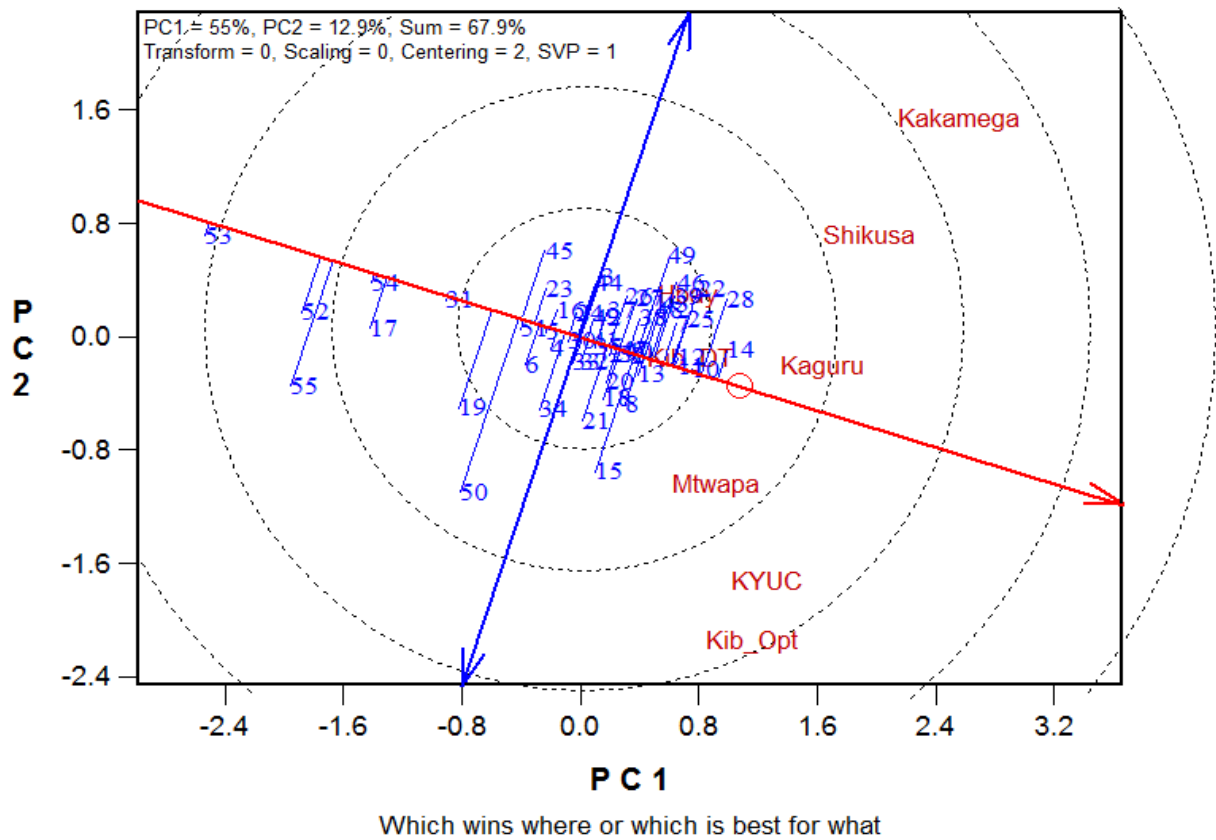


Figure 4.2 Average environment coordination (AEC) of the GGE biplot based on environment scaling for the means performance and stability of genotypes

#### 4.3.4 Winning genotypes and mega-environment

The vertex genotypes in each sector Figure 4.3 portrayed the winning or the poorest in all the environments. Entries 28, 14, 15, 50, 55, 53 and 49 were the vertex entries which gave the highest yield in their respective environments. In this study, the entries fell in seven mega environments but the test environments were in two mega environments with entries 28 and 14 yielding best in the two mega environments of the study locations. The vertex entries 50, 55, 53 were poor yielding in all of the study environments, therefore poorest entries in all environments

followed by entries 15 and 49. This study revealed two mega environments the first consisting of Kakamega, Shikusa and Homabay with entry 28 being the highest yielder (**Error! Reference source not found.**). The second mega-environment consisted of Kiboko\_DT, Kaguru, Mtwapa, KYUC and Kiboko\_Opt, with genotype 14 being the best yielder. Entries 15, 50, 55, 53 and 49 were poor yielders in the study environments.**Error! Reference source not found.**

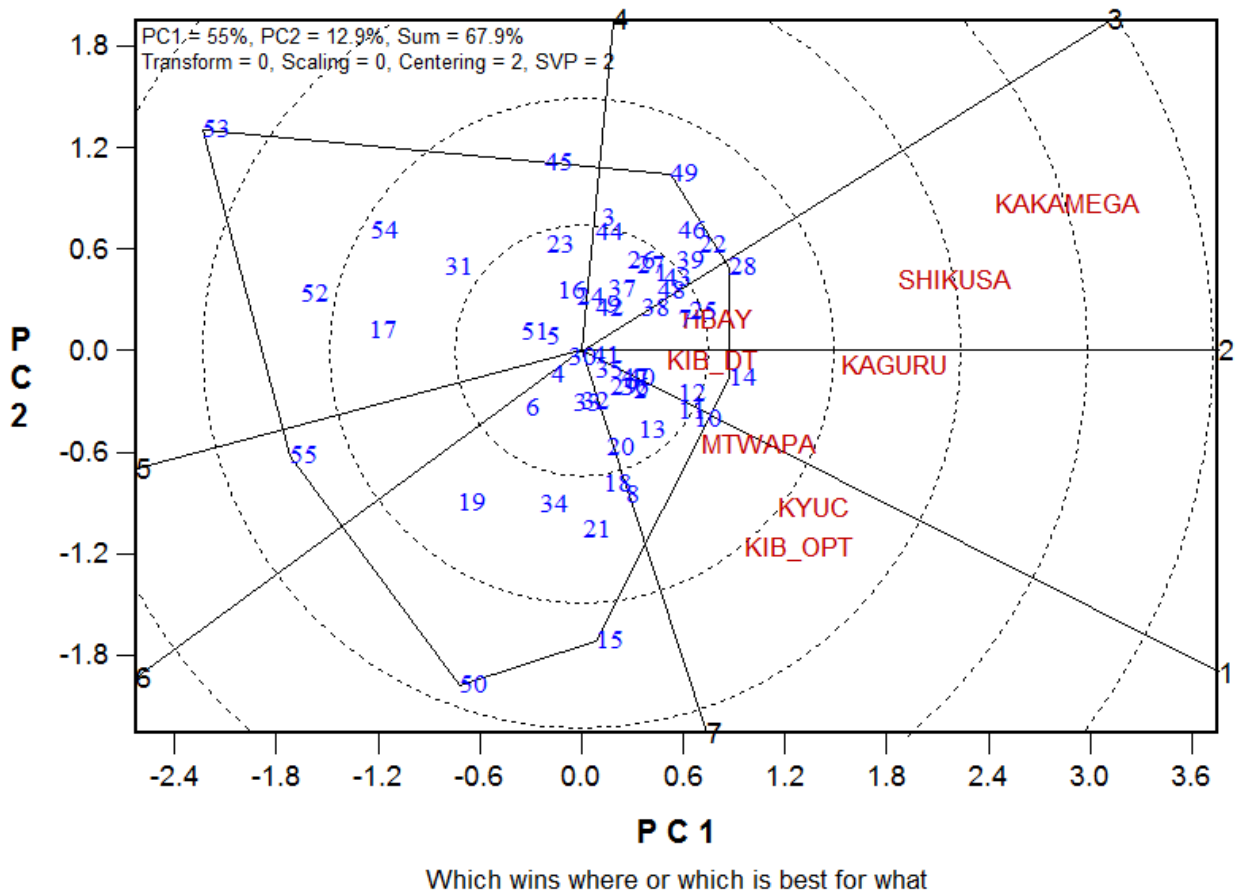


Figure 4.3 Genotypes and Environments (GGE) biplot polygon view based on symmetrical scaling for the which-won-where patter

Table 4.4 Maize grain yield of 55 evaluated genotypes across 8 environments

<b>Entries</b>	<b>Kakamega</b>	<b>KYUC</b>	<b>Hbay</b>	<b>Kib_Opt</b>	<b>Shikusa</b>	<b>Mtwapa</b>	<b>Kaguru</b>	<b>Kib_DT</b>	<b>Mean</b>	<b>CV%<sup>s</sup></b>
<b>1</b>	8.8	6.7	6.6	7.9	9.3	4.1	9.4	3	7	34
<b>2</b>	8.4	6.4	3.9	9.6	8.5	3.3	10.2	3.1	6.7	44
<b>3</b>	8.8	6.1	4.3	6.8	8.9	4.5	8.8	2.3	6.3	40
<b>4</b>	7.7	7.1	3.3	7.8	7.8	4	8	2.9	6.1	37
<b>5</b>	8	6.3	2.9	7.4	7.7	5.3	8	1.8	5.9	41
<b>6</b>	7.2	5.7	4.1	8.9	7	4.3	8.2	2.7	6	37
<b>7</b>	9.4	6.8	4.6	8.6	8.9	4	10.6	2.5	6.9	42
<b>8</b>	7.4	7.7	6	9.5	8.2	4.1	9.5	3.2	7	34
<b>9</b>	8	6.9	5.5	7	8.7	4.8	8.9	3.1	6.6	31
<b>10</b>	8.2	7.2	5.3	9.5	10.3	4.6	10	3.7	7.4	35
<b>11</b>	8.8	7.5	4.4	8.8	8.8	4.6	10.8	2.8	7.1	39
<b>12</b>	9.2	7.2	5.7	9.4	9.3	5	8.8	2.9	7.2	34
<b>13</b>	7.7	8.1	6.6	8.5	9.1	4.5	8.7	2.9	7	32
<b>14</b>	9.3	7.9	4.6	8.1	9.9	5.7	11	3.2	7.5	37
<b>15</b>	7.6	8	3.3	11.1	7.6	5.3	7.4	3.4	6.7	39
<b>16</b>	7.8	6.6	4.8	7.2	8.2	4	8.2	2.2	6.1	36
<b>17</b>	4.9	5	5.3	7.2	6.8	3.7	4.7	1.9	4.9	34
<b>18</b>	7.8	7.6	6.2	9.8	8.4	4.7	7.2	2.2	6.7	35
<b>19</b>	4.6	6.3	4.7	7.9	7.2	5.5	7.7	2.5	5.8	32
<b>20</b>	6.2	7.1	7	8.2	9.9	6	8.4	2.8	7	30
<b>21</b>	7.2	7.3	3.6	10	8.6	4.9	7.6	2.5	6.5	40
<b>22</b>	9.2	6.9	5.2	7.6	10.9	4.6	9.7	2.5	7.1	40
<b>23</b>	8.2	7.3	4.1	6.7	7.6	2.4	7.9	2.6	5.9	42
<b>24</b>	7.9	6.7	5.8	7.8	8.4	3.5	8.3	1.9	6.3	38
<b>25</b>	8.9	7.3	5.8	7	9.1	5.9	10.8	3.2	7.3	33
<b>26</b>	9.8	6.6	4.6	7.7	7.7	4.1	9.1	2.6	6.5	39
<b>27</b>	9	7.1	5.5	8.1	9.5	3.1	8.3	2.4	6.6	41
<b>28</b>	10	6.9	5.2	8.5	11.2	5	9	2.9	7.4	38
<b>29</b>	7.8	6.6	4.3	8.3	8.4	4.7	9.7	3.1	6.6	36
<b>30</b>	7.5	5.8	3.5	8.3	8.8	4.9	8.4	2.3	6.2	40
<b>31</b>	5.1	5.4	4.9	6.6	7.9	2.4	8.1	2.4	5.3	41
<b>32</b>	8.7	6.5	4.1	8.6	6.4	5	9.1	2.5	6.4	38
<b>33</b>	8	6.5	5.4	8.5	7.1	5.3	8.2	2.9	6.5	29
<b>34</b>	5.9	7.3	5	8.9	8.1	4.4	8.3	2.2	6.3	37
<b>35</b>	7.9	7.2	5	8.2	8.8	4.3	8.2	2.2	6.5	37
<b>36</b>	8	7.5	4.6	8.3	9.2	4.5	8.3	3.1	6.7	34
<b>37</b>	8.6	6.1	3.7	7.5	9.4	5.8	7.7	3.1	6.5	35
<b>38</b>	8.2	6.6	4.6	8.2	9.8	3.8	9.6	2.8	6.71	40

Entries	Kakamega	KYUC	Hbay	Kib_Opt	Shikusa	Mtwapa	Kaguru	Kib_DT	Mean	CV% <sup>3</sup>
39	9.8	6.9	5.8	7.8	9	4.6	9.1	3.4	7.1	33
40	8.1	7.3	5.8	8.7	8.1	3.3	10	2.6	6.7	39
41	7.2	7	5	7.2	9	5.1	9.1	2.6	6.5	34
42	8.2	7.8	6.3	6.9	8.1	4.2	8	3.2	6.6	29
43	9.7	5.6	6.8	8.6	8.4	5.5	9.4	2.3	7	35
44	8.6	5	5.4	7	8.7	6.4	8.1	3	6.5	31
45	8.6	5.8	5.9	6.9	8.1	2.8	7	2.7	6	37
46	9.6	5.6	5.1	8	9.4	4.8	10.2	3.1	7	38
47	8.6	5.9	6.4	9	7.5	5.5	9.5	2.4	6.8	34
48	9.4	6	5.5	8.2	9.5	6.1	8.4	2.3	6.9	35
49	9.7	5.6	6.7	7.6	9.9	4.8	8.8	2.9	7	35
50	3.5	8.5	5.1	8.1	6.4	5.9	8.6	1.8	6	41
51	6.7	6.1	5.5	7.5	7.3	3.6	8.7	2.3	6	36
52	3.8	4.1	5.1	6.1	4.7	2.6	7	1.9	4.4	39
53	3.4	2.2	3.3	4.5	4.9	2.6	4.8	1.3	3.4	38
54	4.5	4.4	3.2	5.8	7.4	2.6	7.4	1.6	4.6	46
55	3.4	4.4	3.9	7.2	3.6	4.2	6.8	2.4	4.5	37
<b>LSD5%</b>	2.2	1.4	2.5	1.8	2.3	2.5	2.3	1.1		

Where: KYUC- Kirinyaga University college; Kib\_Opt- Kiboko optimum trial; Kib\_DT- Kiboko drought trial; LSD- least significant difference; CV-coefficiene of variation

#### 4.3.5 Representativeness of test environments

Kaguru was more representative of other test environments in well-watered conditions, while Kiboko\_DT was more representative in water stress conditions Figure 4.4. Kaguru and Kiboko\_DT is representative because of their closeness to the average environment which is a reference benchmark.

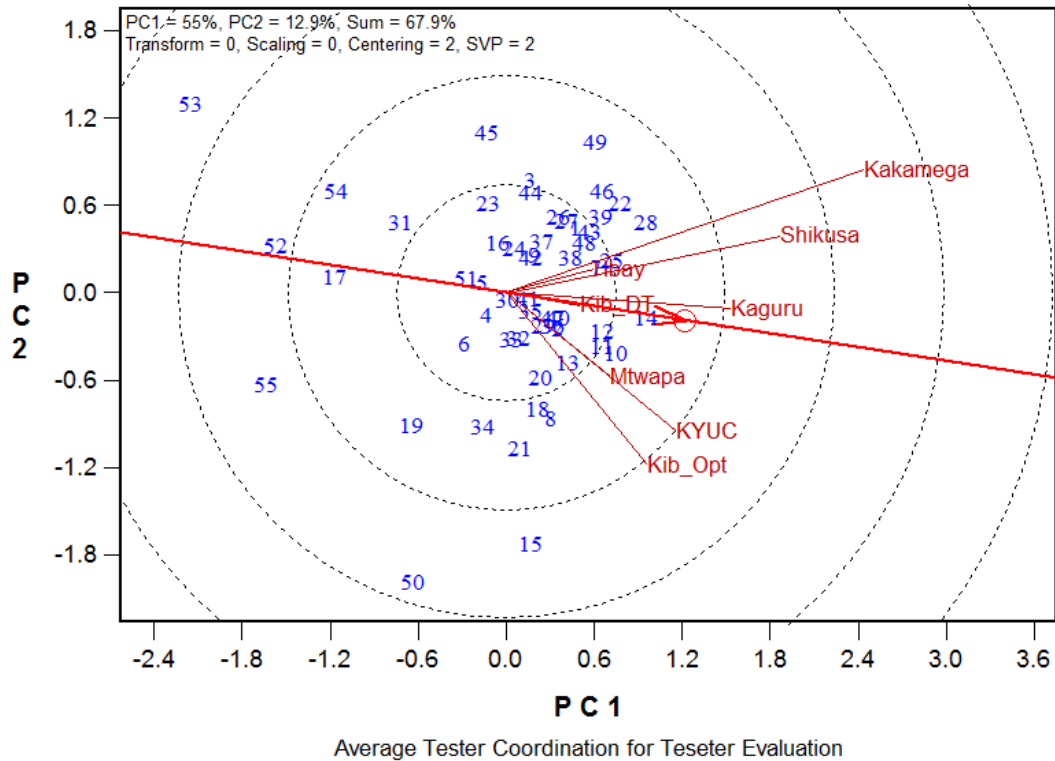


Figure 4.4 GGE biplot showing discrimination and representativeness of the test environments for yield

## 4.4 Discussion

### 4.4.1 Combined analysis of variance and mean comparisons

Combined ANOVA for grain yield and yield related traits (e.g.) showed significant differences among the genotype (G), environment (E) and genotype  $\times$  environment interaction (GEI) at  $p < 0.001$  (Table 4.2). This implied that the genotypes were genetically diverse and a possibility of phenotypic stability in genotypes (Rahnejat and Farshadfar, 2015). The significant interaction of genotype  $\times$  environment effect revealed that the genotypes responded differently to the variation in environmental conditions. Hence, it was necessary to test the tropical/temperate hybrids in multiple locations. The mean of sum of squares (SS) showed genotypic differences for the environments were large (about 67% of the total SS mean). This implies that the



experimental environments were diverse with great differences among environmental means hence the variation in grain yield; therefore, genotypes can be selected for adaptation to specific environments. Other researchers reported similar findings when working with maize inbred lines (Choukan, 2011), barley (Mortazavian *et al.*, 2014) and maize (Farshadfar and Sadeghi, 2014; Rad *et al.*, 2013; Nzuve *et al.*, 2013). The SS of genotype  $\times$  environment interaction was a bit higher than that of genotypes, indicating the importance of this source of variation. Findings by Beyene *et al.* (2011) on stem borer resistant maize in eastern Africa reported higher GEI variance than genotype.

#### **4.4.2 Stability and adaptability for grain yield**

The first two principal components explained a total GGE variation of 67% (PC1 55% and PC2 12.9%) as shown in Figure 4.1. On the x-axis, PC1 was used to estimate yield whereby the genotypes with higher values of PC1 were considered to be more productive. PC2 on y-axis explained the stability of genotypes. The angle between vectors of the genotypes and environment determined the nature of interaction. The angle between Kakamega, Homabay and Shikusa, Kaguru and Kiboko\_DT, Mtwapa, KYUC and Kiboko\_Opt were acute implying a positive interaction. The angle between KARLO Kakamega and Kiboko\_Opt was obtuse therefore a negative interaction (Yan and Tinker, 2006a; Kandus *et al.*, 2010). The right angle was negligible while an angle formed by the vectors of two environments brought out an estimate of their correlation.

#### **4.4.3 Co-relationship among test environments for grain yield**

The relationship is based on an environment centered (centering = 2) G by E table without any scaling (scaling = 0), and it is environment-metric preserving (SVP = 2) and its axes are drawn to scale (default feature of GGE biplot). The biplot of Figure 4.1 explained 67.9% of the environment-centered G by E. In this study, the angle between Kakamega, Shikusa and Kaguru

were positively correlated with regard to well-watered conditions, while Homabay and Kiboko\_DT were positively correlated under drought, therefore similar in their discrimination of genotypes. Mtwapa, KYUC and Kiboko\_Opt (well-watered sites) explained the variability of the data in terms of principle component 2 (PC2). This grouping is based on the cosine angle of vectors theory of genetic correlation (Yan and Tinker, 2006a; Yan *et al.*, 2011). It allows visualization of relationships between environments in ranking genotypes. The wide distance between Kakamega and Kiboko\_Opt measures their dissimilarity in discriminating the genotypes. The presence of close association between KARLO Kakamega and Shikusa; and Mtwapa, KYUC and Kiboko\_Opt suggests that the same information about the entries could be obtained from fewer test environments.

#### **4.4.4 Mean performance and stability of genotypes**

To help in ranking the genotypes based on their performance in environments, a line that passes the biplot origin and the highest yielding environment was drawn. This line is referred to as the average environment axis (AEA) or the average tester coordinate (ATC) was drawn on the x and y-axis (Yan and Tinker, 2006a). Some of the genotypes located on the right hand side of the perpendicular line included the entries 14, 28, 46, 15, 21, 20 and these showed above average yield. Other genotypes located on the left of the perpendicular line showed lower than average yield and they included entries 19, 45, 34, 17, 6 and 23. The genotype which showed nearly average yield was entry 16. Entry 14 and 28 had the highest mean yields while genotype 53 had the poorest mean yield. All the local checks were low yielding with check 50, 55 and 52 demonstrating below average performance (Figure 4.2). The performance of entry 49 and 15 were the most variable, therefore least stable while entries 28, 14, 10, 12, 23, 25, 35 and 41 were more stable with high grain yield in all sites (Figure 4.2; Table 4.4). Entries 30 and 41 showed

performance in both environments (Figure 4.2, Figure 4.3). The presence of close positive association between test environments indicates that similar information could be obtained about the genotypes from a fewer test environments. This is considered as an opportunity to reduce cost of evaluation when resources are minimal (Yan and Tinker, 2006a; Tolessa *et al.*, 2013). The presence of wide obtuse angles and strong negative correlation coefficients indicate existence of a crossover interaction of genotype and environment (Yan and Tinker, 2006a).

#### **4.4.5 Winning genotype and mega-environment**

The average ordinate environment (AOE) represented in the polygon view showed the grouping of genotypes as high or low yielding and their adaptation to the environment (Figure 4.3). Multi-environment trial (MET) data is important for studying the existence of mega-environments in a region through visualization of the which-won-where pattern. The polygon view of a biplot (Yan and Tinker, 2006a) allows a clear interpretation of interaction patterns between genotypes and environments. The vertex genotype in each sector is the one that gave the highest yield in that particular environment. In this study, the vertex entries were 49, 28, 14, 15, 50, 55 and 53. Figure 4.3 also shows grouping of the environments, which suggests the existence of different mega-environments. Therefore, based on this study of eight environments, the biplot analysis suggests that there are two mega-environments. The first mega-environment contains Kakamega, Shikusa and Homabay with entry 28 being the highest yielder (**Figure 4.3, Table 4.4**), while the second mega-environment contained Kiboko\_DT, Kaguru, Mtwapa, KYUC and Kiboko\_Opt, with genotype 14 yielding highest. Entries 15, 50, 55, 53 and 49 though being vertex genotypes were in their own environments which are not in the study, hence showed poorest yields in the study.

#### **4.4.6 Representativeness of test environments**

In well-watered conditions, Kaguru was more representative of other test environments, while Kiboko\_DT was more representative of water stress conditions. Test environments that are both discriminating and representative (e.g. Kiboko\_DT) are good test environments for selecting

generally adapted genotypes. Discriminating but not representative test environments (e.g. KARLO Kakamega and Kiboko\_Opt) are useful for selecting specifically adapted genotypes if the target environments can be divided into mega-environments. Environments with short vectors (non-discriminating environments) are less useful because they provide little discriminating information about the genotypes. The GGE biplot way of measuring representativeness defines an average environment and uses it as a reference or benchmark as observed in Figure 4.3 where the average environment is indicated by small circle. The ideal environment, represented by the small circle with an arrow pointing to it, is the most discriminating of genotypes and yet representativeness of the other tests environments. The correlation for grain yield among locations revealed the highest correlation was in Shikutsa and Kakamega. The two locations can therefore be used interchangeably for yield trial experiments. This however depends on the mean yields of each site as the site with the highest mean yield is most preferred (Table 3.12 and Table 3.13).

Location	Geno	Rep	Mean	Max	SE	LSD5%	SD	Heritability	N_H75	CV%
Kakamega	55	2	7.7	10.0	1.1	2.2	1.7	0.8	1.4	13.7
KYUC	55	2	6.5	8.5	0.7	1.4	1.1	0.8	1.3	10.4
Hbay	55	2	5.0	7.0	1.2	2.5	1.0	0.3	14.6	24.4
Kib_Opt	55	2	8.0	11.1	0.9	1.8	1.1	0.7	2.6	10.9
Shikusa	55	2	8.3	11.2	1.1	2.3	1.4	0.7	3.0	13.7
Mtwapa	55	2	4.5	6.4	1.2	2.5	1.0	0.3	17.5	27.5
Kaguru	55	2	8.6	11.0	1.1	2.3	1.3	0.6	3.8	12.9
Kib_DT	55	2	2.6	3.7	0.6	1.1	0.5	0.4	10.2	21.2

#### 4.5 Conclusion

The present study revealed that the grain yield performances of the tropical/temperate maize hybrids were influenced by the environment. The GEI effect was higher than that of the genotype effect. GGE biplot analysis model was an effective tool for visual interpretation of the magnitude of GEI and stability of the tropical/temperate hybrid maize genotypes. Genotypes with consistently better mean performance were identified (entry 14, 10 and 28). For instance, entry 14 was high yielding and was in the ideal environment, followed by entry 10 then entry 28. Vertex genotypes (28 and 14) were identified as high yielding genotypes for the two different mega-environments of the study. These genotypes positively expressed a highly interactive behavior, contributing more to the GEI effect. These hybrids can be further tested and released for commercial use to hence deal with the recurrent yield losses resulting to food shortage.

High and stable grain yield, appropriate grain quality, earliness, lodging resistance, resistance to diseases, pests and weeds and drought tolerance; are advantageous agronomic traits in maize. The inheritance and heritability of most of these traits have been reported, though some of them are much debated. Tropical maize populations can be improved for these traits using improved maize germplasm.

Table 4.5 Means of top and bottom five tropical-temperate hybrids evaluated under well-watered/optimum conditions during 2014

Entry	Pedigree	BLUE Yield	AD (days)	ASI (days)	Ear Height (cm)	Plant Height (cm)	EPP (#)	GY (GWT) (t/ha)	RL (%)	SL (%)	Turc. Blight (1-5)	GLS (1-5)	MSV (1-5)
14	CKDHL0089/CML395//CKLTI0152	8.5	67.9	0.7	115.0	245.9	1.0	8.1	0.4	3.3	2.0	1.0	0.1
28	CKDHL0089/CML395//CKLTI0200	8.4	66.0	0.6	108.0	241.4	1.0	8.0	1.4	1.8	2.1	1.1	0.0
11	CKDHL0089/CKDHL0333//CKLTI0152	8.3	68.1	0.9	116.6	245.5	1.0	8.5	0.1	1.5	2.0	1.1	0.4
12	CKDHL0089/CKDHL0295//CKLTI0152	8.1	67.9	0.9	112.7	240.9	1.0	9.1	0.7	2.6	2.0	1.1	0.0
7	CKDHL0089/CML395//CKLTI0368	8.1	68.7	0.5	108.8	219.7	1.0	8.2	0.9	2.1	2.0	1.0	0.0
10	CML312/CML395//CKLTI0152	8.0	67.3	1.1	110.6	248.2	1.0	9.2	0.1	1.6	2.0	1.6	0.0
23	CML489/CML444//CKLTI0200	6.6	65.3	0.2	106.6	231.0	0.9	7.3	0.5	2.2	2.1	1.3	0.0
19	CKDHL0089/CKDHL0295//CKLTI0036	6.6	67.7	1.1	131.7	247.1	1.0	7.6	0.0	8.6	2.1	1.5	0.0
45	CML312/CML395//CKLTI0344	6.5	66.0	0.6	118.7	241.9	1.0	7.4	0.0	1.1	2.0	1.1	0.0
31	CML312/CML395//CKLTI0272	6.0	66.6	1.4	109.9	242.2	1.0	6.7	0.8	0.4	2.2	1.5	0.0
17	CML312/CML395//CKLTI0036	5.5	67.7	1.1	116.4	234.7	1.0	7.3	1.2	1.5	2.2	1.5	0.0
54	Pioneer 3253	5.4	67.0	1.6	121.3	245.4	0.9	5.6	0.6	7.1	2.5	1.5	0.4
52	DK8053	4.7	66.4	1.1	116.3	232.5	0.9	6.8	0.8	3.1	3.8	2.0	0.0
55	DH04	4.7	65.8	1.1	114.5	234.2	0.9	6.8	1.9	2.3	3.5	1.4	0.1
53	DK8031	3.6	65.4	4.2	111.9	232.3	0.9	4.2	2.7	3.5	2.3	1.5	0.0
	Loc_Var	2.8	64.4	0.3	979.7	2410.8	0.0	0.0	0.4	22.1	0.0	0.1	0.0
	Ent_Var	0.7	0.9	0.3	80.6	88.8	0.0	0.7	0.0	0.2	0.1	0.0	0.0
	Loc_x_Ent_Var	0.5	0.4	0.1	11.3	8.8	0.0	0.0	0.0	5.5	0.0	0.0	0.0
	Residual_Var	0.7	0.8	0.9	41.0	66.5	0.0	0.5	4.6	12.8	0.1	0.3	0.3
	Grand_Mean	7.3	66.9	0.8	118.1	241.0	1.0	8.0	0.6	2.7	2.2	1.3	0.1
	LSD	1.1	1.1	0.9	6.7	7.9	0.1	1.5	1.8	4.0	0.5	0.7	0.6
	CV	7.5	0.8	60.1	2.9	1.7	3.4	9.6	142.6	75.8	12.3	28.9	267.5
	Heritability	0.8	0.9	0.7	0.9	0.9	0.5	0.7	0.1	0.1	0.7	0.0	0.1

ASI-anthesis silking interval; GLS-gray leaf spot; MSV Maize streak virus; LSD-least significant difference; CV-coefficient of variation; GY grain yield; RL root lodging; SL stem lodging; AD days to 50% anthesis; EPP ears per plant

Table 4.6 Means of top and bottom five tropical-temperate maize hybrids evaluated under water stressed/managed drought conditions during 2014

Entry	Pedigree	BLUE Yield	Yield Rank	AD (days)	ASI (days)	EH (cm)	GY (GWT) (t/ha)	Leaf Senescence (1-9)	Plant Height (cm)	Root Lodging (%)	Plant Stand (#)	Stem Lodging (%)
8	CML395/CML444//CKLTI0152	4.9	1	65.6	1.6	114.2	4.8	5.7	221.9	10.1	38.3	13.2
13	CKDHL0159/CKDHL0295//CKLTI0152	4.8	2	64.6	1.0	112.1	4.7	5.6	217.9	7.7	40.0	31.7
39	CKDHL0089/CKDHL0333//CKLTI0147	4.7	3	64.5	1.0	116.6	4.5	5.1	236.1	2.2	38.5	38.1
1	CML395/CML444//CKLTI0368	4.7	4	64.9	1.0	119.3	4.5	5.0	221.8	5.9	37.6	30.0
42	CKDHL0089/CML395//CKLTI0147	4.6	5	63.5	2.2	117.9	4.5	5.4	233.7	9.2	35.4	30.6
20	CKDHL0159/CKDHL0295//CKLTI0036	4.6	6	63.5	0.5	132.4	4.6	8.1	232.4	4.6	37.9	27.9
28	CKDHL0089/CML395//CKLTI0200	4.1	22	62.1	2.1	106.2	4.1	6.3	225.8	3.8	39.4	27.4
18	CKDHL0089/CKDHL0333//CKLTI0036	4.1	23	64.0	1.5	127.1	4.0	7.6	227.3	10.0	36.4	36.4
22	CML395/CML444//CKLTI0200	4.0	24	61.8	2.5	110.1	4.0	6.3	225.6	10.6	39.7	23.1
41	CKDHL0159/CKDHL0295//CKLTI0147	4.0	25	66.1	0.6	113.3	3.8	5.9	225.0	6.6	37.3	34.4
44	CML489/CML444//CKLTI0344	3.9	26	62.8	0.5	124.4	4.1	6.4	225.8	7.3	37.2	21.3
51	CKDHL0159/CKDHL0295	3.9	27	64.2	1.0	125.5	3.8	5.8	216.4	12.0	38.7	44.4
50	CKDHL0089/CKDHL0295	3.4	41	62.6	4.5	110.4	3.6	8.0	219.3	5.2	34.8	1.1
52	DK8053	3.7	33	66.2	3.1	122.1	3.4	7.0	224.6	6.7	39.7	22.8
55	DH04	2.6	53	58.8	0.3	97.7	3.0	8.9	199.7	5.4	35.0	45.1
54	Pioneer 3253	2.6	54	64.5	4.9	135.2	2.6	7.8	233.9	14.6	40.2	9.2
53	DK8031	2.2	55	61.2	4.4	118.2	2.4	7.6	219.2	7.6	35.2	20.2
	Loc_Var	2.1		9.4	0.1	18.7	2.5	0.0	0.0	141.4	0.5	460.4
	Ent_Var	0.1		1.1	0.4	69.6	0.1	0.6	45.1	0.0	1.3	21.1
	Loc_x_Ent_Var	0.1		2.0	0.4	0.1	0.0	0.1	14.7	0.0	0.4	76.0
	Residual_Var	0.6		1.4	1.7	45.9	0.6	0.4	76.3	70.0	9.6	133.6
	Grand_Mean	3.8		63.6	1.8	116.0	3.8	6.5	224.4	8.5	37.8	28.0
	LSD	1.3		3.4	2.2	10.8	1.3	1.3	16.3	12.8	4.7	26.0
	CV	17.7		2.7	62.6	4.6	16.8	9.8	3.6	75.6	6.2	46.3
	Heritability	0.4		0.4	0.4	0.9	0.4	0.7	0.6	0.0	0.3	0.2

AD days to 50% anthesis; ASI anthesis silking interval; EH ear height; GY grain yield; LSD least significant difference; CV coefficient of variation

## CHAPTER FIVE

### 5 CONCLUSION AND RECOMENDATION

#### 5.1 Conclusion

From the study, it can be concluded that inbred lines CKLT10152 and CKLT10147 were best general combiners for yield increase in well-watered and water stress conditions respectively. Cross L5 × T5 and L2 × T6 exhibited good specific combining ability for grain yield in well-watered and drought conditions respectively, implying that these hybrids can be utilized in heterosis breeding to exploit hybrid vigor. Line 1, line 3 and line 6 could contribute to formation of hybrids consistent earliness; while line 5 contributes to stable high grain yield in both well-watered and water stress conditions. Entries 14, 10 and 28 consistently exhibited better mean grain yield performance and expressed a highly interactive behavior, contributing more to the GEI effect. The two testers used as checks yielded almost similarly in well-watered locations, however, tester CKDHL0159/CKDHL0295 (entry 51) performed better under drought conditions. Shikusa and Kakamega were significantly positively correlated therefore can be used interchangeably for yield trial experiments.

#### 5.2 Recommendation

- For formation of better yielding hybrids in future breeding, testers CKDHL0159/CKDHL0295 and CKDHL0089/CKDHL0295 are highly recommended in formation of hybrids to be used under well-watered and water stress environments.
- The two testers included in this study showed that tester CKDHL0159/CKDHL0295 (entry 51) performed better under drought conditions; therefore, recommended for yield increase in water stress environments.



- The single cross (entry 50) that was used as a check out yielded all other hybrids in Kirinyaga University College, hence it can be recommended to be used to increase grain yields particularly in Kirinyaga (APPENDIX 6).
- The inbred parents used in this study showed good general combining abilities for grain yield and some agronomic traits. These materials consequently have good potential for use as breeding stock in the development of maize hybrids with higher grain yields in various environments
- The tropical-temperate maize hybrids used in this study should be further tested for pests and disease tolerance in future breeding work to further confirm their stability in the tropical ecosystems.
- Future experiments should focus on marker assisted selection for specific genes that influence yield performance traits in the high yielding genotypes.
- The hybrids should be tested for another season to reaffirm the results.

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### APPENDIX 1 ANOVA for hybrids grown under water stress conditions

Source	DF	GY	AD	ASI	EA	EH	EPO	EPP	ER	ET	GLS	GYG
REP	1	41.53***	17.76**	0.02	0.67	3848.43***	0.00	0.08*	78.43*	78.43*	78.43*	41.90***
Site (S)	1	275.03***	1084.29***	4.00	#DIV/0!	5107.14***	0.01***	0.17***	651.03***	651.03***	651.03***	279.23***
Line (L)	6	3.42*	48.28***	4.12*	0.69*	1785.28***	0.03***	0.01	24.07*	24.07*	24.07*	3.58**
Tester (T)	6	0.84	4.59*	3.29*	0.62*	323.87**	0.01***	0.01	16.38	16.38	16.38	0.74
S*L	6	1.80	7.64**	6.95**	#DIV/0!	136.25	0.00*	0.05**	24.07*	24.07*	24.07*	1.50
S*T	6	1.27	0.85	2.32	#DIV/0!	154.09	0.00	0.01	16.38	16.38	16.38	1.31
L*T	36	0.99	2.68	1.72	0.43*	109.34	0.00	0.01	8.50	8.50	8.50	0.99
S*L*T	36	0.97	2.14	1.34	#DIV/0!	78.28	0.00	0.02	8.50	8.50	8.50	0.94
Error	97	1.20	2.05	1.72	0.28	98.39	0.00	0.01	11.71	11.71	11.71	1.17

### APPENDIX 1 ANOVA for hybrids under water stress conditions

Source	DF	HC	LS	MOI	MSV	PA	PH	PS	RL	SAT	SD	SL
REP	1	41.90***	0.65	33.18**	33.18**	33.18**	14425.72***	14425.72***	233.16	0.41	16.58*	18154.41***
Site (S)	1	279.23***	#DIV/0!	4762.38***	4762.38***	4762.38***	10021.44***	10021.44***	14480.23***	72.25**	1220.01***	58880.47***
Line (L)	6	3.58**	6.89***	6.38*	6.38*	6.38*	954.95***	954.95***	101.33	16.38	35.07***	1035.58*
Tester (T)	6	0.74	0.39	3.62	3.62	3.62	421.15*	421.15*	30.98	24.84*	3.18	502.23
S*L	6	1.50	#DIV/0!	5.55	5.55	5.55	529.60*	529.60*	101.33	15.50	4.76	981.16*
S*T	6	1.31	#DIV/0!	7.09*	7.09*	7.09*	383.84	383.84	30.98	6.65	3.93	285.43
L*T	36	0.99	0.59	2.27	2.27	2.27	283.85	283.85	80.54	14.73*	2.94	275.63
S*L*T	36	0.94	#DIV/0!	1.66	1.66	1.66	203.26	203.26	80.54	10.09	2.46	244.43
Error	97	1.17	0.61	3.27	3.27	3.27	229.15	229.15	116.74	9.52	3.07	472.55

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking

## APPENDIX 2 ANOVA for hybrids grown under well-watered environments

Source	DF	GY	AD	ASI	EA	EH	EPO	EPP	ER	ET	GLS	GYG	HC
REP	1	0.36	0.75	2.59*	0.24	9.46	0.01***	0.00	48.67*	0.25	2.00*	0.28	71.83*
Site (S)	5	254.49***	6404.31***	37.00***	6.09***	97474.53***	0.31***	0.29***	1328.86***	0.05	2.22***	#DIV/0!	344.37***
Line (L)	6	8.80***	64.45***	7.63***	2.13***	6757.46***	0.07***	0.02**	58.84***	0.41**	0.54	2.61*	109.15***
Tester (T)	6	10.04***	8.69***	2.14*	1.23**	1472.10***	0.02***	0.01	26.57*	0.27*	0.71*	1.26	46.39***
S*L	30	4.77***	3.67***	1.69**	0.99***	104.06*	0.00***	0.01*	42.68***	0.08	0.89**	#DIV/0!	26.06**
S*T	30	1.43	2.06	0.95	0.37	118.66**	0.00	0.01*	22.38*	0.11	0.38	#DIV/0!	18.27*
L*T	36	2.62***	2.05	0.54	0.75***	197.47***	0.00*	0.01	11.55	0.12	0.18	1.55*	14.85
S*L*T	180	1.13	1.54	0.99	0.25	53.98	0.00	0.00	15.73	0.14	0.21	#DIV/0!	11.61
Error	293	1.12	1.63	0.95	0.37	62.38	0.00	0.01	14.27	0.14	0.30	0.85	11.06

## APPENDIX 2 ANOVA for hybrids grown under Well-watered environments

Source	DF	LS	MOI	MSV	PA	PH	PS	RL	SAT	SD	SL
REP	1	71.83*	20.84*	0.04	0.44	3142.00***	1.00*	7.75	0.04	6.12	45.91*
Site (S)	5	344.37***	1762.79***	1.61**	24.59***	238244.63***	64.00***	35.73***	1006.75***	5763.67***	1960.45***
Line (L)	6	109.15***	31.74***	0.27	6.75***	7225.28***	1.87***	4.88	17.39*	71.49***	40.02**
Tester (T)	6	46.39***	13.11**	0.99*	1.31***	1305.06***	0.21	6.48	46.30***	14.67***	44.13**
S*L	30	26.06**	6.25*	0.36	0.78***	131.57	1.25***	5.36*	3.28	5.20***	35.36***
S*T	30	18.27*	3.48	0.41	0.33	107.62	0.05	5.69*	13.28**	3.95*	51.71***
L*T	36	14.85	2.97	0.33	0.26	322.19***	0.15	2.98	13.21**	2.18	17.83
S*L*T	180	11.61	3.37	0.36	0.29	103.70	0.19	3.82	6.84	2.24	17.82*
Error	293	11.06	3.92	0.35	0.29	113.66	0.21	3.87	6.92	2.36	13.33

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking

**APPENDIX 3 General Combining ability of lines grown under water-stress conditions**

LINE	GY	AD	ASI	EA	EH	EPO	EPP	ER	GYG	LS	MOI
1	0.44*	1.40*	0.01	0.08	11.14***	0.03***	0.01	-0.74	0.51*	-0.37	0.15
2	0.46*	1.74**	-0.24	-0.06	4.63*	0.00	0.03	1.65*	0.48*	-0.44	0.77*
3	-0.01	1.22*	0.33	0.40	8.45**	0.03***	-0.02	-1.33	-0.04	-0.08	0.51
4	0.16	0.99*	-0.45	-0.21	-3.46	0.02**	-0.02	0.07	0.13	-0.44	-0.38
5	0.39	1.13*	0.15	-0.28	-3.38	0.02*	0.01	0.11	0.36	-0.65	0.35
6	-0.35	1.26*	0.58	0.01	-2.82	0.02*	-0.02	-0.04	-0.34	0.85	-0.25
7	-0.16	0.03	-0.38	0.08	11.59***	0.06***	0.00	0.28	-0.13	1.13	0.40

**APPENDIX 3 General Combining ability of lines grown under water-stress conditions**

LINE	PH	RL	SAT	SD	SL
1	9.51*	0.80	0.60	1.39**	-2.06
2	10.24*	1.66	-0.87	1.5**	10.91*
3	-1.53	-1.96	0.74	0.89*	-5.35
4	1.61	-1.94	-0.05	0.54	0.72
5	0.27	2.70	0.53	1.29**	-5.86
6	1.65	0.52	0.28	0.68*	-3.29
7	-1.26	-1.78	1.22*	-0.36	4.93

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turcicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking

**APPENDIX 4 General combining ability of testers grown under water stress environments**

Tester	GY	AD	ASI	EA	EH	EPO	EPP	ER	GYG	LS	MOI
1	-0.10	0.42*	-0.20	0.22	0.88	0.00	-0.01	-0.79	-0.12	0.06	0.19
2	0.03	0.45*	0.19	-0.06	-1.02	-0.01	0.02	1.05	0.00	-0.15	0.49
3	0.07	0.33*	0.05	0.01	0.20	0.00	0.00	-0.60	0.06	-0.01	-0.52
4	0.15	0.28	0.49*	-0.06	2.05	0.01*	-0.01	-0.79	0.14	-0.08	-0.22
5	-0.05	0.62**	0.51*	0.29	6.43*	0.03***	-0.02	0.05	0.00	0.20	0.04
6	0.22	-0.19	0.22	-0.35	4.68*	0.02**	-0.01	0.20	0.21	-0.22	-0.28
7	-0.31	-0.01	-0.28	-0.06	-0.36	0.02**	0.03	0.87	-0.28	0.20	0.31

**APPENDIX 4 General combining ability of testers grown under water stress environments**

Tester	PH	RL	SAT	SD	SL
1	1.63	0.46	0.87*	0.21	1.27
2	0.90	-1.63	1.01*	0.64*	4.33
3	2.02	-1.32	-0.08	-0.29	-0.11
4	-0.49	0.98	-0.22	-0.21	5.59*
5	2.68	0.18	1.81**	-0.11	-0.61
6	1.76	0.41	0.45	0.04	5.86*
7	8.49*	0.92	-0.08	-0.29	-4.61

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turcicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking

**APPENDIX 5 General Combining ability of lines grown under well-watered environments**

LINE	GY	AD	ASI	EA	EH	EPO	EPP	ER	ET	GLS	GYG
1	0.07	0.94***	0.25*	-0.11	7.54***	0.02***	0.02*	0.36	0.12*	-0.11	-0.14
2	-0.09	1.35***	0.32*	0.17	10.05***	0.00	0.02*	0.54	-0.05	-0.06	-0.19
3	0.17	1.04***	-0.17	0.18*	9.10***	0.03***	0.02*	-0.30	0.12*	-0.13	-0.46
4	0.07	0.25	-0.11	0.15	-0.09	0.01**	0.00	0.37	0.02	0.04	-0.36
5	0.54*	0.75***	0.12	-0.07	2.64*	0.02***	0.01	1.07	-0.05	-0.07	0.71
6	-0.35	0.45*	0.22*	-0.15	-0.97	0.01*	0.01	-0.60	0.16**	0.14	-0.02
7	0.41*	0.08	0.52***	-0.17	15.30	0.05***	0.01	1.43*	0.16**	0.16	0.47

**APPENDIX 5 General combining ability of lines grown under well-watered environments**

LINE	HC	LS	MOI	MSV	PA	PH	PS	RL	SAT	SD	SL
1	0.29		0.56*	-0.08	0.09	4.42***	0.42*	-0.17	0.40*	1.19***	-0.56
2	2.13**		0.49*	-0.01	0.33***	-20.18	0.15	0.06	0.31*	1.02***	0.34
3	1.33*		0.36	-0.05	0.29**	2.25*	-0.17	0.13	-0.06	1.21***	-0.53
4	1.09*		0.61*	0.04	0.03	5.77***	0.30	0.45*	0.05	0.14	0.03
5	0.26		-0.25	0.01	0.16*	3.31**	0.08	-0.22	0.72***	0.87***	-0.40
6	1.28*		0.98***	0.13*	0.21*	4.11***	0.22	-0.21	-0.14	-0.23	-0.27
7	1.55*		0.43*	-0.03	0.45***	4.82***	-0.17	-0.04	0.66***	0.60*	1.39*

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turcicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking



**APPENDIX 6 General combining ability of tester grown under well-watered environments**

TESTER	GY	AD	ASI	EA	EH	EPO	EPP	ER	ET	GLS
1	-0.10	0.45**	0.08	0.12*	-0.97	0.00	0.01	-0.22	0.12*	-0.04
2	0.26*	0.07	-0.13	-0.01	0.48	0.00	0.00	0.26	0.13*	0.19*
3	0.38**	0.07	0.08	0.00	-0.99	0.00	-0.01	-0.54	-0.09	-0.13
4	-0.02	0.26*	-0.05	-0.06	2.33*	0.01**	0.00	-0.60	-0.05	0.00
5	0.60***	-0.13	0.25*	0.25***	7.11***	0.03***	-0.01	0.92*	-0.02	0.07
6	0.30*	0.29*	0.02	-0.08	6.83***	0.02***	-0.01	-0.27	0.13*	0.07
7	0.22*	0.49**	0.24*	0.02	-0.58	0.01***	0.01	0.45	0.02	0.17*

**APPENDIX 6 General combining ability of tester grown under well-watered environments**

TESTER	HC	MOI	MSV	PA	PH	PS	RL	SAT	SD	SL
1	1.04*	0.51**	-0.08	0.20**	-0.86	0.05	-0.21	1.59***	0.53*	1.19
2	1.06*	0.45*	0.29**	0.02	1.09	-0.03	-0.13	0.07	-0.06	-0.11
3	0.37	-0.13	-0.08	-0.05	0.76	-0.03	-0.09	0.61	0.15	0.20
4	0.27	0.64**	-0.01	-0.01	0.25	-0.03	0.50*	-0.11	-0.31	0.25
5	1.04*	0.06	-0.05	0.02	-0.28	0.15**	-0.10	0.18	0.12	-0.98
6	-0.71	-0.18	0.01	0.22***	6.24***	0.01	-0.25	0.53	0.31	-0.78
7	0.98*	-0.07	-0.07	0.01	7.19***	0.13**	0.28	0.31	0.73***	0.23

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turcicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking

### APPENDIX 7 Specific combining ability of hybrids grown under well-watered environments

SCA	GY	AD	ASI	EH	ET	GLS	HC	MSV	PH	PS	RL	SAT	SD	SL
L1×T1	0.18	-0.18	-0.07	8.39***	0.09	-0.07	-0.80	0.19	7.09**	0.03	0.15	-0.19	-0.25	-1.41
L1×T2	0.13	0.29	0.15	-2.83	-0.16	0.08	0.99	0.31*	-0.94	0.10	0.21	-0.43	0.43	-0.29
L1×T3	-0.22	-0.05	0.43*	6.49***	0.05	0.36*	0.45	0.07	6.75**	-0.15	-0.28	-0.05	0.38	1.40
L1×T4	0.38	0.29	-0.35	4.19*	0.02	-0.11	-0.22	-0.01	4.36*	0.10	-0.19	1.17*	-0.07	-0.11
L1×T5	-0.43	0.07	-0.07	0.47	-0.02	-0.18	1.22	0.03	4.35*	-0.08	-0.27	-0.37	0.00	0.11
L1×T6	0.00	0.60*	-0.01	-2.68	0.09	-0.18	0.36	-0.02	-0.08	-0.19	0.10	-0.97	-0.60	0.81
L1×T7	-0.03	0.18	-0.08	-1.05	-0.06	0.12	2.00*	0.05	0.66	0.20	0.29	0.84	0.10	-0.52
L2×T1	-0.19	0.29	0.09	-1.15	0.02	-0.12	-0.94	-0.01	-1.00	0.20	-0.40	-0.89	0.37	-0.38
L2×T2	0.60*	0.42	-0.20	6.64***	0.27	0.03	1.81*	0.38*	10.90***	-0.22	0.21	1.12*	0.22	-0.12
L2×T3	0.27	0.58*	0.09	2.11	-0.02	-0.03	-1.45	-0.01	-0.91	0.03	0.42	0.75	0.67*	-1.20
L2×T4	0.51*	-0.08	0.13	-2.20	-0.06	-0.17	0.36	0.17	6.08*	0.03	-0.07	1.87**	0.05	2.33*
L2×T5	0.52*	0.88**	-0.08	5.00**	-0.09	0.27	2.23*	0.21	12.07***	0.35*	-0.51	0.76	0.96**	-0.14
L2×T6	-0.02	-0.38	-0.19	1.03	0.02	-0.23	-0.97	-0.09	3.36	-0.26	0.33	0.57	-0.57	0.77
L2×T7	0.54*	0.06	0.16	1.85	-0.13	0.17	2.59*	0.10	3.45	-0.12	0.01	-0.45	0.22	-1.25
L3×T1	-0.06	-0.08	0.35	-0.36	0.09	0.20	1.03	0.03	-2.45	-0.22	-0.46	1.19*	0.27	-0.12
L3×T2	0.26	0.62*	0.06	2.54	-0.16	0.10	0.54	-0.22	2.71	0.35*	-0.54	-0.55	-0.56	0.21
L3×T3	0.40	0.30	-0.07	-0.45	0.05	0.04	-0.40	0.03	-0.46	0.10	0.76	-0.08	0.23	-0.85
L3×T4	-0.12	0.05	-0.19	-1.12	0.02	-0.10	-0.06	-0.04	-1.81	-0.15	1.30**	-0.45	-0.14	-0.92
L3×T5	0.04	-0.08	0.02	-0.03	0.23	-0.17	-0.78	0.12	0.93	-0.08	-0.36	0.10	-0.07	1.05
L3×T6	0.20	0.50	-0.09	1.75	-0.16	0.08	0.04	0.07	1.11	0.06	-0.20	0.66	0.41	0.78
L3×T7	0.73**	-0.06	-0.08	-2.33	-0.06	-0.07	-0.38	0.01	-0.02	-0.05	-0.50	-0.87	-0.14	-0.15
L4×T1	0.12	0.13	-0.21	-1.22	-0.06	0.03	1.49	-0.06	-2.32	0.31*	-0.31	0.67	-0.08	0.36
L4×T2	0.05	-0.07	-0.08	0.48	0.31*	-0.07	-0.15	0.19	2.47	0.13	0.23	-0.57	-0.15	-1.04
L4×T3	0.75**	-0.15	-0.21	-2.26	-0.09	-0.13	-0.03	-0.06	-1.97	0.13	-0.68	-0.86	-0.37	0.62
L4×T4	-0.12	0.10	-0.08	2.46	0.12	-0.07	-0.74	-0.13	2.60	-0.12	0.27	0.44	0.02	0.45
L4×T5	0.75**	-0.37	0.12	4.64*	0.09	-0.17	-0.76	-0.09	3.20	-0.30	0.03	-0.34	-0.25	-0.21
L4×T6	-0.22	0.05	0.43*	3.64*	0.19	0.26	0.44	0.10	-2.72	-0.15	-0.29	0.30	0.48	-0.66
L4×T7	0.17	0.32	0.03	-0.46	0.05	0.17	-0.24	0.05	-1.26	-0.01	0.76	0.36	0.35	0.48

## APPENDIX 7 Specific combining ability of hybrids grown under well-watered environments

SCA	GY	AD	ASI	EH	ET	GLS	HC	MSV	PH	PS	RL	SAT	SD	SL
L5×T1	0.20	-0.29	0.06	-1.81	0.02	-0.11	-1.10	-0.02	-2.84	-0.22	0.56	1.91**	-0.22	-0.27
L5×T2	-0.06	0.01	0.28	1.10	-0.23	0.04	3.02**	-0.02	1.74	-0.15	0.01	-0.33	0.29	0.07
L5×T3	0.24	-0.07	-0.19	2.11	-0.02	-0.02	0.36	0.10	3.36	0.10	0.22	-0.95	-0.26	0.75
L5×T4	-0.23	0.43	0.11	3.71*	0.19	0.24	-1.10	0.16	-1.67	0.10	-0.35	0.01	0.54	-0.79
L5×T5	0.86**	0.05	0.06	2.39	-0.09	0.27*	-0.89	-0.06	4.05	-0.08	-0.22	0.39	0.11	0.50
L5×T6	0.58*	0.13	-0.29	-1.62	0.27	-0.03	-0.31	-0.11	4.19*	0.31*	-0.06	-0.80	-0.16	-0.92
L5×T7	-0.42	-0.26	-0.03	1.54	-0.13	0.33*	0.03	-0.04	-0.46	-0.05	-0.15	-0.24	-0.29	0.65
L6×T1	0.21	-0.33	-0.13	-2.95	0.05	-0.12	-0.47	-0.15	-1.02	-0.12	0.75	0.86	-0.46	2.14*
L6×T2	-0.02	0.30	-0.16	4.43*	0.30*	-0.18	-1.41	0.85***	5.41*	-0.05	0.25	-0.55	0.13	1.19
L6×T3	-0.10	0.54*	-0.04	1.86	0.02	-0.23	1.74*	-0.15	4.08	-0.05	-0.25	0.17	-0.58	0.34
L6×T4	0.02	0.13	0.00	4.69*	0.27*	0.03	2.52*	-0.22	-3.29	0.20	0.83*	-0.20	0.13	-0.71
L6×T5	0.64*	0.33	0.29	-0.82	-0.06	0.06	-0.16	-0.18	-3.57	0.03	0.52	-0.90	0.62*	-0.14
L6×T6	0.16	0.25	0.10	-0.11	-0.20	0.23	-1.33	0.01	4.72*	0.17	-0.08	0.16	0.35	-0.54
L6×T7	0.36	-0.14	-0.06	2.28	0.16	0.13	-0.89	-0.17	3.11	-0.19	-0.36	0.47	-0.20	2.00*
L7×T1	0.47*	0.46	-0.09	-0.90	-0.20	0.15	0.79	0.01	2.54	0.03	-0.29	3.55***	0.37	3.96***
L7×T2	0.26	-0.32	-0.04	0.92	0.30*	0.05	-1.17	-0.11	-0.49	-0.15	-0.37	1.30*	-0.37	-0.04
L7×T3	0.16	-0.07	-0.01	3.12*	0.02	-0.05	-0.68	0.01	2.65	-0.15	-0.19	1.01	-0.08	-1.06
L7×T4	0.58*	0.90**	0.37	5.07**	-0.02	0.21	-0.75	0.07	5.89*	-0.15	-0.12	0.89	-0.53	-0.25
L7×T5	1.10***	0.88**	-0.34	11.65***	-0.06	-0.06	-0.85	-0.02	12.33***	0.17	0.81*	0.36	0.54	-1.17
L7×T6	0.46*	0.05	0.05	5.27**	-0.20	-0.06	1.78*	0.05	7.24**	0.06	0.21	0.09	0.10	-0.24
L7×T7	0.11	-0.10	0.06	-1.84	0.16	-0.22	0.89	-0.01	5.48*	0.20	-0.04	-0.11	-0.03	-1.20

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking

### APPENDIX 8 Specific combining ability of hybrids grown under water stress environments

SCA	GY	AD	ASI	EA	EH	EPO	EPP	GYG	LS	PH	RL	SAT	SD	SL
L1×T1	0.16	-0.88	0.56	-0.44	7.59*	0.02**	-0.04	0.17	0.94	3.60	-1.19	1.19	-0.32	-0.90
L1×T2	-0.23	0.08	0.92*	0.35	-4.02	-0.01	0.05	-0.23	-0.85	-4.17	-5.87	1.08	1.00	19.76**
L1×T3	0.43	0.37	0.94*	-0.22	2.77	0.00	0.03	0.43	0.51	5.96	-1.55	-0.35	-0.57	-0.67
L1×T4	-0.56	0.51	0.10	-0.16	-2.71	0.00	-0.05	-0.59	-0.42	-3.90	4.87	0.80	0.61	11.23*
L1×T5	0.04	-0.10	0.35	0.49	-0.98	0.00	0.05	0.01	-0.20	-2.20	3.12	0.51	0.25	7.48
L1×T6	0.03	-0.78	-0.12	0.13	-0.71	0.00	0.11*	0.03	0.22	0.10	4.40	-2.13	-0.89	10.84
L1×T7	0.13	0.80	0.87*	-0.15	-1.93	-0.01	0.06	0.18	-0.20	0.60	-3.76	-1.10	-0.07	-8.23
L2×T1	0.99*	1.72**	-0.19	0.71	8.77*	0.00	-0.01	1.00*	0.51	16.02*	2.57	2.85*	1.54*	-0.91
L2×T2	-0.34	0.19	0.17	-0.01	-3.88	-0.01	-0.03	-0.37	0.22	-3.92	0.18	1.55	0.36	-3.90
L2×T3	0.09	-0.03	-0.44	-0.08	1.54	0.00	0.03	0.07	0.58	1.96	0.06	-1.38	-0.46	12.62*
L2×T4	-0.19	0.12	0.35	-0.01	-1.95	0.01	0.03	-0.22	0.15	-5.90	9.59*	2.49*	0.46	2.83
L2×T5	-0.12	-0.99	0.85*	0.13	-3.21	0.02*	-0.04	0.02	-0.13	0.42	8.67*	1.47	-0.14	-10.53
L2×T6	1.15**	-0.92	-0.62	-0.22	7.18*	0.01	0.05	1.15**	-0.70	8.35	-2.79	0.33	1.54*	-5.70
L2×T7	0.39	-0.10	-0.12	-0.51	9.09*	0.01	-0.02	0.35	-0.63	15.10*	-0.95	3.37*	-0.21	5.59
L3×T1	-0.18	0.94	1.51**	-0.26	2.80	0.01*	-0.02	-0.15	-1.35	-0.11	-1.09	0.30	-0.57	-2.57
L3×T2	0.58	0.40	1.15*	-0.48	6.95*	0.01	0.10*	0.57	-0.13	9.87	7.64*	2.31*	-0.75	5.07
L3×T3	0.13	-0.06	0.24	-0.05	-4.27	-0.01	0.02	0.14	0.22	-5.51	-2.12	0.51	0.18	4.67
L3×T4	-0.10	-0.17	0.78	0.52	-2.00	-0.01	0.00	-0.06	-0.20	-2.86	-4.48	-0.35	0.61	-7.44
L3×T5	0.00	0.47	0.03	0.17	7.11*	0.00	-0.06	-0.01	0.01	13.71*	2.06	-0.38	0.50	-8.73
L3×T6	-0.21	-0.45	0.56	0.81	-3.13	0.00	-0.03	-0.23	0.44	-4.99	2.12	0.47	0.11	6.43
L3×T7	-0.23	1.13*	1.06*	-0.48	7.46*	-0.01	-0.01	-0.26	1.01	-10.11	-4.12	1.76	-0.07	2.56
L4×T1	0.23	0.22	0.53	-0.15	-4.55	0.02*	-0.05	0.24	-0.49	-3.13	-2.97	3.58**	0.75	-8.36
L4×T2	0.52	-0.56	-0.37	0.13	5.46	0.01	0.02	0.49	-0.28	6.73	-3.77	1.72	-0.93	9.75
L4×T3	0.63	1.28*	1.03*	0.06	7*	0.02*	0.08	0.61	-0.42	5.60	4.13	-2.20	-0.25	7.63
L4×T4	-0.40	1.12*	-0.19	0.13	-1.36	0.00	-0.07	-0.36	-0.35	-1.63	-0.47	-0.31	0.93	-4.38
L4×T5	-0.29	0.76	0.06	-0.72	1.13	0.01	-0.03	-0.31	0.37	-2.06	6.10	-2.10	0.82	2.12
L4×T6	-0.37	0.08	-0.40	-0.08	-4.36	0.02*	-0.01	-0.36	0.80	1.49	-4.74	1.76	-0.32	-3.26
L4×T7	-0.32	-0.35	-0.65	0.63	-3.32	0.00	0.06	-0.31	0.37	-7.01	1.73	2.45*	-1.00	-3.50

**APPENDIX 8 Specific combining ability of hybrids grown under water stress environments**

SCA	GY	AD	ASI	EA	EH	EPO	EPP	GYG	LS	PH	RL	SAT	SD	SL
L5×T1	0.12	-0.67	-0.08	0.42	-0.02	0.00	0.00	0.10	0.22	3.08	-0.46	2.26*	-0.75	7.50
L5×T2	-0.69	0.05	0.53	0.21	-2.75	0.00	-0.03	-0.66	-0.06	-6.43	-4.54	3.60**	0.57	1.23
L5×T3	-0.45	0.83	0.17	0.13	6.46*	0.02*	-0.02	-0.47	-0.20	-4.68	-0.83	1.97	1.00	-5.28
L5×T4	0.31	-0.53	-0.30	0.20	0.43	0.02*	0.03	0.33	-0.13	-5.29	-4.41	1.87	-0.82	6.10
L5×T5	0.29	-0.88	-0.55	-1.15	3.41	0.01	0.00	0.24	0.08	4.28	5.75	-0.17	1.43*	7.49
L5×T6	0.10	1.19*	-0.26	-0.51	-1.07	0.00	0.02	0.12	0.01	-1.17	-0.20	-0.56	0.93	-9.90
L5×T7	0.32	0.01	0.49	0.71	6.46*	0.00	-0.01	0.33	0.08	10.21*	4.69	-1.78	0.50	-7.12
L6×T1	0.68	0.22	0.24	-0.37	-0.07	-0.01	0.09	0.67	0.22	6.08	-1.64	-1.49	0.46	2.51
L6×T2	-0.27	0.44	-0.15	-0.08	-4.30	0.00	0.09*	-0.26	0.44	-8.81	2.96	1.15	0.29	7.08
L6×T3	-0.05	-0.03	-0.26	0.35	1.73	0.00	-0.02	-0.01	-0.20	3.32	1.37	-0.03	-0.29	13.48*
L6×T4	-0.10	-0.38	-0.47	-0.09	1.00	0.00	0.00	-0.11	0.37	1.83	-2.41	-0.88	-0.86	-1.04
L6×T5	0.17	0.01	0.28	0.06	0.73	-0.01	0.08	0.16	0.08	3.91	-4.53	0.33	0.29	-4.47
L6×T6	-0.08	-0.42	0.56	0.21	5.38	0.02*	-0.02	-0.07	-0.49	2.46	4.14	0.69	0.14	-1.74
L6×T7	-0.35	0.15	-0.19	-0.08	-4.46	0.00	-0.03	-0.38	-0.42	-8.79	0.11	0.22	-0.04	11.15*
L7×T1	-0.03	1.56*	0.45	0.06	3.02	0.00	0.04	-0.03	-0.06	6.49	4.79	2.99*	-1.11	2.73
L7×T2	0.44	-0.60	0.06	-0.15	2.54	-0.01	-0.02	0.47	0.65	6.73	3.40	0.40	-0.54	0.54
L7×T3	0.78*	0.19	0.20	-0.22	-2.30	0.01	0.13*	0.78*	-0.49	-6.65	-1.05	1.47	0.39	-5.49
L7×T4	1.04*	-0.67	-0.26	-0.16	6.59*	-0.01	0.07	1.01*	0.58	17.74**	-2.68	1.37	-0.93	-7.30
L7×T5	-0.09	0.72	1.01*	0.99	8.18*	0.00	-0.01	-0.11	-0.20	18.06**	-3.82	0.33	-0.29	6.65
L7×T6	-0.63	1.30*	0.28	-0.37	-3.29	0.00	0.09*	-0.65	-0.28	-6.26	-2.94	-0.56	1.57*	3.33
L7×T7	0.05	0.62	0.28	-0.15	1.63	0.01	-0.04	0.09	-0.20	-0.01	2.31	-0.03	0.89	-0.46

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turcicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking

APPENDIX 9 Means of tropical-temperate maize hybrids evaluated under well-watered conditions during 2014

Entry	Pedigree	Grain Yield (GWT) (t/ha)	Days to 50% Anthesis (days)	ASI (days)	Ear Height (cm)	Plant Height (cm)	Ears per Plant (#)	Ear Aspect (1-5)	Root Lodg. (%)	Stem Lodg. (%)	Turc. Blight (1-5)	GLS (1-5)	MSV (1-5)
15	CML395/CML444)/(CML539*/OF P27)-3-1-1-2-2-B	10.1	67.7	1.2	144.3	256.3	1	1.8	0.5	2.2	2.2	1.4	0.1
8	CML395/CML444)/(CML495*/OF P9)-6-2-2-2-1-B	9.8	68	0.6	121.1	248.4	1	2.3	0.1	0.4	2.5	1.2	0
18	CKDHL0089/CKDHL0333)/(CML 539*/OFP27)-3-1-1-2-	9.3	66.9	1	134.7	245.8	1	2	0	4.2	2.8	1.3	0.3
21	CKDHL0089/CML395)/(CML539 */OFP27)-3-1-1-2-2-B	9.2	66.9	1.2	135.7	250.3	1	2.2	0.3	3.4	2.3	1.2	0
10	CML312/CML395)/(CML495*/OF P9)-6-2-2-2-1-B	9.2	67.3	1.1	110.6	248.2	1	2.3	0.1	1.6	2	1.6	0
12	CKDHL0089/CKDHL0295)/(CML 495*/OFP9)-6-2-2-2-1	9.1	67.9	0.9	112.7	240.9	1	2.3	0.7	2.6	2	1.1	0
2	CML489/CML444)/([CML312/[T UXPSEQIC1F2/P49-SR]F	9.1	68	0.2	107.8	216.6	1	2.3	0.9	1.8	2	1.5	0.1
40	CKDHL0089/CKDHL0295)/(CML 495*/OFP9)-1-1-2-2-2	9	67.6	0.4	115.7	245.1	1	2.3	0.5	4.1	2	1.3	0
33	CKDHL0089/CKDHL0295)/(CML 537*/OFP106)-5-2-2-3	8.8	66.5	0.9	113.9	243.9	1	1.8	0.9	1.4	2.3	1.3	0
13	CKDHL0159/CKDHL0295)/(CML 495*/OFP9)-6-2-2-2-1	8.8	67.6	0.8	115.2	243.6	1	2.2	0.4	1.9	2.3	1.4	0.3
32	CKDHL0089/CKDHL0333)/(CML 537*/OFP106)-5-2-2-3	8.8	66.8	0.6	122.4	252.6	1	2.2	0.4	3.1	2.8	1.1	1.4
29	CML395/CML444)/(CML537*/OF P106)-5-2-2-3-2-B	8.7	67.1	1	124.4	247.3	1	2.3	0	1.1	2.2	1.6	0.3
36	CML395/CML444)/(CML495*/OF P9)-1-1-2-2-2-B	8.6	67.1	1	122.8	252.7	1	2.4	0.5	1.3	2.5	1.7	0.3
46	CKDHL0089/CKDHL0333)/(CM L312/[TUXPSEQIC1F2/P	8.6	66.3	0.4	123.7	245.9	1	2.3	0.4	2	2	1	0
38	CML312/CML395)/(CML495*/OF P9)-1-1-2-2-2-B	8.5	66.7	0.8	115.4	253.4	0.9	2.5	1	1.6	2.3	1.1	0
47	CKDHL0089/CKDHL0295)/(CM L312/[TUXPSEQIC1F2/P	8.5	66.4	0.5	132	250.8	1	1.8	0.3	1.4	2	1.1	0.1
11	CKDHL0089/CKDHL0333)/(CML 495*/OFP9)-6-2-2-2-1	8.5	68.1	0.9	116.6	245.5	1	2.3	0.1	1.5	2	1.1	0.4
6	CKDHL0159/CKDHL0295)/(CM L312/[TUXPSEQIC1F2/P4	8.4	67.8	0.4	108.5	216.7	1	2.7	1.1	5.6	2	1.1	0.3

Entry	Pedigree	Grain Yield (GWT) (t/ha)	Days to 50% Anthesis (days)	ASI (days)	Ear Height (cm)	Plant Height (cm)	Ears per Plant (#)	Ear Aspect (1-5)	Root Lodg. (%)	Stem Lodg. (%)	Turc. Blight (1-5)	GLS (1-5)	MSV (1-5)
24	CML312/CML395)/(CML495*/OF P14)-8-2-6-1-2-B	8.4	65.8	0.7	103.4	241.4	0.9	2.5	0	2.3	2.2	1.1	0.1
48	CKDHL0159/CKDHL0295)/([CML L312/[TUXPSEQ]C1F2/P	8.3	65.8	0	133	250.8	1	1.9	0.6	2	2	1	0
34	CKDHL0159/CKDHL0295)/(CML 537*/OFP106)-5-2-2-3	8.3	66.2	0.8	116.3	243.5	1	2.1	0	1.5	1.9	1.4	0
20	CKDHL0159/CKDHL0295)/(CML 539*/OFP27)-3-1-1-2-	8.3	66	1.5	139.9	250.1	1	2.1	0.7	4.5	2.3	1.6	0.1
27	CKDHL0159/CKDHL0295)/(CML 495*/OFP14)-8-2-6-1-	8.3	65.7	0.3	110.8	240.2	0.9	2.6	2.5	1.4	2	0.9	0
35	CKDHL0089/CML395)/(CML537 */OFP106)-5-2-2-3-2-	8.2	66.1	0.9	116.6	247.6	1	2.2	0	2.7	2.2	1	0
37	CML489/CML444)/(CML495*/OF P9)-1-1-2-2-2-B	8.2	66.8	0.3	117.7	241.4	1	2.5	2.1	3.1	2.2	1.7	0.1
7	CKDHL0089/CML395)/([CML312 /[TUXPSEQ]C1F2/P49-S	8.2	68.7	0.5	108.8	219.7	1	2.5	0.9	2.1	2	1	0
50	CKDHL0089/CKDHL0295)	8.2	69.9	0.6	114.2	231.3	1	2.1	0.1	3.4	2	1	0.1
14	CKDHL0089/CML395)/(CML495 */OFP9)-6-2-2-2-1-B	8.1	67.9	0.7	115	245.9	1	2.3	0.4	3.3	2	1	0.1
30	CML489/CML444)/(CML537*/OF P106)-5-2-2-3-2-B	8.1	66	0.6	117.6	239.6	1	2.3	0.2	4.5	2.5	1.7	0
1	CML395/CML444)/([CML312/[T UXPSEQ]C1F2/P49-SR]F	8.1	68.4	0.2	115.9	231.1	1	2.5	0.7	2.6	2.2	1	0
28	CKDHL0089/CML395)/(CML495 */OFP14)-8-2-6-1-2-B	8	66	0.6	108	241.4	1	2.2	1.4	1.8	2.1	1.1	0
41	CKDHL0159/CKDHL0295)/(CML 495*/OFP9)-1-1-2-2-2	7.8	66.8	0.4	122.7	250.5	1	2.5	1.8	3.4	2.2	1.3	0
16	CML489/CML444)/(CML539*/OF P27)-3-1-1-2-2-B	7.8	66.4	1	132.3	234.8	1	2.1	0.6	2.6	2.5	1.3	0
3	CML312/CML395)/([CML312/[T UXPSEQ]C1F2/P49-SR]F	7.8	67.4	0.5	106.5	235.6	1	2.4	0	1.1	2	1.5	0.3
39	CKDHL0089/CKDHL0333)/(CML 495*/OFP9)-1-1-2-2-2	7.7	67.4	0.4	118.5	250.1	1	2.5	1.1	1.5	2	1.1	0.6
43	CML395/CML444)/([CML312/[T UXPSEQ]C1F2/P49-SR]	7.6	65.7	0.5	129.2	250.1	0.9	2.3	0.2	2.2	2.2	1	0
19	CKDHL0089/CKDHL0295)/(CML 539*/OFP27)-3-1-1-2-	7.6	67.7	1.1	131.7	247.1	1	2.1	0	8.6	2.1	1.5	0
26	CKDHL0089/CKDHL0295)/(CML 495*/OFP14)-8-2-6-1-	7.6	65.9	0.9	107.4	236.3	1	2.7	0	3.2	2	1.3	0
42	CKDHL0089/CML395)/(CML495	7.5	67	0.4	116.3	248.9	1	2.8	0.2	3.4	2	1.1	0

Entry	Pedigree	Grain Yield (GWT) (t/ha)	Days to 50% Anthesis (days)	ASI (days)	Ear Height (cm)	Plant Height (cm)	Ears per Plant (#)	Ear Aspect (1-5)	Root Lodg. (%)	Stem Lodg. (%)	Turc. Blight (1-5)	GLS (1-5)	MSV (1-5)
	*/OFP9)-1-1-2-2-2-B												
9	CML489/CML444)/(CML495*/OFP9)-6-2-2-2-1-B	7.4	67.1	0.5	115.6	237.1	1	2.3	0.5	2.8	2	1	0
4	CKDHL0089/CKDHL0333)/([CML312/[TUXPSEQ]C1F2/P4	7.4	68.7	-0.1	102.3	212.8	1	2.8	0.7	2.8	2.4	1.1	0
44	CML489/CML444)/([CML312/[TUXPSEQ]C1F2/P49-SR]	7.4	65.3	0.1	124.5	239.9	0.9	2.2	0.9	1.8	1.9	1.4	0
45	CML312/CML395)/([CML312/[TUXPSEQ]C1F2/P49-SR]	7.4	66	0.6	118.7	241.9	1	2.8	0	1.1	2	1.1	0
23	CML489/CML444)/(CML495*/OFP14)-8-2-6-1-2-B	7.3	65.3	0.2	106.6	231	0.9	3	0.5	2.2	2.1	1.3	0
17	CML312/CML395)/(CML539*/OFP27)-3-1-1-2-2-B	7.3	67.7	1.1	116.4	234.7	1	3.1	1.2	1.5	2.2	1.5	0
49	CKDHL0089/CML395)/([CML312/[TUXPSEQ]C1F2/P49-	7.3	66.2	0.9	120.2	241.7	0.9	2.4	0	3.3	2	1.3	0
51	CKDHL0159/CKDHL0295)	7.2	67.9	0.4	123.9	232.7	1	2	2	6.1	1.9	1.1	0.4
5	CKDHL0089/CKDHL0295)/([CML312/[TUXPSEQ]C1F2/P4	7	69.3	0.5	106.9	222.3	1	2.6	0	3.6	2	1	0
22	CML395/CML444)/(CML495*/OFP14)-8-2-6-1-2-B	7	66.6	0.4	117.4	247.7	1	2.3	0.3	2.2	2	1.4	0.1
55	DH04	6.8	65.8	1.1	114.5	234.2	0.9	2.9	1.9	2.3	3.5	1.4	0.1
25	CKDHL0089/CKDHL0333)/(CML495*/OFP14)-8-2-6-1-	6.8	65.7	0.4	111.2	242.6	1	2.4	0	2.4	2	1.1	0.1
52	DK8053	6.8	66.4	1.1	116.3	232.5	0.9	3.2	0.8	3.1	3.8	2	0
31	CML312/CML395)/(CML537*/OFP106)-5-2-2-3-2-B	6.7	66.6	1.4	109.9	242.2	1	2.7	0.8	0.4	2.2	1.5	0
54	Pioneer 3253	5.6	67	1.6	121.3	245.4	0.9	3.2	0.6	7.1	2.5	1.5	0.4
53	DK8031	4.2	65.4	4.2	111.9	232.3	0.9	3.7	2.7	3.5	2.3	1.5	0
	Grand_Mean	8	66.9	0.8	118.1	241	1	2.4	0.6	2.7	2.2	1.3	0.1
	LSD	1.5	1.1	0.9	6.7	7.9	0.1	0.5	1.8	4	0.5	0.7	0.6
	CV	9.6	0.8	60.1	2.9	1.7	3.4	10.4	142.6	75.8	12.3	28.9	267.5



APPENDIX 10 Means of tropical-temperate maize hybrids evaluated under managed drought conditions during 2014

Entry	Pedigree	Grain Yield (GWT) (t/ha)	Days to 50% Anthesis (days)	ASI (days)	Ear Height (cm)	Plant Height (cm)	Root Lodg. (%)	Stem Lodg. (%)	Grain Yield (GWT) (t/ha)	Leaf Senescence (1-9)	Plant Stand (#)
8	(CML395/CML444)//(CML495*/OFP9)-6-2-2-2-1-B	4.8	65.6	1.6	114	222	10.1	13.2	4.8	5.7	38.3
13	(CKDHL0159/CKDHL0295)//(CML495*/OFP9)-6-2-2-2-1	4.7	64.6	1	112	218	7.7	31.7	4.7	5.6	40
20	(CKDHL0159/CKDHL0295)//(CML539*/OFP27)-3-1-1-2-	4.6	63.5	0.5	132	232	4.6	27.9	4.6	8.1	37.9
43	(CML395/CML444)//([CML312/[TUXPSEQ]C1F2/P49-SR]	4.6	60.9	1.8	133	238	13.6	27.2	4.6	6.1	37
39	(CKDHL0089/CKDHL0333)//(CML495*/OFP9)-1-1-2-2-2	4.5	64.5	1	117	236	2.2	38.1	4.5	5.1	38.5
49	(CKDHL0089/CML395)//([CML312/[TUXPSEQ]C1F2/P49-	4.5	62.5	0.8	126	235	6.8	23.3	4.5	5.8	37.8
42	(CKDHL0089/CML395)//(CML495*/OFP9)-1-1-2-2-2-B	4.5	63.5	2.2	118	234	9.2	30.6	4.5	5.4	35.4
1	(CML395/CML444)//([CML312/[TUXPSEQ]C1F2/P49-SR]F	4.5	64.9	1	119	222	5.9	30	4.5	5	37.6
47	(CKDHL0089/CKDHL0295)//([CML312/[TUXPSEQ]C1F2/P	4.4	62.2	1.9	132	232	6.1	18.1	4.4	7	38.4
12	(CKDHL0089/CKDHL0295)//(CML495*/OFP9)-6-2-2-2-1	4.4	64.3	1.5	113	231	10.1	26.1	4.4	6	39.6
9	(CML489/CML444)//(CML495*/OFP9)-6-2-2-2-1-B	4.4	65	1.9	117	226	16.4	16.2	4.4	6.1	36.2
10	(CML312/CML395)//(CML495*/OFP9)-6-2-2-2-1-B	4.3	62.8	1.8	107	229	15.1	27.9	4.3	6.1	40.1
46	(CKDHL0089/CKDHL0333)//([CML312/[TUXPSEQ]C1F2/P	4.3	62.5	2.8	126	234	3.2	12.8	4.3	4.9	38.5
45	(CML312/CML395)//([CML312/[TUXPSEQ]C1F2/P49-SR]	4.3	61.9	2.6	119	231	10.1	30.5	4.3	5.6	40.7
27	(CKDHL0159/CKDHL0295)//(CML495*/OFP14)-8-2-6-1-	4.3	62.1	2.1	107	219	1.3	23.8	4.3	6.1	38.1
40	(CKDHL0089/CKDHL0295)//(CML495*/OFP9)-1-1-2-2-2	4.2	64.9	1.5	111	225	6.6	24.2	4.2	5.6	40.4
36	(CML395/CML444)//(CML495*/OFP9)-1-1-2-2-2-B	4.2	64.3	1	119	238	1	15.5	4.2	6.3	40.4
48	(CKDHL0159/CKDHL0295)//([CML312/[TUXPSEQ]C1F2/P	4.1	62.6	1.4	125	228	14.6	42.7	4.1	5.3	39
28	(CKDHL0089/CML395)//(CML495*/OFP14)-8-2-6-1-2-B	4.1	62.1	2.1	106	226	3.8	27.4	4.1	6.3	39.4
44	(CML489/CML444)//([CML312/[TUXPSEQ]C1F2/P49-SR]	4.1	62.8	0.5	124	226	7.3	21.3	4.1	6.4	37.2
25	(CKDHL0089/CKDHL0333)//(CML495*/OFP14)-8-2-6-1-	4.1	63.7	1	109	227	11.9	30	4.1	5.6	35.2
22	(CML395/CML444)//(CML495*/OFP14)-8-2-6-1-2-B	4	61.8	2.5	110	226	10.6	23.1	4	6.3	39.7
18	(CKDHL0089/CKDHL0333)//(CML539*/OFP27)-3-1-1-2-	4	64	1.5	127	227	10	36.4	4	7.6	36.4
38	(CML312/CML395)//(CML495*/OFP9)-1-1-2-2-2-B	4	64.5	1.8	112	230	12.6	32.8	4	6.3	37.5

Entry	Pedigree	Grain Yield (GWT) (t/ha)	Days to 50% Anthesis (days)	ASI (days)	Ear Height (cm)	Plant Height (cm)	Root Lodg. (%)	Stem Lodg. (%)	Grain Yield (GWT) (t/ha)	Leaf Senescence (1-9)	Plant Stand (#)
14	(CKDHL0089/CML395)//(CML495*/OFP9)-6-2-2-2-1-B	4	64.9	2.1	109	229	8.4	25.8	4	5.6	40.1
26	(CKDHL0089/CKDHL0295)//(CML495*/OFP14)-8-2-6-1-	3.9	63.6	0.2	112	230	7.9	30	3.9	5.3	37.7
19	(CKDHL0089/CKDHL0295)//(CML539*/OFP27)-3-1-1-2-	3.9	61.9	1.6	134	232	14.1	28.4	3.9	7.6	32.6
51	(CKDHL0159/CKDHL0295)	3.8	64.2	1	125	216	12	44.4	3.8	5.8	38.7
41	(CKDHL0159/CKDHL0295)//(CML495*/OFP9)-1-1-2-2-2	3.8	66.1	0.6	113	225	6.6	34.4	3.8	5.9	37.3
37	(CML489/CML444)//(CML495*/OFP9)-1-1-2-2-2-B	3.7	64.2	0.2	111	215	6.7	23.9	3.7	6.4	35.3
11	(CKDHL0089/CKDHL0333)//(CML495*/OFP9)-6-2-2-2-1	3.7	65	2.5	113	226	6.6	26.8	3.7	5	34.1
33	(CKDHL0089/CKDHL0295)//(CML537*/OFP106)-5-2-2-3	3.7	63.4	2.2	109	226	9	28.3	3.7	7.4	35.8
24	(CML312/CML395)//(CML495*/OFP14)-8-2-6-1-2-B	3.7	62.6	2.5	105	236	6.6	19.3	3.7	6.6	40.1
50	(CKDHL0089/CKDHL0295)	3.6	62.6	4.5	110	219	5.2	1.1	3.6	8	34.8
15	(CML395/CML444)//(CML539*/OFP27)-3-1-1-2-2-B	3.6	64.4	1.7	131	225	6.3	29.8	3.6	7.6	36.1
35	(CKDHL0089/CML395)//(CML537*/OFP106)-5-2-2-3-2-	3.6	62.1	2.2	113	229	10.1	15.4	3.6	6.8	37.8
29	(CML395/CML444)//(CML537*/OFP106)-5-2-2-3-2-B	3.5	61.8	3	119	230	12.5	21.2	3.5	6.9	39
17	(CML312/CML395)//(CML539*/OFP27)-3-1-1-2-2-B	3.5	64	0.7	114	211	4.4	38.9	3.5	7.2	39.1
34	(CKDHL0159/CKDHL0295)//(CML537*/OFP106)-5-2-2-3	3.4	62.4	1.2	117	228	9.5	29.9	3.4	7.3	37.4
52	DK8053	3.4	66.2	3.1	122	225	6.7	22.8	3.4	7	39.7
3	(CML312/CML395)//([CML312/[TUXPSEQ]C1F2/P49-SR]F	3.4	63.9	2.8	103	220	2.9	32	3.4	6.2	40.3
2	(CML489/CML444)//([CML312/[TUXPSEQ]C1F2/P49-SR]F	3.4	65.4	0.9	118	219	9.3	42.1	3.4	5.4	39.8
16	(CML489/CML444)//(CML539*/OFP27)-3-1-1-2-2-B	3.4	64	1.3	126	213	9	20.8	3.4	7.6	36.8
31	(CML312/CML395)//(CML537*/OFP106)-5-2-2-3-2-B	3.4	62.3	3.1	103	227	1.4	19.8	3.4	7.8	39.9
32	(CKDHL0089/CKDHL0333)//(CML537*/OFP106)-5-2-2-3	3.3	62.8	2.2	109	221	8.2	31.1	3.3	7.7	38.6
21	(CKDHL0089/CML395)//(CML539*/OFP27)-3-1-1-2-2-B	3.3	63.5	1.3	127	228	6.3	28.8	3.3	6.8	37.6
23	(CML489/CML444)//(CML495*/OFP14)-8-2-6-1-2-B	3.3	61.1	2.8	103	208	4.8	25.6	3.3	8	40.2
6	(CKDHL0159/CKDHL0295)//([CML312/[TUXPSEQ]C1F2/P4	3.2	65.9	1.3	112	210	21	50.1	3.2	6	34.4
7	(CKDHL0089/CML395)//([CML312/[TUXPSEQ]C1F2/P49-S	3.2	65.4	1.1	110	215	5.2	50.9	3.2	6.7	35.6
55	DH04	3	58.8	0.3	98	200	5.4	45.1	3	8.9	35
4	(CKDHL0089/CKDHL0333)//([CML312/[TUXPSEQ]C1F2/P4	2.9	66	1.8	109	215	8	50.4	2.9	6.5	37.7

Entry	Pedigree	Grain Yield (GWT) (t/ha)	Days to 50% Anthesis (days)	ASI (days)	Ear Height (cm)	Plant Height (cm)	Root Lodg. (%)	Stem Lodg. (%)	Grain Yield (GWT) (t/ha)	Leaf Senescence (1-9)	Plant Stand (#)
30	(CML489/CML444)//(CML537*/OFP106)-5-2-2-3-2-B	2.8	62.4	1.6	111	213	12.5	31.4	2.8	6.8	38.5
54	Pioneer 3253	2.6	64.5	4.9	135	234	14.6	9.2	2.6	7.8	40.2
53	DK8031	2.4	61.2	4.4	118	219	7.6	20.2	2.4	7.6	35.2
5	(CKDHL0089/CKDHL0295)//([CML312/[TUXPSEQ]C1F2/P4	2.3	67.2	1	103	202	15.9	32.7	2.3	6.6	33.4
	Grand_Mean	3.8	63.6	1.8	116	224.4	8.5	28	3.8	6.5	37.8
	LSD	1.3	3.4	2.2	10.8	16.3	12.8	26	1.3	1.3	4.7
	CV	16.8	2.7	62.6	4.6	3.6	75.6	46.3	16.8	9.8	6.2

## APPENDIX 11 Means of yield and agronomic traits for Kaguru

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	MOI	PH	RL	SAT	SD	SL	EA	PA	HC
(CKDHL0089/CML395)/(CKLTI0152)	14	11	71.9	0.1	131.8	0.5	1.1	8.1	27.7	263.7	-0.8	37	71.5	0	2.5	1.8	5.1
(CKDHL0089/CKDHL0333)/(CKLTI0152)	11	10.8	72.1	0	133.4	0.5	1	9.4	25.4	268.9	-0.8	36.1	71.5	0	2.5	2	18.2
(CKDHL0089/CKDHL0333)/(CKLTI0200)	25	10.7	71	-1.1	124.2	0.5	1	2	27.8	265.3	0.5	36.2	70	0	1.9	1.5	8.4
(CKDHL0089/CML395)/(CKLTI0368)	7	10.7	74.4	-0.1	113.9	0.5	1.1	0.7	27.5	237.4	0	37.6	74.5	0	1.5	2	5.3
(CKDHL0089/CKDHL0333)/(CKLTI0344)	46	10	70.3	-0.1	144	0.5	1	4.7	27.5	272.8	-0.7	38.2	70	0	2.5	3.1	5
(CML489/CML444)/(CKLTI0368)	2	10	72.7	0.5	122.7	0.5	1.1	4.5	26.1	243.6	2.9	37.5	73.5	0	2	1.5	16.2
(CML395/CML444)/(CKLTI0272)	29	10	71.8	0.5	151.9	0.5	1.1	0.7	21.8	278.4	0.4	38.2	72.5	0	1.5	3.1	2.3
(CML395/CML444)/(CKLTI0152)	8	9.9	71.9	1	144.4	0.5	1	9.5	22.8	275.7	-0.1	37.5	73	0	2.1	3	1.3
(CKDHL0089/CKDHL0295)/(CKLTI0147)	40	9.8	73	-0.1	137.1	0.5	1.1	11.4	26.1	273.4	2	36	73	0	2.4	1.9	-1.1
(CML395/CML444)/(CKLTI0200)	22	9.6	71.1	-1.9	139	0.5	1	2.9	25.1	275.6	0.5	36	69.5	0	2.5	2.5	0.1
(CML395/CML444)/(CKLTI0344)	43	9.5	69.2	-1	142.5	0.5	1	1.5	25.1	274	-0.1	35.9	68.5	1.3	3	2.8	5.1
(CML395/CML444)/(CKLTI0368)	1	9.5	72.1	-0.4	133.5	0.5	1	2.6	24.1	262.5	-0.1	37.9	71.5	0	2	2.8	6.3
(CKDHL0159/CKDHL0295)/(CKLTI0147)	41	9.4	70.4	0.3	138.9	0.5	1	3.3	22.8	273.3	10.9	37.7	70.5	1.3	2.4	3	0.2
(CML312/CML395)/(CKLTI0152)	10	9.3	72	-0.1	126	0.5	1	14.9	25.2	273.2	0	37.9	72	0	2.5	1.5	5.4
(CML312/CML395)/(CKLTI0147)	38	9.2	70.2	1	126.1	0.5	1	12.5	24.8	279.1	0.1	36.3	71.5	0	3	2.5	-0.6
(CKDHL0089/CML395)/(CKLTI0344)	49	9.2	70.2	-0.6	138.9	0.5	1	5.3	23.9	268.4	0.3	38.1	69.5	1.3	2	3.1	6.1
(CKDHL0089/CML395)/(CKLTI0200)	28	9.2	70.4	-1	119	0.5	1	2.6	22.4	265.6	3.8	37.4	70	0	2	2	3.2
(CKDHL0089/CKDHL0333)/(CKLTI0272)	32	9.1	71.3	-0.1	134.8	0.5	1	3.1	26.1	269.8	-0.1	37.5	71.5	0	2	3	4.5
(CKDHL0159/CKDHL0295)/(CKLTI0152)	13	8.9	71.7	0.4	136.8	0.5	1	4.2	24.1	274	-0.4	36.9	72	0	2	2.5	5
(CKDHL0089/CKDHL0295)/(CKLTI0200)	26	8.9	70.2	0.4	118.1	0.4	1	3.2	27.6	268.1	-0.4	37.8	71	0	3	1.9	2.3
(CKDHL0089/CKDHL0333)/(CKLTI0147)	39	8.9	72.5	-0.4	139.2	0.5	1.1	2.8	25.4	276.3	4.8	37.8	72	0	2.5	2.6	3.3
(CML312/CML395)/(CKLTI0368)	3	8.8	71.1	0.2	112.8	0.4	1.1	2.7	25.2	252.6	0.1	37.1	71	0	2.1	1.9	12.8
(CKDHL0089/CKDHL0295)/(CKLTI0344)	47	8.8	71.4	-0.4	161	0.6	1	10.2	27.2	281.7	0.2	37.9	71	0	1.6	2.9	-1.5
(CKDHL0159/CKDHL0295)	51	8.8	71	0.1	146.2	0.6	1	0.5	22.8	263.9	7.1	35.6	71.5	0	1.5	2	0.3
(CKDHL0159/CKDHL0295)/(CKLTI0344)	48	8.8	70	-1.6	144.1	0.5	1	9.5	24.7	263	-0.4	37.8	68.5	0	2.6	3	8.7
(CKDHL0089/CKDHL0295)	50	8.7	76	-0.9	134.9	0.5	1	2.3	28.3	262.2	1.3	37.5	75	0	1.9	2	-0.6
(CML489/CML444)/(CKLTI0152)	9	8.6	71.4	0.1	130.5	0.5	1.1	8.2	24.9	261.3	1.3	37.5	71.5	0	1.5	2.4	4.3
(CKDHL0089/CKDHL0295)/(CKLTI0152)	12	8.5	72.4	0.9	135.7	0.5	1	10.4	26.4	270.3	2.7	37.9	73	1.3	2.5	2.2	-0.4

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	MOI	PH	RL	SAT	SD	SL	EA	PA	HC
(CKDHL0089/CML395)/(CKLTI0147)	42	8.4	71.6	0	126.1	0.5	1	4.5	25.7	273.2	0.4	37.1	72	0	3	2	2.4
(CKDHL0159/CKDHL0295)/(CKLTI0368)	6	8.4	70.9	0.4	123.5	0.5	1.1	6.2	26.9	248.2	0.4	38.3	71.5	0	2.4	1.5	13.5
(CKDHL0089/CML395)/(CKLTI0272)	35	8.4	71.3	0.6	138.7	0.5	1	3.7	23.4	270.1	0.4	36.7	72	0	2	2.9	9.1
(CML312/CML395)/(CKLTI0200)	24	8.4	68.6	-0.6	117.3	0.5	1	1.5	24.2	256.7	-1.1	36.9	67.5	1.4	2.5	2	3.7
(CKDHL0159/CKDHL0295)/(CKLTI0200)	27	8.3	70.7	-1.4	128.6	0.5	1	2.6	22.6	270.6	14.8	37.6	69.5	0	2.5	2.4	1.4
(CML489/CML444)/(CKLTI0272)	30	8.3	69.8	0	131.6	0.5	1	5.1	22.2	269.9	-0.1	37.6	70	2.7	1.5	2.4	6
(CKDHL0089/CKDHL0295)/(CKLTI0368)	5	8.3	75.1	-0.6	121.5	0.5	1.1	7.2	24.6	246.2	-0.3	32.4	74.5	1.6	2	2.2	3.7
(CKDHL0159/CKDHL0295)/(CKLTI0036)	20	8.3	68.1	0.9	154.4	0.6	1	4	25	273.5	4.4	37.5	68.5	3.9	2	2.9	3.2
(CML489/CML444)/(CKLTI0147)	37	8.2	70.1	-1.1	134.8	0.5	1	3	21.8	270.8	9.2	37.4	69	0	2	2.5	0.9
(CML395/CML444)/(CKLTI0147)	36	8.2	71.7	0.5	143.4	0.5	1	6.7	24.6	282.5	0.1	36.5	72.5	0	2.5	2.6	0.5
(CML312/CML395)/(CKLTI0272)	31	8	69.3	1	122.9	0.5	1	4.6	22.6	268.5	0.1	36.8	70	0	2.1	2.5	8
(CML489/CML444)/(CKLTI0200)	23	8	68.2	0.1	121.2	0.5	1	12.4	25	250.5	0.9	38.2	68.5	0	3	2	0.2
(CKDHL0089/CKDHL0295)/(CKLTI0036)	19	7.9	70.6	-0.1	146	0.5	1	8.6	25.6	271.9	-0.5	31.6	71	0	2	3.1	1.2
(CML489/CML444)/(CKLTI0036)	16	7.9	70.2	0.2	151.8	0.6	1	4.9	25	260.4	4.5	34.8	70	0	2	2.4	1.1
(CKDHL0089/CML395)/(CKLTI0036)	21	7.8	70.7	1	157	0.6	1	6.9	24.8	276.8	1.4	38	72	1.3	2	3	-0.2
(CML489/CML444)/(CKLTI0344)	44	7.8	69.6	-1.3	150.4	0.6	1	8.6	25.1	273	1.7	37.5	68.5	0	1.5	3	-0.6
(CKDHL0089/CKDHL0295)/(CKLTI0272)	33	7.7	70.5	1.2	128.7	0.5	1	4.6	26.1	271.4	3.7	36.6	71.5	0	1.4	1.8	1.3
(CKDHL0089/CKDHL0333)/(CKLTI0368)	4	7.7	74.1	-0.5	122	0.5	1.1	4.3	25	250.3	3.7	36.5	73.5	1.4	2.5	2.1	1.8
(CML395/CML444)/(CKLTI0036)	15	7.3	71.9	0	156.3	0.6	1	1.4	23.8	280.2	2.8	37.4	71.5	0	2	2.7	1.7
<b>Pioneer 3253</b>	54	7.3	68.8	1.5	133.3	0.5	0.9	10.8	22.2	261.7	2.7	38	70	0	2.6	2	19.6
(CKDHL0089/CKDHL0333)/(CKLTI0036)	18	7.3	70.3	1.9	154.6	0.6	1	5.2	25.4	274.5	-0.1	38	72	0	2	3.1	0.8
<b>DK8053</b>	52	7.3	69.9	0.1	126.8	0.5	1	7.9	23.1	259.6	0.7	35.9	70	1.5	2.5	2.5	7.9
(CML312/CML395)/(CKLTI0344)	45	7	69.3	-2.1	133.2	0.5	1	4.4	26.4	263.9	-0.5	37.4	67	0	3	2.5	15
<b>DH04</b>	55	6.6	66.6	0.5	136.8	0.5	0.9	2.4	23.1	272.9	3.5	35.9	66.5	1.4	2	2.5	2.7
(CML312/CML395)/(CKLTI0036)	17	5.3	72.2	0.4	124.6	0.5	1	4.2	25.3	260.3	5.2	37.6	73	0	3.5	2.4	1.8
<b>DK8031</b>	53	4.6	67.8	3.6	121.4	0.5	0.9	8.6	22.6	256.9	11.6	35.8	71	0	4	1.6	11.1
<b>Entry_Variance</b>		0.8	2.3	0.3	114.2	0	0	6	0.7	65.3	0	0.8	2	0	0.2	0.1	14.6
<b>Residual_Variance</b>		0.8	1.1	1.1	47.9	0	0	10.3	4	59.5	21.7	1.8	2.2	1.2	0.2	0.2	23.6
<b>Grand_Mean</b>		8.6	71	0	134.6	0.5	1	5.4	24.8	266.9	1.9	36.9	71	0.4	2.3	2.4	4.7
<b>LSD</b>		2.1	2.4	2.2	14.9	0	0.1	6.9	4.3	17.2	9.5	2.8	3.2	2.3	0.9	1	10.3

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	MOI	PH	RL	SAT	SD	SL	EA	PA	HC
CV		12.2	1.7	2959.8	5.4	3.9	6.8	62.6	8.6	3.2	245.7	3.7	2.2	301.4	20.5	21.4	107.6
Heritability		0.6	0.8	0.4	0.8	0.8	0.1	0.5	0.3	0.7	0	0.5	0.6	0	0.6	0.5	0.6

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turcicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking

APPENDIX 12 Means of yield and agronomic traits for Kakamega

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	MOI	PH	RL	SAT	SD	SL	EA	PA	GLS	HC	ET	PS
(CKDHL0089/CKDHL0333)/(CKLTI0344)	46	9.9	76	0	146	0.5	0.9	2.9	32	273	0	40	76	0	1.4	2	0.9	0	2	1.6
(CKDHL0089/CKDHL0333)/(CKLTI0147)	39	9.8	75	1	130	0.5	0.9	7.5	26	274	0	38	77	0	2.6	2	1.1	2.6	2	1.4
(CKDHL0089/CML395)/(CKLTI0344)	49	9.7	76	0	131	0.5	0.8	11	28	262	0	44	76	2.6	1.6	1.5	0.9	0	2	0.9
(CKDHL0089/CML395)/(CKLTI0368)	7	9.7	77	1	117	0.5	0.8	4.8	24	239	0	39	78	0	2.4	1	0.9	0	2	1.2
(CML395/CML444)/(CKLTI0344)	43	9.5	75	-0.5	144	0.5	0.9	4.3	29	272	0	39	74	0	1	2	0.9	0	2	1
(CKDHL0159/CKDHL0295)/(CKLTI0344)	48	9.4	76	0.5	139	0.5	0.8	9.3	25	267	0	40	76	0	1	1.5	0.8	0	2	1
(CML395/CML444)/(CKLTI0200)	22	9.4	76	0	125	0.5	1	13	26	262	0	38	76	0	2	2	1.6	0.1	2	1.5
(CKDHL0089/CML395)/(CKLTI0200)	28	9.3	75	0.5	121	0.5	0.9	7.2	27	265	0	35	75	0	1.5	1.5	1.1	0	2	1.4
(CKDHL0089/CKDHL0295)/(CKLTI0200)	26	9.3	74	0	119	0.5	0.9	5.6	26	257	0	37	74	0	2	1	1.5	-0.1	2	0.8
(CKDHL0089/CML395)/(CKLTI0152)	14	9.3	77	0.5	122	0.5	0.9	8.5	24	265	0	38	77	0	2	1.5	1	0	2	1.4
(CML395/CML444)/(CKLTI0368)	1	9.2	78	0	127	0.5	0.9	8.6	27	255	0	39	77	0	2	1	1	0	2	1
(CML312/CML395)/(CKLTI0368)	3	9.2	77	0.5	120	0.5	0.9	11	26	254	0	40	78	0	2	1.5	1.1	7.9	2	2
(CKDHL0089/CKDHL0295)/(CKLTI0152)	12	9.1	75	2	125	0.5	0.9	7.2	25	258	0	39	77	1.2	1.4	1.5	1	0	2	0.8
(CKDHL0089/CKDHL0333)/(CKLTI0152)	11	9.1	76	2	128	0.5	1	12	26	268	0	38	78	0	1.9	2	0.9	2.5	2	1.1
(CML312/CML395)/(CKLTI0344)	45	8.9	76	1	138	0.5	0.9	7.8	32	267	0	44	77	0	2.1	2	1.2	0.1	2	0.9
(CKDHL0159/CKDHL0295)/(CKLTI0200)	27	8.8	75	0	117	0.4	0.9	10	25	264	0	40	75	0	2	1.5	0.9	0	2	1.2
(CKDHL0089/CKDHL0333)/(CKLTI0272)	32	8.8	76	1	136	0.5	0.9	5.6	24	281	0	40	77	0	2	2.5	1.1	0	3	1.1
(CML489/CML444)/(CKLTI0147)	37	8.7	77	0.5	129	0.5	1.1	2.1	25	260	0	40	77	0	3.1	2	1.6	0	2	1.4
(CKDHL0089/CKDHL0295)/(CKLTI0344)	47	8.6	76	0	145	0.5	0.9	8.4	28	273	0	36	76	0	1	2	1.1	2.7	2	1.1
(CKDHL0089/CKDHL0295)/(CKLTI0147)	40	8.4	78	-0.5	122	0.5	0.9	8.9	23	261	0	34	77	0	1.9	1	1.4	1.3	2	2.1
(CML489/CML444)/(CKLTI0344)	44	8.3	75	0	135	0.5	0.9	6.9	27	259	0	41	75	0	2	1.5	0.9	0	2	1
(CML489/CML444)/(CKLTI0368)	2	8.3	76	1	120	0.5	0.9	6.5	25	241	0	36	77	0	2	2	1	0	2	1.1
(CML395/CML444)/(CKLTI0147)	36	8.2	76	1.5	129	0.5	0.8	13	25	273	0	44	77	0	2.5	3	1.6	1.3	3	0.7
(CKDHL0089/CKDHL0295)/(CKLTI0368)	5	8.2	77	0	107	0.5	0.9	11	29	230	0	38	77	0	2.5	2	0.9	0	2	1.6
(CML312/CML395)/(CKLTI0152)	10	8.2	76	1	121	0.4	1	12	27	277	0	36	78	0	2.5	2	2	-0.1	2	1.4
(CML312/CML395)/(CKLTI0200)	24	8.2	76	0	109	0.4	0.8	13	28	250	1.3	41	76	1.3	2.5	1.5	1	0	3	1.3
(CKDHL0089/CKDHL0333)/(CKLTI0200)	25	8.1	74	0.5	119	0.5	1	3.9	29	259	0	34	74	0	2.5	1.5	1.1	0	2	1.8
(CKDHL0089/CML395)/(CKLTI0147)	42	8.1	76	1	120	0.5	0.9	17	26	257	0	40	77	0	3	2.5	1	0	2	1.7
(CML312/CML395)/(CKLTI0147)	38	8.1	76	1	126	0.5	0.9	7.1	25	270	0	37	77	0	3	2	1.6	2.6	2	1
(CKDHL0089/CKDHL0295)/(CKLTI0272)	33	8	77	1	123	0.5	1	6.1	26	261	0	36	77	0	2.1	2.5	1	2.7	2	1.1
(CML395/CML444)/(CKLTI0036)	15	7.9	77	1	159	0.6	0.9	0	27	276	0	38	78	0	2	3	1.9	0	2	1
(CML395/CML444)/(CKLTI0272)	29	7.9	77	0	129	0.5	0.9	10	24	265	0	39	76	0	2.6	3	1	0.1	2	2
(CML489/CML444)/(CKLTI0200)	23	7.9	75	-0.5	123	0.5	1	11	28	251	0	35	75	0	3	1.5	1.5	0	2	1.3
(CKDHL0159/CKDHL0295)/(CKLTI0152)	13	7.8	76	1	125	0.5	0.9	13	23	264	0	37	77	0	3	2	2	0	3	1.1

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	MOI	PH	RL	SAT	SD	SL	EA	PA	GLS	HC	ET	PS
(CML489/CML444)//(CKLTI0152)	9	7.8	76	1	131	0.5	0.9	8.3	26	262	0	39	77	0	2	1.5	1.1	0	2	1.2
(CML489/CML444)//(CKLTI0272)	30	7.7	75	0.5	129	0.5	1	6.5	30	257	0	44	76	0	3	2.5	1.5	0	2	0.9
(CKDHL0089/CKDHL0333)//(CKLTI0368)	4	7.6	77	0.5	111	0.5	0.9	11	28	229	0	39	77	0	3	2.5	1	8.9	3	1.1
(CML489/CML444)//(CKLTI0036)	16	7.6	76	0.5	150	0.6	1	6.4	26	261	0	39	77	0	2	3	1.5	0	3	1.3
(CKDHL0089/CML395)//(CKLTI0272)	35	7.6	75	0.5	127	0.5	0.7	3.5	23	267	0	40	76	0	2.5	2	0.9	4.9	2	1.1
(CKDHL0089/CKDHL0333)//(CKLTI0036)	18	7.6	76	0.5	142	0.6	0.8	7.6	26	253	0	37	77	0	1.5	2.5	1.6	0	3	0.9
(CML395/CML444)//(CKLTI0152)	8	7.4	77	0.5	125	0.5	0.8	12	25	267	0	38	78	0	2	2.5	1.5	0	3	1.6
(CKDHL0159/CKDHL0295)//(CKLTI0368)	6	7.1	76	0.5	103	0.5	1.2	4.5	27	216	2	32	76	2	2.5	1	1	1.5	2	1.5
(CKDHL0089/CML395)//(CKLTI0036)	21	7.1	76	1.5	148	0.6	0.9	2.9	27	264	0	39	78	0	2.5	3	1.6	0	2	1.1
(CKDHL0159/CKDHL0295)//(CKLTI0147)	41	7	77	0	130	0.5	0.9	8.9	28	262	0	35	77	0	3	2	1	0	2	1.6
(CKDHL0159/CKDHL0295)	51	7	77	0.5	122	0.5	0.9	2.9	26	238	0	33	77	0	1.4	1	1	1.8	2	1.4
(CKDHL0159/CKDHL0295)//(CKLTI0036)	20	6.2	76	1	150	0.6	0.9	0	26	270	0	35	77	0	2.5	2.5	2.5	-0.1	3	1.2
(CKDHL0159/CKDHL0295)//(CKLTI0272)	34	6	76	1	112	0.4	0.9	8.2	23	249	0	37	77	1.4	2.5	2.5	1.5	2.8	2	1.4
(CML312/CML395)//(CKLTI0272)	31	5.1	76	1.5	120	0.5	0.9	12	27	261	1.4	32	77	0	3	3	1.4	3.2	3	1.5
(CKDHL0089/CKDHL0295)//(CKLTI0036)	19	5.1	78	1.5	133	0.5	0.9	6.1	29	254	0	28	80	0	2.5	3	2.1	0	2	1.5
(CML312/CML395)//(CKLTI0036)	17	4.9	77	1.5	121	0.5	0.9	2.8	25	251	0	38	78	0	3.6	3	2	0	2	1.4
Pioneer 3253	54	4.4	76	0.5	130	0.5	0.7	19	24	254	1.2	39	77	0	4	3	2	0	3	1
(CKDHL0089/CKDHL0295)	50	4.4	80	1	107	0.5	1.2	21	32	228	0	21	81	0	2.5	1	0.9	0	2	1.4
DH04	55	3.7	77	-0.5	118	0.5	0.8	26	21	244	0	31	76	0	3.4	3	2	0	3	1.1
DK8053	52	3.5	75	-0.5	129	0.5	0.8	16	25	259	0	40	75	0	4	3	3	0	4	1.2
DK8031	53	3.1	74	7.5	126	0.5	0.8	8	25	258	0	28	82	0	3.5	2.5	1.5	5.3	2	1.9
Entry_Variance		2.3	0.8	0.8	107	0	0	5.9	2	138	0	0.9	1.5	0	0.3	0.3	0.1	1.3	0	0
Residual_Variance		1.1	0.5	0.8	42.4	0	0	37	5.3	64.2	0.3	29	0.9	0.5	0.3	0.3	0.3	4.9	0	0.1
Grand_Mean		7.7	76	0.7	127	0.5	0.9	8.7	26	258	0.1	37	77	0.2	2.3	2.1	1.3	0.9	2	1.3
LSD		2.1	1.5	1.8	14.5	0	0.2	12	4.8	16.3	1.2	11	2.1	1.6	1.1	1.1	1	4.5	1	0.8
CV		13.6	1	128	5.6	4.1	13	70	9	3.1	536	14	1.3	499	23	27	39	235	18	31
Heritability		0.8	0.8	0.7	0.8	0.8	0.1	0.2	0.4	0.8	0	0.1	0.8	0	0.7	0.6	0.3	0.4	1	0.1

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking



APPENDIX 13 Means of yield and agronomic traits for Kiboko well-watered

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	GYG	MOI	PH	SAT	SD	SL	EA	PA
(CML395/CML444)/(CKLTI0036)	15	10.9	58.3	2	143.3	0.6	1	1.4	10.1	20.5	244.8	38.6	60.4	8.6	1.1	3
(CKDHL0089/CML395)/(CKLTI0036)	21	9.5	57.8	2.2	129.9	0.5	1	1.3	9.2	20.8	235.6	38.2	60.1	17.4	1.5	3
(CKDHL0089/CKDHL0333)/(CKLTI0036)	18	9.5	58.5	0.9	132.9	0.6	1	0	9.3	22.1	231.6	37.6	59.3	20.9	1.5	3
(CML489/CML444)/(CKLTI0368)	2	9.4	60.1	0	109.5	0.5	1	1.3	9.1	22.1	207	37.5	60.1	4.3	1.9	1.5
(CML395/CML444)/(CKLTI0152)	8	9.3	59.3	1.3	115	0.5	1	0	9.8	18.9	237.5	39.4	60.7	1.1	1.7	2
(CML312/CML395)/(CKLTI0152)	10	9.2	59	1.3	103.4	0.4	1	0	9.2	20.6	238.2	40.3	60.3	9.6	1.7	2
(CKDHL0089/CKDHL0295)/(CKLTI0152)	12	9.1	59.7	1.5	108.4	0.5	1	1.3	9.1	19.6	227.7	39.4	61.3	12.4	2.1	1
(CKDHL0089/CKDHL0295)/(CKLTI0147)	40	8.9	58.9	1.1	113.1	0.5	1	0	9	19.4	236.1	37.7	60.1	21	2.1	2.5
(CKDHL0089/CKDHL0295)/(CKLTI0272)	33	8.9	57.7	0.9	114	0.5	1	1.4	8.8	19	232.5	37.7	58.8	7.9	0.8	1
(CKDHL0159/CKDHL0295)/(CKLTI0272)	34	8.7	57	1.5	115.7	0.5	1	0	8.3	17.8	230.3	38.2	58.3	6.5	2.2	2
(CKDHL0089/CKDHL0333)/(CKLTI0272)	32	8.7	56.7	2	120.3	0.5	1.1	1.3	8.8	19.9	245	37.5	58.8	10.1	2.6	1.5
(CKDHL0159/CKDHL0295)/(CKLTI0152)	13	8.7	59.8	0.9	111	0.5	1	0	8.8	19	228.5	37.4	60.6	7	2	1.5
(CML395/CML444)/(CKLTI0344)	43	8.7	56.6	1.6	125.7	0.5	0.9	2.9	7.6	17.4	231.7	37.7	58.2	6	2.3	1.5
(CKDHL0159/CKDHL0295)/(CKLTI0368)	6	8.7	59.4	1.2	102.6	0.5	1	1.4	8.4	19.3	201.8	37.5	60.6	23.3	2.8	1.5
(CML395/CML444)/(CKLTI0272)	29	8.6	57.9	1.4	122.9	0.5	0.9	1.5	8.7	19.3	236.2	39.9	59.2	3.3	2	3
(CKDHL0089/CKDHL0333)/(CKLTI0152)	11	8.6	59.3	1.6	113.8	0.5	1	0	8.5	19.3	233.2	39.5	60.8	9.5	2.5	2
(CKDHL0089/CML395)/(CKLTI0368)	7	8.6	60.1	1.9	109.6	0.5	0.9	1.3	8.2	20.6	216.2	38.7	61.7	8.4	2.3	1.5
(CML312/CML395)/(CKLTI0147)	38	8.5	58.5	0.7	115.7	0.5	1	0	8.5	19.7	237.7	37.5	59	6.8	1.8	1.5
(CKDHL0089/CKDHL0295)/(CKLTI0344)	47	8.4	58.2	1.2	123.7	0.5	1	0	8.5	20.9	238.2	38.9	59.4	8.7	2.4	2
(CML395/CML444)/(CKLTI0147)	36	8.4	58.3	1.7	121.3	0.5	1	1.4	8.6	20.6	233.4	37.5	60.1	4.4	2.6	2.5
(CKDHL0089/CKDHL0295)	50	8.4	61.4	0.8	118.2	0.5	0.9	0	8.2	20.2	228.1	35.3	62	15.4	1.8	2
(CML395/CML444)/(CKLTI0368)	1	8.3	60.4	0.9	111.6	0.5	0.9	0	8.1	21.7	215.5	38.1	61.4	11	2.7	1.5
(CKDHL0159/CKDHL0295)/(CKLTI0036)	20	8.3	57.6	2.4	141.5	0.6	1	0	8.3	18	233.8	36	60	17.4	2.1	3
(CKDHL0159/CKDHL0295)/(CKLTI0344)	48	8.2	56.9	-0.2	125.1	0.5	1	0	8.3	19	231.3	40.1	56.8	6.4	2.4	2.5
(CKDHL0089/CML395)/(CKLTI0200)	28	8.1	57.2	1.2	101.9	0.5	1	0	8	21.5	224.5	37.9	58.6	8.7	2.8	2
(CKDHL0159/CKDHL0295)/(CKLTI0200)	27	8.1	56.3	1.1	114.2	0.5	1	0	8.3	20.6	224.8	34.5	57.5	7.2	2.1	1
(CKDHL0089/CML395)/(CKLTI0272)	35	8.1	57.1	1.5	109.3	0.5	1	0	8.2	18.5	230.4	39.1	58.8	13.2	2.4	2
(CKDHL0089/CKDHL0333)/(CKLTI0368)	4	8.1	59.2	1.1	97.8	0.5	1	1.3	7.4	19.7	200.3	38.9	60.2	13.5	2.9	1
(CKDHL0089/CKDHL0333)/(CKLTI0344)	46	8	56.7	0.4	119.6	0.5	1	0	8.6	18.5	235.2	37.5	56.9	10.9	1.9	2

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	GYG	MOI	PH	SAT	SD	SL	EA	PA
(CKDHL0089/CML395)/(CKLTI0152)	14	8	58.3	2.6	110	0.5	1	0	8.1	19.8	232.9	37.8	61	18.1	1.8	2
(CML489/CML444)/(CKLTI0147)	37	7.9	58.1	1.5	112	0.5	1.1	0	8.2	18.3	220.8	38	59.8	13.2	2.3	2.5
(CML489/CML444)/(CKLTI0272)	30	7.9	57.4	1.2	116.2	0.5	1	0	8.1	18.3	224.4	37.9	58.7	19.3	2.5	2.5
(CML312/CML395)/(CKLTI0200)	24	7.8	57.5	2	105.7	0.4	1	0	8.4	21.3	234.5	38.4	59.6	11.9	2.7	2
(CKDHL0089/CKDHL0295)/(CKLTI0368)	5	7.8	61.8	0.8	106.1	0.5	1	0	7	19.4	216	33.2	62.3	20.2	2.2	1.5
(CKDHL0089/CKDHL0333)/(CKLTI0147)	39	7.8	58.5	1.2	109.7	0.5	1	1.4	7.7	20.5	222.8	36.9	59.7	9	2.5	2
(CKDHL0159/CKDHL0295)/(CKLTI0147)	41	7.7	58.3	1.5	117.2	0.5	1	1.3	7.8	17.7	230.6	36.3	59.9	14	2.5	2
(CKDHL0089/CKDHL0295)/(CKLTI0036)	19	7.7	58.8	1.9	140.9	0.6	1.2	0	7.6	21.2	249.8	31.1	60.7	50.5	2.3	1.5
(CKDHL0089/CKDHL0295)/(CKLTI0200)	26	7.5	58	1.5	110.7	0.5	1	1.3	7.6	19.8	226.3	40.4	59.5	19.4	3.1	1
(CML489/CML444)/(CKLTI0036)	16	7.5	57.5	2.5	126.3	0.6	1	1.4	7.8	18.3	213.4	37.3	60.1	9.7	2.2	3
(CKDHL0089/CML395)/(CKLTI0344)	49	7.5	56.2	1	118.1	0.5	0.9	0	7.3	17.3	229	38.4	56.9	12.7	2.5	2
(CKDHL0089/CML395)/(CKLTI0147)	42	7.4	57.8	1.5	117.5	0.5	1	0	7.5	18.5	233.6	37.4	59.3	13.2	2.8	2.5
(CML312/CML395)/(CKLTI0368)	3	7.4	57.4	2	100.9	0.5	0.9	0	7.8	19.6	224	38.7	59.4	8.4	2.1	1.5
(CML312/CML395)/(CKLTI0036)	17	7.4	59.7	1.5	118.6	0.5	1	0	7.3	18.7	224.1	37.7	61.1	9.2	3	3
(CKDHL0159/CKDHL0295)	51	7.3	59.9	1	135.2	0.6	1	1.4	7.2	17.4	227.2	37.3	60.6	32.1	2.5	3
(CML489/CML444)/(CKLTI0152)	9	7.3	59.1	2	106.3	0.5	1	1.4	7.4	17	215.4	39.1	61	9.6	3.1	2
(CML395/CML444)/(CKLTI0200)	22	7.1	58.4	2.4	112.7	0.5	1	0	7	20.2	233.8	39	60.8	12	2.7	2.5
(CKDHL0089/CKDHL0333)/(CKLTI0200)	25	7	57.9	1.3	102.4	0.5	1	1.3	6.8	18	215.4	36.4	59.3	9.2	3.1	2
(CML489/CML444)/(CKLTI0344)	44	7	55.3	1.1	118.6	0.5	0.9	0	7.4	17.1	220.8	37.8	56.5	4	3.1	2
(CML312/CML395)/(CKLTI0344)	45	7	56.7	2.1	111.7	0.5	1	0	7.4	19.1	220.7	38.1	59	4.5	2.9	2
(CML489/CML444)/(CKLTI0200)	23	6.8	56.9	1.5	104.7	0.5	1	0	7.3	20.4	217.5	37.3	58.5	11	2.8	1.5
(CML312/CML395)/(CKLTI0272)	31	6.7	58.9	2	107.9	0.5	1.1	0	6.7	19.9	227.5	36.5	60.9	3.2	2.5	2.5
<b>DH04</b>	55	6.7	58	2.6	110.6	0.5	1	0	6.8	17.8	226.7	37.9	60.6	6.9	3.1	3
<b>DK8053</b>	52	6.6	57.9	2.4	120.4	0.6	0.9	1.6	6.8	17.3	216.4	38.9	60.4	12.7	2.9	3
<b>Pioneer 3253</b>	54	5.6	59.7	3.5	128.7	0.5	0.9	1.6	5.6	18.1	243	38.1	63.3	27.7	3.2	3
<b>DK8031</b>	53	4.3	59.4	5.1	113.1	0.5	1	1.4	4.2	17.1	220.7	37.4	64.6	15	3.5	3
<b>Entry_Variance</b>		0.8095	1.3	0.3	94.1	0	0	0	0.7	0.8	61.3	0.9	1.8	31.7	0.1	0.3
<b>Residual_Variance</b>		0.4624	0.6	0.7	22.7	0	0	1.4	0.5	1.6	55.4	3.4	0.8	64.9	0.3	0.3
<b>Grand_Mean</b>		7.9888	58.3	1.6	115.9	0.5	1	0.6	8	19.3	227.5	37.8	59.9	12.3	2.4	2.1
<b>LSD</b>		1.6669	1.6	1.7	10.8	0	0.1	2.7	1.6	2.9	17.7	3.7	2	17.9	1.1	1.1
<b>CV</b>		10.2557	1.3	52.6	4.6	3.8	5	229.2	9.6	7.4	3.8	4.9	1.6	71.6	22.6	25.3

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	GYG	MOI	PH	SAT	SD	SL	EA	PA
Heritability		0.7779	0.8	0.5	0.9	0.9	0.5	0	0.7	0.5	0.7	0.3	0.8	0.5	0.5	0.7

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turcicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking

#### APPENDIX 14 Means of yield and agronomic traits for Mtwapa

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	MOI	PH	RL	SAT	SD	SL	EA	MSV	PA	HC
(CKDHL0089/CML395)/(CKLTI0036)	21	6.1	57.2	2.5	74.5	0.4	1	1.2	20	167.4	0.1	38	59	1.2	2.8	0	3.2	0
(CKDHL0089/CKDHL0295)/(CKLTI0036)	19	6.1	58	2	74.5	0.4	1	2.2	20.7	174.5	0	41	59.6	1.5	2.4	0	3.2	1.3
(CKDHL0089/CKDHL0295)	50	5.9	58.2	1.5	61	0.4	1	2.8	20.9	147.8	0.2	39	59.7	1.7	2.6	0	3.5	1.2
(CML489/CML444)/(CKLTI0147)	37	5.7	54.1	-0.5	56.5	0.4	0.9	3.2	20.9	146.4	0.4	39	54.3	2.8	2.5	0.5	3	0
(CKDHL0089/CKDHL0295)/(CKLTI0368)	5	5.6	57.9	1	55.8	0.4	1	1.2	20.1	148.5	0	37.5	58.7	-0.2	2.4	0	3.2	1.3
(CML312/CML395)/(CKLTI0368)	3	5.5	55.5	-0.5	65.7	0.4	1	2.6	20.2	166.6	-0.1	38	55.4	-0.6	2.2	0	3	2.6
(CML395/CML444)/(CKLTI0147)	36	5.3	55	1.5	60.1	0.4	1	2.5	21	167.5	1.3	38.5	56.5	2.4	2.3	0	3.2	1.3
(CML395/CML444)/(CKLTI0368)	1	5.3	59	0.5	58	0.4	1	1.2	21.5	137.2	1.9	38.5	59.3	1	2.2	0	3.2	0
(CML395/CML444)/(CKLTI0036)	15	5.3	58.1	2	76.3	0.5	0.9	4.1	21.1	165.1	0.1	38	60.4	0.2	2.5	0	3.5	3.9
(CML489/CML444)/(CKLTI0344)	44	5.2	53.5	-0.5	64.4	0.4	1	0.4	20.5	150.8	0	39	53.2	0	2.2	0	2.8	0
(CKDHL0089/CKDHL0295)/(CKLTI0344)	47	5.2	55.7	1	69.9	0.4	1	1.4	21.3	170.6	-0.2	37	56.2	0.9	2.6	0	2.7	0
(CKDHL0159/CKDHL0295)/(CKLTI0368)	6	5.1	58	1	59.2	0.4	1	1.2	21	135.9	0.2	37.5	58.9	1.5	2.7	1	3.4	1.3
(CKDHL0159/CKDHL0295)	51	5.1	56.6	0.5	59.9	0.4	0.9	1.1	19.6	143.6	3.6	34	57.6	0.8	2.6	1	3.9	1.4
(CKDHL0089/CKDHL0295)/(CKLTI0272)	33	5.1	52.8	1	64.8	0.4	1	1.4	19.6	165.1	0.4	38	54.6	0.1	2.4	0	3.3	1.3
(CML489/CML444)/(CKLTI0036)	16	5	56.1	1	60.3	0.4	1	1.2	20.9	141	-0.8	37.5	56.8	4.9	2.7	0	3.5	2.7
(CKDHL0089/CML395)/(CKLTI0147)	42	5	56.6	-0.5	49.1	0.3	0.9	-0.4	21	154.5	0.1	36	56.1	3.4	2.8	0	3.2	0
(CKDHL0089/CKDHL0295)/(CKLTI0152)	12	5	57.8	1	48	0.3	1	1.5	21.1	152.8	0.2	38.5	58.1	1.6	3	0	3.2	0
(CKDHL0159/CKDHL0295)/(CKLTI0036)	20	4.9	55.1	1.5	75.3	0.4	0.9	0.2	22.3	168.1	0.3	39	57	0.5	2.9	0	3	0
(CKDHL0159/CKDHL0295)/(CKLTI0344)	48	4.9	53.8	0.5	69.9	0.4	0.9	4.5	18.6	168.4	1.3	38.5	54.4	1.4	2.3	0	2.6	1.3

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	MOI	PH	RL	SAT	SD	SL	EA	MSV	PA	HC
(CKDHL0159/CKDHL0295)/(CKLTI0272)	34	4.8	55.7	1	56.9	0.3	0.9	3.3	19.1	159.4	0.1	39	57.3	0	2.3	0	3.2	0
(CML489/CML444)/(CKLTI0272)	30	4.7	56.2	0	55.7	0.4	1	2.8	19.6	155.6	0.1	37	56	1.3	2.1	0	3.1	0
(CKDHL0089/CKDHL0333)/(CKLTI0036)	18	4.7	55.2	1.5	71.5	0.4	0.9	4.8	21.6	156	0.1	36.5	57.2	4	3	0	3.5	0
(CML489/CML444)/(CKLTI0152)	9	4.7	54.5	0	51.5	0.3	1	0	21.5	150.2	0.2	39	55	6.4	2.5	0	3	1.3
(CML395/CML444)/(CKLTI0152)	8	4.6	56.4	1	55.5	0.4	1	3.9	21.3	147.7	-0.2	37.5	57.7	0.6	3.3	0	3.2	1.3
(CKDHL0089/CKDHL0333)/(CKLTI0200)	25	4.6	54	0	53.5	0.4	1	1.4	20.5	152.6	-0.1	37.5	54	1.8	2.7	0.5	3.3	0
(CKDHL0089/CML395)/(CKLTI0152)	14	4.6	56.7	0	50.8	0.3	1	1.5	20.5	146.3	1.4	36.5	57.2	0.4	2.9	0.5	2.9	1.3
(CKDHL0089/CML395)/(CKLTI0200)	28	4.6	54	1	52.4	0.3	0.9	1.3	19.8	158.4	1.2	38	55.6	0.6	2.5	0	3.5	1.3
(CKDHL0089/CKDHL0333)/(CKLTI0344)	46	4.6	56.5	1	53.8	0.3	1	9.3	22.1	155.8	1.4	38	58.1	2.2	3.2	0	3.5	7.9
(CML395/CML444)/(CKLTI0272)	29	4.6	58.3	1.5	60.2	0.4	1	0.2	20.6	157.6	-0.2	37.5	59.5	0.1	3	0	3.3	2.7
(CKDHL0159/CKDHL0295)/(CKLTI0152)	13	4.6	55.8	1.5	52.2	0.3	0.9	1.6	19.6	155.1	0.1	39	56.7	1.5	2.4	0	3.2	0
(CKDHL0089/CKDHL0333)/(CKLTI0147)	39	4.6	56.5	0	56.9	0.4	0.9	-0.1	21	157.6	1.9	38.5	56.6	0.8	2.5	2.5	3.5	1.3
(CML312/CML395)/(CKLTI0152)	10	4.6	55.6	1.5	54.1	0.3	0.9	1.4	20.6	158.1	0.2	37	57.4	0.2	2.4	0	3	0
(CKDHL0159/CKDHL0295)/(CKLTI0147)	41	4.5	54	0	64	0.4	1	-0.1	21.1	173.1	0.2	38.5	54.3	1.3	2.5	0	3.3	1.3
(CKDHL0089/CKDHL0333)/(CKLTI0272)	32	4.3	55	1.5	58.1	0.4	0.9	-0.1	19.9	163.9	1.3	38	56.8	1.2	2.6	0.5	3.3	1.3
(CML395/CML444)/(CKLTI0344)	43	4.3	56	1.5	61.1	0.4	1	5.4	20.4	157.8	1.5	38.5	57.8	4.2	3.4	0	3.3	2.6
(CKDHL0089/CML395)/(CKLTI0344)	49	4.1	56	4	51	0.3	1	5.2	21.1	145.8	0.2	39	59.6	0	3.6	0	3.3	3.8
(CKDHL0089/CKDHL0295)/(CKLTI0200)	26	4.1	54.9	4.5	44.5	0.3	0.9	2.8	21.1	142.9	0.4	38	59	0	3.3	0	3.5	0
(CKDHL0089/CKDHL0333)/(CKLTI0368)	4	4	59.7	-1	44.3	0.4	0.9	7.1	20.6	121.5	0.4	38	57.8	0.1	3.1	0	3.3	1.4
(CKDHL0159/CKDHL0295)/(CKLTI0200)	27	4	53.1	0.5	47.9	0.3	0.8	1.2	21	150.2	0.2	37.5	54.2	-0.3	3.2	0	3.2	0
(CML312/CML395)/(CKLTI0147)	38	3.9	55	2	53.5	0.3	0.9	2.9	20	162.7	5.6	37	55.9	1	2.9	0	3.5	0
(CML395/CML444)/(CKLTI0200)	22	3.8	55.2	1	53	0.3	1	7.6	21.8	156	1.3	38.5	56.3	1.1	3.8	0	3.3	1.3
(CKDHL0089/CKDHL0333)/(CKLTI0152)	11	3.8	57.6	0	50.8	0.3	0.9	1.5	20.7	145.2	1.1	39.5	58	0.3	3.3	0.5	3.1	1.3
(CKDHL0089/CML395)/(CKLTI0272)	35	3.8	57.3	0	64.2	0.4	1	4.3	20.9	170	0.1	37.5	57.1	3	2.8	0	3.3	2.7
DH04	55	3.7	56.5	0.5	65.3	0.4	0.9	1.7	20.3	151.2	1.4	38	57.1	0.4	2.6	0	3.3	1.4
DK8031	53	3.7	55.7	2	61.6	0.4	0.9	4.6	17.5	159.4	2.9	35.5	57.5	2.3	3.2	0	3.7	2.8
(CML312/CML395)/(CKLTI0272)	31	3.6	57.2	3	55.9	0.4	1	-0.1	21	156.9	-0.4	38	59.8	0.5	3.2	0	3.9	1.3
(CML312/CML395)/(CKLTI0036)	17	3.6	56.3	2	64.5	0.4	0.9	15.9	21	158.6	0	38	58.3	0.7	3.5	0	3.7	2.6
(CML489/CML444)/(CKLTI0368)	2	3.6	57.4	0.5	39.2	0.3	0.9	3	21.7	119.6	2	38	57.8	2.3	3.1	0	3.3	0
(CML312/CML395)/(CKLTI0200)	24	3.6	55	2	44.5	0.3	1	8.3	21.2	153.1	-0.5	38	56.3	-0.6	2.9	0	3.2	0

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	MOI	PH	RL	SAT	SD	SL	EA	MSV	PA	HC
(CKDHL0089/CML395)/(CKLTI0368)	7	3.5	58.4	0	62.1	0.5	1	0.4	20.4	122.9	0	40.5	58.6	0.2	3.9	0	3.3	1.3
(CKDHL0089/CKDHL0295)/(CKLTI0147)	40	3.3	56	1.5	50.1	0.3	1	7	20.3	155	-0.2	38	56.9	1	3.2	0	3	1.3
(CML312/CML395)/(CKLTI0344)	45	3	55.8	0.5	51.9	0.3	1	6.6	20.1	152.1	0.3	37	56	1.1	3.9	0	3.5	4.2
<b>Pioneer 3253</b>	54	2.9	56.9	0	60.9	0.4	0.8	22.3	19.1	159.7	-0.2	37	57.4	9.7	3.4	1	3.5	2.7
<b>DK8053</b>	52	2.2	57.6	2	44.1	0.3	0.9	4.7	19.6	134.6	-0.1	38.5	59.1	1.3	3.6	0	3.3	3.9
(CML489/CML444)/(CKLTI0200)	23	1.8	53.7	0	39.3	0.3	0.7	5.9	21.1	136.4	1.5	37	53.4	-0.2	4.1	0	3.6	0
<b>Entry_Variance</b>		0.5	1.2	0.3	43	0	0	10	0.4	87.3	0	0.3	1.3	1.2	0	0.1	0	0
<b>Residual_Variance</b>		0.4	1.5	1.5	57.4	0	0	8.3	0.6	88.3	2.3	1.8	2.7	3.8	0.4	0.2	0.1	5
<b>Grand_Mean</b>		4.5	56.1	1	57.5	0.4	0.9	3.3	20.6	153.3	0.6	37.9	57.1	1.4	2.9	0.1	3.3	1.3
<b>LSD</b>		1.5	2.7	2.6	17.8	0.1	0.2	6.3	1.7	21.9	3.4	2.7	3.8	4	1.5	0.8	0.7	4.8
<b>CV</b>		16.9	2.3	128.7	15.2	11.3	8.1	92.7	4.1	7	263.3	3.5	3.3	143.2	25.5	278.1	10.3	175
<b>Heritability</b>		0.7	0.6	0.3	0.6	0.6	0.2	0.7	0.6	0.7	0	0.2	0.5	0.4	0	0.5	0.2	0

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turcicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking

## APPENDIX 15 Means of yield and agronomic traits for Shikusa

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	MOI	PH	RL	SAT	SD	SL	EA	MSV	PA	GLS	HC	ET	PS
(CKDHL0089/CML395)/(CKLTI0200)	28	10.8	71.5	-0.9	128.8	0.5	1.1	1.8	30.8	246.9	1.4	31.5	70.9	0	2	0	1	1	1.3	2	2
(CML395/CML444)/(CKLTI0200)	22	10.6	71.6	-0.5	122.5	0.5	1	0.3	29.1	248.6	0	34.1	71.5	0.2	1.5	0	1	1	1.7	2	2
(CKDHL0089/CML395)/(CKLTI0152)	14	10.3	73.3	0.4	128.3	0.5	1.1	1.5	30.5	249.5	0	31.4	73.6	0.2	2	0	1.5	1	8.4	2	2.4
(CML312/CML395)/(CKLTI0152)	10	10	73.5	0.3	126.5	0.5	1	0.2	30	243.1	0	33.1	73.2	0.6	2	0	1.5	1	6.1	2	2.5
(CKDHL0089/CML395)/(CKLTI0344)	49	9.9	72.2	0	138.3	0.6	1	0.3	30.6	242.2	0	32.4	72.4	0	2	0	2	1	6.1	2	1.4
(CKDHL0159/CKDHL0295)/(CKLTI0036)	20	9.8	72.8	-0.2	145.8	0.6	1.1	0.1	29.9	246.9	0	32.9	72.1	0.5	2	0	2	1	-0.5	2	1.8
(CKDHL0159/CKDHL0295)/(CKLTI0200)	27	9.7	71.3	0.1	120.8	0.5	1.1	5.2	30.4	238.2	0	30	71.8	0	2.5	0	1.5	1	3.4	2	2
(CML489/CML444)/(CKLTI0147)	37	9.7	73.5	-0.3	134.5	0.5	1.1	0.5	30.5	245.6	1.5	33.2	73	0	2.5	0	1.5	1	1.4	2.5	2.6
(CML312/CML395)/(CKLTI0147)	38	9.6	72.3	-0.7	130.8	0.5	1	0.2	30.2	261.3	0	30.7	71.7	0.2	2	0	1.5	1	4.2	2.5	3
(CKDHL0089/CKDHL0295)/(CKLTI0152)	12	9.5	74	-0.1	122.8	0.5	1.1	1.1	30.5	240.5	0	30.5	73.6	0.3	2.5	0	1	1	2.3	2	2.4
(CML395/CML444)/(CKLTI0368)	1	9.4	72.9	-1.1	120.3	0.5	1.1	1.4	31.6	234.6	0	32.3	71.4	-0.1	3	0	1.5	1	7.2	2.5	2.6
(CKDHL0159/CKDHL0295)/(CKLTI0344)	48	9.3	71	0.1	137	0.6	1	1.6	32.1	249.5	0	34	71.2	1.4	1.5	0	2	1	3.3	2	2
(CKDHL0159/CKDHL0295)/(CKLTI0147)	41	9.2	73	-0.2	128.5	0.5	1	3.1	27.5	249.7	0	30.8	72.6	1.3	2	0	2.5	1	3.2	2.5	2.5
(CKDHL0089/CKDHL0333)/(CKLTI0152)	11	9.2	73.1	0.5	129.8	0.5	1	5.1	29.6	250.6	0	33.8	73.7	-0.2	2	0	2	1	6.4	2	2.3
(CKDHL0089/CKDHL0333)/(CKLTI0147)	39	9.1	72.2	-0.4	132.8	0.5	1.1	2.7	28.3	257.7	0	28.6	71.9	-0.4	2.5	0	1.5	1	1.9	2	3
(CML395/CML444)/(CKLTI0147)	36	9	72.3	0	131.3	0.5	1.1	3.7	27.7	253.7	0	31.7	72.1	0	2.5	0.5	1.5	1.5	2.8	2	3
(CML395/CML444)/(CKLTI0152)	8	9	74.2	-0.5	134.8	0.5	1	3.6	29.4	250	0	31	73.7	0	3	0	2.5	1	5	2.5	3
(CKDHL0089/CKDHL0333)/(CKLTI0200)	25	9	71.7	-0.5	127.4	0.5	1	1.9	32.4	244.3	0	34	71.5	1.6	2	0	1.5	1	2.5	2	2
(CKDHL0089/CKDHL0333)/(CKLTI0344)	46	9	72.5	-0.1	133.8	0.5	1.1	1.3	32.1	251.8	0	28.2	72.3	-0.4	2	0	2	1	8.7	2	1.5
(CKDHL0089/CML395)/(CKLTI0368)	7	8.9	73.8	-0.1	117.8	0.5	1.1	-0.3	32.2	232.2	1.7	28.8	73.4	3.4	2	0	1.5	1	8.4	2	3.1
(CKDHL0159/CKDHL0295)/(CKLTI0152)	13	8.9	72.9	0	121.8	0.5	1	2.9	32.8	246.1	0	31.6	72.9	1.5	2	0	2.5	1	2.7	2	3
(CML312/CML395)/(CKLTI0368)	3	8.9	73	0.1	114.5	0.5	1	0.6	32	229.9	0	31.7	73.2	-0.3	2.5	0	1	1	7.8	2	2.9
(CKDHL0089/CML395)/(CKLTI0036)	21	8.8	72.1	0.5	150.8	0.6	1	-0.1	31.2	258	0	31.2	72.7	0	2	0	2	1	3.6	2.5	2
(CML489/CML444)/(CKLTI0344)	44	8.7	72.2	0.6	125	0.5	1.1	2.6	32.5	231.5	0	35.3	72.6	3.4	2	0	2	1	0.5	2	2.2
(CML395/CML444)/(CKLTI0344)	43	8.7	71.2	0.7	138.8	0.6	1	1.5	31.4	255.4	0	30.6	72.2	0.2	2	0	2	1	4.1	2	1.6
(CML489/CML444)/(CKLTI0272)	30	8.5	70.9	0	126.3	0.5	1.1	5.2	26.5	228.6	0	34.7	70.8	0.4	2.5	0	2.5	1	4.5	3	2.6
(CML489/CML444)/(CKLTI0036)	16	8.5	73.1	0.6	139.8	0.6	1.1	-0.6	28.4	242.8	0	27.8	73.8	1.2	2	0	2.5	1.5	0	2.5	2
(CML489/CML444)/(CKLTI0368)	2	8.5	73	-0.5	118.5	0.5	1.1	3.7	31.1	217.1	0	30.2	72.6	0	2	0	2	1	8.5	2	2.5

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	MOI	PH	RL	SAT	SD	SL	EA	MSV	PA	GLS	HC	ET	PS
(CKDHL0089/CKDHL0333)/(CKLTI0036)	18	8.5	72.4	0.7	142.8	0.6	1	2.2	31.9	258	0	31.4	73.2	-0.2	2	0	2.5	1	2.7	3	2.1
(CML395/CML444)/(CKLTI0272)	29	8.4	71.7	0.6	124	0.5	1.1	-0.1	28.5	229.7	0	29.7	72.4	1.7	2.5	0	2.5	1	3.5	2.5	2.7
(CML312/CML395)/(CKLTI0200)	24	8.3	70.6	-0.3	110.5	0.4	1	1.6	31.2	249.7	0	27.8	70.8	0.1	2	0	1.5	1	4.1	2	2.1
<b>Pioneer 3253</b>	54	8.3	73.3	2.1	133.5	0.5	1	1.6	26.5	246.5	0	32.9	75.7	0	3	0	3	1	5.1	2	2
(CKDHL0159/CKDHL0295)/(CKLTI0272)	34	8.3	70.9	0.5	124.3	0.5	1	2	26.8	238.7	0	31.7	71.3	1.3	2	0	2	1	8.3	2	3.2
(CML489/CML444)/(CKLTI0152)	9	8.2	72.6	-0.1	130.8	0.5	1.2	2.8	30	245.5	0	27.2	72.7	0.2	2.5	0	2.5	1	3.6	2	2.5
(CML395/CML444)/(CKLTI0036)	15	8.2	72.8	0.1	149	0.6	1.1	-0.4	30.7	258.1	0	26.8	73.4	4.3	1.5	0	3	1	2.6	2.5	2.4
(CKDHL0089/CML395)/(CKLTI0272)	35	8.1	71	0.1	121.5	0.5	1.1	0.1	28.9	241.4	0	27.7	71.3	0.2	1.5	0	1.5	1	8.1	2.5	3
(CKDHL0089/CKDHL0333)/(CKLTI0368)	4	8	74.4	-0.2	111.5	0.5	1	2.1	32.2	215.8	0	31.8	73.8	0	2.5	0	2	1	4.9	2.5	2.5
(CKDHL0089/CKDHL0295)/(CKLTI0147)	40	7.9	71.8	-0.4	129.8	0.5	1.1	1.1	30.2	252	0	25.4	71.2	-0.1	2	0	2.5	1	5.7	2	3.1
(CKDHL0089/CML395)/(CKLTI0147)	42	7.7	72.3	0.1	134.8	0.5	1	3.7	28.9	259.5	0	27.2	72.3	0	2.5	0	2.5	1	5.6	2	3
(CML312/CML395)/(CKLTI0036)	17	7.7	73.2	0.2	119.5	0.5	1.1	-0.6	33.3	231.7	1.9	29.2	73.7	-0.3	2.5	0	2.5	1	0.4	2	2.5
(CKDHL0089/CKDHL0295)/(CKLTI0036)	19	7.7	74	0	140.8	0.6	1.1	0.2	33	245.9	0	22.6	74	0	1.5	0	1.5	1	2.6	2	1.9
(CKDHL0089/CKDHL0295)/(CKLTI0200)	26	7.6	72	-1.1	122.5	0.5	1	0	30.4	234.3	0	24.8	70.8	0	2	0	1.5	1	2.9	2	2
(CKDHL0089/CKDHL0295)/(CKLTI0368)	5	7.6	73.9	0.1	114	0.5	1.1	2.2	32	216.7	0	22.4	74	-0.3	3	0	1	1	7	2	3
(CML312/CML395)/(CKLTI0272)	31	7.5	72.6	0	121.5	0.5	1.1	1.2	29.8	245	1.7	29.7	72.1	0.4	2.5	0	2	1	8	2	3.1
(CKDHL0089/CKDHL0295)/(CKLTI0344)	47	7.5	71.1	0.2	140.8	0.6	1	0.7	34.9	250.2	1.9	26.8	71.6	-0.4	1.5	0	2	1	1.3	2	2
(CML312/CML395)/(CKLTI0344)	45	7.5	72	0.4	130.5	0.5	1	0.2	29.9	244.3	0	27.1	72.3	0	2	0	1.5	1	2.4	2	2
(CML489/CML444)/(CKLTI0200)	23	7.5	72	-0.1	108.3	0.5	1.1	1.4	34.8	234.8	0	27.6	71.7	0.2	2.5	0	1.5	1	-0.9	2	1.5
(CKDHL0159/CKDHL0295)	51	7.3	74	-0.2	124.5	0.5	1.1	0.2	30.3	229.5	0	22.6	73.6	0.4	1.5	0	1	1	1.8	2	2.9
(CKDHL0089/CKDHL0295)/(CKLTI0272)	33	7.3	71.1	0	116.5	0.5	1	-0.8	31.4	238.5	0	26.7	71.2	-0.2	2	0	2	1	4.3	2.5	2.9
(CKDHL0159/CKDHL0295)/(CKLTI0368)	6	7.2	72.6	-0.4	120	0.5	1.1	3.5	30.1	226.1	0	24.7	72.4	-0.2	2.5	0	2	1	6.1	2	2.4
(CKDHL0089/CKDHL0333)/(CKLTI0272)	32	6.6	72.6	-1.5	135.8	0.6	1.1	5.8	28.2	245.3	0	26.2	71	8.3	2	0	3	1	6.7	2.5	2.9
(CKDHL0089/CKDHL0295)	50	6.5	73.9	0.2	120	0.5	1.2	-0.2	35.5	229.2	0	17.7	74.3	-0.1	1.5	0	1	1	0.2	2	2
<b>DK8053</b>	52	4.3	71.5	0.3	127.5	0.6	1.2	5.9	23.7	226.6	2.6	21.7	71.5	0.2	3	0	3	1	2.1	3.5	2.9
<b>DK8031</b>	53	4	70.8	3.5	120.3	0.5	1.2	2	26.8	228.6	0	21.6	74.1	0	3.5	0	3	1	8.8	2.5	3
<b>DH04</b>	55	3.3	70.8	1	118.5	0.5	1.1	3.3	27.5	225.5	0	15.6	71.6	3.7	3	0	3	1	0.3	4	2.9
<b>Entry_Variance</b>		1.4	0.7	0.3	72.6	0	0	0.3	2.1	87.7	0	10	1	0.6	0	0	0.2	0	2.4	0.1	0.1
<b>Residual_Variance</b>		1	0.5	0.4	39	0	0	5.2	5.7	70.4	0.8	11.2	0.4	3.1	0.4	0	0.4	0	9	0.1	0.2
<b>Grand_Mean</b>		8.3	72.4	0.1	127.6	0.5	1.1	1.7	30.3	241.7	0.2	29	72.5	0.6	2.2	0	1.9	1	4.1	2.2	2.4

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	MOI	PH	RL	SAT	SD	SL	EA	MSV	PA	GLS	HC	ET	PS
<b>LSD</b>		2.2	1.6	1.3	12.7	0	0.2	4.6	4.9	18.9	1.9	7.3	1.5	3.7	1.3	0.2	1.3	0.3	6	0.7	0.9
<b>CV</b>		12.9	1.1	986.4	4.9	4	8.2	135.3	8	3.9	404.6	12.4	1	292.6	28.7		32.3	13.1	72.4	16.5	17.9
<b>Heritability</b>		0.7	0.7	0.6	0.8	0.8	0	0.1	0.4	0.7	0	0.6	0.8	0.3	0.1	0	0.5	0	0.4	0.6	0.6

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turcicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking



APPENDIX 16 KYUC means of grain yield and agronomic traits

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	MOI	PH	RL	SAT	SD	SL	EA	MSV	PA	GLS
(CKDHL0089/CKDHL0295)	50	8.6	69.6	1	147	0.5	1	3.5	19.7	295.9	0	37.2	70.8	1.4	1.9	0.5	2.1	1
(CKDHL0159/CKDHL0295)/(CKLTI0152)	13	8.2	69.4	1	145.1	0.5	1.1	0.6	19.4	298.9	2.7	36	70.4	1.1	2	1	2.5	1
(CKDHL0089/CML395)/(CKLTI0152)	14	8.1	70	0.5	145.9	0.5	1	11.2	20.3	312.2	1.4	36.5	70.6	-0.2	2.4	0	2.5	1
(CML395/CML444)/(CKLTI0036)	15	7.9	67.2	2.6	183.8	0.6	1	4.3	21	320.5	0	37.8	70.2	1.4	1.4	0.5	2.5	1
(CKDHL0089/CML395)/(CKLTI0147)	42	7.9	67.8	0.5	148.1	0.5	1	7.8	20.6	317.2	1.4	36.8	68.3	2.7	2.3	-0.1	2.9	
(CML395/CML444)/(CKLTI0152)	8	7.7	68.9	0	153.9	0.5	1	13.6	20.1	313.1	0	36	68.8	0.1	2	0	2	1
(CKDHL0089/CKDHL0333)/(CKLTI0152)	11	7.6	70.4	1.5	144.4	0.5	1	7.7	20.9	305.8	0	36.6	71.7	-0.1	1.9	1	2	
(CKDHL0089/CKDHL0333)/(CKLTI0036)	18	7.6	67.7	0.5	163.9	0.5	1	1	22.4	300.5	0	38	68.3	0.1	2.1	1	2.5	
(CML395/CML444)/(CKLTI0147)	36	7.4	70.1	1	150.4	0.5	1	3.6	21.6	305.9	1.4	36.1	71	1.2	2.1	0.5	2.5	2
(CML489/CML444)/(CKLTI0200)	23	7.3	65.9	0	139	0.5	1	7.5	21	295.8	1.4	34.7	66	1.6	2.5	-0.1	2	1
(CKDHL0089/CML395)/(CKLTI0036)	21	7.3	67.8	-0.1	155.6	0.5	1	7.1	22.8	300.8	0	37.2	67.5	0.2	2	0	2	1
(CKDHL0089/CKDHL0295)/(CKLTI0147)	40	7.3	68.9	1	139.9	0.5	0.9	1.8	20.3	292.6	1.3	37.1	69.9	1.3	2.6	0	2	
(CML312/CML395)/(CKLTI0152)	10	7.3	68	2	135.2	0.4	1	13.8	21.4	305.1	0	37.2	69.9	0.1	2.3	-0.1	2.5	
(CKDHL0159/CKDHL0295)/(CKLTI0272)	34	7.3	66.5	1.1	154.3	0.5	1	5.5	21.3	308.8	0	37	67.8	-0.1	1.4	0	2.5	2
(CKDHL0089/CKDHL0333)/(CKLTI0200)	25	7.2	66.3	2	140.5	0.5	0.9	9.7	21.1	311.6	0	36.4	68.2	1.5	2.5	0	2	
(CKDHL0089/CKDHL0295)/(CKLTI0152)	12	7.2	68.4	0	135.7	0.5	1	11	21.6	295.3	1.3	36.6	68.3	0.9	2.1	0	2	
(CKDHL0159/CKDHL0295)/(CKLTI0036)	20	7.2	66.4	3	170.9	0.6	1	5	20.5	308	0	36.4	69.4	4.3	1.4	0.4	3	1
(CKDHL0159/CKDHL0295)/(CKLTI0200)	27	7.2	66.3	1.5	140.5	0.5	0.9	9.9	19.5	299.8	0	36.1	67.7	1.1	2.9	0	2	1
(CKDHL0089/CML395)/(CKLTI0272)	35	7.1	64.9	3.1	137.6	0.4	1	8	20.4	308.7	-0.1	37.7	68.3	0.1	2	0	2	1
(CKDHL0089/CKDHL0333)/(CKLTI0368)	4	7	68.3	0.1	126.1	0.5	1	15.2	20.8	257.8	0	37.6	68.7	1.4	2.6	0	2	
(CKDHL0089/CML395)/(CKLTI0200)	28	7	68.6	2.5	127.9	0.4	1	7	20.7	291.4	1.4	36	71.2	1.2	2.4	0	2.5	
(CKDHL0089/CKDHL0333)/(CKLTI0147)	39	7	69.4	0.5	141.2	0.5	1	16.5	20.3	310.7	0	35.4	70.1	0.2	2.6	0	2.1	1
(CML489/CML444)/(CKLTI0152)	9	6.9	69.1	0	147.7	0.5	1	20.3	21.8	295.2	1.4	37.4	69.1	1.4	2.6	0	2	1
(CML395/CML444)/(CKLTI0200)	22	6.9	67.7	1.5	151.6	0.5	0.9	7	21.2	304.7	0	37.8	69	0.5	2.1	0.6	3.1	
(CKDHL0159/CKDHL0295)/(CKLTI0147)	41	6.9	69	0.5	156.2	0.5	1	10	20.4	312.9	0	36.7	69.5	1.3	2.7	0	2	2
(CKDHL0089/CML395)/(CKLTI0368)	7	6.9	70.3	0	135.2	0.5	0.9	14.6	22	276.5	3.9	36.5	70.3	1.3	3	0	2	
(CML312/CML395)/(CKLTI0200)	24	6.8	66.4	1.5	128.3	0.4	0.9	6.7	20.8	297.7	-0.1	37.6	67.9	-0.2	2.4	0.5	2.4	1
(CML395/CML444)/(CKLTI0368)	1	6.7	68.4	1.1	145.1	0.5	0.9	11.1	22.1	282.9	1.4	35.6	69.8	3.2	2.6	0.1	2.5	1
(CKDHL0089/CKDHL0295)/(CKLTI0200)	26	6.6	66.8	0	133.8	0.5	1	1.1	20	295.1	0	35.5	66.7	-0.3	2.8	0	2	
(CML312/CML395)/(CKLTI0147)	38	6.6	68.5	1	147.8	0.5	0.9	14.7	20	313.5	0	35.3	69.3	1.8	2.2	0.1	2.5	1
(CKDHL0089/CKDHL0333)/(CKLTI0272)	32	6.6	69.3	0.5	150.6	0.5	1	12.5	21.6	312.4	1.4	36.3	69.9	0.4	2	5	2	1
(CML395/CML444)/(CKLTI0272)	29	6.6	66.4	1.9	157.3	0.5	1	12.5	20.5	316.4	-0.1	35.3	68	1.1	1.9	1	3	3
(CML489/CML444)/(CKLTI0036)	16	6.5	65.2	1.5	162.8	0.6	1	11.3	21.3	294.4	0.1	34.8	66.8	-0.1	1.4	0	2.5	1

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	MOI	PH	RL	SAT	SD	SL	EA	MSV	PA	GLS
(CKDHL0089/CKDHL0295)/(CKLTI0272)	33	6.5	68.6	1	140.4	0.5	1	10.8	20.7	296.2	1.4	37.2	69.8	0.2	1.9	0	2.5	2
(CML489/CML444)/(CKLTI0368)	2	6.5	69.2	0	136.8	0.5	1	12.2	20.5	273.9	0	35.3	69.1	4.4	2.4	0.5	2	2.5
(CKDHL0089/CKDHL0295)/(CKLTI0036)	19	6.3	67.4	1.5	157.3	0.5	1	3.1	21.5	297.9	0	30.2	68.8	-0.2	1.8	0	3	1.5
(CKDHL0089/CKDHL0295)/(CKLTI0368)	5	6.2	69.5	1.5	136.3	0.5	1	16.7	20.7	276.4	0	36.2	71.2	0.1	3	0	2	1
(CML489/CML444)/(CKLTI0147)	37	6.2	67.6	1.5	140.3	0.5	1	13.6	21.9	302.5	1.4	36.5	68.8	2.6	2.4	0	2.5	3
(CKDHL0159/CKDHL0295)	51	6.1	68.8	0.5	154.6	0.5	0.9	7	21.6	285.7	1.3	35.9	69.2	2.6	2	0.5	3	1
(CML312/CML395)/(CKLTI0368)	3	6.1	69.3	1	127.5	0.4	1	23.7	22.4	286.7	0	37	70.4	-0.1	2.9	1	2.5	2.5
(CKDHL0159/CKDHL0295)/(CKLTI0344)	48	6	67.8	0.5	175.4	0.6	1	11.8	20.8	317.1	2.8	37.2	68.4	2.9	2	0	3	1
(CKDHL0089/CKDHL0295)/(CKLTI0344)	47	5.9	65.8	1	150.1	0.5	0.9	11.4	22.5	289.1	0	36.6	66.9	-0.2	2.5	0.5	2.9	
(CML312/CML395)/(CKLTI0344)	45	5.8	65.4	1.5	149.4	0.5	1	7.9	20.2	303.2	0	37	66.9	0.1	2.9	0	2.5	1
(CKDHL0159/CKDHL0295)/(CKLTI0368)	6	5.7	70.5	-0.1	145.5	0.5	0.9	12.4	21.3	276.7	4.1	35.6	70.2	5.5	3.1	0	2.5	1
(CML489/CML444)/(CKLTI0272)	30	5.7	67.1	2	146.8	0.5	1	9.8	20.2	296.4	1.5	32.7	68.9	3	2.1	0	3	2.5
(CML395/CML444)/(CKLTI0344)	43	5.6	65.8	0.5	156.2	0.5	0.9	9.5	21.7	308.5	0.1	35.8	66.5	1.2	2.5	0	3	1
(CKDHL0089/CML395)/(CKLTI0344)	49	5.5	65.8	1	144.2	0.5	0.9	13	21.5	292.4	0	34.6	67	3	3.2	0.1	2.5	2
(CKDHL0089/CKDHL0333)/(CKLTI0344)	46	5.4	66.2	1	144.8	0.5	0.9	10.2	21.7	292.3	1.4	34.6	67.2	-0.1	2.5	0	3.4	1
(CML312/CML395)/(CKLTI0272)	31	5.2	66.2	1	131.5	0.4	0.9	12.9	20.1	295.5	1.5	35.6	67.4	-0.1	2.7	0	3	2
(CML312/CML395)/(CKLTI0036)	17	5.1	68.5	1	145.5	0.5	1	4.7	20.8	278.6	0	37.5	69.6	0.1	2.6	0	3	1
(CML489/CML444)/(CKLTI0344)	44	5	66.2	0.9	152.3	0.5	0.8	13.3	20.7	298.4	4.3	35.9	66.8	4.1	2.5	0	2.5	3
<b>Pioneer 3253</b>	54	4.5	66.8	2	143.6	0.5	0.8	23.6	20.1	309.8	0	35.6	68.8	4.3	2.9	0.5	2.5	1.5
<b>DH04</b>	55	4.3	66.4	2.5	137.7	0.5	0.9	17.2	19.8	287.4	6.1	32.6	68.8	1.7	3.1	0.5	2.5	1
<b>DK8053</b>	52	4	66.1	2.5	147.2	0.5	0.8	19.7	19.8	294.2	1.6	33.1	68.4	1.9	3.2	0	2.5	2
<b>DK8031</b>	53	2.1	65.2	3.5	131.7	0.5	0.7	9.4	18.3	275.8	1.5	34.2	68.6	4.3	4.5	0	3	2
<b>Entry_Variance</b>		0.9	1.8	0.3	120.5	0	0	12.9	0.3	148	0.4	0.6	1.1	0.6	0.2	0	0.1	0
<b>Residual_Variance</b>		0.5	1	0.9	28.1	0	0	25.2	0.8	46	2.4	2.6	1.1	3.1	0.2	1.1	0.2	0.8
<b>Grand_Mean</b>		6.5	67.7	1.1	146.2	0.5	1	10.3	20.9	298.1	0.9	36	68.9	1.3	2.4	0.3	2.5	1.5
<b>LSD</b>		1.4	2.1	1.9	12.2	0	0.1	9.9	1.9	15.4	3.3	3.4	2.2	3.6	0.9	2.2	0.9	3.1
<b>CV</b>		10.6	1.5	83.3	4.1	3.2	6.2	47.1	4.4	2.5	178.8	4.6	1.5	132.3	18.8	380.7	18.5	106.6
<b>Heritability</b>		0.8	0.8	0.4	0.9	0.9	0.6	0.5	0.5	0.9	0.3	0.3	0.7	0.3	0.6	0	0.4	0

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turcicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking

APPENDIX 17 Kiboko well-watered means of grain yield and other agronomic traits

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	GYG	MOI	PH	SAT	SD	SL	EA	LS
(CML312/CML395)/(CKLTI0152)	10	3.7	65.5	2	107.3	0.5	0.9	0	3.6	13.1	226.3	40	67.5	49.1	1.4	6.1
(CKDHL0089/CKDHL0333)/(CKLTI0147)	39	3.3	67	0	128.3	0.5	0.9	0	3.2	12.2	248.8	37	67	68.3	2.1	5.1
(CML395/CML444)/(CKLTI0036)	15	3.3	66.2	1.5	141.5	0.6	0.9	0	3.4	13.4	242.4	37.5	68	50.5	1.8	7.6
(CKDHL0089/CKDHL0333)/(CKLTI0200)	25	3.2	66.1	1	116.3	0.5	1	0	3.1	13.4	247.8	33.5	67	41.2	2	5.6
(CKDHL0089/CML395)/(CKLTI0147)	42	3.2	65.5	2	119.8	0.5	0.9	0	3.1	12.5	232.5	37	67.4	36.2	2	5.4
(CML395/CML444)/(CKLTI0152)	8	3.1	67.5	3.5	118	0.5	0.9	0	3.1	11.4	225.9	36.5	70.8	20.7	1	5.7
(CML395/CML444)/(CKLTI0272)	29	3.1	63.8	3	123.8	0.5	0.9	0	3.1	14.6	230.6	37.5	67	43	2.2	6.9
(CKDHL0089/CKDHL0333)/(CKLTI0344)	46	3.1	65.3	1	129.3	0.5	1	0	3.2	12.1	240.7	37.5	66.5	15	2.7	4.9
(CML395/CML444)/(CKLTI0147)	36	3.1	66.7	2	119.8	0.5	0.9	0	3.1	12	243.5	39.5	69	23.3	1.4	6.3
(CKDHL0089/CML395)/(CKLTI0152)	14	3.1	67.9	3	116	0.5	0.8	0	3	13.5	237.9	38.5	71.1	37.3	2	5.6
(CML489/CML444)/(CKLTI0147)	37	3.1	67.1	-0.5	117.5	0.5	1	0	3.1	12.5	226.5	37.5	66.6	42.3	1.9	6.4
(CML489/CML444)/(CKLTI0152)	9	3	67	2.5	118	0.5	0.9	0	3.1	12	228.7	36.5	69.4	24.2	2.5	6.1
(CKDHL0089/CML395)/(CKLTI0344)	49	3	63.9	1.5	129	0.6	0.8	0	3	12.4	232.6	36	65.6	34.2	2	5.8
(CKDHL0089/CML395)/(CKLTI0200)	28	3	63.6	2.5	116.8	0.5	0.8	0	2.8	12.5	240.6	38.5	66	40.3	2.5	6.3
(CML489/CML444)/(CKLTI0344)	44	3	65	0.5	127.8	0.5	0.9	0	3.2	13.7	232.6	37.5	65.4	33.1	2.1	6.4
(CML489/CML444)/(CKLTI0368)	2	3	68.5	0.5	129.5	0.5	0.9	0	3	12.9	234.8	36.5	69	76.2	1.8	5.4
(CKDHL0089/CKDHL0295)/(CKLTI0272)	33	2.9	64.6	2.5	110	0.5	1	0	2.8	11.7	230.1	38	67	44.9	2.1	7.4
(CML395/CML444)/(CKLTI0368)	1	2.9	69.1	0	124.5	0.6	0.9	0	2.9	12.5	227.4	37	68.9	61.5	1.1	5
(CKDHL0089/CKDHL0333)/(CKLTI0368)	4	2.8	68.4	0.5	115	0.5	1	0	2.7	13	229.5	36	69	84.7	2.2	6.5
(CKDHL0089/CKDHL0295)/(CKLTI0152)	12	2.8	67.5	2	117.8	0.5	0.8	0	2.7	12.6	230.4	38.5	69.4	35.9	2.4	6
(CKDHL0159/CKDHL0295)/(CKLTI0152)	13	2.8	67	2	116.8	0.5	0.8	0	2.8	12.5	217.8	38	68.9	48.6	1.9	5.6
(CML312/CML395)/(CKLTI0344)	45	2.8	64	2.5	116.3	0.5	0.9	0	2.9	11.4	232.3	38.5	66.6	39.3	3.1	5.6
(CML312/CML395)/(CKLTI0147)	38	2.8	65.5	2	112.3	0.5	0.8	0	2.8	13.5	234.9	37.5	67.5	55.6	1.7	6.3
(CKDHL0159/CKDHL0295)/(CKLTI0036)	20	2.8	66.4	0.5	136	0.6	0.9	0	2.8	11.5	238.2	34.5	67	53.8	1.8	8.1
(CKDHL0089/CKDHL0333)/(CKLTI0152)	11	2.8	67.6	3	122	0.5	0.9	0	2.7	13.1	236.1	35	70.5	43.3	2	5
<b>DH04</b>	55	2.7	55.1	0	91	0.5	0.8	0	2.4	11.8	191.3	38.5	55	85.4	2.1	8.9

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	GYG	MOI	PH	SAT	SD	SL	EA	LS
(CML489/CML444)/(CKLTI0200)	23	2.6	63.9	2.5	102.5	0.5	0.8	0	2.5	15.6	214.1	37.5	66.5	39.8	2.5	8
(CML395/CML444)/(CKLTI0200)	22	2.6	63.5	2.5	115.5	0.5	0.8	0	2.4	12.5	233.3	38.5	66	34.3	2.9	6.3
(CKDHL0089/CKDHL0295)/(CKLTI0200)	26	2.6	66	0.5	119	0.5	0.8	0	2.5	12.7	244.2	36.5	66.4	52.2	2.4	5.3
(CKDHL0159/CKDHL0295)/(CKLTI0368)	6	2.6	68.6	0	120.8	0.5	0.9	0	2.5	11.1	219	36	68.5	77.6	1.8	6
(CKDHL0089/CKDHL0333)/(CKLTI0272)	32	2.6	64.9	2	113.3	0.5	0.7	0	2.5	13.3	232.3	40.5	66.9	50.7	2	7.7
(CKDHL0089/CKDHL0295)/(CKLTI0147)	40	2.5	66.5	3	119	0.5	0.8	0	2.5	12.5	233.1	38.5	69.5	34.4	1.8	5.6
(CKDHL0159/CKDHL0295)/(CKLTI0147)	41	2.5	67	1	125	0.5	0.8	0	2.6	12.2	231.2	38.5	68	62.1	2.1	5.9
(CKDHL0089/CKDHL0295)/(CKLTI0036)	19	2.5	65.9	1.5	140.3	0.6	0.9	0	2.5	12.7	242.4	37	67.6	43.7	2.4	7.6
(CKDHL0089/CML395)/(CKLTI0036)	21	2.5	65.6	1.5	132	0.6	0.7	0	2.5	11.2	233.1	38	67	56.3	2.1	6.8
(CML312/CML395)/(CKLTI0272)	31	2.5	64	4	105.3	0.5	0.9	0	2.5	13.4	231.3	38.5	68.2	31.5	2.4	7.8
(CKDHL0159/CKDHL0295)/(CKLTI0200)	27	2.4	63.7	2.5	115	0.5	0.8	0	2.3	11.7	230	36.5	66	36.3	3	6.1
(CML395/CML444)/(CKLTI0344)	43	2.4	63.4	2	135.5	0.6	0.5	0	2.4	15.5	240.5	36	65.5	46.9	2	6.1
(CKDHL0089/CML395)/(CKLTI0368)	7	2.4	69.5	1	110.5	0.5	1	0	2.4	12.1	219.6	34.5	70.5	82.7	2.2	6.7
(CKDHL0089/CKDHL0295)/(CKLTI0344)	47	2.4	65.1	2	141	0.6	0.6	0	2.4	11.7	242.3	38.5	67	27.9	1.9	7
(CKDHL0159/CKDHL0295)/(CKLTI0344)	48	2.3	65.6	1	135	0.6	0.8	0	2.4	11.3	240.5	37	66.6	69.7	1.7	5.3
(CML489/CML444)/(CKLTI0272)	30	2.3	65.7	2.5	113.3	0.5	0.8	0	2.3	12.4	215.3	37	67.9	48.7	2.2	6.8
(CKDHL0159/CKDHL0295)	51	2.3	66.7	0.5	139.5	0.6	0.7	0	2.2	13.6	232.7	36	67.5	80.7	2.2	5.8
(CKDHL0159/CKDHL0295)/(CKLTI0272)	34	2.3	64.2	2.5	118.5	0.5	0.7	0	2.2	14.3	230.2	36.5	66.5	53.6	2.2	7.3
(CKDHL0089/CKDHL0333)/(CKLTI0036)	18	2.2	65.1	2	130.8	0.6	0.8	0	2.3	10.7	235.7	36.5	67.1	57.6	2	7.6
(CKDHL0089/CML395)/(CKLTI0272)	35	2.2	64.4	3	113.8	0.5	0.8	0	2.2	12.8	227.4	37.5	67.5	31.3	2.1	6.8
(CML489/CML444)/(CKLTI0036)	16	2.2	65.4	2	138.8	0.6	0.7	0	2.3	14.2	227.5	38	67.4	31	2.1	7.6
(CML312/CML395)/(CKLTI0368)	3	2.1	67.1	1.5	105.3	0.5	0.8	0	2.5	12.5	228.9	38.5	68.5	48.8	2.4	6.2
(CML312/CML395)/(CKLTI0200)	24	2	63.6	3	103.3	0.4	0.7	0	1.9	14.6	242.9	37.5	66.5	30.4	2.7	6.6
(CKDHL0089/CKDHL0295)	50	1.9	62	6	103	0.5	0.7	0	2	14.8	222.3	34.5	68.1	-5.4	2.6	8
(CML312/CML395)/(CKLTI0036)	17	1.8	66.7	1.5	117	0.6	0.8	0	2	14.1	211.2	37.5	67.9	71.5	3.6	7.2
DK8053	52	1.7	69.8	4	128	0.6	0.7	0	1.8	13.8	227.6	38.5	73.6	38.4	2.3	7
Pioneer 3253	54	1.6	66.8	6	144.8	0.6	0.6	2.4	1.7	13.1	242.8	37.5	72.6	7.8	3.1	7.8
(CKDHL0089/CKDHL0295)/(CKLTI0368)	5	1.6	70.3	1	111.8	0.5	1	0	1.7	13.1	213.6	33	71.5	49.8	2.9	6.6
DK8031	53	1.4	63.6	6.5	132.8	0.5	0.6	0	1.4	10.5	242.5	37	70	27.8	3.1	7.6
Entry_Variance		0.1	5.1	1.4	88.5	0	0	0	0.1	0	52	0.8	5.7	208	0.2	0.7

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	GYG	MOI	PH	SAT	SD	SL	EA	LS
<b>Residual_Variance</b>		0.3	0.7	1.3	53.8	0	0	0.2	0.2	1.8	82.3	2.6	1	200.9	0.2	0.4
<b>Grand_Mean</b>		2.6	65.7	2	120.9	0.5	0.8	0	2.6	12.8	231.4	37.2	67.7	45.6	2.2	6.5
<b>LSD</b>		1.2	1.8	2.4	16.1	0	0.2	0.9	1.1	2.6	20.8	3.3	2.1	31.7	0.9	1.3
<b>CV</b>		23.4	1.3	58	6.5	4.2	12.9	1048.8	19.9	9.8	4.4	4.4	1.5	34.2	20.6	9.8
<b>Heritability</b>		0.3	0.9	0.7	0.8	0.9	0.5	0	0.3	0	0.6	0.4	0.9	0.7	0.6	0.8

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turcicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking

APPENDIX 18 Homabay means of grain yield and other agronomic traits

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	GYG	MOI	PH	RL	SAT	SD	SL
(CML395/CML444)//(CKLTI0152)	8	6.7	63.6	0	110.6	0.5	0.8	6.8	6.3	22.3	219.4	19.1	40	63.8	3.8
(CKDHL0159/CKDHL0295)//(CKLTI0152)	13	6.6	62	0	108.5	0.5	0.9	2.8	6.4	24.3	215	16.3	42	62.2	14.5
(CKDHL0159/CKDHL0295)//(CKLTI0036)	20	6.5	61.3	0.5	128.8	0.6	0.8	1.8	6.4	22	228	7.1	41	61.3	2.5
(CKDHL0089/CKDHL0295)//(CKLTI0147)	40	6.4	63.2	0	101.2	0.4	0.7	0.1	6	23.4	221.1	16.3	42.5	63.5	8.5
(CKDHL0089/CML395)//(CKLTI0344)	49	6.3	61.4	0	123.6	0.5	0.9	1.7	6.2	23.3	241.2	14.8	40	60.9	10.5
(CKDHL0089/CKDHL0333)//(CKLTI0036)	18	6.2	62.7	1	122.3	0.6	0.8	8.1	5.9	24.3	218.5	18.2	35.5	63.2	16.4
(CKDHL0159/CKDHL0295)//(CKLTI0147)	41	6.2	65.3	0	107.8	0.5	0.7	0.1	5.3	23.9	225	9.4	36	65.2	9
(CKDHL0089/CKDHL0333)//(CKLTI0147)	39	6.1	62.1	2	111.9	0.5	0.8	-0.5	5.9	24	226.3	2	40	63.9	6.2
(CKDHL0089/CML395)//(CKLTI0147)	42	6	61.5	2.5	116.8	0.5	0.8	-0.1	6	20.1	230.6	16.5	34	63.7	29.5
(CML395/CML444)//(CKLTI0344)	43	6	58.6	1.5	125.2	0.5	0.8	1.7	6.6	22.9	234.3	29.5	37.5	60.2	7.1
(CML395/CML444)//(CKLTI0368)	1	5.9	60.6	2	111.6	0.5	0.8	3	6	20.1	212.2	12.1	38.5	62.2	10.5
(CML489/CML444)//(CKLTI0152)	9	5.8	62.7	1.5	116.2	0.5	0.8	3.7	5.5	23.4	223.7	31.6	36.5	64.1	11.5
(CKDHL0089/CKDHL0295)//(CKLTI0344)	47	5.8	59.6	2	124	0.5	0.9	-0.3	6.3	24.8	225	11	39	61	4.9
(CKDHL0159/CKDHL0295)//(CKLTI0200)	27	5.7	60.3	2	101.6	0.5	0.8	0.2	6.1	22.7	211.8	2.1	39.5	62.9	8.8
(CKDHL0089/CKDHL0295)//(CKLTI0152)	12	5.7	61.2	1	107.8	0.5	0.8	1.1	5.7	24	229.3	21.9	41	62.5	15.8
(CKDHL0159/CKDHL0295)	51	5.6	61.8	1.5	118.3	0.6	0.7	0.2	5.5	22.5	206	23	42.5	63	4.7
(CML312/CML395)//(CKLTI0147)	38	5.6	63.4	1.5	106.1	0.5	0.7	9.1	5.2	22.6	224.1	25.7	37.5	65.1	7.8
(CML312/CML395)//(CKLTI0200)	24	5.5	61.4	2	102.2	0.5	0.8	1.5	5.4	21.8	223.4	12.4	42.5	63.4	17.6
(CKDHL0089/CKDHL0295)	50	5.5	63.2	3	113	0.5	0.8	4.5	4.9	25.1	212	13.9	35.5	66.3	1.1
(CML312/CML395)//(CKLTI0344)	45	5.4	60.1	2.5	122.6	0.5	0.8	3	5.8	21.5	232.1	17.9	43	62.1	20.8
(CKDHL0159/CKDHL0295)//(CKLTI0344)	48	5.4	59.4	1.5	116.7	0.5	0.8	2.7	5.9	21.6	218.3	30.1	41	61.8	23.2
<b>DK8053</b>	52	5.3	62.3	2	121.3	0.5	0.7	0	5	20.3	226.4	15	41	64.9	10.9
(CKDHL0089/CKDHL0333)//(CKLTI0200)	25	5.3	61.1	1	104.2	0.5	0.8	-0.1	5.2	23.9	208.4	22.1	37	62.2	18
(CKDHL0089/CML395)//(CKLTI0200)	28	5.2	60.6	2	94.4	0.4	0.8	3	5.6	23.6	209.3	4.9	39.5	62.3	8.9
(CML312/CML395)//(CKLTI0036)	17	5.2	61.6	0	108.3	0.5	0.8	2.1	5.1	23.2	206.4	5.8	40	61.4	3.7
(CML395/CML444)//(CKLTI0147)	36	5.1	62.1	0	116.3	0.5	0.7	5.6	5	19.2	230.5	0.9	40.5	61.8	3.8

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	GYG	MOI	PH	RL	SAT	SD	SL
(CML312/CML395)/(CKLTI0152)	10	5.1	60.2	1.5	108.1	0.5	0.7	1.3	5.3	23.2	233.7	29.7	40	62.3	13.7
(CKDHL0089/CKDHL0333)/(CKLTI0152)	11	5.1	62.1	2	102.9	0.5	0.7	11.1	5	23.3	214.1	12.5	32.5	64.2	10.3
(CKDHL0089/CML395)/(CKLTI0152)	14	5.1	62	1	100.4	0.5	0.8	-0.1	5	22.9	218.5	16.6	42	63.1	16.9
(CML395/CML444)/(CKLTI0200)	22	5.1	60.1	3	102.9	0.5	0.7	0.6	5.5	23.3	213.2	20.4	40.5	62.4	5.6
(CML489/CML444)/(CKLTI0344)	44	5.1	60.7	0.5	122	0.6	0.9	1	5.1	23.3	219.7	14.6	37	61.8	10.5
(CKDHL0089/CKDHL0295)/(CKLTI0272)	33	5	62	2	108.6	0.5	0.8	0.1	4.7	21.1	225.9	18.7	33.5	63.9	7.3
(CML489/CML444)/(CKLTI0036)	16	5	63	0.5	117.4	0.6	0.8	3.3	4.4	22.9	198.6	16.2	35	63.6	8.7
(CKDHL0089/CKDHL0333)/(CKLTI0344)	46	5	59.5	4.5	116.5	0.5	0.8	4.9	5.5	24.4	224	9.7	39.5	64.2	5.1
(CKDHL0089/CKDHL0295)/(CKLTI0200)	26	4.9	61.3	0	105.8	0.5	0.8	0.1	5.1	22.6	213.4	17.6	39.5	61.3	7.5
(CKDHL0159/CKDHL0295)/(CKLTI0272)	34	4.7	60.9	0	111.1	0.5	0.8	4.6	4.7	21.3	220.5	18.7	37.5	60.7	6.3
(CKDHL0089/CML395)/(CKLTI0272)	35	4.5	59.6	1	106.7	0.5	0.8	1.6	4.8	20.6	225.1	23.7	38.5	61	8
(CML312/CML395)/(CKLTI0272)	31	4.4	60.7	2	101.7	0.5	0.8	1.5	4.5	21.6	225.2	0.8	42	62.1	13.1
(CKDHL0089/CKDHL0295)/(CKLTI0036)	19	4.3	57.7	1.5	129.5	0.6	0.9	4.8	5.4	25	227.9	29.8	28.5	59.8	9.3
(CML489/CML444)/(CKLTI0368)	2	4.3	62.4	1.5	107.6	0.5	0.8	10.2	4.2	21.6	204.8	20.2	44	63.2	5.7
(CKDHL0159/CKDHL0295)/(CKLTI0368)	6	4.3	63	2.5	107.8	0.5	0.8	2.8	3.7	23.4	201.7	41.6	32.5	65.6	24.4
(CML312/CML395)/(CKLTI0368)	3	4.2	60.8	4	100.5	0.5	0.8	7.9	4.4	22.4	210.8	1.9	42	64.9	14.5
(CKDHL0089/CML395)/(CKLTI0368)	7	4.2	61.2	1	105.9	0.5	0.7	9.1	4	19.6	208.7	10.3	36.5	62.1	25.2
(CKDHL0089/CKDHL0333)/(CKLTI0272)	32	4.1	61	2.5	105.7	0.5	0.7	9.5	4.3	22.6	210.6	16.1	36	63.5	12.5
(CML395/CML444)/(CKLTI0036)	15	4	62.8	2	125	0.6	0.9	7.7	3.8	22.9	211.8	11.4	35.5	64.5	8.6
(CML489/CML444)/(CKLTI0147)	37	3.9	61	1	102.5	0.5	0.8	10.7	4.1	22.5	201.3	12	33	61.9	4.4
<b>DH04</b>	55	3.9	62.5	0.5	103.3	0.5	0.6	7	3.4	21.6	205.6	10.4	31.5	63.3	7.6
(CKDHL0089/CML395)/(CKLTI0036)	21	3.9	61.5	1.5	119.6	0.6	0.7	2.7	4	22.8	216.2	14.1	38	62.5	1.3
(CML395/CML444)/(CKLTI0272)	29	3.8	60	3	117.7	0.5	0.7	3.3	4.2	21.3	231.3	24.7	41	62.4	2.4
(CKDHL0089/CKDHL0295)/(CKLTI0368)	5	3.7	64.4	1	98.5	0.5	0.6	7.6	2.9	20.8	194.1	32.1	33.5	65.1	11.1
(CML489/CML444)/(CKLTI0200)	23	3.6	58.2	3	100.7	0.5	0.8	3.2	4.5	22.6	203.4	8.9	43	61.4	8.2
(CKDHL0089/CKDHL0333)/(CKLTI0368)	4	3.6	63.5	3	98	0.5	0.7	7	3	23	194.6	18.7	39	66.5	15
<b>Pioneer 3253</b>	54	3.5	61.9	3.5	128.8	0.6	0.5	10.4	3.3	22.1	230.2	32.8	43	66.5	11.6
(CML489/CML444)/(CKLTI0272)	30	2.7	58.8	1	106.4	0.5	0.8	5.3	3.2	22.3	207.2	27.2	39.5	60.2	11.4
<b>DK8031</b>	53	2.6	58.7	2	107.8	0.5	0.4	10.6	3.1	19.5	201	19.5	33.5	61.4	11.3
<b>Entry_Variance</b>		0.3	1.1	0.1	56.5	0	0	1.4	0.3	0.2	67.8	0	2.6	0.5	0.2

Pedigree	Entry	BLUE	AD	ASI	EH	EPO	EPP	ER	GYG	MOI	PH	RL	SAT	SD	SL
Residual_Variance		1	2.2	2.2	39.6	0	0	21	1	2.6	72.8	139.9	16.6	4	54.6
Grand_Mean		5	61.4	1.6	111.1	0.5	0.8	3.8	5	22.5	217.3	16.9	38.4	62.9	10.5
LSD		2.2	3.3	3	15.4	0	0.2	9.7	2.2	3.6	21.1	25.8	8.8	4.5	16.3
CV		22.1	2.6	94.8	6.8	4.1	14.6	124.3	22	7.9	4.8	75	11.3	3.5	76.5
Heritability		0.4	0.5	0.1	0.7	0.9	0.3	0.1	0.4	0.1	0.7	0	0.2	0.2	0

KEY: GY Grain yield; AD Days to 50% anthesis; ASI Anthesis silking interval; EA Ear aspect; EH Ear height; EPO ear position; EPP ears per plant; ER number of rotten ears; ET *Turcicum* leaf blight; GLS *Gray* leaf spot; GYG grain yield-field weight; HC husk cover; LS leaf senescence; MOI grain moisture; MSV *Maize streak virus*; PA plant aspect; PH plant height; PS *Puccini sorghi*; RL root lodging; SL stem lodging; SAT plant stand; SD days to 50% silking

#### APPENDIX 19 Phenotypic correlation for grain yield among locations

_NAME_	Homabay	KYUC	Kaguru	Kakamega	Kiboko_DR	Kiboko_Opt	Mtwapa	Shikutsa
Homabay	1	0.2335101	0.2334304	0.274998	0.2283388	0.0959026	0.1638454	0.3287776
KYUC	0.2335101	1	0.509097	0.4077521	0.4797298	0.6119686	0.328112	0.5003845
Kaguru	0.2334304	0.509097	1	0.6215361	0.5380371	0.387733	0.2994584	0.5722208
Kakamega	0.274998	0.4077521	0.6215361	1	0.5560242	0.3566498	0.2962053	0.7233784
Kiboko_DR	0.2283388	0.4797298	0.5380371	0.5560242	1	0.434652	0.3283699	0.5173751
Kiboko_Opt	0.0959026	0.6119686	0.387733	0.3566498	0.434652	1	0.3756704	0.3159711
Mtwapa	0.1638454	0.328112	0.2994584	0.2962053	0.3283699	0.3756704	1	0.3305663
Shikutsa	0.3287776	0.5003845	0.5722208	0.7233784	0.5173751	0.3159711	0.3305663	1

KYUC Kirinyaga University College; Kiboko\_DR Kiboko drought trial; Kiboko\_Opt Kiboko well-watered



## APPENDIX 20 Genetic correlation for grain yield among locations

COL1	Homabay	KYUC	Kaguru	Kakamega	Kiboko_DR	Kiboko_Opt	Mtwapa	Shikutsa
Homabay	1	0.4224924	0.4671154	0.4900636	0.64536	0.1745929	0.3186337	0.6164599
KYUC	0.4224924	1	0.7149753	0.5099679	0.9515744	0.7818966	0.4478198	0.6584611
Kaguru	0.4671154	0.7149753	1	0.8597387	1	0.5479066	0.4520342	0.8328053
Kakamega	0.4900636	0.5099679	0.8597387	1	1	0.4488195	0.3981839	0.9375651
Kiboko_DR	0.64536	0.9515744	1	1	1	0.8675028	0.7000896	1
Kiboko_Opt	0.1745929	0.7818966	0.5479066	0.4488195	0.8675028	1	0.515907	0.4183664
Mtwapa	0.3186337	0.4478198	0.4520342	0.3981839	0.7000896	0.515907	1	0.4675511
Shikutsa	0.6164599	0.6584611	0.8328053	0.9375651	1	0.4183664	0.4675511	1

KYUC Kirinyaga University College; Kiboko\_DR Kiboko drought trial; Kiboko\_Opt Kiboko well-watered

## APPENDIX 21 Heritability of tropical-temperate maize hybrids evaluated during 2014

Trait	Managed Drought	Optimum
Grain yield	0.449090564	0.747541995
Days to anthesis	0.4479	0.8635
Anthesis silking interval	0.383020303	0.728647878
Plant height	0.630592942	0.926743357
Ear height	0.857967282	0.938401312
Leaf senescence	0.664627324	
Grain moisture	0.068116176	0.729972626
Root lodging	0	0.085000709
Stem lodging	0.228400957	0.101951341
Ear aspect	0.498562375	0.777381233
<i>Turcicum</i> leaf blight		0.705994244
<i>Gray leaf spot</i>		0.040847653
<i>Maize streak virus</i>		0.114419148