GENETIC ANALYSIS OF DROUGHT TOLERANCE AND EARLINESS IN TROPICAL MAIZE (*Zea mays* L.) GERMPLASM

WACHENJE DOROTHY WANJALA

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DECLARATION AND RECOMMENDATION

Declaration

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

Signature: Date 26.03.2023…….

Wachenje Dorothy Wanjala

KM21/11762/16

Recommendation

This thesis has been submitted with our approval as University supervisors.

Signature: Date …12/04/2023……

Dr. Pascal Okwiri Ojwang (PhD)

Department of Crops, Horticulture and Soils

Egerton University, Njoro.

Signature Date…27/03/2023…..

Dr. Murenga Mwimali (PhD)

Maize Programme

Kenya Agricultural and Livestock Research Organization

Nairobi, Kenya

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DEDICATION

I dedicate this work to the Wachenje family, for their love and steadfast support throughout my study period.

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ABSTRACT

Drought is a major production constraint limiting maize production in sub-Saharan Africa. Adoption of improved hybrid maize cultivars with resilience to drought stress is necessary for enhanced productivity in the semi-arid areas. The objectives of this study were; (i) identify elite single-cross maize hybrids that are drought tolerant and early maturing for semi-arid Kenya and (ii) to estimate the combining ability effects for drought tolerance and earliness among single-cross maize hybrids in semi-arid Kenya. Two experiments were carried out at the Kenya Agricultural and Livestock Research organization Katumani Research Centre and Kiboko sub-Centre. The first experiment involved evaluation of ninety-one single-cross maize hybrids alongside seven commercial checks for drought tolerance under random and managed drought conditions in two replications. In the second experiment, eleven parents were crossed a half diallel mating design excluding self's and reciprocals to generate fifty-five crosses. The fifty-five crosses were evaluated alongside two commercial checks in an alpha-lattice design with two replications. Results from the first experiment revealed significant differences ($p<0.05$) for genotypes, locations and genotype by location interactions for yield and yield related traits studied. Broad sense heritability for grain yield trait of 61.93% was recorded under managed drought and 1.95% under to random drought while anthesis-silking interval recorded 3.02% and 8.2% respectively. Genotypes KAT-DT-EE-02, KAT-DT-EE-04 and KAT-DT-EE-05 recorded the lowest cultivar superiority values of 0.20, 0.23 and 0.26 respectively on the cultivar superiority index hence were consistently well ranked across the test environments. From the second experiment, crosses KAT-DT-EE-07×KAT-DT-EE-14 (6.18t ha^{-1}) and KAT-DT-EE-07×KAT-DT-EE-04 (6.16t ha^{-1}) had superior grain yield while KAT-DT-EE-07×KAT-DT-EE-14 showed significant low values for anthesis silking interval (0.5) hence adapted to drought. Genetic analysis revealed significant ($p<0.05$) general combining ability and specific combining ability mean squares for most measured traits which underscored the importance of both additive and non-additive genetic variance in their inheritance. Significant interaction of general combining ability with location effects demonstrated the need for multi-location testing of potential cultivars. Cross KAT-DT-E-06×KAT-DT-EE-04 (-0.27^{*}) had significant specific combining ability for a reduction in anthesis silking interval in managed drought conditions. Significant specific combining ability effects for grain yield were recorded in KAT-DT-M-31×KAT-DT-EE-07(1.72^{*}) which demonstrated the potential of obtaining drought tolerant hybrids for possible future deployment to farmers in drought endemic areas.

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LIST OF ABBREVIATIONS AND ACRONYMS

ANOVA	Analysis of variance
ASAL's	Arid and semi-arid lands
ASI	Anthesis -silking interval
CIMMYT	International Maize and Wheat Improvement Center
CML	CIMMYT maize lines
FAO	Food and Agriculture Organization of the United Nations
GCA	General combining ability
GEI	Genotype by environment interactions
HSD	Honestly significant difference
KALRO	Kenya Agricultural and Livestock Research Organization
Kcal	Kilocalories
OPV	Open pollinated variety
QTLs	Quantitative trait loci
SCA	Specific combining ability
SSA	Sub-Saharan Africa

CHAPTER ONE

INTRODUCTION

1.1 Background of the study

Maize is a major cereal crop worldwide. However, drought causes a significant negative impact on global food supply resulting in an estimated 34% yield loss each year, with dry areas facing more serious challenges (FAOSTAT, 2021). It is projected that major maize producing areas will become drier besides experiencing warmer temperatures and attacks by new pests and diseases (Ahsan *et al.*, 2015). The enormous impact of drought is in sub-Saharan Africa where 97% of the crop is grown under rain-fed conditions and up to 25% of cultivated land suffers frequent droughts (Mutiso & Kimtai, 2022; Worku *et al.*, 2020). Subsequently, farmers dependent on rain-fed farming are being pushed to marginal growing areas where they are more vulnerable to drought and unpredictable weather patterns resulting from climate change (FAOSTAT, 2019). In Kenya, the arid and semi-arid lands (ASAL's) constitute more than 80% of the total land area, host about 10 million people and are exposed to climate variability (Herero *et al.*, 2010). In recent decades, pronounced rainfall variability in ASAL's has resulted in unpredictable lengths of growing seasons Omoyo *et al.* (2015), where an estimated 2.4 million people are severely food insecure (FAO, 2021).

Farming in Kenya is mainly practiced by small-scale farmers who produce about 75% of total maize consumed and 75% of the market output (Mutiso & Kimtai, 2022). However, these farmers have limited access to irrigation technology exposing them to rainfall variation risk (Kalungu *et al.*, 2013). In addition, there is an increasing pressure on land with agricultural potential which is likely to drive population migration to the ASAL's (Mutiso & Kimtai, 2022). Farmers in ASAL's have limited access to suitable maize varieties prompting them to grow varieties recommended for medium to high potential areas, which are less adapted to drought conditions thereby leading to crop failures (Muli *et al.*, 2017). Access to suitable varieties adapted to target agro-ecologies may potentially increase maize production and improve food security among small-scale farmers in dry areas.

Genetic variation for drought tolerance has been exploited to develop genotypes that are better adapted to drought stress (Badu-Apraku *et al.*, 2013). Important traits such as plant growth and development, plant phenology, grain-filling and translocation of photo-assimilate reserves are targeted (Ahsan *et al.*, 2015). The most widely used strategy in selection for drought tolerance is to select for grain yield in optimal conditions and then later evaluate selections in multiple sites with variable moisture conditions termed random stress (Magorokosho *et al*., 2003).

Genetic gains for drought tolerance in the tropical maize germplasm are associated with a reduced anthesis silking interval, days to 50% tasseling, days to 50% silking, plant height, ear height, grain yield per plant and earliness (Ali *et al*., 2017; Dar *et al.,* 2017; Ngugi *et al*., 2013). Hybrid maize gives a higher yield under both random and managed drought conditions in comparison to open pollinated varieties (OPVs) of maize (Blum, 2011b).

Drought tolerant hybrids and OPVs of maize have been in cultivation in many countries in the continent of Africa. However, to improve food security, the level of adaptability towards drought requires further improvement (Aslam *et al*., 2015). Significant genotype by environment interactions (GEI) in response to drought stress show that there is substantial genetic variation in breeding populations (Ali *et al*., 2017). Significant GEI and in particular, the presence of cross over type of interaction complicates the identification of superior genotypes (Nyombayire *et al*., 2018). Developing drought tolerant germplasm has demonstrated to be effective, efficient and feasible method to improve maize yields in drought prone regions (Rezende *et al*., 2019).

1.2 Statement of the problem

Drought is a serious challenge in maize production in the world. In Kenya, maize production has been on a decline over the last decade due to low and irregular rainfall. The frequency and severity of extreme climatic events has been aggravated by climate change leading to perennial crop failure. Apart from climate variability, deployment of genetic resistance to curb yield losses arising from drought has been restricted by absence of drought resistant varieties that yield high under semi-arid conditions. Yield losses have caused food shortages and malnutrition thus impacting negatively on Kenya's food security requirements. The breeding programme at Kenya Agricultural and Livestock Research organization (KALRO) Katumani in collaboration with the International Maize and Wheat Improvement Centre (CIMMYT) have in the past released early maturing varieties with 50 to 60 days to flowering as a drought escape strategy to manage drought. Through such initiatives, drought escaping varieties namely; Katumani and Makueni composites were developed for commercial exploitation in mid and low altitude agro-ecological zones, but their yields are far below average compared to hybrids. In addition, released hybrids currently under cultivation are not resilient to marginal growing zones. Low cultivar adoption may be attributed to earlier breeding objectives that largely prioritized selection for drought escape without considering drought tolerance. The development of drought tolerant maize varieties will improve food security and climate resilience hence will improve the live hoods of resource constrained farmers.

1.3 Objectives

1.3.1 Broad objective

To contribute towards food security by developing double cross-cross hybrids that are drought tolerant and early maturing with good average grain yield in Kenya.

1.3.2 Specific objectives

i. To identify elite single-cross maize hybrids that are drought tolerant and early maturing for semi-arid Kenya.
ii. To estimate the combining ability effects for drought tolerance and earliness among single-cross maize hybrids in semi-arid Kenya.

1.4 Hypotheses

For the germplasm assembled for this study;

i. There is no significant variation for drought tolerance and earliness among single-cross maize hybrids for semi-arid Kenya.
ii. There are no significant combining ability effects for drought tolerance and earliness among single-cross maize hybrids in semi-arid Kenya.

1.5 Justification of the study

Maize is a staple food and the most important in Kenya’s strategic food reserve (Kange’the *et al*., 2020). It accounts for 35% of the population’s total calorific intake (FAO, 2019). Maize shows great sensitivity to drought stress resulting in pronounced yield losses. Kenya experiences major droughts in every decade while minor droughts occur once in about four years (Herero *et al.*, 2010). Extreme drought stress results in failure of maize crop with a significant impact on national food security (Daryanto *et al*., 2016). Maize crop failures cause a decline in the per capita calorie availability and general human well-being. For instance, maize production declined from 3.789 M tonnes in 2020 to 3.303M tonnes in 2021, translating to 12.8% decrease (Mutiso & Kimtai, 2022). Consequently, a decline in calorie availability is exhibited by an increase in malnutrition especially among young children (Herero *et al*., 2010). Projections show an increase in the demand for food resulting from a population rise together with economic development (Shiferaw *et al*., 2011).

Resource constrained farmers prefer drought tolerant and early maturing maize varieties due to their limited capacity to access irrigation (Cairns *et al.*, 2013). Early maturity and grain yield are considered the most important traits to farmers when selecting maize seeds for drought endemic areas (Worku *et al.*, 2020). Hybrid varieties produce higher grain yields compared to OPVs (Kutka, 2011). However, limited access to suitable drought tolerant maize varieties necessitate the development of drought tolerant maize varieties adapted to arid and semi-arid lands.

The development of drought tolerant maize and early maturing varieties will contribute towards the attainment of sustainable development goal two whose aim is to have a world free of hunger by 2030. Additionally, drought tolerant hybrid maize varieties with improved grain yield will lead to the attainment of the African Union goal of improved agricultural production and productivity by 2063. This work is also aligned to the Kenya government's manifesto on reducing food imports by increasing agricultural productivity.

CHAPTER TWO
LITERATURE REVIEW

2.1 Origin, genetics and botany of maize

Maize (*Zea mays* L.) production dates to about 5,000 years ago (Hallauer *et al*., 1988). It was introduced to the continent of Africa in the 16th Century by Portuguese explorers (Halluer *et al*., 1988). It is postulated that its progenitor may be a domesticated version of teosinte, a wild grass that is cultivated in Mexico and Guatemala (Ullrich, 2007). Hallauer *et al*. (1988) described maize as a diploid (2n=20) monocotyledon of the family *poaceae,* also called *graminaeae,* the grass family. The genus has four species; *Zea mays* which is cultivated maize, *Zea diploperennis* which is diplo perennial teosinte, *Zea luxurians* and *Zea perennis* which are both perennial teosintes. *Zea mays* is the most widely cultivated among these four species.

Maize is an allogamous species with heterogeneous natural populations (Ali *et al.*, 2014). It contains a female part referred to as ear and male part referred to as tassel flowers in separate places on the plant (Sheikh *et al*., 2017). According to Hallauer *et al*. (1988), staminate flowers are borne on the tassel and pistillate flowers are borne midway of the stalk. The main stem of the maize plant terminates into a tassel flower that bears two flowered staminate spikelets, each flower bears three anthers. A single tassel from a normal plant produces an average of 25,000 pollen grains. The principal agent of pollen transfer in open maize pollination is wind. Pollen is carried for great distances however, most of the pollen that pollinates an ear of a maize plant comes from plants in the immediate vicinity. Pollen shedding begins about three days after the silk becomes receptive to pollen. Temperatures above 35°C may kill pollen during the pollination period, however, seed set is unaffected if 10% of the pollen grains survive. The kernel of maize has a pericarp of the fruit fused with the seed coat, it is close to a multiple fruit in structure, except that the individual fruits never fuse into a single mass (Ali *et al*., 2014). Maize grain constitutes about 42% of the total plant's dry weight which depends on genetic, environmental and cultural conditions (Sheikh *et al*., 2017).

2.2 Importance of maize production

Maize is the third most important food crop in the world with a production of about 3.89 million metric tonnes of maize annually on over 2.2 million hectares of cultivated land area (FAOSTAT, 2021). It is a staple food for about 1.2 billion in the world and about 300 million people in sub-Saharan Africa (Shiferaw, 2011). About 95% of the maize produced in Africa is primarily for human consumption accounting for 42% of world's food calories, with per capita caloric intake ranging from 52 to 328 g per day (FAOSTAT, 2021).

Maize is also used as livestock feed and as a raw material in medicine and textile industries. Maize, wheat, rice, barley, sorghum, oat and rye provide about 56% of the total food energy and the protein consumed on earth (Cordain, 1999). The nutritional value of maize includes 72% starch, 10% protein, 4% fat, B vitamins, essential minerals and fibre which supply 365 Kcal/100 g of energy (Ranum *et al.*, 2014).

In Kenya, maize is a major food crop, accounting for 40% of the crop area and more than 51% of all staples grown (CIMMYT, 2015). It accounts for more than 30% of agricultural production and 57% of employment in the agricultural sector (FAOSTAT, 2019; Mutiso & Kimtai, 2022). Maize contributes up to 3% of the agricultural gross domestic product and 21% of the total value of agricultural commodities (FAOSTAT, 2019). The per capita consumption of maize in Kenya is 64 kg/person/year with a national consumption of about 29 million 90 kg bags annually (FAOSTAT, 2019; Ranum *et al.*, 2014).

2.3 Maize production constraints

The major problem facing maize production in Kenya is low yields per hectare of about 1,440 to 1,836 kg compared to 5,751 kg globally (FAOSTAT, 2019). Thus, Africa accounts for only 6.5% of the total global maize produced, while importing more than 20% of its total maize consumed (FAO, 2019). Low maize yields are attributed to limited ability of farmers to cope with drought due to an inadequate capacity to accurately predict rainfall patterns, poor adaptation of maize varieties, climate variability, high cost of irrigation, low input supply, poor agronomic practices, insect pests, infectious maize diseases and poor infrastructure (Ertiro *et al.*, 2017; Worku *et al.*, 2020).

Maize is a versatile crop that is grown from altitudes below sea level to altitudes exceeding 3000 m, in areas that receive annual rainfall of between 250 mm to more than 5000 mm and has a growing cycle that ranges from 4 to 10 months (Sheikh *et al.*, 2017). Maize requires a large amount of water to achieve optimal growth compared to other crops. It requires between 350 to 450 mm of rainfall per annum and at maturity, each maize plant would have consumed 250 litres of water in the absence of water stress to produce 3,152 kg ha^{-1} of grain yield (Zain, 2014). In the semi-arid tropics, irregular rainfall, high temperatures, high levels of solar radiation and poor soil productivity intensify drought effects (Sheikh *et al.*, 2017). Maize production is mainly rain fed, coupled with limited access to irrigation technology which has led to successions of fluctuating maize production and overall low maize productivity in Africa (Oseni & Masarirambi, 2011).

2.4 Physiological basis of yield reduction in maize under drought stress

All developmental stages of maize between germination and reproduction are susceptible to drought (Blum, 2011a). Drought stress reduces seed viability and germination potential of maize seeds by inhibiting metabolic activation required to break down dormancy or convert stored food into consumable form (Aslam *et al*., 2015). Severe drought stress results in poor absorption and seedling germination (Achakzai, 2009).

Growth and development which is important to establish a normal maize plant structure required to undertake all physiological and metabolic processes is seriously hindered by drought (Aslam *et al*., 2015). Visual symptoms of drought stress in maize are; a change in colour from green to green-grey, rolling of the lower leaves followed by the upper leaves and closed stomates, which sharply reduce photosynthesis and slow down growth (Aslam *et al*., 2015). Drought brings about a reduction in plant biomass as well as harvest-able yield in plants (Anjum *et al*., 2011).

Cell division, cell elongation and a reduction in leaf area result from drought (Aslam *et al*., 2015). Drought effects are progressive stomatal closure coupled with a decline in photosynthesis and water use efficiency resulting in reduced crop yield. Photosynthetic pigments and photosynthetic organs are damaged by drought stress (Anjum *et al*., 2011).

During the flowering stage, drought causes barrenness by reducing assimilate flux to the developing ear below a minimum amount required to sustain optimal grain growth (Yadav *et al*., 2004). Embryo abortion results when drought occurs during early embryonic development (Setter *et al.*, 2011). Ear growth is slowed down more as compared to tassel growth when drought stress occurs simultaneously within the 7 to10 day period prior to flowering, resulting in a delay in silk extrusion relative to pollen shed known as Anthesis-silking interval which is an important cause of yield failure (Aslam *et al*., 2015). Few and poorly filled kernels are produced when drought is extended during the grain filling period (Edmeades *et al*., 2000). Morphological traits such as; fresh root weight, dry root weight, fresh shoot weight, dry shoot weight, fresh root length and fresh shoot length are used when selecting for improve grain yield (Ahsan *et al*., 2013).

2.5 Maize improvement for drought tolerance

Drought tolerance is the yield of a genotype as compared to other genotypes when subjected to the same severity of drought (Rosielle & Hamblin, 1981). Drought tolerant cultivars show an increase in production under drought, thus the ability of a genotype to survive is only useful at seedling stage (Bänziger *et al.*, 2000). Earlier genetic improvement in maize involved selection based on plant phenotype, where seeds from the best maize plants would be stored and used to improve subsequent generations (Beyene e*t al*., 2015; Mhike *et al*., 2011). Currently, breeding efforts to characterize the most ideal drought tolerant maize genotypes have put an emphasis on combining classical procedures with molecular tools to speed up deployment of genes and development of improved varieties (Araus *et al*., 2008).

Grain yield is the principal trait in a breeding population under drought and optimal conditions (Bänziger *et al.*, 2000). Breeding for high maize yield can be achieved by breeding under optimum conditions in the initial stages. It is expected that maximum genetic potential of yields is achieved under optimum conditions and there is a high positive correlation between performance in optimum and drought conditions (Murthada *et al*., 2018). During maize breeding for drought stress, it is important to evaluate a breeding population because drought stress alleles occur at very low frequencies, limiting the development of drought resistant maize cultivars (Blum, 2011a). Unique alleles may exist in natural populations; however, they are often limited by pleiotropic gene effects such as low yields and poor adaptability (Aslam *et al*., 2015).

The most frequently used parameters to select for high grain yield are mean yield, mean productivity and relative yield in drought and non-drought conditions (Rashid *et al*., 2003). Aslam *et al*. (2015) noted that the effectiveness of breeding, either through classical or molecular approaches, depends on identification of vital physiological processes related to yield improvement and determining an association between a gene and the phenotype. Yield improvements under drought stress have been proven to carry no yield penalty under optimum conditions. However, grain yield is slowed by low heritability in trials under random and managed drought that is linked to soil variation and severe levels of managed drought.

Maize breeding for drought tolerance has been achieved using both conventional and marker assisted selection methods in collaborative projects in sub-Saharan Africa (Araus *et al*., 2008; Aslam *et al*., 2015). The use of new maize varieties with superior adaptability traits alongside improved management practices redeem yield losses by 40% (Thornton *et al*., 2009). Breeding for drought tolerance in maize has reduced chronic food deficit levels and provided stability to rural economies (Edemeades & Bänziger, 1997).

2.6 Maize improvement for earliness

Earliness is the potential of a genotype to conclude its life cycle within a given season length to escape drought conditions (Bänziger *et al*., 2000). It is a drought avoidance strategy that can be used to enhance crop yield under terminal drought conditions (Blum, 2011a). Earliness is important in tropical zones especially in countries where maize cultivation is dependent on rains (Abadasi, 2015). Early maturing maize hybrids are required for successful development in short growing season regions because under such conditions, period to maturity and yield traits are positively correlated (Hallauer *et al*., 1988). Therefore, matching the growth period of plants to soil moisture supply is important to achieve high grain yield (Ngugi *et al*., 2013).

Earliness traits include; number of leaves, days to anthesis, days to silking and days to maturity (Abadasi, 2015). Leaf rolling, leaf waxy layer, root length and root branching pattern are used to determine the extent of drought avoidance (Blum, 2011a). Anthesis-silking interval (ASI) trait has been utilized in recent crop improvement efforts to increase flow of assimilates to the developing ear to stabilize kernel set for increased grain yield (Aslam *et al*., 2015). Days to female flowering and grain moisture at harvest traits are targeted for selection because both traits have medium heritability and predominance of additive effects (Hallauer *et al*., 1988).

Earliness has been effectively used to come up with drought escaping maize varieties such as Katumani and Makueni composites (Ngugi *et al*., 2013). Makueni composite flowers in 52 days while Katumani composite flowers in 57 days. Although Katumani and Makueni composites are widely adapted to drought conditions, they were not early maturity enough to escape drought in semi-Arid Kenya (Ngugi *et al*., 1982). Substantial early maturity and increased grain yield in F_1 generation as compared to their parental cultivars has been documented (Ali *et al*., 2017). Hoque *et al*. (2016) found parents that were good combiners for earliness, while Ngugi *et al*. (2013) found that ASI in maize is a dependable and heritable secondary trait for use in phenotypic selection for drought tolerance.

2.7 Drought stress breeding

Drought is water deficit in the soil required for adequate growth of a plant that can reduce crop yield (Bänziger *et al*., 2000). It could result from rainfall shortage, rough soil texture that retains little water in the root zone or drying winds (Bänziger *et al*., 2000). Drought causes considerable agricultural losses because crops sensitive to drought fail to grow (Athar & Ashraf, 2009). Selection of maize for high yield potential in both drought and non-drought conditions has led to sustained increases in grain yield (Mageto *et al*., 2017). An annual genetic gain of 1.1% in random drought conditions and 1.33% in optimum conditions has been realized. Genetic gain in recent maize hybrids is attributed to higher resistance to; drought, low night temperatures during the grain filling period, weed infestation and high plant population density (Badu-Apraku *et al*., 2013). Maize grain yield has been improved by 124 kg ha^{-1} per year when drought occurred during flowering, 91 kg ha^{-1} per year at mid-grain filling period resulting in improved drought tolerance (Blum, 2011b). Drought tolerance in maize has been made possible by targeting genes which reduce the anthesis-silking interval and enabling seed set under drought conditions (Ngugi *et al*., 2013). Genomic approaches have been employed to locate relevant genes and quantitative trait loci (QTLs) responsible for drought tolerance (Varshney *et al*., 2011). To discover genes controlling drought tolerance, maize plants are experimentally subjected to drought stress. Genes that are up-regulated are compared to known maize genetic profiles to identify genes that code for drought tolerance (Blum, 2011a). Mapping of quantitative trait loci that regulate drought responses have provided a useful way to enhance tolerance of maize germplasm to drought (Zhu *et al*., 2011). The QTLs are applied in crop improvement through molecular breeding while candidate genes are utilized in genetic engineering to generate transgenics (Varshney *et al*., 2011).

2.8 Drought stress management

2.8.1 On-farm drought stress management

In rain fed agriculture, the onset of rains is an important factor determining time of planting crops, when farmers plant too early, soil moisture may be inadequate for seed germination while too late planting may cause the seeds to be swept away by rains (Reason *et al*., 2005). In response to varying annual rainy season onset, several maize farmers in sub-Saharan Africa (SSA) move planting dates to ensure that crops fully utilize available soil moisture (Bryan *et al*., 2013; Fosu-Mensah *et al*., 2012). In addition to this, farmers adopt soil and water conservation practices, grow a variety of crops or opt to plant different species of crops (Bryan *et al*., 2013). They opted to plant cassava (*Manihot esculentum* L.), sweet potato (*Ipomea batatas* L.), pigeon pea (*Cajanus cajan* L.), potato (*Solanum tuberosum* L.), yam (*Dioscorea alata L.*) and bananas (*Musa spp*.) over maize due to low yields associated with low rainfall (Kalungu *et al*., 2013). These strategies have had a positive impact on productivity however, the most preferred strategy is selection of drought tolerant varieties which are either not easily accessible to farmers or are under development (Cairns *et al*., 2013).

2.8.2 Experimental drought stress management

Random drought is an environment which depends solely on natural rainfall as the source of soil moisture while managed drought is an environment which is prevented from drought stress by irrigating whenever required (Kumar *et al*., 2016). Choice of test environment is vital and has a large bearing on the rate of achievable genetic gain. It should typify the target environment in rainfall distribution, soil physical and chemical properties and predictable evapotranspiration rates. To ensure that genetic gain realized in the test environment is replicated in the intended environment, genotype by environment interactions should be insignificant (Ribaut *et al.*, 2009).

Drought stress is managed by supplementing soil moisture through irrigation (Bänziger *et al*., 2000). Irrigation is a major means to tackle drought in agricultural intensification and the creation of stable incomes; however, when practiced without exclusion, hazards such as erosion, salinization, leaching and disease, infected soil may occur (Blum, 2011a).

Managed drought targets growth stages that are vulnerable to the stress and have a high likelihood of being affected by that stress in the target environment (Sheikh *et al.*, 2017). According to Bänziger *et al*. (2000), drought may be induced at flowering to accelerate leaf senescence. When induced at this stage, it affects kernel weight due to reduced photosynthetic rate at grain filling. Effectively managed drought should be able to reduce yields by 50% of the yield potential.

2.9 Heritabilty, combining ability and gene action

Heritability is the proportion of the observed variation that is inherited. Heritability is a function of the trait, the population and the environment. There are two different estimates of heritabilty which are broad sense heritabilty and narrow sense heritability. Broad sense heritabilty is estimated using the total genetic variance while narrow sense heritabilty is estimated using the additive genetic variance. The additive genetic variance determines the response to selection, therefore narrow sense heritabilty estimate is more useful to plant breeders than the broad sense heritability (Acquaah, 2007).

Combining ability is a cultivar’s capacity to combine among each other during hybridization to enable transmission of genes to offspring (Fasahat, 2016). General combining ability is the expected value of the sum of two parental lines of a cross while specific combining ability is the deviation from the expected value (Allard, 1960). General combining ability (GCA) and specific combining ability (SCA) are crucial in crop improvement for they characterize the kind and extent of genetic effects controlling yield and yield traits (Dar *et al*., 2017). Parents that show a high average combining ability in crosses are regarded to have good GCA while good SCA is when the potential to combine well is specific to a certain cross (Acquaah, 2007).

There are four types of gene action namely; additive, dominance, epistasis, and over-dominance. However, genes do not fall into clear cut categories and quantitative traits are governed by genes with small and individual effects, they are described by their gene action rather than by the number of genes encoding it. Gene action concept is the same for both major and minor genes nevertheless, the action of a minor gene is small and significantly influenced by the environment.

The effect of a gene is said to be additive when an additional gene enhances the expression of the trait by equal increments. Dominance effects are deviations from additivity that make the heterozygous resemble one parent more than the other. Over dominance on the other hand exists when each allele at a locus produces a separate effect on the phenotype and their combined effect exceeds the independent effect of the alleles. Epistasis is described as the masking effect of the expression of one gene by another at a different locus. In other words, the allelic effects at one locus depend on the genotype at a second locus (Acquaah, 2007). Gene action enables a plant breeder to gain understanding of the breeding material by estimating genetic parameters (Shah *et al*., 2015).

The importance of GCA and SCA is computed by the Bakers' ratio (Baker, 1978). As this ratio approaches unity, it shows high precision in predicting and selecting superior progeny based on GCA. Additionally, Baker's ratio indicates the primary type of gene effects for a trait of interest where a large ratio implies that additive gene effects are responsible for controlling a character while a low ratio implies that dominant and or epistatic gene effects are important (Griffing, 1956). Additive genetic variance was responsible for the inheritance of earliness and grain yield (Hosary, 2014). Contrastingly, both additive and non- additive gene actions were involved in the control of grain yield traits (Mogesse *et al*., 2020).

2.10 Mating designs

North Carolina mating designs were described by Comstock & Robinson, (1952). The North Carolina design I is popular and multipurpose (Acquaah, 2012). It is used to estimate additive and non-additive variances. It is a hierarchical design with non-common parents nested in common parents. However, it requires sufficient seed for replicated trials and hence not practical in species that are not capable of producing large amounts of seeds. The progenies include full-sibs and half-sibs. Full sibs are sets of families with the both parents in common while half-sibs have the same father in common (Kearsey & Pooni, 1996). The North Carolina design 1 has been used in maize breeding to estimate genetic variances (Acquaah, 2012).

The North Carolina Design II is a factorial mating scheme. In this design, each member of a group of parents is used as males is mated to each member of another group used as females. It is used to evaluate inbred lines for combining ability. This design allows the breeder to measure both GCA and SCA however, NCII does not provide for a test of epistasis nor genotype by environment interaction (Kearsey & Pooni, 1996).

A full diallel mating design is one that allows parents to be crossed in all possible combinations including selfs and reciprocals (Sharma, 2006). There are two models for diallel analysis; random and fixed models (Griffing, 1956). A random model involves parents that are random members of a random mating population. A random model is useful in estimating GCA and SCA variances. In a fixed effects model, the aim is to measure for each parent and the SCA for each pair of parents. These effects only apply to the set of parents in the diallel.

In a half diallel, each parent is mated with every other parent, excluding selfs and reciprocals, resulting to only one set of F_1's (Hayman, 1954). In a diallel analysis, there are two models namely; random and fixed models (Griffing, 1956). A random effects model involves parents that are considered a representative random sample from a random mating population. In contrast, in a fixed effects model, parents are non-randomly selected with an aim to measure GCA effects for each parent and the SCA effects for each pair of parents (Fasahat *et al.*, 2018). The GCA and SCA effects of parents in a fixed effects model only apply to the set of parents in the diallel (Acquaah, 2012).

Diallel crosses are used to study genetic parameters of combining ability and gene action which are integral in character expression and predicting the behaviour of parents (Fasahat *et al.*, 2018). Half diallel is suitable in estimating GCA and SCA variances and is used to identify parents and crosses with high combining abilities (Murenga *et al.*, 2015). Moreover, diallel crosses are used to predict the best heterotic combinations for hybrid maize production (Hauller, 2010).

Half diallel mating design has been widely used in maize breeding programmes for example, documented control of additive gene action in the inheritance of ear height (Amana

& Hadi, 2021). Contrastingly, significant SCA effects showed that non-additive gene action was responsible for the inheritance of ear height, ear diameter and 1000 kernel weight (Aslam *et al.*, 2015). Additive gene action for anthesis-silking interval and ear height trait have been reported (Raihani *et al.*, 2019).

2.11 Genotype by environment interactions

Genotype by environment interactions (GEI) are consequences of different cultivars that show contrasting responses to a given environment (Becker & Leon, 1988). The environment consists of all non-genetic factors that influence the expression of a trait (Basford & Cooper, 1998). In the analysis of GEI, the necessary elements are; different genotypes, different environments and yield measurements. Assessing the relative contribution of the genotype, the environment and GEI to cultivar performance is essential in determining the adaptation capacity of a cultivar (Crossa, 1990).

The adaptation capacity of a cultivar is the ability of a genotype to reach its full potential in a specific environment despite the constraints imposed on the cultivar (Blum, 2011a). To determine the genetic potential of a breeding material, assessments should be carried out in multi environmental trials because genetic facts are inferred from phenotypic observations (Crossa, 1990). The most important agronomic and economic traits observed such as grain yield are quantitative in nature and routinely exhibit GEI (Fan *et al.*, 2007).

Various statistical approaches have been employed in the analysis of the GEI. They include analysis of variance and regression analysis. Pattern analysis of multivariate analytical methods like the principal components analysis, principal coordinates analysis and the additive main effects and multiplicative interaction (AMMI) model and the genotype plus genotype by environment interaction (GGE) biplots (Crossa, 1990; Yan &Tinker, 2006).

Cultivar superiority is a measure of a cultivar’s general lead in a cultivar by location data. It is the distance mean square between the cultivar’s response and the maximum response averaged over all locations. The maximum response in each location is also the upper boundary where a small mean square indicates general superiority of the test cultivar. The advantage of using this method is that commercial checks are not required in each location to assess the test cultivars. Additionally, cultivar superiority is a measure which consists of only one parameter that greatly simplifies the screening process. To identify a cultivar’s specific adaptation graphically, the maximum and test cultivar responses are plotted against location means (Linn & Binns, 1988).

Genotype by environment interactions studies have been documented by various researchers. Significant genotype by environment interactions were observed on inbred lines and hybrid maize. The presence of significant GEI shows inconsistent performance of maize genotypes across environments (Ali *et al.*, 2017; Karim *et al*., 2013; Li *et al*., 2018).

CHAPTER THREE

IDENTIFICATION OF DROUGHT TOLERANT ELITE SINGLE-CROSS MAIZE (*Zea mays* L.) HYBRIDS FOR SEMI-ARID KENYA

Abstract

Drought is a major production constraint limiting maize production in sub-Saharan Africa. Improving maize for resilience to drought stress is essential for deployment of drought tolerant varieties in semi-arid areas. The objective of this study was to identify elite single-cross maize hybrids which are drought tolerant and early maturing under semi-arid conditions. Ninety-one single-cross maize hybrids and seven commercial checks were evaluated for drought tolerance under field conditions at the Kenya Agricultural and Livestock Research organization (KALRO) Katumani research centre and Kiboko sub-centre in an alpha-lattice design. This experiment was carried out under both random and managed drought conditions in two replications. Combined analysis of variance across locations revealed significant ($p<0.05$) main effects for genotypes, locations and genotype by location interactions of most yield and yield related traits studied. The highest performing hybrid for grain yield was KAT-DT-E-06 with 6.45 t ha^{-1} against the best performing check variety DK8031 which yielded 4.66 t ha-^{1}. Anthesis-silking interval trait, values of 0 and 0.5 were recorded for genotype KAT-DT-M-25 and KAT-DT-M-29 while the best performing commercial check variety in terms of ASI was PAN 4M-19 with 1.0. Broad sense heritability for grain yield trait of 61.93% was recorded under managed drought compared to 1.95% under to random drought while anthesis-silking interval recorded 3.02% and 8.2% respectively. Genotypes KAT-DT-EE-02, KAT-DT-EE-04, KAT-DT-EE-05 and KAT-DT-E-06 recorded the lowest cultivar superiority (P_i) values between 0.20 and 0.26 on the cultivar superiority index demonstrating their high grain yield and wide adaptability to drought prone conditions. These identified genotypes are drought tolerant, high yielding and stable hence suitable candidates for deployment to farmers in semi-arid areas.

3.1 Introduction

Drought is a major constraint limiting maize production in sub-Saharan Africa (SSA) where cultivation is mainly under rain fed conditions (Shiferaw *et al*., 2011). Drought causes a significant negative impact on global food supply resulting in an estimated 34% yield loss annually (FAO, 2021). In the arid and semi-arid lands (ASAL's), there is pronounced rainfall variability which is characterized by unpredictable onset and length of the growing season. As a consequence, terminal drought sets in because maize varieties planted in the ASAL's are late maturing. In addition, the ASAL's experience major droughts every five years causing total crop failure (Omoyo *et al*., 2015). Climate change effects of extreme natural events are becoming more frequent thereby aggravating drought stress on maize yield. Despite SSA recording the lowest maize yield in the world, the production in this region is bound to decline further partly due to the negative effects of climate change (Setimela *et al*., 2017).

Farming in Kenya is predominantly practised by small-scale farmers with limited access to irrigation technology exposing them to rainfall variability (Kalungu *et al*., 2013). In addition to this, farmers in ASAL's have limited access to suitable maize varieties prompting them to grow varieties recommended for medium to high potential areas (Muli *et al*., 2017). The widely cultivated open pollinated varieties are less adapted to drought conditions however, the basis of this choice is mainly due to their plasticity to survive drought hence assured yields despite having lower productivity compared to hybrid cultivars (Kutka, 2011). Selection of quality seed is a critical factor in successful maize cultivation (Zaidi *et al*., 2017). Resource poor farmers prefer drought tolerant maize varieties due to their limited capacity to access irrigation (Cairns *et al*., 2013). Drought tolerance and high grain yield are considered the most important traits to farmers when selecting maize seeds (Worku *et al*., 2020). Farmers show willingness to buy drought tolerant hybrid maize seeds because of guaranteed higher yields (Gharib *et al*., 2021).

Screening of elite genotypes in target production environments has been conducted to provide suitable drought tolerant maize varieties to farmers in ASAL's (Lunduka *et al*., 2019). Adequate genotype variation in maize breeding populations for key agronomic traits show the potential to identify elite drought tolerant germplasm (Aslam *et al*., 2015; Heakel & Wafa, 2019). Grain yield is considered the primary trait for selection under drought stress (Bänziger *et al*., 2000). However, grain yield is a complex trait controlled by many genes acting additively to express the trait and its selection is hindered by low heritability under drought stress (Blum, 2011a). As an intervention, secondary traits which are correlated with grain yield, are easy to measure and highly heritable are used (Araus *et al*., 2008). They are leaf rolling at seedling stage, anthesis-silking interval at flowering, stay-green capacity under moisture stress and ears per plant (Aslam *et al*., 2015: Cairns *et al*., 2013). Maize when affected by drought stress at flowering period leads to low yields (Ngugi *et al*., 2013). Drought at this stage reduces assimilate flux to the developing ear below the minimum required level to sustain optimal production (Yadav *et al*., 2004). Consequently, ear growth is slowed down resulting in a delay in silk protrusion relative to pollen shed known as anthesis-silking interval (ASI) (Aslam *et al*., 2015). ASI is the most useful secondary trait used to improve drought tolerance in maize (Edmeades, 2000). Previous studies have shown that under drought stress, ASI is negatively correlated with grain yield (Ngugi *et al*., 2013).

Significant genotype by environment interactions (GEI) in response to drought stress show that genotypes perform differently in varied environments (Ali *et al*., 2017). The presence of cross over type of interaction complicates the identification of superior genotypes (Nyombayire *et al*., 2018). To address this challenge, cultivar superiority which is a measure of a cultivar's general top performance based on a cultivar by location data obtained from a multi-environment trial. A small mean square indicates general superiority of the test cultivar (Linn & Binns, 1988). Cultivar superiority has been used successfully to identify tef (*Eragrostis tef*. Zucc) varieties which showed wide adaptability (Worede *et al*., 2020). Similarly, high yielding and stable triticale (*Triticosecale* Wittmack) varieties with wide adaptation as well as varieties narrowly adapted to specific test environments were identified (Derejko *et al*., 2020). The present study was therefore carried out to identify elite single-cross maize hybrids which are drought tolerant in semi-arid conditions.

3.2 Materials and methods

3.2.1 Site description

The experiment was carried out at Kenya Agricultural and Livestock Research Organization (KALRO), Katumani Research Centre in Machakos County and KALRO Kiboko sub-Centre in Makueni County. The agro-climatic description of the two sites is presented in Table 1, while the distribution of monthly rainfall and average temperature during the experimental period is presented in Figures 1 and 2.

The mean annual rainfall is 830 and 675 mm for Katumani and Kiboko, respectively. Kiboko is hotter with a maximum temperature of 30.6 ^{o}C and a minimum of 16.6 ^{o}C compared to Katumani with a maximum temperature of 24.7^{o}C and a minimum of 16.5 ^{o}C (Table 3.1). The highest amount of rainfall during the performance evaluation was received in December 2018 with very little rainfall being received in January and February (Figures 1 and 2) indicating poor distribution.

Table 3.1.Geographical and climatic data for the study sites.

Location	**Longitude**	**Latitude**	**Altitude**	**Mean annual rainfall**	**Temp Min**	**Temp Max**	**Soil type**
Katumani	37^{o} 14' E	1^{o} 35' S	1600 m	830 mm	16.5^{o}C	24.7^{o}C	Eutricnitrosol
Kiboko	37^{o} 37' E	1^{o} 48' S	975 m	675 mm	16.6^{o}C	30.6^{o}C	Sandy clay

Source: Jaetzold *et al*. (2012).

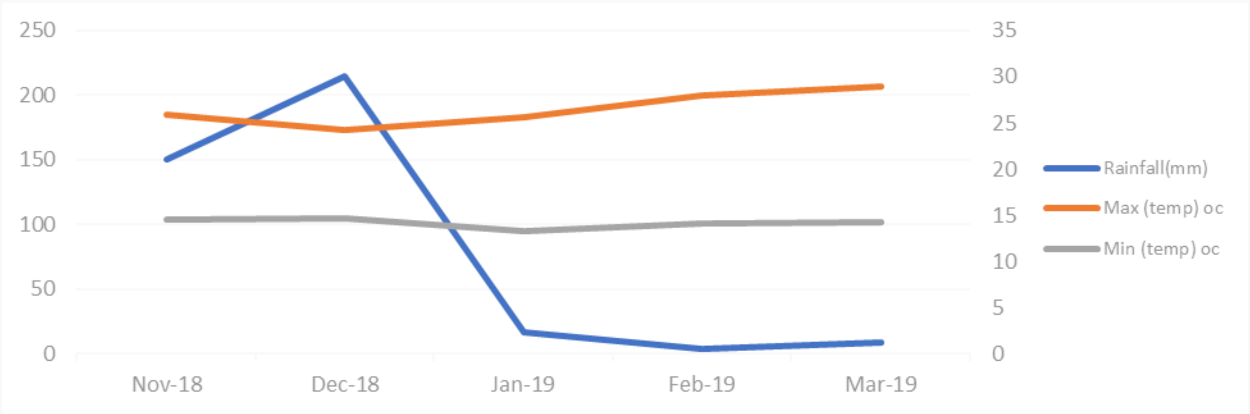

Figure 1.Total monthly rainfall, average minimum and maximum temperature for 2018/2019 growing season in Katumani-random drought site, data obtained from Machakos meteorological station.

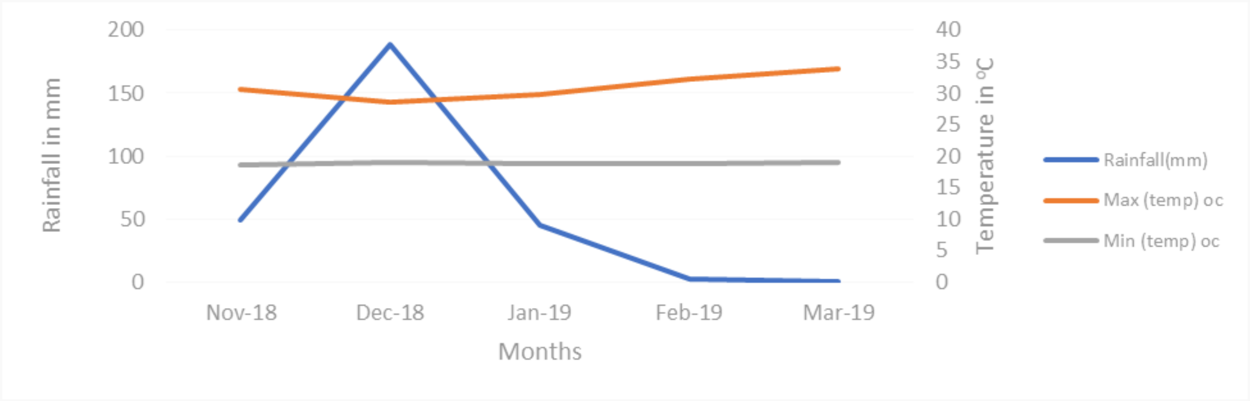

Figure 2.Total monthly rainfall, average minimum and maximum temperature for 2018/2019 growing season in Kiboko-managed drought environment, data obtained from Makindu meteorological station.

3.2.2 Germplasm for study

Ninety-one single-cross maize hybrids sourced from KALRO and CIMMYT germplasm banks and seven commercial maize varieties were used in this study (Table 3.2). The genotypes were selected based on their selection histories for maturity duration and drought tolerance.

Table 3.2. Germplasm for the study with maturity duration and drought response.

Category	Genotype code	Attribute	Drought response
1	KAT-EE-DT-01 to KAT-EE-DT-20	Extra-early	Tolerant
2	KAT-E-DT-01 to KAT-E-DT-30	Early	Tolerant
3	KAT-M-DT-01 to KAT-M-DT-41	Medium-early	Tolerant
Checks			
1	DUMA 43	Extra-early	Tolerant
2	DK 8031	Extra-early	Tolerant
3	DH 04	Early	Tolerant
4	PH3253	Early	Tolerant
5	PAN 4M-19	Medium-early	Tolerant
6	WE1101	Medium-early	Tolerant
7	DK 8033	Medium-early	Tolerant

Table 3.2. Contd…

3.2.3 Experimental design

Ninety-one single-cross maize hybrids alongside seven control genotypes were evaluated during the 2018/2019 October/November/January rainy season. The trial was planted in an alpha-lattice design as shown in appendix A. Each genotype was sown in two-row plots measuring 5 m each, replicated twice in two locations for one season. Row spacing of 0.75 m and spacing of 0.25 m within the rows was used. Two seeds were planted in each hill and later thinned to one. To screen genotypes for drought tolerance the experiment was conducted in two environments namely; random drought at Katumani Research Centre and managed drought environments at the Kiboko sub-Centre. In the random drought environment, the trial depended on natural rainfall while in the managed drought environment, supplemental irrigation was applied using drip irrigation as recommended (Bänziger *et al*., 2000). Water stress was achieved by withholding irrigation for two weeks before 50% male flowering to the end of the flowering period.

Phosphate fertilizer was applied at the recommended rate 60 kg P_20_5 ha^{-1} and nitrogen at the rate of 60 kg N ha^{-1} to ensure healthy and vigorous plants. Weed management practices were carried out to keep plots free of weeds. Fall army worms were controlled using emamectin benzoate 19g L^{-1}.

3.3 Data collection

Data were collected on days to anthesis (DTA), days to silking (DTS), ear height (EH), plant height (PH), anthesis-silking interval (ASI), number of ears per plot (EPP) and grain yield (GY) as described by Bänziger *et al*. (2000). Anthesis-silking interval (ASI) was the difference between the date of tussling and the date at which 50% of plant produced silk from six randomly selected plants. Ear height in cm was determined by measuring from ground level to the node bearing the uppermost ear. Number of plants at harvest was determined by counting the number of plants that survive to physiological maturity. Ears per plant was determined by counting the number of ears with at least fully developed grains and divided by the number of plants per plot at harvest. At physiological maturity, heights of six randomly selected plants in a plot were measured using a meter scale from the soil surface to the base of the tassel. Grain yield was measured in tonnes per hectare adjusted to grain moisture content of 13% and assuming a shelling percentage of 80%. All ears harvested from each plot were weighed and representative samples of ears were shelled to determine the percentage moisture of the grain using a Dickey John™ moisture meter.

3.4 Data analyses

Data collected were subjected to combined analysis of variance for agronomic traits over two locations using GenStat (VSN, 2014). To obtain entry plot-based, heritability in broad sense (h^2_{bs}) estimates, replication and location were treated as fixed effects while genotype and block effects were treated as random. The model below was used;

$$Y_{ijk} = \mu + G_i + R_l + B_{l(k)} + L_j + GL_{ij} + \varepsilon_{ijk}$$

Where Y_{ijk} is the observed trait for the i^{th} genotype in the k^{th} block within the lth replicate, μ = overall mean, G_i is the effect of the i^{th} genotype, R_l is the effect of the l^{th} replicate, $B_{l}(_{k})$ is the effect of the k^{th} block in the l^{th} replicate, L_j effect of the j^{th} location GL_{ij} is the interaction effect between the i^{th} genotype and jth location and ε_{ijk} is the random error term.

Mean comparison was performed using Tukey's honestly significant difference (HSD) test at ($p \leq 0.05$). Heritability in broad sense was calculated as described by Holland *et al*. (2003).

$$H^2 = \frac{\sigma^2_g}{\sigma^2_g + {\sigma^2_{gy}}/{y} + {\sigma^2_e}/{r}}$$ ……………………………………………………………………………………… (Equation 1).

where σ^2_g is the variance component for genotype, σ^2_{gy} is the variance component for genotype-by-year interaction, σ^2_e variance component for the residual, y is the harmonic number of years per genotype and r is the harmonic mean number of replications per genotype (Holland *et al*., 2003).

In order to assess genotypic stability of maize genotypes cultivar superiority method was used (Linn & Binns, 1988). Superiority of genotypes was based on P_i values which represent mean squares (MS) due to genotype $[n(\bar{X}_{i.} - \bar{M})^2]$, genotype-by-environment interaction (GEI) $\left[\sum_{j=1}^{n}\left(X_{ij} - \bar{X}_{i.} - M_j + \bar{M}\right)^2\right]$ and genotypes' general adaptability (Linn & Binns, 1985; Linn & Binns, 1988). Pairwise genotype by interaction (GEI) mean squares (MS) between minimum and test genotype were used to avoid discarding genotypes with specific adaptability. Critical values for significance of Pi and GEI were the product of pooled residual MS from combined analyses and tabulated F-values for corresponding degrees of freedom (df), where the df for P_i was 1 and error MS df was 194, respectively (Linn & Binns, 1988). In addition, the *b* value which is regression coefficient was calculated and taken as a genotype’s stability parameter (Finlay &Wilkinson’s, 1963). It was used to guard against discarding narrowly adapted cultivars.

3.5 Results

3.5.1 Combined analysis of variance for grain yield and yield contributing traits

Results from combined analysis of variance over locations revealed significant ($p < 0.05$) genotype main effect for all the traits measured except plant height (Table 3.3). Location main effect was significant ($p < 0.05$) for ears per plant trait. On the other hand, there was significant ($p < 0.05$) genotype by location interaction effect in all measured traits.

Table 3.3. Mean squares from combined analysis of variance for grain yield and yield related traits.

Source	**df**	**GY**	**ASI**	**PH**	**EH**	**EPP**	**DTA**	**DTS**
Location	1	3255.68	907.74	729608.3	177259.09	12.55^*	12056.83	8782.6
Residual	2	4.97	1.38	1129.4	759.20	0.17	0.66	13.51
Genotype	97	3.23^*	6.05^*	1084.9	470.64^*	0.08^*	98.48^*	143.7^*
Loc×geno	97	2.98^*	5.43^*	341.2^*	145.16^*	0.06^*	191.67^*	147.2^*
Error	182	1.04	5.75	212.5	81.58	0.05	14.77	18.24
CV %		5.3	4.4	2.4	4.4	4.8	0.1	0.6
Mean		4.26	2.67	140.21	63.57	0.86	56.95	60.79
s.e.d		0.72	1.72	10.31	6.39	0.15	2.72	3.02

GY = Grain yield, ASI=anthesis-silking interval, PH=plant height, EH=ear height, EPP=ears per plant, DTA=days to anthesis, DTS=days to silking, * = significant at *($p<0.05$)*.

3.5.2 Mean performance of maize hybrids for grain yield and yield contributing traits

Mean performance of maize hybrids for yield and yield related traits for the top single-cross maize hybrids which outperformed the best yielding commercial check variety in terms of grain-yield are presented in table 3. 4, table 3.5 and appendix 1 and 2. Mean grain yield (GY) across locations ranged from 1.07 t ha^{-1} to 6.45 t ha^{-1} in comparison to the best performing commercial check variety whose yield was 4.66 t ha^{-1}. Individual grain mean yields for each environment ranged between 0.07 t ha^{-1} and 3.7 t ha^{-1} in the random drought conditions while in the managed drought conditions it was 1.55 t ha^{-1} to 10.59 t ha^{-1}. The overall best performing genotypes for GY was KAT-DT-E-06 while the best performing commercial check variety was DK8031. Anthesis-silking interval trait, values of 0 and 0.5 were recorded for genotypes KAT-DT-M-25 and KAT-DT-M-29 while the best performing commercial check variety in terms of ASI was genotype PAN 4M-19 with 2.0.

Table 3.4. Mean performance of grain yield and yield contributing traits in managed and random drought environments.

	Managed drought							**Random drought**						
Genotype	**ASI**	**PH**	**EH**	**EPP**	**DTA**	**DTS**	**GY**	**ASI**	**PH**	**EH**	**EPP**	**DTA**	**DTS**	**GY**
KAT-DT-E-15	1	163.2	80.3	1.34	52	53	5.31	8.5	109.9	49.8	1.17	69.5	40	1.10
KAT-DT-M-26	1	187.5	80	1.06	50	59	5.36	6	102.3	42.5	0.63	66	72	1.97
KAT-DT-EE-02	1	167.7	69.5	0.82	52.5	53.5	8.90	4	82.8	29.5	0.90	70	74	2.02
KAT-DT-E-14	1	166.8	82.5	1.14	53.5	54.5	7.44	4	97.5	43.8	0.53	45	47	1.10
KAT-DT-M-25	1	206.5	91.8	1.00	46.5	55.5	7.09	-1	107.4	57.0	0.58	70.5	69.5	1.49
KAT-DT-EE-03	1	177	76.5	0.84	54.5	55.5	6.81	5	65.3	23.0	0.83	74	77	1.40
KAT-DT-E-26	1	197.5	105.5	0.62	61	62	5.05	-2	123.3	52.0	0.60	47	45	1.73
KAT-DT-M-24	1	190.2	78	0.99	47.5	56.5	7.59	0.5	121.5	54.5	0.85	68.5	69	1.98
KAT-DT-EE-05	1	156.2	70	1.05	52	53	9.72	5.5	73.0	22.5	0.81	66	71.5	1.85
KAT-DT-E-25	1	186.5	92.5	0.99	57	58	8.65	3.5	114.8	50.5	0.78	45	47	1.10
KAT-DT-M-23	1	200	82.5	1.11	47	56	6.97	1	108.0	54.0	0.71	68	69	2.00
Commercial checks														
DK 8031	1	189	96.5	0.9	59.5	60.5	8.49	5	95.8	28.5	0.6	78.5	83	0.83
DH 04	1	160	79.5	1.2	59	60	5.84	2.5	64.5	31.5	0.6	78.5	81	0.30
Mean	1.1	183	84.9	1.0	51.3	56.0	7.14	4.2	97.1	42.3	0.7	62.5	65.5	1.38
CV%	6.9	2.6	3.9	1.4	0	0.1	4.3	3.6	0.4	5.1	8.2	0.2	0.8	5.7
HSD (0.05)	0.02	0.55	0.39	0.0	0.22	0.07	0.02	0.1	0.63	0.65	0.04	0.21	0.24	0.04

ASI=anthesis-silking interval, PH=plant height, EH=ear height, EPP=ears per plant, DTA=days to anthesis, DTS=days to silking, GY = grain yield

Table 3.5. Mean performance of maize hybrids for grain yield and yield contributing traits combined across environments.

Geno	**GY**	**ASI**	**PH**	**EH**	**EPP**	**DTA**	**DTS**
KAT-DT-E-06	6.45	2.5	144	67	0.86	48.75	51.25
KAT-DT-EE-04	6.31	1.5	131.4	54.38	0.93	64.5	66
KAT-DT-E-18	5.84	1.5	162.8	81	0.82	48.5	50
KAT-DT-EE-05	5.78	3.3	114.6	46.25	0.93	59	62.25
KAT-DT-EE-16	5.75	2.5	110.5	39	0.88	60.25	62.75
KAT-DT-EE-14	5.60	2.0	124.8	53	1.14	60.25	62.25
KAT-DT-M-39	5.49	3.0	145.5	64.12	0.93	57.25	64.25
KAT-DT-EE-02	5.46	2.5	125.2	49.5	0.86	61.25	63.75
KAT-DT-EE-11	5.39	3.5	116.4	46.62	0.92	59.75	63.5
KAT-DT-E-17	5.38	1.7	138.8	65.5	0.76	52.75	50.75
KAT-DT-EE-07	5.37	2.3	117.4	47.5	1.14	59.25	61.5
KAT-DT-E-28	5.26	3.8	130.9	65.88	0.76	48.75	52.5
KAT-DT-EE-15	5.26	2.8	124.1	53	1.03	60.25	62.75
KAT-DT-EE-08	5.25	3.0	120.8	48.38	1.00	60.25	63.25
KAT-DT-M-31	5.24	3.0	151.8	62.62	0.79	56.5	63.5
KAT-DT-EE-20	5.21	4.8	112.4	43.38	0.87	60.25	65
KAT-DT-M-38	5.20	3.5	148	69	0.92	58.75	66.25
KAT-DT-EE-18	5.15	2.5	111.9	43.75	0.99	59.25	61.75
KAT-DT-E-20	5.07	1.3	153	69.25	0.76	50.25	52.67
KAT-DT-E-29	5.02	4.0	165.6	83.75	0.92	53	57
KAT-DT-E-22	4.95	3.0	145.5	69.38	0.83	49.75	52.75
KAT-DT-M-02	4.98	6.8	150.9	70.25	0.85	62	69.75
KAT-DT-M-28	4.89	2.3	131.5	66.75	0.85	56.75	63
KAT-DT-E-03	4.88	2.3	143.4	60.62	0.88	48.75	51
KAT-DT-E-25	4.87	2.3	150.6	71.5	0.92	51	54.33
KAT-DT-M-30	4.84	2.5	146.8	62	0.78	60	66.5
KAT-DT-EE-10	4.83	2.5	117.5	48.5	0.90	57.25	59.75
KAT-DT-EE-09	4.79	2.0	119.4	47.62	0.86	60.75	62.75

Table 3.5. Contd…

Geno	**GY**	**ASI**	**PH**	**EH**	**EPP**	**DTA**	**DTS**
KAT-DT-EE-10	4.83	2.5	117.5	48.5	0.90	57.25	59.75
KAT-DT-EE-09	4.79	2.0	119.4	47.62	0.86	60.75	62.75
KAT-DT-E-13	4.79	3.5	139.4	70	0.69	47.5	51
KAT-DT-M-24	4.78	0.8	155.9	66.25	0.92	58	62.75
KAT-DT-E-30	4.77	0.7	146.6	68.75	0.74	51.25	53.33
KAT-DT-E-12	4.75	1.8	149.1	72.12	1.05	50	51.75
KAT-DT-EE-19	4.75	2.3	126.2	49.62	0.95	61.5	63.5
Checks							
DUMA 43	4.01	4.8	158.8	73	0.66	59.5	69.75
DK8031	4.66	3.0	142.5	62.5	0.74	69	71.75
DH 04	3.07	1.8	112.2	55.5	0.88	68.75	70.5
PH3253	3.69	2.8	145.6	63	0.64	58.25	65.75
PAN 4M-19	1.07	2.0	103.6	50.75	1.04	65.25	67
WE1101	3.70	5.8	141.1	69.38	0.81	63	67.75
DK 8033	3.70	6.5	142.8	58.5	0.71	73.75	72.5
HSD (0.05)	0.04	0.10	0.59	0.01	0.37	0.16	0.17

ASI=anthesis-silking interval, PH=plant height, EH=ear height, EPP=ears per plant, DTA=days to anthesis, DTS=days to silking, GY = grain yield.

3.5.3 Broad sense heritability estimates for grain yield and yield contributing traits per environment

Broad sense heritability estimates among the studied traits as presented in table 3.6. The study revealed a range of heritability estimates as categorized by Robinson *et al*. (1949) as follows; 0-30 % low, 31-60 % moderate and > 61 % high. Under managed drought conditions, heritability ranged between 3 to 84 %. High broad sense heritability was exhibited by hybrids for GY, DTA and DTS, moderate estimates were exhibited for PH and EH while low heritability estimates were observed for ASI and EPP. Under random drought conditions, heritability estimates ranged from 1 to 81%. Notably, ASI and DTS traits recorded higher heritability in random drought environment as compared to managed drought conditions. In addition, high broad sense heritability was observed for DTA and DTS, moderate estimates by PH and EH while low estimates were obtained for GY, ASI and EPP.

Table 3.6. Heritability in broad sense estimates of single-cross maize hybrids for yield and yield contributing traits.

Parameter	Managed drought (%)	Random drought (%)
GY	61.93	1.95
ASI	3.20	8.02
PH	54.28	53.60
EH	54.60	41.30
DTA	84.19	81.28
DTS	69.84	75.40
EPP	23.89	1.82

GY = grain yield, ASI=anthesis-silking interval, PH=plant height, EH=ear height, DTA=days to anthesis DTS=days to silking, EPP = ears per plant.

3.5.4 Stability analysis using cultivar superiority measure

The superiority measure (Pi) and genotype by environment interaction mean square MS(GE) for maize hybrids are presented in Table 3.7 and appendix D. Results show that genotype KAT-DT-EE-02, KAT-DT-EE-04, KAT-DT-EE-05 and KAT-DT-E-06 recorded the lowest (P_i) values. Hybrids KAT-DT-M-03, KAT-DT-M-14, KAT-DT-M-07 and DH 04 and PAN 5M-19 with (Pi) values greater than the cut-off point of 4.03 value were considered different.

Table 3.7. Superiority measure P_i, genotype by environment interaction mean squares MS(GE) and regression coefficient (*b*) single-cross maize hybrids and 3 commercial checks arranged in the order of Pi

Genotype	**Genotype mean**	**P_i**	**MS(GE)**	***b* value**
KAT-DT-EE-02	5.46	0.20	1.66	1.19
KAT-DT-EE-04	6.31	0.20	1.82	1.36
KAT-DT-EE-05	5.78	0.23	1.84	1.37
KAT-DT-E-06	6.45	0.26	1.84	0.94
KAT-DT-M-39	5.49	0.34	1.82	1.36
KAT-DT-EE-14	5.60	0.34	1.89	1.39
KAT-DT-EE-07	5.37	0.36	1.77	1.32
KAT-DT-M-31	5.24	0.43	1.73	1.29
KAT-DT-EE-15	5.26	0.48	1.80	0.97
KAT-DT-M-38	5.20	0.51	1.78	1.33
DH 04	3.07	4.67*	1.81	0.96
KAT-DT-E-26	3.39	4.98*	3.04	0.58
KAT-DT-E-08	2.96	5.10*	1.92	0.90
KAT-DT-EE-12	3.05	5.13*	2.21	0.79
KAT-DT-M-05	3.46	5.32*	3.57*	0.47
KAT-DT-E-02	2.83	6.88*	3.28*	0.53
KAT-DT-M-41	2.81	7.13*	3.46*	0.49
PAN 4M-19	1.07	16.57*	5.71*	0.17

3.6 Discussion

Significant differences at ($p<0.05$) among genotypes, locations and genotype by location interaction were observed in this study. Similar results were reported by Murthadha *et al*. (2018) and Rezende *et al*. (2019) where significant differences in genotype, location and genotype by location interactions among test hybrids were reported. Genotypic performance varied across the locations. Significant genotype main effect for yield and related traits revealed the existence of enough genetic variation within the germplasm under study hence a basis for yield improvement under drought (Islam *et al*., 2020; Murtadha *et al.*, 2018). Significant location mean squares suggests heterogeneity of growing conditions and geographic separation (Rezende *et al*., 2019). Presence of genotype by location interactions for grain yield, plant height, ear height, days to silking and ears per plant indicate that genetic expressions of these traits were affected by environmental conditions in the study locations. These findings agree with those of Katsenios *et al.* (2021) and Rezende *et al*. (2019) who reported significant GEI for grain yield trait which explain the existence of environmental variations across the study sites. Environmental variation in the study sites was occasioned by the difference in moisture levels.

The average GY of experimental hybrids was higher than the best commercial check variety under both environments. In this experiment, hybrids KAT-DT-E-06 and KAT-DT-EE-04 recorded the highest results on GY trait. These findings indicate that most of the experimental hybrids were superior for drought tolerance than the commercial checks. High and stable GY under both management conditions are considered high-priority criteria for selecting genotypes (Setimela *et al*., 2017). Grain yield is influenced by combined effects due to genotype and environmental conditions, therefore, high GY results recorded indicate that the maize varieties are tolerant to drought due to minimal environmental influences (Ray *et al*., 2020). Similar results were reported by Etiro *et al*. (2017) and Rezende *et al*. (2020) where hybrids adapted to both random drought and managed drought environments were identified. Genotypes KAT-DT-M-25 and KAT-DT-M-29 with the shortest ASI showed considerable high grain yield values. Previous reports revealed that a short ASI contributes to a greater chance of successful seed set, increased kernel numbers thereby contributing to increased yields (Ngugi *et al*., 2013).

Broad sense heritability varied significantly between test environments indicating the role of genotype by environment effects for conditioning these traits. Broad sense heritability was generally higher in managed drought conditions as compared to random drought conditions. High broad sense heritability may be inflated by non-additive gene action or may be due to a positive environmental effect which is not heritable. Consequently, it lowers the prediction accuracy of progeny performance in subsequent generations (Ali *et al.*, 2017). In this study, decreased heritability with increased drought stress was observed on grain yield trait. This finding indicates that selection for grain yield trait under drought conditions slows down genetic improvement (Umar *et al.*, 2015). Low heritability for grain yield trait in random drought conditions could be attributed to the characteristic of maize being a water demanding plant hence slowing down ear growth, causing a delay in anthesis-silking interval which causes notable yield reduction (Ngugi *et al.*, 2013). These findings were consistent with results by Etiro *et al*. (2017) and Rezende *et al*. (2019).

On the other hand, anthesis-silking interval recorded increased heritability under drought conditions. Selection for reduced anthesis silking interval (ASI) under drought conditions results to an increase in yield (Benchikh-Lehocine *et al.*, 2021). ASI is highly heritable under random drought conditions and is an important indicator of drought tolerance (Ngugi *et al.*, 2013). Further, results show the need to select maize for ASI in random drought conditions for rapid yield improvement. Increased heritability of ASI in random drought environment has been documented (Etiro *et al.*, 2017; Ngugi *et al*., 2013).

Findings from this study show cultivars with low P_i values show general adaptation over the test locations while high P_i values show genotypes with specific adaptation to a particular environment (Linn & Binns, 1988). Based on this statistic, hybrid KAT-DT-EE-02, KAT-DT-EE-04, KAT-DT-EE-05 and KAT-DT-E-06 were the most stable and high yielding across the study locations. In contrast, genotypes KAT-DT-M-05, KAT-DT-M-02, KAT-DT-M-41 and DH 04 were above the MS (GEI) cut off point. Low P_i values indicate that a large part of the total variation is attributable to the genetic component (Eze *et al*., 2020; Linn & Binns, 1988) while genotypes with above MS (GEI) cut off point were specifically adapted to manage drought conditions (Linn & Binns, 1988). These findings are consistent with Derejko *et al*. (2020) and Worede *et al*. (2020) where genotypes widely and narrowly adapted to study locations were identified.

3.7 Conclusion

Analysis of variance across environments for grain yield revealed that genotype by environment interaction played an important part in the selection of the best genotypes for high grain yield and stability. In this study, elite genotypes with outstanding genetic performance for drought tolerance and high grain yield were identified. Single cross hybrids KAT-DT-EE-02, KAT-DT-EE-04, KAT-DT-EE-05 and KAT-DT-E-06 were superior for grain yield and stable under drought conditions. The genotypes identified are promising hence demonstrate potential for deployment as new cultivars for semi-arid areas. However, further testing on-farm with key stakeholders would accelerate adoption.

CHAPTER FOUR

COMBINING ABILITY ANALYSIS FOR DROUGHT TOLERANCE AMONG SINGLE-CROSS TROPICAL MAIZE (*Zea mays* L.) HYBRIDS IN SEMI-ARID KENYA

Abstract

Drought stress is a major production challenge of maize (*Zea mays* L.) causing negative impact on its production in semi-arid areas of eastern Africa. Breeding hybrid cultivars for dry areas is essential for reducing yield losses commonly incurred under rain fed maize production. The objective of is study was to estimate combining ability effects for drought tolerance among single-cross tropical maize hybrids in semi-arid Kenya. Eleven parents with known drought resistance and maturity duration were crossed in a half diallel mating design to generate 55 crosses. The F_1s alongside two local checks were evaluated in an alpha-lattice design with two replications during the 2020/2021 cropping season. Combined analysis of variance over environments revealed significant ($p < 0.05$) main effects for genotypes, locations and genotype by location interaction in most studied traits. Significant ($p<0.05$) general combining ability and specific combining ability for GY, EH and PH demonstrated the role of both additive and non-additive genetic variance in the inheritance of these traits. The interaction of GCA effects with location effects revealed the necessity for advanced trials in multi-locations for the identification of potential cultivars. Crosses KAT-DT-EE-07×KAT-DT-EE-14 (6.18 t ha^{-1}) and KAT-DT-EE-07×KAT-DT-EE-04 (6.16 t ha^{-1}) had superior grain yield while KAT-DT-EE-07×KAT-DT-EE-14 showed significant low values for ASI (0.5) hence adapted to drought. Cross KAT-DT-E-06×KAT-DT-EE-04 had significant SCA for a reduction in ASI. Significant SCA effects for grain yield were recorded in KAT-DT-M-31×KAT-DT-EE-07(1.72^{*}) which demonstrated the potential of obtaining drought tolerant hybrids cultivars for possible future deployment to farmers.

4.1 Introduction

Maize (*Zea mays* L.) is an important food crop in sub-Saharan Africa (SSA) due to its high yielding capacity and adaptability to a wide range of agro-ecological zones (Akaogu *et al*., 2017; Sheikh *et al*., 2017). Drought has been reported to cause major yield reduction of up to 34% (FAO, 2021). In the ASAL's, frequent droughts cause crops failures once in every three seasons (Quandt, 2021). Drought induced losses are common in subsistence agricultural production system and reported to impact negatively on a number of crops including maize (Bänziger *et al*., 2000; Daryanto *et al*., 2016). Climate change has further exacerbated drought stress by altering weather patterns causing irregular and unpredictable rainfall quantities (Badu-Apraku *et al*., 2013).

Maize production in the semi-arid areas of eastern Africa is largely carried by small-scale farmers under rain-fed conditions. The use of hybrid seeds in the ASAL's is low due to high prices and poor access to input stores. Maize being a low value crop has not attracted investment in irrigation facilities (Mutiso & Kimtai, 2022). Besides, the socio-economic reasons have compelled farmers to produce maize with low input application thereby further plummeting the yield (Mutiso & Kimtai, 2022). Currently, the average production under semi-arid conditions stands at 1400 kg ha^{-1} against a potential of 5600 kg ha^{-1} (FAO, 2019).

Previous maize breeding efforts in Kenya mainly focused on developing open pollinated varieties (OPVs) for semi-arid areas (Njoroge, 1982). Such varieties are known to have adequate inherent genetic variability that allow them survive under adverse conditions. However, OPVs are inherently low yielding compared to hybrid varieties (Kutka, 2011). Thus, continuous cultivation of the OPVs by maize farmers in dry areas is partly the major cause of perennial low yields realized (Schroeder *et al*., 2013). The need for increased productivity in semi-arid areas to meet the demand for food has thus necessitated the realignment of the breeding strategy to focus on developing hybrid varieties (Banziger *et al*., 2000). This is because hybrid cultivars have been shown to have the genetic potential for high productivity compared to OPVs (Kutka, 2011). Development and deployment of hybrid cultivars that mature within the duration available within a cropping season and with the available moisture can improve productivity under semi-arid conditions hence improve food security (Ngugi *et al*., 2013).Grain yield is a key trait in breeding maize under drought stress conditions (Bänziger *et al*., 2000). It is controlled by many genes acting additively to express the trait. Under drought stress conditions, selection for grain yield is slowed down by low heritability, low yields and poor adaptability (Aslam *et al*., 2015; Blum, 2011a). To solve this challenge, secondary traits are targeted in the selection of drought tolerance provided they are positively correlated to grain yield, easy to measure and highly heritable (Araus *et al*., 2008).

Knowledge of gene action modulating drought tolerance and the genes present in the germplasm are key in the attainment of desirable breeding objectives. Effective maize genetic improvement programme for production in drought stress conditions lays emphasis on exploiting drought tolerant genes (Badu-Apraku *et al*., 2013). A diallel technique for estimating the combining ability of lines and characterizing the nature and extent of both additive and dominance effects was suggested by Griffing (1956). Significance of both specific combining ability (SCA) general combining ability (GCA) in control of drought tolerance and related agronomic traits in maize have been reported (Aswin *et al*., 2020; Ilyas *et al*., 2019; Makanda *et al*., 2010 ; Murthadha *et al*., 2018). For example, studies on diallel mating design on single-cross maize hybrids showed that inheritance of ear diameter, grain rows per ear and ear length were governed by non-additive gene action (Aslam *et al*., 2015). Raihani *et al*. (2019) reported significant general combining ability variances for ear height, number of kernels per row as controlled by additive gene action while specific combining ability for grain yield, plant height and ear height controlled by non-additive gene action. However, more information on combining ability is needed to facilitate germplasm enhancement for drought tolerance in drought conditions. The objective of this study was therefore to estimate combining ability effects for drought tolerance in maize germplasm.

4.2 Materials and methods.

4.2.1 Site description

The experiment was carried out at Kenya Agricultural and Livestock Research Organization (KALRO), Agricultural Mechanization Research Institute (AMRI) Katumani in Machakos County and its sub-centre at Kiboko in Makueni County. The agro-climatic description of the two sites is presented in Table 1, while the distribution of monthly rainfall and average temperature during the experimental period is presented in figures 3 and 4. The mean annual rainfall is 830 and 675 mm for Katumani and Kiboko, respectively. Kiboko is hotter with a maximum temperature of 30.6^{o}C and a minimum of 16.6^{o}C compared to Katumani with a maximum temperature of 24.7^{o}C and a minimum of 16.5^{o}C. The highest amount of rainfall during the performance evaluation was received in November 2020 with very little rainfall being received between December and March (Figures 3 and 4) indicating poor distribution.

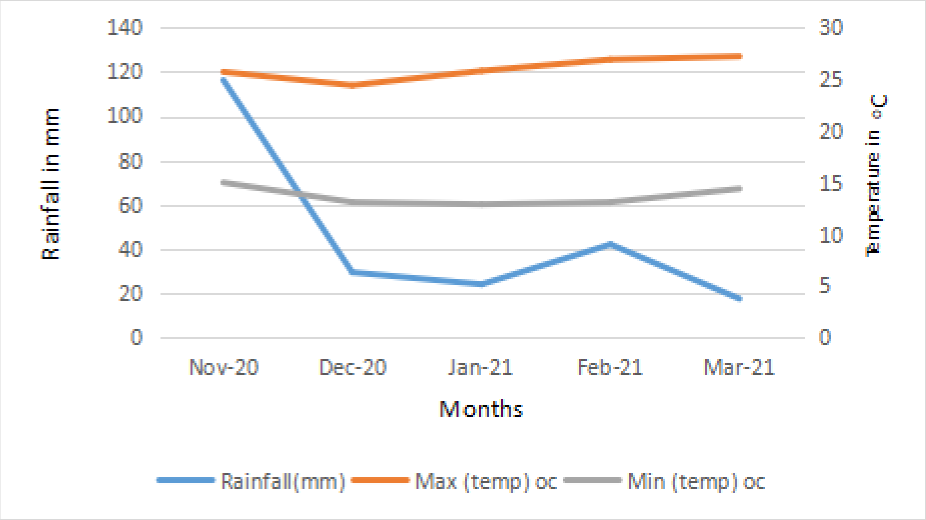

Figure 3. Total monthly rainfall, average minimum and maximum temperature for 2019/2020 growing season in Katumani-random drought site, data obtained from Machakos meteorological station.

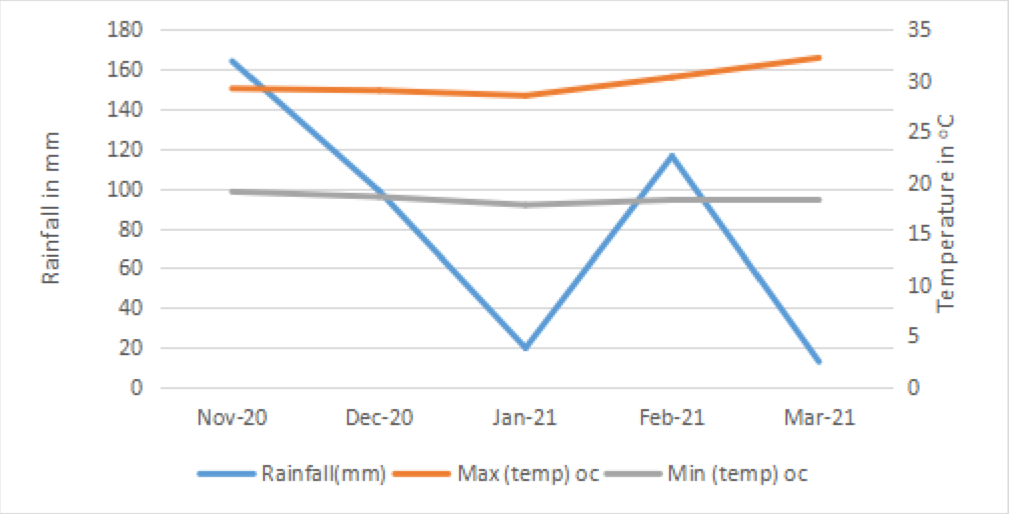

Figure 4. Total monthly rainfall, average minimum and maximum temperature for 2019/2020 growing season in Kiboko-managed drought site, data obtained from Makindu meteorological station.

4.2.2 Germplasm for study

Eleven single-cross maize hybrids were used in this study as both male and female parents. The parental materials were selected based on high grain yield and adaptability to drought prone conditions following the results of preliminary evaluation conducted under drought conditions during the 2018/2019 October/November cropping season. Two commercial checks namely, DUMA 43 and PAN 4M-19 were included to benchmark the performance with the test material (Table 4.1).

Table 4.1. Classification of genotypes used in the study by maturity duration

No	Genotype	Maturity duration
1	KAT-DT-EE-02	Extra-early
2	KAT-DT-EE-04	Extra-early
3	KAT-DT-EE-05	Extra-early
4	KAT-DT-E-06	Early
5	KAT-DT-M-39	Medium early
6	KAT-DT-EE-14	Extra-early
7	KAT-DT-EE-07	Extra-early
8	KAT-DT-M-31	Medium early
9	KAT-DT-EE-15	Extra-early
10	KAT-DT-M-38	Medium early
11	KAT-DT-EE-18	Extra-early
	Checks	
12	DUMA 43	Extra-early maturity
13	PAN 4M-19	Medium early maturity

4.2.3 Field operations

Land preparation was carried out using a mould board plough followed by harrowing. Two seeds per hill were sown and later thinned to one seed per hill. During planting, di-ammonium phosphate fertilizer (DAP) with an N:P: K ratio of 18:46:0 was applied at a recommended rate of 150 kg ha^{-1} to supply 6.45 kg of P for the total area of 0.15 ha. At 21 days after emergence, top-dressing with 150 kg ha^{-1} of calcium ammonium nitrate (CAN) with nitrogen (N) composition of 26% was applied to supply a total of 5.85 kg of N. Weed management practices were carried out to keep plots free of weeds. Fall army worms were controlled using emamectin benzoate 19 g L^{-1}.

4.2.4 Experimental design

Eleven parents (single-cross maize hybrids) were crossed in half-diallel mating scheme to generate 55 F_1 progenies (double crosses). The 55 F_1's alongside two checks were screened for drought tolerance in alpha-lattice design with two replications at two locations for one cropping season (Appendix E). Each genotype was sown in two-row plots measuring 5 m each. Spacing of 0.75 m between the rows and 0.25 m within the rows was used. Each genotype was sown in two-row plots measuring 5 m each. Spacing of 0.75 m between the rows and 0.25 m within the rows was used. To evaluate hybrids for drought tolerance, the experiment was conducted in two environments *viz*; random drought at Katumani Research Centre and managed drought environments at the Kiboko sub-Centre. In the random drought environment, the trial relied on natural rainfall while in the managed drought environment, supplemental irrigation was applied using drip irrigation as recommended (Bänziger *et al*., 2000). Water stress was achieved by withholding irrigation for two weeks before 50% male flowering to the end of the flowering period.

4.3 Data collection

Data were collected on grain yield (GY), plant height (PH), ear height (EH), number of plants (NP) and number of ears per plant (EPP) as described by Bänziger *et al*. (2000). Grain (GY) yield was measured in tonnes per hectare adjusted to grain moisture content of 13% and assuming a shelling percentage of 80%. All ears harvested from each plot were weighed and representative samples of ears were shelled to determine the percentage moisture of the grain using a Dickey John™ moisture meter. Anthesis-silking interval (ASI) was the difference between the date of tussling and the date at which 50% of plant produced silk from six randomly selected plants. Ear height in cm (EH) was determined by measuring from ground level to the node bearing the uppermost ear. Number of plants (NP) at harvest was determined by counting the number of plants that survive to physiological maturity. At physiological maturity, heights of six randomly selected plants in a plot were measured using a metre scale from the soil surface to the base of the tassel. Ears per plant (EPP) was determined by counting the number of ears with at least fully developed grains and divided by the number of plants per plot at harvest. The conversion equation by Badu-Apraku *et al*. (2012) was used to correct for moisture content.

4.3.1 Phenotypic data analysis

Data collected was subjected to residual/restricted maximum likelihood (REML) where replication, genotypes, location and interaction between genotype and location was considered fixed while the random term was block nested within replication using GenStat (Patterson & Thompson 1971; VSN, 2014). Data analysis was conducted for single environments and combined over environments to show the influence of the environment on genotypic expression. The model below was used;

$Y_{ijk} = \mu + G_i + R_l + B_{l(k)} + L_j + GL_{ij} + \varepsilon_{ijk}$.. (Equation 2).

Where Y_{ijk} is the observed trait for the ith genotype in the kth block within the lth replicate, μ = overall mean, G_i is the effect of the ith genotype, R_l is the effect of the lth replicate, $B_l({}_k)$ is the effect of the kth block in the lth replicate, L_j is the effect of the jth location GL_{ij} is the interaction effect between the ith genotype and jth location and ε_{ijk} is the random error term. Mean separation was carried out using LSD at 5% significance level using suitable error terms.

4.3.2 Genetic data analysis

Combining ability was estimated based on Griffing (1956) method IV, model II, analysis using the Diallel-SAS programme as described by Zhang & Kang (1997). The genetic model for the combining ability analysis is given by;

$y_{ij} = \mu + g_i + g_j + s_{ij}$…………………………………………………………… (Equation 3).

where μ is the overall mean of all crosses in the diallel design, g_i is the general combining ability of the ith parent, g_j is the general combining ability of the *j*th parent while s_{ij} is the specific combining ability between the ith and the jth parents (Singh & Chaudhary, 1985).

Heritability in narrow sense (h^2) was estimated on a plot basis,

$h^2 = \frac{\sigma_A^2}{\sigma_A^2+\sigma_D^2+\sigma_e^2}$……………………………………………………………………..…. (Equation 4).

Where h^2 is heritability in narrow sense, σ_A^2 is the additive variance, σ_D^2 is the dominance variance and σ_e^2 is the environmental (Singh & Chaudhary, 1985).

Baker's ratio (BR) was calculated using the following formula;

$BR = \frac{2\sigma_{GCA}^2}{2\sigma_{GCA}^2+\sigma_{SCA}^2}$ ……………………………………………………………… (Equation 5).

where σ^2_{GCA} refers to general combining ability variance and σ^2_{SCA} refers to specific combining ability variance (Baker, 1979).

4.4 Results

4.4.1 Variance components for grain yield and yield contributing traits

Residual maximum likelihood (REML) analyses for managed drought environment revealed ($p<0.05$) main effects of genotypes for all measured traits except ASI. In the random drought environment, significant ($p<0.05$) main effects for genotype were observed for PH and EH traits only (Table 4.2 and Table 4.3). Combined analysis of variance over environments revealed significant ($p<0.01$) main effects for genotypes for all traits except ASI and EPP. In addition, significant ($p<0.01$) location main effects were observed for all traits studied. Genotype by location interactions were significant ($p<0.01$) for all traits except ASI (Table 4.4).

Table 4.2. REML table of variance components of all entries including crosses and checks for grain yield and yield contributing traits of maize hybrids in managed drought environment

GY			**PH**			**EH**			**EPP**		
Fixed	Wald (df)	*P*	Fixed	Wald (df)	*P*	Fixed	Wald (df)	*P*	Fixed	Wald (df)	*P*
Rep	9.41 (1)	0.129	Rep	1.04 (1)	0.309	Rep	1.86 (1)	0.172	Rep	0.29 (1)	0.642
Geno	117.7 (56)	0.010	Geno	232.78 (56)	<0.001	Geno	196.53 (56)	<0.001	Geno	63.67 (56)	0.327
Random	Estimate	SE	Random	Estimate	SE	Random	Estimate	SE	Random	Estimate	SE
Rep.bloc	0.048	0.142	Rep.bloc	-6.3	11.2	Rep.bloc	-0.08	7.76	Rep.bloc	0.002	0.0004
Residual	1.388	0.272	Residual	195.2	38.4	Residual	92.23	18.53	Residual	0.002	0.005

GY=grain yield, PH=plant height, EH=ear height, EPP=ears per plant, Rep=replication, Geno=Genotype, Rep.bloc=Replication*Block, p=probability, DF=degrees of freedom, SE= standard error.

Table 4.3. REML table of variance components for all entries including crosses and checks for grain yield and yield contributing traits in random drought environment

GY			**PH**			**EH**			**EPP**		
Fixed	Wald (df)	*P*	Fixed	Wald (df)	*P*	Fixed	Wald (df)	*P*	Fixed	Wald (df)	*P*
Rep	0.01 (1)	0.9	Rep	0.03 (1)	0.8	Rep	0.7 (1)	0.4	Rep	0.00 (1)	*
Geno	6.25 (56)	0.9	Geno	130.5 (56)	<0.001	Geno	134.03 (56)	<0.001	Geno	20.92 (56)	0.4
Random	Estimate	SE	Random	Estimate	SE	Random	Estimate	SE	Random	Estimate	SE
Rep.bloc	0.004	0.01	Rep.bloc	-23	25.7	Rep.bloc	0.17	0.10	Rep.bloc	0.002	0.0004
Residual	0.309	0.05	Residual	501.3	102.1	Residual	0.08	0.01	Residual	0.002	0.005

GY=grain yield, PH=plant height, EH=ear height, EPP=ears per plant, Rep=replication, Geno=Genotype, Rep.Bloc=Replication*Bloc, p=probability, DF=degrees of freedom, SE= standard error.

Table 4.4. REML table of variance components of all entries including crosses and checks for grain yield and yield contributing combined across environments.

ASI			PH			EH			EPP		
Fixed	Wald (df)	*P*	Fixed	Wald (df)	*P*	Fixed	Wald (df)	*P*	Fixed	Wald (df)	*P*
Rep	1.45 (1)	0.23	Rep	3.25 (1)	0.07	Rep	23.92 (1)	<0.001	Rep	0.25 (1)	0.62
Geno	0.79 (56)	0.87	Geno	4.09 (56)	<0.001	Geno	12.80 (56)	<0.001	Geno	1.30 (56)	0.06
Loc	24.37 (1)	<0.001	Loc	3613.9 (1)	<0.001	Loc	4460.5 (1)	<0.001	Loc	657.61 (1)	<0.001
Loc.geno	50.39(56)	0.68	Loc.geno	82.25 (56)	0.0013	Loc.geno	148.3 (56)	<0.001	Loc.geno	75.54 (56)	0.042
Random	Estimate	SE	Random	Estimate	SE	Random	Estimate	SE	Random	Estimate	SE
L.R.B	0.127	0.217	L.R.B	-11.5	0.01	L.R.B	127.5	18	L.R.B	-0.001	0.001
Residual	3.53	0.498	Residual	7.7	46.5	Residual	-5.7	2.1	Residual	0.05	0.007

GY=grain yield, PH=plant height, EH=ear height, EPP=ears per plant, Rep=replication, Geno=Genotype, Loc.geno =Location*genotype interaction, p=probability, DF=degrees of freedom, SE= standard error.

Table 4.4. Contd…

GY		
Fixed	Wald (df)	*P*
Rep	6.02 (1)	<0.001
Geno	1.97 (56)	<0.001
Loc	945.4 (1)	<0.001
Loc.geno	93.28(56)	0.001
Random	Estimate	SE
L.R.B	0.09	0.084
Residual	0.948	0.135

GY=grain yield, PH=plant height, EH=ear height, EPP=ears per plant, Rep=replication, Geno=Genotype, Rep.Bloc=Replication*Bloc, p=probability, DF=degrees of freedom, SE= standard error.

4.4.2 Mean performance of grain yield and yield contributing traits

In the managed drought environment, higher GY values were recorded as compared to the random drought environment (Table 4.5, Appendix E and F). The highest GY was KAT-DT-EE-14×KAT-DT-EE-05 which yielded 9.82 t ha^{-1} and KAT-DT-M-38×KAT-DT-EE-15 yielding 2.03 t ha^{-1} in the managed and random drought conditions, respectively. For GY, the best performing check variety PAN 5M-19 which yielded 8.73 t ha^{-1} and DUMA 43 yielding 1.19 t ha^{-1} in the managed and random drought environments, respectively, despite the checks having a higher mean number of ears per plant. For ASI trait, a wider interval was observed in the random drought experiment. Furthermore, longer ear heights and increased ears per plant were observed in the managed drought experiment.

The least anthesis-silking interval of 0.5 was observed in KAT-DT-M-39×KAT-DT-E-06, KAT-DT-M-38×KAT-DT-M-31, KAT-DT-EE-18×KAT-DT-M-31 and DUMA 43 in the managed drought experiment. Overall results show that commercial check varieties had reduced plant height means compared to crosses in both environments. Crosses KAT-DT-M-38×KAT-DT-EE-07, KAT-DT-M-39×KAT-DT-EE-04, KAT-DT-M-31×KAT-DT-EE-14 had significantly lower plant heights of 41.2, 47.8 and 55.5, respectively in random drought experiment. In managed drought experiment, KAT-DT-M-38×KAT-DT-EE-15, KAT-DT-EE-18×KAT-DT-M-31 and KAT-DT-M-31×KAT-DT-EE-02 recorded plant heights of 128.2, 147 and 156.8, respectively.

Higher ear height values were observed in the managed drought environment which translated possibly to higher GY values. KAT-DT-EE-14×KAT-DT-E-06, KAT-DT-EE-18×KAT-DT-M-39 and KAT-DT-EE-07×KAT-DT-E-06 with 118.75 cm, 117.75 cm and 115.25 cm, respectively. In the random drought experiment, shorter ear height values were recorded in KAT-DT-EE-07×KAT-DT-E-06, KAT-DT-M-39×KAT-DT-EE-05 and KAT-DT-EE-18×KAT-DT-EE-02 with values of 74.25 cm, 70.5 cm and 67 cm, respectively possibly contributing to lower GY. Further, it was evident that genotypes with similar numbers of ears per plant had different GY values depending on the test environments. For example, in the managed drought environment cross KAT-DT-EE-18×KAT-DT-EE-05 with 0.93 EPP yielded 8.78 t ha^{1} while cross KAT-DT-M-31×KAT-DT-EE-02 had 0.92 EPP and a GY of 1.59 t ha^{-1} in the random drought experiment.

Mean performance of measured traits in combined environments is shown in Table 6. Mean GY of crosses outperformed commercial checks for example, cross KAT-DT-EE-07×KAT-DT-EE-14, KAT-DT-EE-07×KAT-DT-EE-04 and KAT-DT-E-06×KAT-DT-EE-05 yielded 6.18 t ha^{-1}, 6.16 t ha^{-1} and 6.10 t ha^{-1}, respectively while commercial checks PAN 5M-19 and DUMA 43 yielded 4.82 t ha^{-1} and 4.31 t ha^{-1}, respectively. Mean ASI values of experimental hybrids was shorter than the checks. Comparatively, commercial checks recorded lower plant height values as compared to crosses while crosses showed higher ear heights than the checks. Greater ears per plant were observed in commercial checks however, the checks had lower GY as compared to crosses. EPP of 0.82 and 0.83 against a GY of 4.82 and 4.31t ha^{-1} respectively was observed for commercial check PAN 5M-19 and DUMA 43 while comparable EPP of 0.81 KAT-DT-EE-15×KAT-DT-EE-02 and 0.83 yielded GY of 5.29 and 5.51 t ha^{-1}, respectively by the crosses.

Table 4.5. Mean performance for measured traits in managed and random drought environment, the cut-off point was the best performing check for GY

	Managed drought					**Random drought**				
Genotype	**ASI**	**PH**	**EH**	**EPP**	**GY**	**ASI**	**PH**	**EH**	**EPP**	**GY**
KAT-DT-EE-14×KAT-DT-EE-05	1.5	210.4	113	1.04	9.82	2	102	57.25	0.35	0.81
KAT-DT-EE-04×KAT-DT-EE-02	1	203.5	91	1.11	9.67	1.5	117.5	51	0.55	1.34
KAT-DT-EE-18×KAT-DT-EE-14	2.5	217	90.75	1.4	9.35	-2	109.2	61	0.17	0.26
KAT-DT-EE-15×KAT-DT-E-06	1	196.8	82	1.01	9.13	5.5	100.2	52	0.38	0.7
KAT-DT-E-06×KAT-DT-EE-04	1	203.1	86.75	1.02	9.04	1	125.2	56.5	0.73	1.54
KAT-DT-EE-07×KAT-DT-EE-04	1	193	97	1.08	8.99	2	84.2	23.5	0.18	0.5
KAT-DT-M-39×KAT-DT-EE-02	1	197.5	83.75	1.09	8.98	0.5	111.2	49	0.28	0.46
KAT-DT-E-06×KAT-DT-EE-05	1	205.8	84.75	1.02	8.92	3.5	118.5	58.25	0.21	0.47
KAT-DT-EE-15×KAT-DT-EE-02	1	175.8	85.75	0.99	8.91	3.5	109.5	51	0.63	1.67
KAT-DT-EE-07×KAT-DT-EE-14	1	196.2	111.75	1	8.88	0	60.8	34.75	0.27	0.78
KAT-DT-EE-18×KAT-DT-EE-05	1.5	210.1	102.25	0.93	8.78	3	117.5	41	0.08	0.21
KAT-DT-EE-18×KAT-DT-EE-02	1	209.2	97.5	1.03	8.76	4.5	143.2	67	0.84	1.75
PAN 5M-19	1	197.2	101.75	1.05	8.73	4.5	81	8.1	0.58	0.9
Lsd (0.05)	1.00	28.94	21.47	0.4	2.5	6.5	54	33.2	0.53	1.3
CV%	15.4	7.13	11.21	16.5	15.4	19.1	25.9	37.1	13.2	26

ASI=anthesis-silking interval, GY= grain yield, PH=plant height, EH=ear height, EPP=ears per plant, LSD = Least significant difference, CV% = coefficient of variation.

Table 4.6. Mean performance of hybrids for measured traits combined over study environments, cut of point is the best performing check for GY.

Genotype	**ASI**	**PH**	**EH**	**EPP**	**GY**
KAT-DT-EE-07×KAT-DT-EE-14	0.5	128.5	73.25	0.64	6.18
KAT-DT-EE-07×KAT-DT-EE-04	1.5	138.6	60.25	0.63	6.16
KAT-DT-E-06×KAT-DT-EE-05	2.25	162.1	71.5	0.62	6.10
KAT-DT-EE-15×KAT-DT-EE-14	1.5	138.5	65	0.56	5.74
KAT-DT-EE-04×KAT-DT-EE-02	1.25	160.5	71	0.83	5.51
KAT-DT-M-39×KAT-DT-EE-04	2.25	120.9	46.62	0.53	5.50
KAT-DT-EE-14×KAT-DT-E-06	3	176.9	72.38	0.60	5.35
KAT-DT-EE-14×KAT-DT-EE-05	1.75	156.2	85.12	0.70	5.32
KAT-DT-E-06×KAT-DT-EE-04	1	164.2	71.62	0.88	5.29
KAT-DT-EE-15×KAT-DT-EE-02	2.25	142.6	68.38	0.81	5.29
KAT-DT-EE-18×KAT-DT-EE-02	2.75	176.2	82.25	0.94	5.26
KAT-DT-M-38×KAT-DT-EE-14	1.25	146.6	65	0.76	4.89
KAT-DT-EE-15×KAT-DT-EE-04	1.5	161.6	73	0.78	4.83

ASI=anthesis-silking interval, GY= grain yield, PH=plant height, EH=ear height, EPP=ears per plant, LSD = Least significant difference, CV% = coefficient of variation.

Table 4.6. Contd…

Genotype	**ASI**	**PH**	**EH**	**EPP**	**GY**
PAN 5M-19	2.75	139.1	54.92	0.82	4.82
DUMA 43	2.75	129.5	57.23	0.83	4.31
Trial mean	1.86	149.7	68.98	0.47	4.24
Lsd (0.05)	3.19	30.21	19.42	0.32	30.21
CV %	27.1	0.6	1.5	1.9	0.6

ASI=anthesis-silking interval, GY= grain yield, PH=plant height, EH=ear height, EPP=ears per plant, LSD = Least significant difference, CV% = coefficient of variation.

4.4.3 Mean squares due to GCA and SCA for measured traits in a half diallel mating design of 11 parents across test environments

Mean square of double cross hybrids was significant (p<0.05) for all measured traits except ASI and EPP. Combining ability analysis showed significant (p<0.05) mean squares due to GCA and SCA for GY, EH and PH. Significant GCA by environment (p <0.05) mean squares were observed for all measured traits except ASI. In contrast, SCA by environment interaction mean squares were not significant for all studied traits (Table 4.7).

Table 4.7. Mean squares due to GCA and SCA for measured traits in a half diallel of 11 parents.

Source of variation	**df**	**ASI**	**GY**	**PH**	**EH**	**EPP**
Hybrids	54	2.88	1.75*	944.89*	1429.3*	0.06
GCA	10	4.19	4.29*	1742.21*	3.89*	0.06
SCA	44	2.59	2.12*	784.30*	459.12*	1.31
Environment × hybrids						
ENV x GCA	10	2.97	2.00*	945.65*	304.6*	0.11*
ENV x SCA	44	3.00	0.58	365.41	157.63	0.05
Error	108	4.12	16.46	320.68	118.11	0.05
CV%		10.9	22.3	11.7	15.1	30.1
Mean		1.89	4.32	152.85	71.95	0.05

* Significant at (p<0.05), ASI=anthesis-silking interval, GY= grain yield, PH=plant height, EH=ear height, EPP=ears per plant, CV% = coefficient of variation.

4.4.4 Specific combining ability of crosses across locations for grain yield and yield contributing traits

Results of specific combining ability (SCA) for grain yield and yield related traits are presented in Table 4.8. In random drought conditions, significant negative SCA estimates for reduced plant heights were observed. Cross KAT-DT-M-39×KAT-DT-EE-04 and KAT-DT-M-38×KAT-DT-EE-07 in random drought and KAT-DT-EE-14×KAT-DT-EE-02 and KAT-DT-EE-14×KAT-DT-EE-04 under managed drought conditions. Specific combining ability estimates revealed significant and positive increase in ear height under managed drought conditions. Significant positive SCA for ear height was recorded in crosses KAT-DT-M-31×KAT-DT-EE-04, KAT-DT-M-39×KAT-DT-E-06, KAT-DT-EE-14×KAT-DT-E-06 and KAT-DT-M-38×KAT-DT-M-39 in managed drought environment while KAT-DT-M-38×KAT-DT-EE-04, KAT-DT-M-38×KAT-DT-M-39 in random drought environment. Notably, KAT-DT-M-38×KAT-DT-M-39 has good specific combining ability for increased ear height in both study environments.

Increase in grain yield was observed in KAT-DT-M-31×KAT-DT-EE-07 under managed drought conditions with a significant and positive SCA. The potential to increase ears per plant among hybrids under random drought environment was also revealed. Significant positive SCA was recorded for genotype KAT-DT-E-06×KAT-DT-EE-02, KAT-DT-EE-07×KAT-DT-E-06 and KAT-DT-EE-15×KAT-DT-M-39 in managed drought conditions and KAT-DT-E-06×KAT-DT-EE-02, KAT-DT-EE-07×KAT-DT-E-06 under random drought conditions. Evidently, KAT-DT-E-06×KAT-DT-EE-02 and KAT-DT-EE-07×KAT-DT-E-06 showed significant increase in EPP in both study environ

Table 4.8. Specific combining ability (SCA) estimates of crosses for yield and yield related traits according to test environment.

Cross	**ASI**		**PH**		**EH**		**GY**		**EPP**	
	MD	**RD**	**MD**	**RD**	**MD**	**RD**	**MD**	**RD**	**MD**	**RD**
KAT-DT-EE-04×KAT-DT-EE-02	-0.27	-0.50	8.20	9.20	6.88	-0.75	1.25	0.26	0.00	0.01
KAT-DT-EE-05×KAT-DT-EE-02	-0.04	0.50	5.56	-2.66	6.55	-4.92	-0.75	0.30	0.00	-0.01
KAT-DT-E-06×KAT-DT-EE-02	0.96	-0.39	7.09	-2.69	7.99	0.53	0.13	-0.72	0.21*	0.29*
KAT-DT-M-39×KAT-DT-EE-02	0.07	-1.11	7.38	-4.61	-3.09	-9.11	1.40	-0.45	0.00	-0.01
KAT-DT-EE-14×KAT-DT-EE-02	-0.26	1.44	-21.21*	-0.66	-10.40	-3.39	-0.71	-0.32	0.03	-0.12
KAT-DT-EE-07×KAT-DT-EE-02	-0.04	1.11	-11.66	-18.24	-18.20	-16.72	-1.85	-0.45	0.00	0.00
KAT-DT-M-31×KAT-DT-EE-02	-0.10	-2.94	-16.91	2.28	-10.42	3.27	-1.32	0.40	0.00	-0.04
KAT-DT-EE-15×KAT-DT-EE-02	0.01	1.28	1.79	1.51	9.71	4.14	0.71	0.25	0.01	-0.05
KAT-DT-M-38×KAT-DT-EE-02	-0.04	-0.50	2.91	-15.11	2.66	5.26	0.56	-0.02	0.00	-0.01
KAT-DT-EE-18×KAT-DT-EE-02	0.44	-0.2	25.40	2.679	14.47	-4.19	0.86	0.13	-0.02	0.1
KAT-DT-EE-05×KAT-DT-EE-04	-0.27	-0.11	-3.07	9.56	-2.05	-2.25	-1.68	0.11	0.28	-1.06
KAT-DT-E-06×KAT-DT-EE-04	-0.27	-2.50	-12.50	13.28	-9.10	-0.81	0.55	0.85	0.05	0.30
KAT-DT-M-39×KAT-DT-EE-04	0.34	1.28	-11.75	-57.63*	-11.44	-35.95	0.50	-0.55	0.00	1.08
KAT-DT-EE-14×KAT-DT-EE-04	-0.49	3.83	-19.94*	24.06	-11.90	2.026	-2.09	0.27	0.01	-1.44
KAT-DT-EE-07×KAT-DT-EE-04	-0.27	0.50	-16.29	-15.27	-2.30	-26.56	0.90	-0.19	0.01	1.35
KAT-DT-M-31×KAT-DT-EE-04	1.18	-0.56	27.45	3.01	23.73*	8.687	0.83	-0.46	0.01	-0.03
KAT-DT-EE-15×KAT-DT-EE-04	-0.21	-0.33	15.40	20.73	2.62	15.80	-0.09	0.32	0.03	-0.24
KAT-DT-M-38×KAT-DT-EE-04	-0.27	-1.11	-0.22	11.37	-2.69	19.93*	-0.38	-0.12	0.00	-0.37

Table 4.8. Contd…

Cross	**ASI**		**PH**		**EH**		**GY**		**EPP**	
	MD	**RD**	**MD**	**RD**	**MD**	**RD**	**MD**	**RD**	**MD**	**RD**
KAT-DT-E-06×KAT-DT-EE-05	-0.04	0.00	-13.69	-10.33	-17.19	-9.72	0.44	-0.07	0.03	-0.10
KAT-DT-M-39×KAT-DT-EE-05	0.07	-1.22	-2.14	14.01	3.73	5.89	-0.45	0.11	0.01	-0.06
KAT-DT-EE-14×KAT-DT-EE-05	0.23	-0.67	-2.13	-18.05	8.52	-8.64	1.50	0.23	0.00	0.00
KAT-DT-EE-07×KAT-DT-EE-05	-0.04	-1.50	2.57	15.12	-0.38	6.03	-0.40	0.11	0.01	-0.05
KAT-DT-M-31×KAT-DT-EE-05	-0.10	0.94	0.06	-25.61*	1.15	-1.73	0.89	0.01	0.01	-0.06
KAT-DT-M-31×KAT-DT-E-06	-0.10	-0.44	5.34	-15.13	-5.16	2.45	0.99	0.05	0.00*	-0.02
KAT-DT-EE-15×KAT-DT-E-06	0.01	1.78	2.54	-11.41	-5.77	-0.33	0.85	-0.33	0.01	-0.07
KAT-DT-M-38×KAT-DT-E-06	-0.04	2.00	-14.59	-7.27	-11.07	-0.43	-0.57	-0.43	0.00	-0.01
KAT-DT-EE-18×KAT-DT-E-06	0.69	0.54	2.7	9.27	0.84	5.68	-0.29	0.26	-0.17	0.001
KAT-DT-EE-14×KAT-DT-M-39	-0.16	1.22	-12.51	2.01	-14.87	-12.34	-0.70	0.57	0.01	-0.07
KAT-DT-EE-07×KAT-DT-M-39	0.07	2.39	-20.61	1.67	-15.02	2.58	-1.69	0.17	0.01	0.05
KAT-DT-M-31×KAT-DT-M-39	0.01	2.33	8.14	21.70	-3.99	15.58	1.31	0.46	0.10	0.20
KAT-DT-EE-15×KAT-DT-M-39	0.12	-3.44	-0.91	-1.33	-3.60	2.19	-0.48	-0.47	0.00	0.04
KAT-DT-M-38×KAT-DT-M-39	0.07	0.28	15.11	19.81	17.09*	20.06*	0.68	0.20	0.04	-0.13
KAT-DT-EE-18×KAT-DT-M-39	-0.61	-0.39	13.88	1.08	13.24	3.91	0.43	-0.31	-0.08	-0.04
KAT-DT-EE-07×KAT-DT-EE-14	-0.27	-2.06	-10.80	6.62	7.02	5.80	0.07	0.07	0.00	-0.04

Table 4.8. Contd…

Cross	**ASI**		**PH**		**EH**		**GY**		**EPP**	
	MD	**RD**	**MD**	**RD**	**MD**	**RD**	**MD**	**RD**	**MD**	**RD**
KAT-DT-M-31×KAT-DT-EE-14	0.68	-2.61	15.00	5.64	10.80	8.55	-0.57	-0.57	0.00	-0.04
KAT-DT-EE-15×KAT-DT-EE-14	-0.21	-0.89	3.90	-17.13	7.69	13.66	-0.13	-0.13	0.00	-0.04
KAT-DT-M-38×KAT-DT-EE-14	-0.27	-1.17	16.52	-7.74	-1.62	-4.97	0.32	0.32	0.02	0.09
KAT-DT-EE-18×KAT-DT-EE-14	0.27	0.21	4.88	4.71	-4.37	8.28	0.2	0.33	-0.02	-0.03
KAT-DT-M-31×KAT-DT-EE-07	-0.10	1.56	-11.40	0.31	-8.10	7.96	1.72^*	0.48	0.01	-0.05
KAT-DT-EE-15×KAT-DT-EE-07	0.01	0.28	18.80	12.78	7.54	8.58	0.27	-0.15	0.03	-0.11
KAT-DT-M-38×KAT-DT-EE-07	0.96	0.00	20.92	-31.58^*	7.73	-7.80	-0.78	-0.67	0.02	-0.09
KAT-DT-EE-18×KAT-DT-EE-07	-0.32	-0.43	7.22	4.25	4.32	-2.92	0.28	0.07	-0.09	0.03
KAT-DT-EE-15×KAT-DT-M-31	-0.04	-1.28	20.79^*	11.81	4.56	-15.63	-0.48	-0.48	0.00	-0.04
KAT-DT-M-38×KAT-DT-M-31	-0.60	0.44	-9.09	1.20	7.26	0.35	0.35	0.35	0.01	0.05
KAT-DT-EE-18×KAT-DT-M-31	0.88	0.1	-23.92	-6.71	-22.53	-9.61	-1.13	0.07	0.06	0.00
KAT-DT-M-38×KAT-DT-EE-15	0.86	-0.06	-17.67	3.7	-21.70	-21.7	0.32	0.33	0.1	0.00
KAT-DT-EE-18×KAT-DT-EE-15	-0.19	-0.18	-27.03	8.64	-8.98	-8.98	-0.22	0.34	0.19	0.01
KAT-DT-EE-18×KAT-DT-M-38	-1.93	0.13	-4.34	8.86	-14.77	4.48	0.36	-0.5	0	0.02

ASI=anthesis=silking interval, PH=plant height, EH=ear height, GY= grain yield, EPP=ears per plant, RD=random drought, MD=managed drought.

4.4.5 Heritability and Baker’s ratio

Bakers’ ratios of 0.2 for anthesis-silking interval, 0.2 for plant height, 0.5 for ear height, 0.8 for ears per plant and 0.2 for grain yield were obtained as shown in Table 4.9. Low heritability in narrow sense estimates of 0.28%, 3.81%, 31.68% and 4.07% were recorded for anthesis-silking interval, plant height, ear height and grain yield, respectively.

Table 4.9. Baker’s ratios of additive and non-additive gene effects on yield and yield contributing traits.

Variances	**ASI**	**PH**	**EH**	**EPP**	**GY**
σ^2_{gca}	0.0046	10.49	337.82	0.02	0.0000028
σ^2_{sca}	0.044	104.72	6691.	0.01	0.00002
Baker's Ratio	0.2	0.2	0.5	0.8	0.2

ASI=anthesis-silking interval, PH=plant height, EH=ear height, EPP ears per plant, GY= grain yield, σ^2_{gca} = variance due to general combining ability, σ^2_{sca} = variance due to specific combining ability**.**

Baker’s Ratio = $\frac{2\sigma^2_{GCA}}{2\sigma^2_{GCA}+\sigma^2_{SCA}}$

Table 4.10. Estimates of genetic parameters and heritability in grain yield and yield related traits

Trait	σ^2_A	σ^2_D	σ^2_G	σ^2_e	σ^2_P	h^2
ASI	0.0046	0.044	0.0486	3.21	1.6536	0.28
PH	10.49	104.72	115.21	320.68	275.55	3.81
EPP	337.82	669.42	1007.24	118.11	1066.295	31.68
GY	0.02	0.001	0.021	0.94	0.491	4.07

ASI = anthesis-silking interval, PH= Plant height, EH= ear height, EPP = ears per plant and GY = grain yield, σ^2_A Additive variance, σ^2_D = dominance variance, σ^2_e= Additive variance, σ^2_D Error variance, σ^2_P = Phenotypic variance, h^2 = Narrow sense heritability.

4.5 Discussion

The magnitude of genetic variance for drought tolerance can be quantified based on yield and correlated characters with high heritability and ease of measurement (Araus *et al.*, 2008; Bänziger *et al.*, 2000). Significant genotype differences observed for most of the phenotypic traits studied suggest the presence of high genetic variability within the germplasm (Begum *et al.*, 2018). Furthermore, significant (p<0.05) location effects and genotype-by-location interactions in this study show that the environment contributed significantly to the total variation observed in hybrid performance. Similar findings of significant main effects for genotypes, location and genotype-by-environment interactions were reported (Mbuvi *et al.*, 2018).

Superior performance of the F_1 hybrids over the commercial checks for grain yield, anthesis-silking interval and ear height across environments was observed in this study. Grain yield is a key trait in selection for drought tolerance while ASI is important for drought escape (Bänziger *et al.*, 2000; Ngugi *et al.*, 2013). Similar results were reported by Rezende *et al.* (2019) and Murtadha *et al.* (2018) where experimental materials outperformed commercial checks on plant height and anthesis-silking-interval traits. Improved performance of these traits could be explained by the heterosis phenomenon. The presence of heterotic patterns further showed their potential for adaption to drought conditions (Issa *et al.*, 2018). Conclusions on the relevance of heterosis in increasing performance in hybrids for agronomic traits under drought were also drawn by Ilyas *et al.* (2019), Kenga *et al.* (2004), Li & Li (1998) and Mogesse *et al.* (2020) in maize and soghum (*Sorghum bicolor* L.). Presence of heterosis presents an opportunity to exploit hybrid cultivars for semi-arid Kenya.

The high reduction in GY under drought stress environment could be attributed to a wider ASI under stress. Wider ASI's in the random drought environment is undesirable to breeding for drought tolerance because ASI is negatively correlated with yield (Ngugi *et al.*, 2013). Anthesis-silking interval negatively impacts grain yield due to an increase between days to pollen shed and silk emergence resulting to a low seed set (Etiro *et al.*, 2017). Selecting genotypes for reduced ASI under drought stress is an effective approach to improve drought tolerance (Ngugi *et al.*, 2013). In addition, shorter ear heights and higher ears per plant values could be linked to the reduction in grain yield in random drought conditions. Results point to small and poorly filled ears contributing to reduced grain yield.

In a breeding programme focused on developing hybrid cultivars, knowledge of combining ability of the parental genotypes and the inheritance of traits is key. In the present study, significant general combining ability (GCA) and specific combining ability (SCA) mean squares were observed for most measured traits but not for GY, EH and PH traits. Significant GCA and SCA show the presence of additive and non-additive gene action in governing the inheritance of the traits. The inheritance of traits during selection of maize hybrids for drought tolerance has been reported by various researchers (Ali *et al*., 2018; Ilyas *et al*., 2019; Issa *et al*., 2018). GCA by environment interactions for grain yield, plant height, ear height and number of ears indicated varied expression of additive genetic variance in different locations due to the role of environment in genotypic expression (Mogesse *et al*., 2020; Mwimali *et al*., 2015). Findings on differential expression of genes across environments for given traits show the importance of carrying out selection in specific target environments (Mwimali *et al*., 2015). Therefore, hybrids may need to be subjected to advanced trials in multi-locations to test for SCA and select crosses with potential for good performance.

Results from this study show the potential to increase grain yield trait under managed drought conditions with a significant and positive SCA. Significant combining ability for grain yield trait is useful in developing high yielding maize hybrids. Positive SCA for improved grain yield in maize has been documented by various researchers (Dar *et al*., 2017; Mogesse *et al*., 2020). Further, it corroborates that drought adversely affects growth and causes a reduction on maize yields (Murtadha *et al*., 2018). Superior hybrids with improved ASI under drought stress were identified. These results agree with other studies where drought tolerant maize was identified using ASI (Ngugi *et al*., 2013). Reports of significant negative SCA for plant height have been documented (Hoque *et al*., 2016; Mbuvi *et al*., 2018). Crosses with good specific combining ability for short plant stature are potential candidates for selection of desirable maize genotypes for drought tolerance because shorter plants are resistant to lodging (Hoque *et al*., 2016). Good SCA for increased ear height was observed under both random and managed drought environments. Significant positive SCA for ear height is desirable because it allows more ears to develop below the nodes however, there is a risk of breaking when the ear is too high (Amana & Hadi, 2021). These findings demonstrate the potential to increase ears per plant under random drought environment. Hybrids were prolific because they yielded a higher number of ears per plant. Higher ears per plant is a preferred trait since it is directly associated with improved grain yield (Mogesse *et al*., 2020).

Low Bakers' ratios (BRs) alongside low narrow sense heritability were recorded for most traits in this study. Narrow sense heritability is a useful statistic because it measures the proportion of variation that is fixable (Kearsey & Pooni, 1996). Low narrow sense heritability coupled with low BR demonstrates the role of dominant and or epistatic gene effects in inheritance of traits, hence difficult to be transmitted to the progenies. ASI, PH and GY had BR of less than 0.5, implying that non-additive gene action was more important in the inheritance of these traits. However, BR for ears per plant was close to unity suggesting the predominance of additive genetic variance hence heritable (Biswas *et al.*, 2019). Low heritability estimates in this study indicate that the inheritance of traits is largely influenced by non-genetic factors arising from environmental impact (Issa *et al.*, 2018). Therefore, adoption of selection procedures that result in accumulation of positive genes modulating drought tolerance would be plausible.

4.6 Conclusion

Genotype-by-environment interaction affected grain yield and yield contributing traits significantly. Among the traits studied, non-additive gene effects predominated over the additive gene effects in the inheritance of grain yield, ear height and plant height. Specific combining ability was observed for reduced plant heights, increased ear heights and increased ears per plant. The study revealed the potential to develop hybrid cultivars with improved grain yield, reduced plant height, increased ear height and ears per plant superior compared to those currently in the market for future deployment in semi-arid areas.

CHAPTER FIVE

GENERAL DISCUSSION, CONCLUSIONS AND RECOMMENDATIONS

5.1 General Discussion

Drought is a serious challenge in maize production in the world today. In response to this challenge, the breeding programme at Kenya Agricultural and Livestock Research Organization (KALRO) Katumani in collaboration with the International Maize and Wheat Improvement Centre (CIMMYT) released early maturing varieties as a drought escape strategy to manage drought. The varieties yields are far below average compared to hybrids. Moreover, the frequency and severity of extreme climatic events due to climate change necessitates breeding for improved drought tolerance. Therefore, this study was carried out to evaluate drought tolerance and combining ability analysis in tropical maize germplasm.

Screening of genotypes was conducted under random drought and managed drought environments which were ideal in identifying drought tolerance traits. Results from combined analysis of variance over locations showed significant ($p<0.05$) differences among genotypes or grain yield, anthesis-silking interval (ASI), ear height and ears per plant while location main effect was significant ($p<0.05$) for ears per plant trait. On the other hand, there was significant ($p <0.05$) genotype by location interaction effect in all measured traits.

Findings from combining ability analysis revealed the importance of additive and non-additive genetic variance was observed in the inheritance of grain yield, ear height and plant height through significant GCA and SCA mean squares. Additionally, significant GCA by environment was observed for GY, EH, PH and EPP. Significant negative SCA estimates of reduced plant heights, significant positive SCA for ear height, increased ears per plant under drought. The implications of these findings are; differences among genotypes exists for most of the traits under study. Selection can be made on these traits for further crop improvement. Mean performance for most studied traits across environments revealed that some crosses outperformed environmental checks and could be deployed for use by farmers. In addition, low narrow sense heritability and significant SCA showed the presence of non-additive gene effects which makes these traits unreliable for selection.

5.2 Conclusions

Drought tolerant single-cross maize hybrids with high and stable grain yield were successfully identified. Among the experimental hybrids evaluated, desirable agronomic traits of increased ear height, reduced plant height and increased ears per plant were identified and these are key for selection to improve grain improvement. Valuable experimental hybrids that were stable and high yielding across sites which may be recommended for further evaluation in multi-environmental trials for possible release in semi-arid Kenya. From the combining ability analysis, non-additive genetic effects were important in the inheritance of ASI, PH, EH and GY while additive gene action was responsible in the inheritance of EPP. Distinctive crosses that could be utilized directly are KAT-DT-EE-14×KAT-DT-EE-02, KAT-DT-M-39×KAT-DT-EE-04, KAT-DT-M-31×KAT-DT-EE-05, KAT-DT-M-38×KAT-DT-M-39, KAT-DT-EE-15×KAT-DT-M-31, KAT-DT-M-31×KAT-DT-EE-07 and KAT-DT-M-31×KAT-DT-E-06. This study showed that there is genetic potential to obtain superior hybrids for grain yield, plant heights, ear height and ears per plant for deployment in semi-arid Kenya.

5.3 Recommendations

i. Distinct performers for drought tolerance and high grain yield should be advanced to National Performance Trials (NPT) and varietal release to combat yield failures occasioned by drought.
ii. Low narrow sense heritability of key traits; anthesis silking interval, grain yield, plant height and ear height should be utilized to guide the choice of a selection towards yield improvement under drought conditions.
iii. Significant GCA by environment indicate that multi-location testing experiments should be conducted to identify genotypes for adaptability to target environment.
iv. Crosses that showed good specific combining ability for grain yield and ears per plant should be used directly or exploited for future hybrid breeding programmes to achieve considerable increase in maize improvement.

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APPENDICES

Appendix A. Field layout for evaluation of single cross maize hybrids in experiment one

Loc	Rep	Bloc	Plot	Geno	Loc	Rep	Bloc	Plot	Geno	Loc	Rep	Bloc	Plot	Geno	Loc	Rep	Bloc	Plot	Geno
1	1	1	1	68	1	1	8	50	67	1	2	15	99	23	1	2	22	148	87
1	1	1	2	93	1	1	8	51	34	1	2	15	100	4	1	2	22	149	84
1	1	1	3	89	1	1	8	52	74	1	2	15	101	21	1	2	22	150	43
1	1	1	4	2	1	1	8	53	35	1	2	15	102	83	1	2	22	151	35
1	1	1	5	85	1	1	8	54	56	1	2	15	103	58	1	2	22	152	36
1	1	1	6	88	1	1	8	55	9	1	2	15	104	91	1	2	22	153	6
1	1	1	7	32	1	1	8	56	66	1	2	15	105	61	1	2	22	154	72
1	1	2	8	37	1	1	9	57	19	1	2	16	106	25	1	2	23	155	24
1	1	2	9	97	1	1	9	58	21	1	2	16	107	39	1	2	23	156	59
1	1	2	10	28	1	1	9	59	14	1	2	16	108	16	1	2	23	157	37
1	1	2	11	25	1	1	9	60	48	1	2	16	109	38	1	2	23	158	32
1	1	2	12	82	1	1	9	61	76	1	2	16	110	13	1	2	23	159	22
1	1	2	13	57	1	1	9	62	60	1	2	16	111	67	1	2	23	160	19
1	1	2	14	92	1	1	9	63	53	1	2	16	112	31	1	2	23	161	42
1	1	3	15	83	1	1	10	64	27	1	2	17	113	8	1	2	24	162	26
1	1	3	16	73	1	1	10	65	15	1	2	17	114	33	1	2	24	163	18

Loc	Rep	Bloc	Plot	Geno	Loc	Rep	Bloc	Plot	Geno	Loc	Rep	Bloc	Plot	Geno	Loc	Rep	Bloc	Plot	Geno
1	1	3	17	75	1	1	10	66	11	1	2	17	115	79	1	2	24	164	29
1	1	3	18	24	1	1	10	67	69	1	2	17	116	45	1	2	24	165	2
1	1	3	19	31	1	1	10	68	36	1	2	17	117	44	1	2	24	166	75
1	1	3	20	45	1	1	10	69	63	1	2	17	118	12	1	2	24	167	27
1	1	3	21	72	1	1	10	70	13	1	2	17	119	74	1	2	24	168	94
1	1	4	22	61	1	1	11	71	33	1	2	18	120	40	1	2	25	169	65
1	1	4	23	77	1	1	11	72	46	1	2	18	121	81	1	2	25	170	69
1	1	4	24	55	1	1	11	73	18	1	2	18	122	11	1	2	25	171	66

Loc=Location, Rep=Replication, Geno=Genotype

Key to appendix A

Genotype	Description	Genotype	Description	Genotype	Description
1	KAT-DT-EE-11	34	KAT-DT-EE-04	67	KAT-DT-E-07
2	KAT-DT-E-06	35	KAT-DT-E-15	68	KAT-DT-M-14
3	KAT-DT-M-13	36	KAT-DT-M-26	69	KAT-DT-E-28
4	KAT-DT-EE-10	37	KAT-DT-EE-02	70	KAT-DT-M-02
5	KAT-DT-E-05	38	KAT-DT-E-14	71	KAT-DT-E-27

Genotype	Description	Genotype	Description	Genotype	Description
6	KAT-DT-M-11	39	KAT-DT-M-25	72	KAT-DT-M-01
7	KAT-DT-EE-06	40	KAT-DT-EE-03	73	KAT-DT-E-18
8	KAT-DT-E-21	41	KAT-DT-E-26	74	KAT-DT-M-03
9	KAT-DT-M-12	42	KAT-DT-M-24	75	KAT-DT-E-20
10	KAT-DT-EE-17	43	KAT-DT-EE-05	76	KAT-DT-M-10
11	KAT-DT-E-09	44	KAT-DT-E-25	77	KAT-DT-E-19
12	KAT-DT-M-18	45	KAT-DT-M-23	78	KAT-DT-M-31
13	KAT-DT-EE-16	46	KAT-DT-EE-08	79	KAT-DT-E-08
14	KAT-DT-E-04	47	KAT-DT-E-02	80	KAT-DT-M-32
15	KAT-DT-M-19	48	KAT-DT-M-22	81	KAT-DT-M-33
16	KAT-DT-EE-13	49	KAT-DT-EE-20	82	KAT-DT-M-34
17	KAT-DT-E-29	50	KAT-DT-E-01	83	KAT-DT-M-41
18	KAT-DT-M-09	51	KAT-DT-M-21	84	KAT-DT-M-37

Genotype	**Description**	**Genotype**	**Description**	**Genotype**	**Description**
19	KAT-DT-EE-15	52	KAT-DT-EE-19	85	KAT-DT-M-35
20	KAT-DT-E-24	53	KAT-DT-E-11	86	KAT-DT-M-36
21	KAT-DT-M-07	54	KAT-DT-M-20	87	KAT-DT-M-40
22	KAT-DT-EE-09	55	KAT-DT-EE-18	88	KAT-DT-M-39
23	KAT-DT-E-23	56	KAT-DT-E-10	89	KAT-DT-M-38
24	KAT-DT-M-08	57	KAT-DT-M-17	90	KAT-DT-M-29
25	KAT-DT-EE-14	58	KAT-DT-EE-01	91	KAT-DT-M-30
26	KAT-DT-E-30	59	KAT-DT-E-13	92	CHECK 4
27	KAT-DT-M-04	60	KAT-DT-M-27	93	CHECK 1
28	KAT-DT-EE-07	61	KAT-DT-E-12	94	CHECK 7
29	KAT-DT-E-17	62	KAT-DT-M-28	95	CHECK 5
30	KAT-DT-M-05	63	KAT-DT-E-22	96	CHECK 3
31	KAT-DT-EE-12	64	KAT-DT-M-16	97	CHECK 2
32	KAT-DT-E-16	65	KAT-DT-E-03	98	CHECK 6

Appendix B. Mean performance single-cross maize hybrids for grain yield and yield contributing traits in the managed drought experiment

Genotype	ASI	PH	EH	EPP	DTA	DTS	GY
KAT-DT-EE-16	1.5	153	59	1.04	50	52	10.59
KAT-DT-EE-04	1	178.2	74.25	0.96	54	55	10.22
KAT-DT-E-17	1	186.5	98	1.01	55.5	57	9.89
KAT-DT-EE-05	1	156.2	70	1.05	52	53	9.72
KAT-DT-EE-14	0.5	178.2	81	1.50	51.5	52	9.61
KAT-DT-EE-11	1.5	161.2	70.5	0.97	50.5	52	9.54
KAT-DT-M-39	1	193	81	1.07	47.5	56.5	9.40
KAT-DT-EE-08	3	160.5	66.5	1.12	50	53	9.38
KAT-DT-EE-20	1.5	167.2	67	1.00	50	51.5	9.34
KAT-DT-E-28	1	164.2	87.5	0.99	53.5	54.5	9.23
KAT-DT-EE-07	2	161	68	1.35	49.5	51.5	9.17
KAT-DT-E-18	1	191	100.75	0.96	54	55	9.16
KAT-DT-E-06	1	183	91	0.98	54.5	55.5	9.16
KAT-DT-M-02	1	189	88.25	1.05	48	57	9.09
KAT-DT-M-38	1	194.8	89	1.03	50.5	59.5	9.02
KAT-DT-M-31	1	180.5	77	1.01	46	55	8.96
KAT-DT-EE-02	1	167.7	69.5	0.82	52.5	53.5	8.90
KAT-DT-EE-18	1	151.2	63.75	1.15	51	52	8.89
KAT-DT-E-13	1	178.8	93	0.94	53.5	54.5	8.76
KAT-DT-E-25	1	186.5	92.5	0.99	57	58	8.65
KAT-DT-E-29	2	207	113	1.09	57.5	59.5	8.53
DUMA 43	1	189.2	96.5	0.90	59.5	60.5	8.49
KAT-DT-E-23	1.5	199	102	1.01	59	60.5	8.38
KAT-DT-E-22	1	178	91.5	1.05	55.5	57	8.34
KAT-DT-M-28	1	166.8	83.25	1.01	46.5	55.5	8.25
KAT-DT-E-09	1	196.2	106.5	0.91	55	56	8.21
KAT-DT-M-36	1	183	87	1.20	47.5	56.5	8.10
KAT-DT-EE-06	1	147.5	59	1.02	52.5	53.5	8.09
KAT-DT-EE-15	1	157.2	74.5	1.23	52	53	8.05

Genotype	**ASI**	**PH**	**EH**	**EPP**	**DTA**	**DTS**	**GY**
KAT-DT-E-03	1	186.5	80.75	0.88	54	55	7.99
KAT-DT-EE-10	1.5	159.8	69.75	1.00	48.5	50	8.03
KAT-DT-M-30	1	186.5	78	1.03	49.5	58.5	7.93
KAT-DT-E-27	1	177	84	0.87	54.5	55.5	7.85
KAT-DT-EE-19	0.5	166.5	69.5	1.10	54	54.5	7.85
KAT-DT-EE-09	0.5	165.8	68.5	0.97	50	50.5	7.84
KAT-DT-E-04	2	184.2	98.25	1.05	58	60	7.64
KAT-DT-M-24	1	190.2	78	0.99	47.5	56.5	7.59
KAT-DT-M-04	1	238.8	94.75	1.27	47.5	56.5	7.58
KAT-DT-E-01	1	181	99.75	0.96	54.5	55.5	7.51
KAT-DT-M-33	1	189	79	1.06	47.5	56.5	7.51
KAT-DT-E-12	1	184.8	90.75	1.04	54	55	7.50
KAT-DT-E-14	1	166.8	82.5	1.14	53.5	54.5	7.44
KAT-DT-M-06	1	199.2	94.75	1.00	46.5	55.5	7.42
KAT-DT-M-22	1	196	80.5	0.97	46.5	55.5	7.31
KAT-DT-M-01	1	180.8	90	0.93	46	55	7.30
KAT-DT-E-10	1.5	182.8	98	1.05	55	56.5	7.28
KAT-DT-M-40	1.5	182.8	77.25	0.97	49	58.5	7.28
KAT-DT-M-11	1	198.2	92.75	1.09	47	56	7.25
KAT-DT-M-25	1	206.5	91.75	1.00	46.5	55.5	7.09
KAT-DT-M-34	1.5	176.5	78.5	1.00	48.5	58	7.09
PAN 4M-19	1	190.2	82	0.94	47.5	56.5	7.08
KAT-DT-M-23	1	200	82.5	1.11	47	56	6.97
KAT-DT-E-21	0.5	177.8	85	1.09	54.5	55	6.97
KAT-DT-E-05	1.5	169.2	83.25	1.08	56	57.5	6.88
KAT-DT-EE-03	1	177	76.5	0.84	54.5	55.5	6.81
KAT-DT-EE-13	1.5	150.5	67	1.17	50	51.5	6.79
KAT-DT-M-32	1	184.5	81.5	0.94	49.5	58.5	6.74
KAT-DT-M-16	1	210.2	87	1.00	46	55	6.73
PH3253	2.5	225.2	105.25	0.90	51	61.5	6.72
KAT-DT-M-12	1	195.8	88.5	0.99	46	55	6.70
WE1101	2.5	189.2	80.75	0.95	61.5	64	6.68

Genotype	**ASI**	**PH**	**EH**	**EPP**	**DTA**	**DTS**	**GY**
KAT-DT-E-19	1	177.5	92	0.99	53	54	6.54
DK 8031	1.5	189	105.5	0.95	59	58.5	6.53
KAT-DT-M-15	1	191.5	87.5	0.99	45	54	6.46
KAT-DT-E-11	1.5	195.2	95	1.08	60.5	62	6.39
KAT-DT-M-09	1	206	105.5	1.09	47	56	6.37
KAT-DT-M-27	1	172.5	78.5	1.52	45.5	54.5	6.35
KAT-DT-M-37	1	181.8	78.75	1.02	48	57	6.23
KAT-DT-M-21	1	204.2	97.75	1.02	47.5	56.5	6.20
KAT-DT-E-30	1	184.8	93.75	1.01	54	55	6.08
KAT-DT-M-17	1	212.2	101.25	1.07	46	55	5.97
KAT-DT-EE-17	1	142	56.5	1.03	47.5	48.5	5.94
KAT-DT-M-13	1	189	83.5	0.94	46.5	55.5	5.92
KAT-DT-M-35	1	181	74.5	1.00	46.5	55.5	5.91
DK8033	1	160	79.5	1.18	59	60	5.84
KAT-DT-M-20	1	190.5	78.5	1.32	47	56	5.81
KAT-DT-M-18	1	196.8	82.25	1.09	47.5	56.5	5.69
KAT-DT-E-24	1	178.8	100.75	0.94	55.5	56.5	5.63
KAT-DT-E-08	1	202.2	94.5	1.09	54.5	55.5	5.56
KAT-DT-E-16	1	194.8	100.25	0.91	61	62	5.53
KAT-DT-M-08	1	222.2	119.75	0.98	48.5	57.5	5.53
KAT-DT-M-10	1	183.2	75.25	1.00	47	56	5.49
KAT-DT-EE-01	1.5	177.5	81.75	1.05	50.5	52	5.42
KAT-DT-M-26	1	187.5	80	1.06	50	59	5.36
KAT-DT-M-29	1	182.8	77	1.01	51.5	60.5	5.34
KAT-DT-E-07	1	163.2	80.25	1.06	55	56	5.32
KAT-DT-EE-12	1	143.2	57.75	1.18	50.5	51.5	5.32
KAT-DT-E-15	1	163.2	80.25	1.34	52	53	5.31
KAT-DT-M-19	2	208.5	90.75	0.96	49	59	5.27
KAT-DT-M-03	1	176.2	75	1.17	47.5	56.5	5.17
KAT-DT-E-26	1	197.5	105.5	0.62	61	62	5.05
KAT-DT-M-05	1	207	89	1.09	49.5	58.5	4.83
KAT-DT-E-02	1	184	91.5	0.84	54.5	55.5	4.36

Genotype	ASI	PH	EH	EPP	DTA	DTS	GY
KAT-DT-M-41	0.5	201	76.25	1.46	50.5	59	4.24
KAT-DT-M-07	2	193.2	95.25	1.05	49	59	3.76
KAT-DT-M-14	1	185.5	77	0.97	46.5	55.5	3.68
DH04	1.5	174.5	90.5	0.91	63	64	1.55

ASI=anthesis-silking interval, PH=plant height, EH=ear height, EPP=ears per plant, DTA=days to anthesis, DTS=days to silking, GY = grain yield

Appendix C. Mean performance single-cross maize hybrids for grain yield and yield contributing traits in the random drought experiment

Genotype	ASI	PH	EH	NP	NE	EPP	DTA	DTS	GY
KAT-DT-E-06	4	105	43	34	25	0.74	43	47	3.74
KAT-DT-E-30	0	108.5	43.75	31.5	15	0.46	48.5	50	3.47
KAT-DT-M-35	1	120	55.75	19	17.5	0.96	66	67	2.75
KAT-DT-E-18	2	134.5	61.25	27	18	0.67	43	45	2.51
KAT-DT-EE-15	4.5	91	31.5	32	26.5	0.82	68.5	72.5	2.47
KAT-DT-EE-04	2	84.5	34.5	42	37.5	0.89	75	77	2.41
KAT-DT-M-21	2	113	58.5	26	22.5	0.87	67	69	2.35
KAT-DT-M-09	6.5	102.3	56.25	23	11	0.53	68	74.5	2.15
KAT-DT-M-14	4	107.3	60	19.5	16	0.81	67	67	2.11
KAT-DT-M-05	2.5	108.5	52.75	17	16.5	1.30	68	70.5	2.10
KAT-DT-M-27	2	116.3	51.5	27	28.5	1.06	86	63.5	2.08
KAT-DT-EE-02	4	82.8	29.5	40	36	0.90	70	74	2.02
KAT-DT-E-12	2.5	113.5	53.5	27.5	29	1.07	46	48.5	2.00
KAT-DT-M-12	7.5	99.5	48.75	29	19.5	0.67	64.5	72	2.00
KAT-DT-M-23	1	108	54	31.5	21.5	0.71	68	69	2.00
KAT-DT-M-24	0.5	121.5	54.5	32	27	0.85	68.5	69	1.98
KAT-DT-M-26	6	102.3	42.5	21	13	0.63	66	72	1.97
KAT-DT-EE-05	5.5	73	22.5	36.5	30	0.81	66	71.5	1.85
KAT-DT-M-16	3.5	109	54.5	20.5	21	1.03	67	70.5	1.82
KAT-DT-E-03	3.5	100.3	40.5	35.5	31.5	0.89	43.5	47	1.76
KAT-DT-M-30	4	107	46	30	16.5	0.54	70.5	74.5	1.75
KAT-DT-EE-09	3.5	73	26.75	38	28.5	0.75	71.5	75	1.74
KAT-DT-EE-13	1.5	75	27	30	31.5	1.05	68.5	70	1.73
KAT-DT-E-26	-2	123.3	52	30	18	0.60	47	45	1.73
KAT-DT-M-08	5	112.8	63	25	16	0.63	68	73	1.69
KAT-DT-M-32	2.5	108.3	49.25	37	28.5	0.77	73.5	76	1.69
KAT-DT-EE-19	4	86	29.75	33	26	0.79	69	72.5	1.65
KAT-DT-EE-01	2.5	88	30	32.5	30.5	0.95	68	70	1.65
KAT-DT-M-34	6.5	108.3	52.75	28.5	19	0.67	69	75.5	1.64
KAT-DT-EE-10	3.5	75.25	27.25	36.5	28.5	0.80	66	69.5	1.63

Genotype	ASI	PH	EH	NP	NE	EPP	DTA	DTS	GY
KAT-DT-E-07	3	97.5	38.5	30.5	24.5	0.82	47	50	1.61
KAT-DT-E-11	3	108.5	47	29.5	19	0.74	47	50	1.61
KAT-DT-EE-14	3.5	71.25	25	33.5	26	0.77	69	72.5	1.60
KAT-DT-M-39	5	98	47.25	27.5	22	0.78	67	72	1.59
KAT-DT-EE-07	2.5	73.85	27	33.5	31.5	0.93	69	71.5	1.57
KAT-DT-E-22	5	113	47.25	32.5	20.5	0.62	44	48.5	1.56
KAT-DT-M-28	3.5	96.25	50.25	33	22.5	0.68	67	70.5	1.53
KAT-DT-M-31	5	94.5	48.25	32	18	0.57	67	72	1.52
KAT-DT-E-29	6	124.25	54.5	28	21	0.75	48.5	54.5	1.50
KAT-DT-M-04	6.5	97.75	50.5	30	15.5	0.51	66	68.5	1.49
KAT-DT-M-25	-1	107.4	57	33.5	19.5	0.58	70.5	69.5	1.49
KAT-DT-M-01	4	119.5	55	30	19	0.63	68.5	65	1.48
KAT-DT-E-16	2.5	109	44	30	25	0.83	53.5	56	1.48
KAT-DT-M-20	7.5	122	56.25	33	25	0.77	64.5	72	1.46
KAT-DT-EE-18	4	72.5	23.75	34.5	28.5	0.83	67.5	71.5	1.41
KAT-DT-E-10	2.5	102	44.75	33.5	21	0.64	44.5	47	1.40
KAT-DT-EE-03	5	65.25	23	21	17.5	0.83	74	77	1.40
KAT-DT-M-41	2.5	112.75	49.5	14	10	0.71	69.5	72	1.39
KAT-DT-M-38	6	101.25	49	31.5	24.5	0.81	67	73	1.38
KAT-DT-M-03	2.5	79.5	37.5	26.5	11	0.57	68	70.5	1.35
KAT-DT-M-40	4.5	106.5	52.25	29.5	24	0.82	68.5	73	1.32
KAT-DT-M-07	6	110.5	56	27	16	0.58	66	72	1.32
KAT-DT-E-02	6	117.25	53	28	33	1.18	42.5	48.5	1.31
CHECK 4	7	92.25	40.75	12	5	0.42	68	78	1.30
KAT-DT-E-28	6.5	97.5	44.25	33	18	0.54	44	50.5	1.30
KAT-DT-EE-11	5.5	71.5	22.75	32	28	0.87	69	75	1.24
KAT-DT-M-15	2	100.25	47.5	21.5	16.5	0.76	67	69	1.23
KAT-DT-M-10	4	104.25	50	22	9	0.41	68	72	1.17
KAT-DT-EE-17	4.5	43.75	14.75	21	17	0.83	68	72.5	1.15
KAT-DT-M-22	3.5	102.75	48.25	37.5	22	0.60	67	70.5	1.12
KAT-DT-M-33	8	152.65	50.75	19	15	0.80	65	73	1.12

Genotype	ASI	PH	EH	NP	NE	EPP	DTA	DTS	GY
KAT-DT-M-33	8	152.65	50.75	19	15	0.80	65	73	1.12
KAT-DT-EE-08	3	81	30.25	30	26	0.88	70.5	73.5	1.12
KAT-DT-M-29	0	94.25	22.5	28	5.5	0.23	72	72	1.11
KAT-DT-M-06	3.5	101	48.75	35	17	0.48	67	70.5	1.10
KAT-DT-E-25	3.5	114.75	50.5	32	25	0.78	45	47	1.10
KAT-DT-E-14	4	97.5	43.75	32	15	0.53	45	47	1.10
KAT-DT-M-18	3.5	106	49.75	25.5	16	0.64	67	70.5	1.10
KAT-DT-E-15	8.5	109.9	49.75	24	28	1.17	69.5	40	1.10
KAT-DT-EE-20	8	57.5	19.75	39.5	29	0.73	70.5	78.5	1.09
KAT-DT-M-19	1.5	103	50.75	28	16.5	0.59	69	70.5	1.08
KAT-DT-EE-06	5	67.25	20.85	33.5	25	0.75	72.5	77.5	1.08
KAT-DT-E-21	4	108.25	44.75	27	18	0.66	43	47	1.06
KAT-DT-E-27	4	103	42.75	34.5	26.5	0.79	45	47	1.04
KAT-DT-E-09	3	96	42.5	33	14.5	0.42	43.5	50	0.99
KAT-DT-M-13	3	99.25	50.75	22.5	12.5	0.57	68	67	0.98
KAT-DT-M-37	7	100.75	46	26	15.5	0.63	66	73	0.93
KAT-DT-EE-16	3.5	68	19	29.5	20.5	0.72	70.5	73.5	0.91
KAT-DT-E-20	2	112.75	50.25	31.5	17	0.51	46	47	0.90
KAT-DT-M-11	8	102.25	56.75	28	13.5	0.49	70	78	0.89
KAT-DT-E-17	3	91	33	33.5	16.5	0.52	50	44.5	0.88
DK 8031	10	93.25	33.25	31.5	20.5	0.67	67	77	0.87
KAT-DT-M-02	12.5	112.75	52.25	30.5	19	0.65	76	82.5	0.87
DUMA 43	5	95.75	28.5	13.5	8	0.59	78.5	83	0.83
KAT-DT-E-13	6	100	47	33	14.5	0.44	41.5	47.5	0.82
KAT-DT-EE-12	3.5	53	14.75	23.5	16.5	0.69	70.5	73.5	0.79
WE1101	10.5	96.25	36.25	7	3.5	0.48	86	81	0.72
KAT-DT-M-36	6.5	102.5	48.5	33	17.5	0.53	70.5	77	0.71
KAT-DT-M-17	5	101.25	50.25	26	13	0.50	67	72	0.61
DH 04	2.5	32.75	11	2.5	3	1.17	67.5	70	0.60
KAT-DT-E-01	6	67	26.5	31.5	8.5	0.29	50	46	0.46
KAT-DT-E-24	4	106.5	51	34	16	0.47	46	50	0.41

Genotype	**ASI**	**PH**	**EH**	**NP**	**NE**	**EPP**	**DTA**	**DTS**	**GY**
KAT-DT-E-05	6	77.75	32	32.5	9	0.28	47	53	0.39
KAT-DT-E-05	6	77.75	32	32.5	9	0.28	47	53	0.39
KAT-DT-E-08	3	43.75	22.25	34.5	9.5	0.28	47	50	0.37
PAN 4M-19	4.5	101	44	30.5	10.5	0.34	69	75	0.31
DK 8033	2.5	64.5	31.5	14	2.5	0.57	78.5	81	0.30
KAT-DT-E-23	6	125.5	45.25	36	12	0.33	47	53	0.23
KAT-DT-E-04	*	90	40.75	36	2	0.06	51.5	*	0.08
KAT-DT-E-19	2	113.75	50.25	33	6	0.18	52	55	0.08

ASI=anthesis-silking interval, PH=plant height, EH=ear height, EPP=ears per plant, DTA=days to anthesis, DTS=days to silking, GY = grain yield, * missing value

Appendix D. Superiority measure Pi, genotype by environment interaction mean squares and regression coefficient single-cross maize hybrids and 7 commercial checks arranged in the order of Pi

Genotype	Geno mean	pi	MS(GE)	*b* value
KAT-DT-EE-02	5.46	0.20	1.66	1.19
KAT-DT-EE-04	6.31	0.20	1.82	1.36
KAT-DT-EE-05	5.78	0.23	1.84	1.37
KAT-DT-E-06	6.45	0.26	1.84	0.94
KAT-DT-M-39	5.49	0.34	1.82	1.36
KAT-DT-EE-14	5.60	0.34	1.89	1.39
KAT-DT-EE-07	5.37	0.36	1.77	1.32
KAT-DT-M-31	5.24	0.43	1.73	1.29
KAT-DT-EE-15	5.26	0.48	1.80	0.97
KAT-DT-M-38	5.20	0.51	1.78	1.33
KAT-DT-EE-18	5.15	0.51	1.74	1.30
KAT-DT-E-28	5.26	0.54	1.86	1.38
KAT-DT-E-29	5.02	0.58	1.67	1.22
KAT-DT-EE-11	5.39	0.58	2.00	1.44
KAT-DT-E-22	4.95	0.64	1.66	1.18
KAT-DT-EE-08	5.25	0.67	1.98	1.43
KAT-DT-EE-20	5.21	0.69	1.97	1.43
KAT-DT-M-28	4.89	0.71	1.65	1.17
KAT-DT-E-03	4.88	0.74	1.68	1.08
KAT-DT-EE-10	4.83	0.78	1.66	1.11
KAT-DT-M-30	4.84	0.79	1.68	1.07
KAT-DT-E-25	4.87	0.82	1.75	1.31
KAT-DT-E-20	5.07	0.86	2.01	1.45
KAT-DT-EE-09	4.79	0.86	1.69	1.06
KAT-DT-EE-19	4.75	0.90	1.68	1.08
KAT-DT-M-02	4.98	0.91	1.96	1.43
KAT-DT-E-17	5.38	0.94	2.35	1.56
KAT-DT-M-24	4.78	0.97	1.79	0.97

Genotype	Geno mean	pi	MS(GE)	b value
KAT-DT-E-13	4.79	1.04	1.86	1.38
KAT-DT-E-12	4.75	1.04	1.82	0.95
DUMA 43	4.66	1.13	1.78	1.33
KAT-DT-E-09	4.60	1.13	1.69	1.25
KAT-DT-EE-06	4.58	1.13	1.67	1.22
KAT-DT-EE-16	5.75	1.20	2.80	1.68
KAT-DT-M-04	4.53	1.23	1.69	1.06
KAT-DT-E-27	4.45	1.33	1.66	1.18
KAT-DT-M-36	4.40	1.47	1.72	1.28
KAT-DT-M-01	4.39	1.51	1.74	1.01
KAT-DT-M-33	4.32	1.56	1.66	1.11
KAT-DT-E-10	4.34	1.58	1.73	1.02
KAT-DT-E-18	5.83	1.58	1.65	1.16
KAT-DT-M-23	4.49	1.62	2.01	0.86
KAT-DT-M-40	4.30	1.63	1.71	1.03
KAT-DT-M-34	4.37	1.64	1.83	0.95
KAT-DT-E-14	4.27	1.64	1.67	1.10
KAT-DT-M-06	4.26	1.67	1.67	1.10
KAT-DT-M-25	4.29	1.73	1.79	0.97
KAT-DT-M-22	4.22	1.75	1.68	1.07
KAT-DT-E-23	4.30	1.85	1.94	1.41
KAT-DT-M-12	4.35	1.97	2.13	0.81
KAT-DT-EE-13	4.26	1.97	1.97	0.88
KAT-DT-M-16	4.27	2.00	2.03	0.85
KAT-DT-M-11	4.07	2.02	1.66	1.10
KAT-DT-M-32	4.21	2.05	1.97	0.88
KAT-DT-EE-03	4.10	2.14	1.85	0.94
KAT-DT-E-21	4.02	2.19	1.72	1.02
KAT-DT-E-01	3.98	2.21	1.67	1.22
PH3253	4.01	2.33	1.84	0.94
KAT-DT-M-09	4.26	2.39	2.39	0.73
KAT-DT-M-27	4.22	2.43	2.36	0.74

Genotype	Geno mean	pi	MS(GE)	b value
KAT-DT-M-15	3.84	2.54	1.90	0.91
KAT-DT-E-04	3.86	2.56	1.76	1.31
KAT-DT-E-11	4.00	2.60	2.09	0.83
KAT-DT-M-21	4.27	2.61	2.63	0.67
PAN 4M-19	3.69	2.84	1.66	1.17
WE1101	3.70	2.88	1.71	1.04
KAT-DT-E-30	4.77	2.89	3.69	0.45
DK 8031	3.70	2.94	1.78	0.98
KAT-DT-E-05	3.63	2.99	1.66	1.13
KAT-DT-M-35	4.33	3.04	3.17	0.55
KAT-DT-M-37	3.58	3.34	1.88	0.92
KAT-DT-EE-17	3.55	3.63	2.08	0.83
KAT-DT-M-20	3.63	3.64	2.32	0.75
KAT-DT-M-13	3.45	3.81	2.02	0.86
KAT-DT-E-19	3.31	3.82	1.66	1.12
KAT-DT-M-08	3.61	4.03	2.64	0.67
KAT-DT-M-17	3.29	4.09	1.86	0.93
KAT-DT-M-18	3.39	4.13	2.18	0.80
KAT-DT-E-16	3.50	4.15	2.49	0.70
KAT-DT-M-26	3.67	4.23	2.98	0.59
KAT-DT-EE-01	3.53	4.27	2.69	0.65
KAT-DT-M-10	3.33	4.45	2.33	0.75
KAT-DT-E-07	3.47	4.49	2.74	0.64
DK8033	3.07	4.67	1.81	0.96
KAT-DT-M-29	3.23	4.79	2.38	0.73
KAT-DT-E-15	3.20	4.86	2.39	0.73
KAT-DT-E-24	3.02	4.92	1.91	0.91
KAT-DT-M-19	3.18	4.95	2.41	0.73
KAT-DT-E-26	3.39	4.98	3.04	0.58
KAT-DT-E-08	2.96	5.10	1.92	0.90
KAT-DT-EE-12	3.05	5.13	2.21	0.79
KAT-DT-M-05	3.46	5.32	3.57	0.47

Genotype	**Geno mean**	**pi**	**MS(GE)**	**b value**
KAT-DT-M-05	3.46	5.32	3.57	0.47
KAT-DT-E-02	2.83	6.88	3.28	0.53
KAT-DT-M-41	2.81	7.13	3.46	0.49
KAT-DT-M-03	3.26	7.17	2.66	0.66
KAT-DT-M-14	2.90	8.28	4.88	0.27
KAT-DT-M-07	2.54	8.46	3.86	0.34
DH04	1.07	16.57	5.71	0.17

Geno mean= genotype mean, pi= cultivar superiority statistic, MS (GE) = genotype by environment interaction mean squares, *b value*=slope of regression

Appendix E: Field layout for evaluation of crosses between single cross maize hybrids in experiment two

Location	Replication	Block	Plot	Genotype	Parents
1	1	1	1	6	KAT-DT-EE-07×KAT-DT-EE-02
1	1	1	2	34	KAT-DT-EE-18×KAT-DT-E-06
1	1	1	3	32	KAT-DT-EE-15×KAT-DT-E-06
1	1	1	4	30	KAT-DT-EE-07×KAT-DT-E-06
1	1	1	5	37	KAT-DT-M-31×KAT-DT-M-39
1	1	1	6	51	KAT-DT-M-38×KAT-DT-M-31
1	1	1	7	43	KAT-DT-EE-15×KAT-DT-EE-14
1	1	1	8	2	KAT-DT-EE-05×KAT-DT-EE-02
1	1	1	9	45	KAT-DT-EE-18×KAT-DT-EE-14
1	1	1	10	9	KAT-DT-M-38×KAT-DT-EE-02
1	1	1	11	18	KAT-DT-M-38×KAT-DT-EE-04
1	1	1	12	41	KAT-DT-EE-07×KAT-DT-EE-14
1	1	1	13	24	KAT-DT-M-31×KAT-DT-EE-05
1	1	1	14	26	KAT-DT-M-38×KAT-DT-EE-05
1	1	1	15	52	KAT-DT-EE-18×KAT-DT-M-31
1	1	1	16	48	KAT-DT-M-38×KAT-DT-EE-07
1	1	1	17	21	KAT-DT-M-39×KAT-DT-EE-05
1	1	1	18	1	KAT-DT-EE-04×KAT-DT-EE-02
1	1	1	19	29	KAT-DT-EE-14×KAT-DT-E-06

Location	**Replication**	**Block**	**Plot**	**Genotype**	**Parents**
1	1	2	20	50	KAT-DT-EE-15×KAT-DT-M-31
1	1	2	21	39	KAT-DT-M-38×KAT-DT-M-39
1	1	2	22	17	KAT-DT-EE-15×KAT-DT-EE-04
1	1	2	23	49	KAT-DT-EE-18×KAT-DT-EE-07
1	1	2	24	54	KAT-DT-EE-18×KAT-DT-EE-15
1	1	2	25	4	KAT-DT-M-39×KAT-DT-EE-02
1	1	2	26	38	KAT-DT-EE-15×KAT-DT-M-39
1	1	2	27	56	DUMA 43
1	1	2	28	55	KAT-DT-EE-18×KAT-DT-M-38
1	1	2	29	46	KAT-DT-M-31×KAT-DT-EE-07
1	1	2	30	27	KAT-DT-EE-18×KAT-DT-EE-05
1	1	2	31	44	KAT-DT-M-38×KAT-DT-EE-14
1	1	2	32	57	PAN 5M-19
1	1	2	33	13	KAT-DT-M-39×KAT-DT-EE-04
1	1	2	34	23	KAT-DT-EE-07×KAT-DT-EE-05
1	1	2	35	33	KAT-DT-M-38×KAT-DT-E-06
1	1	2	36	5	KAT-DT-EE-14×KAT-DT-EE-02
1	1	2	37	31	KAT-DT-M-31×KAT-DT-E-06
1	1	2	38	10	KAT-DT-EE-18×KAT-DT-EE-02
1	1	3	39	22	KAT-DT-EE-14×KAT-DT-EE-05

Location	Replication	Block	Plot	Genotype	Parents
1	1	3	40	47	KAT-DT-EE-15×KAT-DT-EE-07
1	1	3	41	28	KAT-DT-M-39×KAT-DT-E-06
1	1	3	42	42	KAT-DT-M-31×KAT-DT-EE-14
1	1	3	43	14	KAT-DT-EE-14×KAT-DT-EE-04
1	1	3	44	53	KAT-DT-M-38×KAT-DT-EE-15
1	1	3	45	20	KAT-DT-E-06×KAT-DT-EE-05
1	1	3	46	8	KAT-DT-EE-15×KAT-DT-EE-02
1	1	3	47	36	KAT-DT-EE-07×KAT-DT-M-39
1	1	3	48	35	KAT-DT-EE-14×KAT-DT-M-39
1	1	3	49	11	KAT-DT-EE-05×KAT-DT-EE-04
1	1	3	50	40	KAT-DT-EE-18×KAT-DT-M-39
1	1	3	51	7	KAT-DT-M-31×KAT-DT-EE-02
1	1	3	52	3	KAT-DT-E-06×KAT-DT-EE-02
1	1	3	53	19	KAT-DT-EE-18×KAT-DT-EE-04
1	1	3	54	12	KAT-DT-E-06×KAT-DT-EE-04
1	1	3	55	15	KAT-DT-EE-07×KAT-DT-EE-04
1	1	3	56	25	KAT-DT-EE-15×KAT-DT-EE-05
1	1	3	57	16	KAT-DT-M-31×KAT-DT-EE-04
1	2	4	58	54	KAT-DT-EE-18×KAT-DT-EE-15
1	2	4	59	40	KAT-DT-EE-18×KAT-DT-M-39

Location	Replication	Block	Plot	Genotype	Parents
1	2	4	60	4	KAT-DT-M-39×KAT-DT-EE-02
1	2	4	61	13	KAT-DT-M-39×KAT-DT-EE-04
1	2	4	62	14	KAT-DT-EE-14×KAT-DT-EE-04
1	2	4	63	53	KAT-DT-M-38×KAT-DT-EE-15
1	2	4	64	6	KAT-DT-EE-07×KAT-DT-EE-02
1	2	4	65	22	KAT-DT-EE-14×KAT-DT-EE-05
1	2	4	66	38	KAT-DT-EE-15×KAT-DT-M-39
1	2	4	67	17	KAT-DT-EE-15×KAT-DT-EE-04
1	2	4	68	1	KAT-DT-EE-04×KAT-DT-EE-02
1	2	4	69	43	KAT-DT-EE-15×KAT-DT-EE-14
1	2	4	70	9	KAT-DT-M-38×KAT-DT-EE-02
1	2	4	71	12	KAT-DT-E-06×KAT-DT-EE-04
1	2	4	72	10	KAT-DT-EE-18×KAT-DT-EE-02
1	2	4	73	16	KAT-DT-M-31×KAT-DT-EE-04
1	2	4	74	44	KAT-DT-M-38×KAT-DT-EE-14
1	2	4	75	34	KAT-DT-EE-18×KAT-DT-E-06
1	2	4	76	41	KAT-DT-EE-07×KAT-DT-EE-14
1	2	5	77	39	KAT-DT-M-38×KAT-DT-M-39
1	2	5	78	15	KAT-DT-EE-07×KAT-DT-EE-04
1	2	5	79	5	KAT-DT-EE-14×KAT-DT-EE-02

Location	Replication	Block	Plot	Genotype	Parents
1	2	5	80	36	KAT-DT-EE-07×KAT-DT-M-39
1	2	5	81	45	KAT-DT-EE-18×KAT-DT-EE-14
1	2	5	82	50	KAT-DT-EE-15×KAT-DT-M-31
1	2	5	83	29	KAT-DT-EE-14×KAT-DT-E-06
1	2	5	84	49	KAT-DT-EE-18×KAT-DT-EE-07
1	2	5	85	7	KAT-DT-M-31×KAT-DT-EE-02
1	2	5	86	25	KAT-DT-EE-15×KAT-DT-EE-05
1	2	5	87	52	KAT-DT-EE-18×KAT-DT-M-31
1	2	5	88	21	KAT-DT-M-39×KAT-DT-EE-05
1	2	5	89	37	KAT-DT-M-31×KAT-DT-M-39
1	2	5	90	19	KAT-DT-EE-18×KAT-DT-EE-04
1	2	5	91	27	KAT-DT-EE-18×KAT-DT-EE-05
1	2	5	92	28	KAT-DT-M-39×KAT-DT-E-06
1	2	5	93	35	KAT-DT-EE-14×KAT-DT-M-39
1	2	5	94	2	KAT-DT-EE-05×KAT-DT-EE-02
1	2	5	95	31	KAT-DT-M-31×KAT-DT-E-06
1	2	6	96	47	KAT-DT-EE-15×KAT-DT-EE-07
1	2	6	97	30	KAT-DT-EE-07×KAT-DT-E-06
1	2	6	98	46	KAT-DT-M-31×KAT-DT-EE-07
1	2	6	99	57	PAN 5M-19

Location	**Replication**	**Block**	**Plot**	**Genotype**	**Parents**
1	2	6	100	56	DUMA 43
1	2	6	101	3	KAT-DT-E-06×KAT-DT-EE-02
1	2	6	102	20	KAT-DT-E-06×KAT-DT-EE-05
1	2	6	103	11	KAT-DT-EE-05×KAT-DT-EE-04
1	2	6	104	48	KAT-DT-M-38×KAT-DT-EE-07
1	2	6	105	42	KAT-DT-M-31×KAT-DT-EE-14
1	2	6	106	33	KAT-DT-M-38×KAT-DT-E-06
1	2	6	107	51	KAT-DT-M-38×KAT-DT-M-31
1	2	6	108	18	KAT-DT-M-38×KAT-DT-EE-04
1	2	6	109	32	KAT-DT-EE-15×KAT-DT-E-06
1	2	6	110	24	KAT-DT-M-31×KAT-DT-EE-05
1	2	6	111	26	KAT-DT-M-38×KAT-DT-EE-05
1	2	6	112	55	KAT-DT-EE-18×KAT-DT-M-38
1	2	6	113	8	KAT-DT-EE-15×KAT-DT-EE-02
1	2	6	114	23	KAT-DT-EE-07×KAT-DT-EE-05
2	1	1	1	21	KAT-DT-M-39×KAT-DT-EE-05
2	1	1	2	24	KAT-DT-M-31×KAT-DT-EE-05
2	1	1	3	2	KAT-DT-EE-05×KAT-DT-EE-02
2	1	1	4	10	KAT-DT-EE-18×KAT-DT-EE-02
2	1	1	5	39	KAT-DT-M-38×KAT-DT-M-39

Location	Replication	Block	Plot	Genotype	Parents
2	1	1	6	32	KAT-DT-EE-15×KAT-DT-E-06
2	1	1	7	38	KAT-DT-EE-15×KAT-DT-M-39
2	1	1	8	45	KAT-DT-EE-18×KAT-DT-EE-14
2	1	1	9	18	KAT-DT-M-38×KAT-DT-EE-04
2	1	1	10	28	KAT-DT-M-39×KAT-DT-E-06
2	1	1	11	29	KAT-DT-EE-14×KAT-DT-E-06
2	1	1	12	23	KAT-DT-EE-07×KAT-DT-EE-05
2	1	1	13	20	KAT-DT-E-06×KAT-DT-EE-05
2	1	1	14	55	KAT-DT-EE-18×KAT-DT-M-38
2	1	1	15	15	KAT-DT-EE-07×KAT-DT-EE-04
2	1	1	16	52	KAT-DT-EE-18×KAT-DT-M-31
2	1	1	17	37	KAT-DT-M-31×KAT-DT-M-39
2	1	1	18	12	KAT-DT-E-06×KAT-DT-EE-04
2	1	1	19	17	KAT-DT-EE-15×KAT-DT-EE-04
2	1	2	20	22	KAT-DT-EE-14×KAT-DT-EE-05
2	1	2	21	27	KAT-DT-EE-18×KAT-DT-EE-05
2	1	2	22	19	KAT-DT-EE-18×KAT-DT-EE-04
2	1	2	23	4	KAT-DT-M-39×KAT-DT-EE-02
2	1	2	24	7	KAT-DT-M-31×KAT-DT-EE-02
2	1	2	25	33	KAT-DT-M-38×KAT-DT-E-06

Location	Replication	Block	Plot	Genotype	Parents
2	1	2	26	54	KAT-DT-EE-18×KAT-DT-EE-15
2	1	2	27	57	PAN 5M-19
2	1	2	28	11	KAT-DT-EE-05×KAT-DT-EE-04
2	1	2	29	34	KAT-DT-EE-18×KAT-DT-E-06
2	1	2	30	1	KAT-DT-EE-04×KAT-DT-EE-02
2	1	2	31	48	KAT-DT-M-38×KAT-DT-EE-07
2	1	2	32	6	KAT-DT-EE-07×KAT-DT-EE-02
2	1	2	33	47	KAT-DT-EE-15×KAT-DT-EE-07
2	1	2	34	40	KAT-DT-EE-18×KAT-DT-M-39
2	1	2	35	31	KAT-DT-M-31×KAT-DT-E-06
2	1	2	36	46	KAT-DT-M-31×KAT-DT-EE-07
2	1	2	37	51	KAT-DT-M-38×KAT-DT-M-31
2	1	2	38	43	KAT-DT-EE-15×KAT-DT-EE-14
2	1	3	39	36	KAT-DT-EE-07×KAT-DT-M-39
2	1	3	40	14	KAT-DT-EE-14×KAT-DT-EE-04
2	1	3	41	9	KAT-DT-M-38×KAT-DT-EE-02
2	1	3	42	25	KAT-DT-EE-15×KAT-DT-EE-05
2	1	3	43	53	KAT-DT-M-38×KAT-DT-EE-15
2	1	3	44	13	KAT-DT-M-39×KAT-DT-EE-04
2	1	3	45	41	KAT-DT-EE-07×KAT-DT-EE-14

Location	Replication	Block	Plot	Genotype	Parents
2	1	3	46	35	KAT-DT-EE-14×KAT-DT-M-39
2	1	3	47	26	KAT-DT-M-38×KAT-DT-EE-05
2	1	3	48	30	KAT-DT-EE-07×KAT-DT-E-06
2	1	3	49	3	KAT-DT-E-06×KAT-DT-EE-02
2	1	3	50	44	KAT-DT-M-38×KAT-DT-EE-14
2	1	3	51	50	KAT-DT-EE-15×KAT-DT-M-31
2	1	3	52	42	KAT-DT-M-31×KAT-DT-EE-14
2	1	3	53	16	KAT-DT-M-31×KAT-DT-EE-04
2	1	3	54	56	DUMA 43
2	1	3	55	5	KAT-DT-EE-14×KAT-DT-EE-02
2	1	3	56	49	KAT-DT-EE-18×KAT-DT-EE-07
2	1	3	57	8	KAT-DT-EE-15×KAT-DT-EE-02
2	2	4	58	50	KAT-DT-EE-15×KAT-DT-M-31
2	2	4	59	33	KAT-DT-M-38×KAT-DT-E-06
2	2	4	60	52	KAT-DT-EE-18×KAT-DT-M-31
2	2	4	61	12	KAT-DT-E-06×KAT-DT-EE-04
2	2	4	62	34	KAT-DT-EE-18×KAT-DT-E-06
2	2	4	63	44	KAT-DT-M-38×KAT-DT-EE-14
2	2	4	64	53	KAT-DT-M-38×KAT-DT-EE-15
2	2	4	65	6	KAT-DT-EE-07×KAT-DT-EE-02

Location	Replication	Block	Plot	Genotype	Parents
2	2	4	66	38	KAT-DT-EE-15×KAT-DT-M-39
2	2	4	67	23	KAT-DT-EE-07×KAT-DT-EE-05
2	2	4	68	28	KAT-DT-M-39×KAT-DT-E-06
2	2	4	69	13	KAT-DT-M-39×KAT-DT-EE-04
2	2	4	70	42	KAT-DT-M-31×KAT-DT-EE-14
2	2	4	71	2	KAT-DT-EE-05×KAT-DT-EE-02
2	2	4	72	31	KAT-DT-M-31×KAT-DT-E-06
2	2	4	73	57	PAN 5M-19
2	2	4	74	7	KAT-DT-M-31×KAT-DT-EE-02
2	2	4	75	9	KAT-DT-M-38×KAT-DT-EE-02
2	2	4	76	30	KAT-DT-EE-07×KAT-DT-E-06
2	2	5	77	17	KAT-DT-EE-15×KAT-DT-EE-04
2	2	5	78	8	KAT-DT-EE-15×KAT-DT-EE-02
2	2	5	79	39	KAT-DT-M-38×KAT-DT-M-39
2	2	5	80	49	KAT-DT-EE-18×KAT-DT-EE-07
2	2	5	81	24	KAT-DT-M-31×KAT-DT-EE-05
2	2	5	82	51	KAT-DT-M-38×KAT-DT-M-31
2	2	5	83	19	KAT-DT-EE-18×KAT-DT-EE-04
2	2	5	84	36	KAT-DT-EE-07×KAT-DT-M-39
2	2	5	85	1	KAT-DT-EE-04×KAT-DT-EE-02

Location	Replication	Block	Plot	Genotype	Parents
2	2	5	86	25	KAT-DT-EE-15×KAT-DT-EE-05
2	2	5	87	40	KAT-DT-EE-18×KAT-DT-M-39
2	2	5	88	37	KAT-DT-M-31×KAT-DT-M-39
2	2	5	89	4	KAT-DT-M-39×KAT-DT-EE-02
2	2	5	90	43	KAT-DT-EE-15×KAT-DT-EE-14
2	2	5	91	41	KAT-DT-EE-07×KAT-DT-EE-14
2	2	5	92	32	KAT-DT-EE-15×KAT-DT-E-06
2	2	5	93	47	KAT-DT-EE-15×KAT-DT-EE-07
2	2	5	94	35	KAT-DT-EE-14×KAT-DT-M-39
2	2	5	95	21	KAT-DT-M-39×KAT-DT-EE-05
2	2	6	96	48	KAT-DT-M-38×KAT-DT-EE-07
2	2	6	97	56	DUMA 43
2	2	6	98	45	KAT-DT-EE-18×KAT-DT-EE-14
2	2	6	99	54	KAT-DT-EE-18×KAT-DT-EE-15
2	2	6	100	15	KAT-DT-EE-07×KAT-DT-EE-04
2	2	6	101	10	KAT-DT-EE-18×KAT-DT-EE-02
2	2	6	102	55	KAT-DT-EE-18×KAT-DT-M-38
2	2	6	103	22	KAT-DT-EE-14×KAT-DT-EE-05
2	2	6	104	26	KAT-DT-M-38×KAT-DT-EE-05
2	2	6	105	46	KAT-DT-M-31×KAT-DT-EE-07

Location	**Replication**	**Block**	**Plot**	**Genotype**	**Parents**
2	2	6	106	27	KAT-DT-EE-18×KAT-DT-EE-05
2	2	6	107	3	KAT-DT-E-06×KAT-DT-EE-02
2	2	6	108	16	KAT-DT-M-31×KAT-DT-EE-04
2	2	6	109	29	KAT-DT-EE-14×KAT-DT-E-06
2	2	6	110	14	KAT-DT-EE-14×KAT-DT-EE-04
2	2	6	111	20	KAT-DT-E-06×KAT-DT-EE-05
2	2	6	112	18	KAT-DT-M-38×KAT-DT-EE-04
2	2	6	113	5	KAT-DT-EE-14×KAT-DT-EE-02
2	2	6	114	11	KAT-DT-EE-05×KAT-DT-EE-04

Appendix E. Mean performance of crosses for grain yield and yield contributing traits in managed drought conditions

Genotype	ASI	PH	EH	EPP	GY
KAT-DT-EE-14×KAT-DT-EE-05	1.5	210.4	113	1.04	9.82
KAT-DT-EE-04×KAT-DT-EE-02	1	203.5	91	1.11	9.67
KAT-DT-EE-18×KAT-DT-EE-14	2.5	217	90.75	1.40	9.35
KAT-DT-EE-15×KAT-DT-E-06	1	196.8	82	1.01	9.13
KAT-DT-E-06×KAT-DT-EE-04	1	203.1	86.75	1.02	9.04
KAT-DT-EE-07×KAT-DT-EE-04	1	193	97	1.08	8.99
KAT-DT-M-39×KAT-DT-EE-02	1	197.5	83.75	1.09	8.98
KAT-DT-E-06×KAT-DT-EE-05	1	205.8	84.75	1.02	8.92
KAT-DT-EE-15×KAT-DT-EE-02	1	175.8	85.75	0.99	8.91
KAT-DT-EE-07×KAT-DT-EE-14	1	196.2	111.75	1.00	8.88
KAT-DT-EE-18×KAT-DT-EE-05	1.5	210.1	102.25	0.93	8.78
KAT-DT-EE-18×KAT-DT-EE-02	1	209.2	97.5	1.03	8.76
PAN 5M-19	1	197.2	101.75	1.05	8.73
KAT-DT-EE-18×KAT-DT-EE-07	1	226.2	113	0.93	8.60
KAT-DT-EE-18×KAT-DT-EE-04	2	220.8	104.25	1.00	8.54
KAT-DT-M-38×KAT-DT-EE-14	1	204.8	93.5	1.09	8.48
KAT-DT-E-06×KAT-DT-EE-02	2	207	95	1.49	8.48
KAT-DT-EE-15×KAT-DT-EE-04	1	205	87.5	0.88	8.26
KAT-DT-M-39×KAT-DT-EE-04	1.5	194	84.25	1.05	8.23
KAT-DT-EE-18×KAT-DT-M-39	1	216.5	117.75	1.01	8.22
KAT-DT-EE-15×KAT-DT-EE-07	1	206.8	98.75	0.86	8.14
KAT-DT-EE-15×KAT-DT-EE-14	1	191.2	98	0.94	8.12
KAT-DT-M-31×KAT-DT-EE-07	1	176.2	82.75	0.97	8.11
KAT-DT-EE-15×KAT-DT-EE-05	1	196.5	96.75	1.01	8.07
KAT-DT-EE-07×KAT-DT-E-06	1	222.5	115.25	1.48	8.05
KAT-DT-M-31×KAT-DT-E-06	1	199.2	82.25	1.11	7.80
KAT-DT-M-31×KAT-DT-EE-05	1	193.2	91.75	0.95	7.76
KAT-DT-M-31×KAT-DT-EE-04	2.5	216.8	108.25	0.99	7.71
KAT-DT-EE-14×KAT-DT-E-06	1	233.2	118.75	1.07	7.69

Genotype	ASI	PH	EH	EPP	GY
KAT-DT-EE-18×KAT-DT-E-06	1.5	206.2	96.5	0.94	7.68
KAT-DT-EE-07×KAT-DT-EE-05	1	215.8	105	0.96	7.67
KAT-DT-M-38×KAT-DT-EE-02	1	177.8	83.5	1.03	7.66
KAT-DT-EE-05×KAT-DT-EE-02	1	204.8	96.75	1.06	7.65
KAT-DT-M-38×KAT-DT-EE-05	1	206	91.5	0.98	7.50
KAT-DT-EE-14×KAT-DT-EE-02	1	171.8	79.15	0.99	7.47
DUMA 43	0.5	172	105.75	1.12	7.42
KAT-DT-EE-18×KAT-DT-EE-15	1	162.2	82.5	1.18	7.36
KAT-DT-M-31×KAT-DT-M-39	1	192.2	83.25	1.22	7.35
KAT-DT-M-39×KAT-DT-EE-05	1	207.5	105.5	0.96	7.27
KAT-DT-M-38×KAT-DT-M-39	1	200.4	109.5	0.87	7.10
KAT-DT-M-38×KAT-DT-EE-15	1.5	128.2	60.5	1.05	7.05
KAT-DT-EE-15×KAT-DT-M-39	1	183.5	84	1.02	7.04
KAT-DT-EE-05×KAT-DT-EE-04	1	211.8	97	1.36	6.87
KAT-DT-M-38×KAT-DT-EE-04	1	190.2	87	1.00	6.87
KAT-DT-EE-14×KAT-DT-M-39	1	191	86.25	0.98	6.80
KAT-DT-M-38×KAT-DT-E-06	1	180.5	81.5	1.08	6.61
KAT-DT-EE-18×KAT-DT-M-38	1	185.2	100.75	0.97	6.52
KAT-DT-EE-15×KAT-DT-M-31	1	188.8	81	0.92	6.40
KAT-DT-M-39×KAT-DT-E-06	0.5	214	112.75	1.15	6.35
KAT-DT-EE-14×KAT-DT-EE-04	1	188.8	86.5	1.00	6.24
KAT-DT-EE-07×KAT-DT-EE-02	1	182	72.25	1.09	6.08
KAT-DT-M-38×KAT-DT-EE-07	2	209.8	103.75	0.88	5.99
KAT-DT-EE-07×KAT-DT-M-39	1	183.5	87	1.07	5.56
KAT-DT-M-31×KAT-DT-EE-14	2	202.1	100.75	0.99	5.45
KAT-DT-M-31×KAT-DT-EE-02	1	156.8	65.25	1.04	5.41
KAT-DT-M-38×KAT-DT-M-31	0.5	159.8	88.5	1.03	4.81
KAT-DT-EE-18×KAT-DT-M-31	0.5	147	69.75	1.08	4.43

ASI=anthesis-silking interval, PH=plant height, EH=ear height, EPP=ears per plant, GY = grain yield

Appendix F. Mean performance of crosses for grain yield and yield contributing traits in random drought conditions

Genotype	ASI	PH	EH	EPP	GY
KAT-DT-M-38×KAT-DT-EE-15	3.5	101.5	10.15	0.67	2.03
KAT-DT-EE-18×KAT-DT-EE-02	4.5	143.2	67	0.84	1.75
KAT-DT-EE-15×KAT-DT-EE-02	3.5	109.5	51	0.63	1.67
KAT-DT-M-31×KAT-DT-EE-02	-0.5	112.8	46.25	0.93	1.59
KAT-DT-E-06×KAT-DT-EE-04	1	125.2	56.5	0.73	1.54
KAT-DT-M-38×KAT-DT-M-31	3	94.2	9.43	0.57	1.42
KAT-DT-EE-15×KAT-DT-EE-04	2	118.2	58.5	0.68	1.39
KAT-DT-EE-18×KAT-DT-EE-15	3.5	71.8	7.17	0.64	1.38
KAT-DT-EE-04×KAT-DT-EE-02	1.5	117.5	51	0.55	1.34
KAT-DT-M-38×KAT-DT-EE-14	1.5	88.5	36.5	0.44	1.30
KAT-DT-M-38×KAT-DT-EE-02	1.5	86.2	43.25	0.71	1.30
KAT-DT-M-31×KAT-DT-EE-07	3.5	102	49.25	0.85	1.29
KAT-DT-EE-07×KAT-DT-E-06	-2	142	74.25	0.57	1.25
KAT-DT-EE-05×KAT-DT-EE-02	2.5	122.5	57.5	0.80	1.22
DUMA 43	5	87	8.7	0.53	1.19
KAT-DT-EE-14×KAT-DT-M-39	3.5	112.8	49.25	0.64	1.15
KAT-DT-M-31×KAT-DT-M-39	4.5	129.2	60.75	0.74	1.14
KAT-DT-EE-14×KAT-DT-EE-04	6.5	127.2	57.25	0.55	1.02
KAT-DT-M-38×KAT-DT-M-39	2	118.2	60.25	0.41	1.01
KAT-DT-EE-15×KAT-DT-EE-14	2	85.8	32	0.19	0.96
KAT-DT-EE-18×KAT-DT-M-38	1.5	96	9.6	0.59	0.94
PAN 5M-19	4.5	81	8.1	0.58	0.90
KAT-DT-EE-15×KAT-DT-EE-07	2	112	53.75	0.73	0.88
KAT-DT-M-31×KAT-DT-E-06	3.5	99	47.25	0.15	0.85
KAT-DT-M-38×KAT-DT-EE-04	4.5	102.2	53.75	0.35	0.85
KAT-DT-EE-14×KAT-DT-EE-05	2	102	57.25	0.35	0.81
KAT-DT-EE-15×KAT-DT-EE-05	4	116.2	62.25	0.52	0.80
KAT-DT-EE-18×KAT-DT-E-06	6	124.8	60.5	0.33	0.78
KAT-DT-EE-07×KAT-DT-EE-14	0	60.8	34.75	0.27	0.78
KAT-DT-EE-14×KAT-DT-EE-02	4	113	56	0.49	0.77

Genotype	ASI	PH	EH	EPP	GY
KAT-DT-EE-15×KAT-DT-M-31	1.5	63.5	31	0.27	0.70
KAT-DT-EE-15×KAT-DT-E-06	5.5	100.2	52	0.38	0.70
KAT-DT-EE-07×KAT-DT-M-39	3.5	108.8	59	0.37	0.70
KAT-DT-M-31×KAT-DT-EE-05	3.5	91.2	47.75	0.39	0.69
KAT-DT-EE-05×KAT-DT-EE-04	2	124.2	56	0.38	0.68
KAT-DT-EE-14×KAT-DT-E-06	5	120.5	26	0.13	0.66
KAT-DT-EE-07×KAT-DT-EE-05	4	131.5	66.75	0.36	0.64
KAT-DT-EE-18×KAT-DT-EE-07	2.5	103.8	49.25	0.39	0.64
KAT-DT-EE-07×KAT-DT-EE-02	2.5	91.8	37.5	0.40	0.59
KAT-DT-EE-18×KAT-DT-M-39	2	120.5	60.5	0.29	0.53
KAT-DT-EE-18×KAT-DT-M-31	6.5	98.8	9.88	0.49	0.52
KAT-DT-M-39×KAT-DT-EE-05	0.5	136.2	70.5	0.27	0.52
KAT-DT-EE-07×KAT-DT-EE-04	2	84.2	23.5	0.18	0.50
KAT-DT-M-38×KAT-DT-E-06	5.5	97.8	46	0.49	0.49
KAT-DT-E-06×KAT-DT-EE-05	3.5	118.5	58.25	0.21	0.47
KAT-DT-M-39×KAT-DT-EE-02	0.5	111.2	49	0.28	0.46
KAT-DT-M-39×KAT-DT-E-06	2.5	112.8	61.75	0.34	0.46
KAT-DT-EE-15×KAT-DT-M-39	-1.5	103.8	51.25	0.34	0.44
KAT-DT-M-38×KAT-DT-EE-05	-2.5	125	61.75	0.28	0.42
KAT-DT-M-31×KAT-DT-EE-04	2	103	47.5	0.18	0.38
KAT-DT-E-06×KAT-DT-EE-02	3	119.8	62	0.21	0.32
KAT-DT-M-31×KAT-DT-EE-14	0.5	55.5	27.5	0.17	0.28
KAT-DT-M-38×KAT-DT-EE-07	1.5	41.2	19.25	0.58	0.26
KAT-DT-EE-18×KAT-DT-EE-14	-2	109.2	61	0.17	0.26
KAT-DT-EE-18×KAT-DT-EE-05	3	117.5	41	0.08	0.21
KAT-DT-EE-18×KAT-DT-EE-04	3	83.5	30.5	0.11	0.18
KAT-DT-M-39×KAT-DT-EE-04	3	47.8	9	0.01	0.03

ASI=anthesis-silking interval, PH=plant height, EH=ear height, EPP=ears per plant, DTA=days to anthesis, DTS=days to silking, GY = grain yield

Appendix G. Mean performance of crosses for grain yield and yield contributing traits combined over study locations

Genotype	ASI	PH	EH	EPP	GY
KAT-DT-EE-04×KAT-DT-EE-02	1.25	160.5	71	0.83	5.51
KAT-DT-EE-05×KAT-DT-EE-02	1.75	163.6	77.12	0.93	4.43
KAT-DT-E-06×KAT-DT-EE-02	2.5	163.4	78.5	0.85	4.40
KAT-DT-M-39×KAT-DT-EE-02	0.75	154.4	66.38	0.68	4.72
KAT-DT-EE-14×KAT-DT-EE-02	2.5	142.4	67.58	0.74	4.12
KAT-DT-EE-07×KAT-DT-EE-02	1.75	136.9	54.88	0.74	3.33
KAT-DT-M-31×KAT-DT-EE-02	0.25	134.8	55.75	0.98	3.50
KAT-DT-EE-15×KAT-DT-EE-02	2.25	142.6	68.38	0.81	5.29
KAT-DT-M-38×KAT-DT-EE-02	1.25	132	63.38	0.87	4.48
KAT-DT-EE-18×KAT-DT-EE-02	2.75	176.2	82.25	0.94	5.26
KAT-DT-EE-05×KAT-DT-EE-04	1.5	168	76.5	1.03	3.78
KAT-DT-EE-14×KAT-DT-EE-04	3.75	158	71.88	0.77	3.63
KAT-DT-EE-07×KAT-DT-EE-04	1.5	138.6	60.25	0.63	6.16
KAT-DT-M-31×KAT-DT-EE-04	2.25	159.9	77.88	0.58	4.05
KAT-DT-EE-15×KAT-DT-EE-04	1.5	161.6	73	0.78	4.83
KAT-DT-M-38×KAT-DT-EE-04	2.75	146.2	70.38	0.68	3.86
KAT-DT-EE-18×KAT-DT-EE-04	2.5	152.1	67.38	0.56	4.36
KAT-DT-E-06×KAT-DT-EE-05	2.25	162.1	71.5	0.62	6.10
KAT-DT-M-39×KAT-DT-EE-05	0.75	171.9	88	0.62	3.90
KAT-DT-EE-14×KAT-DT-EE-05	1.75	156.2	85.12	0.70	5.32
KAT-DT-EE-07×KAT-DT-EE-05	2.5	173.6	85.88	0.66	4.16
KAT-DT-M-31×KAT-DT-EE-05	2.25	142.2	69.75	0.67	4.23
KAT-DT-EE-15×KAT-DT-EE-05	2.5	156.4	79.5	0.76	4.44
KAT-DT-M-38×KAT-DT-EE-05	-0.75	165.5	76.62	0.63	3.96
KAT-DT-EE-18×KAT-DT-EE-05	2.25	163.8	71.62	0.50	4.50
KAT-DT-M-39×KAT-DT-E-06	1.5	163.4	87.25	0.74	3.41
KAT-DT-EE-14×KAT-DT-E-06	3	176.9	72.38	0.60	5.35
KAT-DT-EE-07×KAT-DT-E-06	-0.5	182.2	94.75	1.03	4.65
KAT-DT-M-31×KAT-DT-E-06	2.25	149.1	64.75	0.63	4.33

Genotype	**ASI**	**PH**	**EH**	**EPP**	**GY**
KAT-DT-EE-15×KAT-DT-E-06	3.25	148.5	67	0.70	4.92
KAT-DT-M-38×KAT-DT-E-06	3.25	139.1	63.75	0.78	3.55
KAT-DT-EE-18×KAT-DT-E-06	3.75	165.5	78.5	0.64	4.23
KAT-DT-EE-14×KAT-DT-M-39	2.25	151.9	67.75	0.81	3.98
KAT-DT-EE-07×KAT-DT-M-39	2.25	146.1	73	0.72	3.13
KAT-DT-M-31×KAT-DT-M-39	2.75	160.8	72	0.98	4.25
KAT-DT-EE-15×KAT-DT-M-39	-0.25	143.6	67.62	0.68	3.74
KAT-DT-M-38×KAT-DT-M-39	1.5	159.3	84.88	0.64	4.05
KAT-DT-EE-18×KAT-DT-M-39	1.5	168.5	89.12	0.65	4.38
KAT-DT-EE-07×KAT-DT-EE-14	0.5	128.5	73.25	0.64	6.18
KAT-DT-M-31×KAT-DT-EE-14	1.25	128.8	64.12	0.58	2.87
KAT-DT-EE-15×KAT-DT-EE-14	1.5	138.5	65	0.56	5.74
KAT-DT-M-38×KAT-DT-EE-14	1.25	146.6	65	0.76	4.89
KAT-DT-EE-18×KAT-DT-EE-14	0.25	163.1	75.88	0.79	4.80
KAT-DT-M-31×KAT-DT-EE-07	2.25	139.1	66	0.91	4.70
KAT-DT-EE-15×KAT-DT-EE-07	1.5	159.4	76.25	0.80	4.51
KAT-DT-M-38×KAT-DT-EE-07	1.75	125.5	61.5	0.73	3.13
KAT-DT-EE-18×KAT-DT-EE-07	1.75	165	81.12	0.66	4.62
KAT-DT-EE-15×KAT-DT-M-31	1.25	126.1	56	0.59	4.50
KAT-DT-M-38×KAT-DT-M-31	1.75	127	48.96	0.80	3.12
KAT-DT-EE-18×KAT-DT-M-31	3.5	122.9	39.81	0.79	2.47
KAT-DT-M-38×KAT-DT-EE-15	2.5	114.9	35.33	0.86	4.54
KAT-DT-EE-18×KAT-DT-EE-15	2.25	117	44.84	0.91	4.37
KAT-DT-EE-18×KAT-DT-M-38	1.25	140.6	55.17	0.78	3.73
DUMA 43	2.75	129.5	57.23	0.83	4.31
PAN 5M-19	2.75	139.1	54.92	0.82	4.82

ASI=anthesis-silking interval, PH=plant height, EH=ear height, EPP=ears per plant, DTA=days to anthesis, DTS=days to silking, GY = grain yield

Appendix H: Mean performance for measured traits in managed and random drought environments

	Managed drought					Random drought				
Genotype	**ASI**	**PH**	**EH**	**EPP**	**GY**	**ASI**	**PH**	**EH**	**EPP**	**GY**
KAT-DT-EE-14×KAT-DT-EE-05	1.5	210.4	113	1.04	9.82	2	102	57.25	0.35	0.81
KAT-DT-EE-04×KAT-DT-EE-02	1	203.5	91	1.11	9.67	1.5	117.5	51	0.55	1.34
KAT-DT-EE-18×KAT-DT-EE-14	2.5	217	90.75	1.4	9.35	-2	109.2	61	0.17	0.26
KAT-DT-EE-15×KAT-DT-E-06	1	196.8	82	1.01	9.13	5.5	100.2	52	0.38	0.7
KAT-DT-E-06×KAT-DT-EE-04	1	203.1	86.75	1.02	9.04	1	125.2	56.5	0.73	1.54
KAT-DT-EE-07×KAT-DT-EE-04	1	193	97	1.08	8.99	2	84.2	23.5	0.18	0.5
KAT-DT-M-39×KAT-DT-EE-02	1	197.5	83.75	1.09	8.98	0.5	111.2	49	0.28	0.46
KAT-DT-E-06×KAT-DT-EE-05	1	205.8	84.75	1.02	8.92	3.5	118.5	58.25	0.21	0.47
KAT-DT-EE-15×KAT-DT-EE-02	1	175.8	85.75	0.99	8.91	3.5	109.5	51	0.63	1.67
KAT-DT-EE-07×KAT-DT-EE-14	1	196.2	111.75	1	8.88	0	60.8	34.75	0.27	0.78
KAT-DT-EE-18×KAT-DT-EE-05	1.5	210.1	102.25	0.93	8.78	3	117.5	41	0.08	0.21
KAT-DT-EE-18×KAT-DT-EE-02	1	209.2	97.5	1.03	8.76	4.5	143.2	67	0.84	1.75
PAN 5M-19	1	197.2	101.75	1.05	8.73	4.5	81	8.1	0.58	0.9

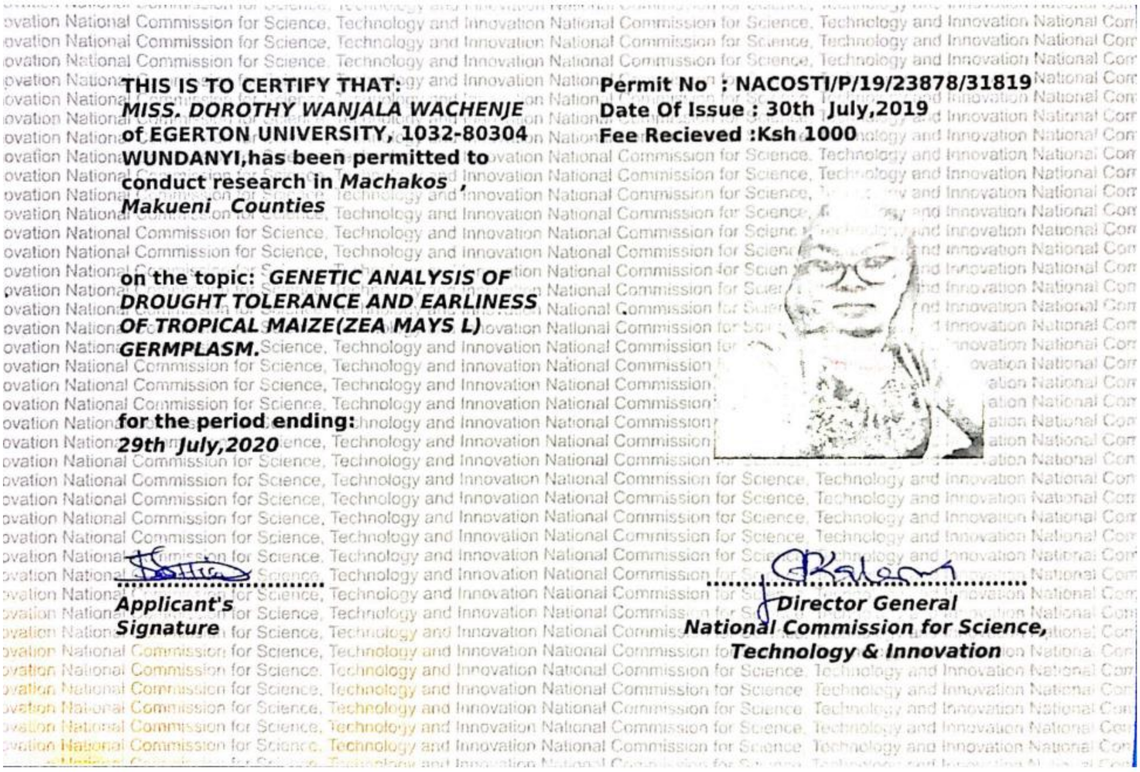
	Managed drought					Random drought				
Genotype	**ASI**	**PH**	**EH**	**EPP**	**GY**	**ASI**	**PH**	**EH**	**EPP**	**GY**
KAT-DT-EE-18×KAT-DT-EE-07	1	226.2	113	0.93	8.6	2.5	103.8	49.25	0.39	0.64
KAT-DT-EE-18×KAT-DT-EE-04	2	220.8	104.25	1	8.54	3	83.5	30.5	0.11	0.18
KAT-DT-E-06×KAT-DT-EE-02	2	207	95	1.49	8.48	3	119.8	62	0.21	0.32
KAT-DT-M-38×KAT-DT-EE-14	1	204.8	93.5	1.09	8.48	1.5	88.5	36.5	0.44	1.3
KAT-DT-EE-15×KAT-DT-EE-04	1	205	87.5	0.88	8.26	2	118.2	58.5	0.68	1.39
KAT-DT-M-39×KAT-DT-EE-04	1.5	194	84.25	1.05	8.23	3	47.8	9	0.01	0.03
KAT-DT-EE-18×KAT-DT-M-39	1	216.5	117.75	1.01	8.22	2	120.5	60.5	0.29	0.53
KAT-DT-EE-15×KAT-DT-EE-07	1	206.8	98.75	0.86	8.14	2	112	53.75	0.73	0.88
KAT-DT-EE-15×KAT-DT-EE-14	1	191.2	98	0.94	8.12	2	85.8	32	0.19	0.96
KAT-DT-M-31×KAT-DT-EE-07	1	176.2	82.75	0.97	8.11	3.5	102	49.25	0.85	1.29
KAT-DT-EE-15×KAT-DT-EE-05	1	196.5	96.75	1.01	8.07	4	116.2	62.25	0.52	0.8
KAT-DT-EE-07×KAT-DT-E-06	1	222.5	115.25	1.48	8.05	-2	142	74.25	0.57	1.25
KAT-DT-M-31×KAT-DT-E-06	1	199.2	82.25	1.11	7.8	3.5	99	47.25	0.15	0.85
KAT-DT-M-31×KAT-DT-EE-05	1	193.2	91.75	0.95	7.76	3.5	91.2	47.75	0.39	0.69

	Managed drought					Random drought				
Genotype	**ASI**	**PH**	**EH**	**EPP**	**GY**	**ASI**	**PH**	**EH**	**EPP**	**GY**
KAT-DT-M-31×KAT-DT-EE-04	2.5	216.8	108.25	0.99	7.71	2	103	47.5	0.18	0.38
KAT-DT-EE-14×KAT-DT-E-06	1	233.2	118.75	1.07	7.69	5	120.5	26	0.13	0.66
KAT-DT-EE-18×KAT-DT-E-06	1.5	206.2	96.5	0.94	7.68	6	124.8	60.5	0.33	0.78
KAT-DT-EE-07×KAT-DT-EE-05	1	215.8	105	0.96	7.67	4	131.5	66.75	0.36	0.64
KAT-DT-M-38×KAT-DT-EE-02	1	177.8	83.5	1.03	7.66	1.5	86.2	43.25	0.71	1.3
KAT-DT-EE-05×KAT-DT-EE-02	1	204.8	96.75	1.06	7.65	2.5	122.5	57.5	0.8	1.22
KAT-DT-M-38×KAT-DT-EE-05	1	206	91.5	0.98	7.5	-2.5	125	61.75	0.28	0.42
KAT-DT-EE-14×KAT-DT-EE-02	1	171.8	79.15	0.99	7.47	4	113	56	0.49	0.77
DUMA 43	0.5	172	105.75	1.12	7.42	5	87	8.7	0.53	1.19
KAT-DT-EE-18×KAT-DT-EE-15	1	162.2	82.5	1.18	7.36	3.5	71.8	7.17	0.64	1.38
KAT-DT-M-31×KAT-DT-M-39	1	192.2	83.25	1.22	7.35	4.5	129.2	60.75	0.74	1.14
KAT-DT-M-39×KAT-DT-EE-05	1	207.5	105.5	0.96	7.27	0.5	136.2	70.5	0.27	0.52
KAT-DT-M-38×KAT-DT-M-39	1	200.4	109.5	0.87	7.1	2	118.2	60.25	0.41	1.01

	Managed drought					**Random drought**				
	ASI	**PH**	**EH**	**EPP**	**GY**	**ASI**	**PH**	**EH**	**EPP**	**GY**
KAT-DT-M-38×KAT-DT-EE-15	1.5	128.2	60.5	1.05	7.05	3.5	101.5	10.15	0.67	2.03
KAT-DT-EE-15×KAT-DT-M-39	1	183.5	84	1.02	7.04	-1.5	103.8	51.25	0.34	0.44
KAT-DT-EE-05×KAT-DT-EE-04	1	211.8	97	1.36	6.87	2	124.2	56	0.38	0.68
KAT-DT-M-38×KAT-DT-EE-04	1	190.2	87	1	6.87	4.5	102.2	53.75	0.35	0.85
KAT-DT-EE-14×KAT-DT-M-39	1	191	86.25	0.98	6.8	3.5	112.8	49.25	0.64	1.15
KAT-DT-M-38×KAT-DT-E-06	1	180.5	81.5	1.08	6.61	5.5	97.8	46	0.49	0.49
KAT-DT-EE-18×KAT-DT-M-38	1	185.2	100.75	0.97	6.52	1.5	96	9.6	0.59	0.94
KAT-DT-EE-15×KAT-DT-M-31	1	188.8	81	0.92	6.4	1.5	63.5	31	0.27	0.7
KAT-DT-M-39×KAT-DT-E-06	0.5	214	112.75	1.15	6.35	2.5	112.8	61.75	0.34	0.46
KAT-DT-EE-14×KAT-DT-EE-04	1	188.8	86.5	1	6.24	6.5	127.2	57.25	0.55	1.02
KAT-DT-EE-07×KAT-DT-EE-02	1	182	72.25	1.09	6.08	2.5	91.8	37.5	0.4	0.59
KAT-DT-M-38×KAT-DT-EE-07	2	209.8	103.75	0.88	5.99	1.5	41.2	19.25	0.58	0.26
KAT-DT-EE-07×KAT-DT-M-39	1	183.5	87	1.07	5.56	3.5	108.8	59	0.37	0.7

	Managed drought					Random drought				
	ASI	**PH**	**EH**	**EPP**	**GY**	**ASI**	**PH**	**EH**	**EPP**	**GY**
KAT-DT-M-31×KAT-DT-EE-14	2	202.1	100.75	0.99	5.45	0.5	55.5	27.5	0.17	0.28
KAT-DT-M-31×KAT-DT-EE-02	1	156.8	65.25	1.04	5.41	-0.5	112.8	46.25	0.93	1.59
KAT-DT-M-38×KAT-DT-M-31	0.5	159.8	88.5	1.03	4.81	3	94.2	9.43	0.57	1.42
KAT-DT-EE-18×KAT-DT-M-31	0.5	147	69.75	1.08	4.43	6.5	98.8	9.88	0.49	0.52

Appendix I: Research permit



THIS IS TO CERTIFY THAT:
MISS. DOROTHY WANJALA WACHENJE
of EGERTON UNIVERSITY, 1032-80304
WUNDANYI,has been permitted to
conduct research in *Machakos ,*
Makueni Counties

Permit No : NACOSTI/P/19/23878/31819
Date Of Issue : 30th July,2019
Fee Recieved :Ksh 1000

on the topic: *GENETIC ANALYSIS OF DROUGHT TOLERANCE AND EARLINESS OF TROPICAL MAIZE(ZEA MAYS L) GERMPLASM.*

for the period ending:
29th July,2020

……………………………
Applicant's Signature

……………………………
Director General
National Commission for Science, Technology & Innovation

Appendix J: Abstract of a paper published from objective one

E. Afri. Agri. For. J (2021,Volume 85, 1-4, Pg. 69-80)

IDENTIFICATION OF DROUGHT TOLERANT ELITE SINGLE-CROSS MAIZE (ZEA MAYS L.) HYBRIDS FOR SEMI-ARID KENYA

D. W.Wachenje [1], P. P. O. Ojwang [1] and M. Mwimali [2]

[1]Department of Crops, Horticulture and Soils, Egerton University, P.O Box 536-20115, Egerton, Kenya.

[2]Kenya Agricultural and Livestock Research Organization, P.O Box 57811-0200, Nairobi, Kenya.

ABSTRACT

Drought is a major production constraint limiting maize production in sub-Saharan Africa. Improving maize for resilience to drought stress is essential for deployment of drought tolerant varieties in semi-arid areas. The objective of this study was to identify elite single-cross maize hybrids which are drought tolerant under semi-arid conditions. Ninety-one single-cross maize hybrids and seven commercial checks were evaluated for drought tolerance under field conditions at the Kenya Agricultural and Livestock Research organization (KALRO) Katumani research centre and Kiboko sub-centre in an α-lattice design. This experiment was carried out under both random and managed drought conditions in two replications. Combined analysis of variance across locations revealed significant ($p<0.05$) main effects for genotypes, locations and genotype by location interactions of most yield and yield related traits studied. The highest performing hybrid for grain yield was KAT-DT-E-06 with 6.45 t/ha against the best performing check variety DK8031 which yielded 4.66 t/ha. Anthesis-silking interval trait, values of 0 and 0.5 were recorded for genotype KAT-DT-M-25 and KAT-DT-M-29 while the best performing commercial check variety in terms of ASI was PAN 4M-19 with 1.0. Broad sense heritability for grain yield trait of 61.93% was recorded under managed drought compared to 1.95% under to random drought while anthesis-silking interval recorded 3.02% and 8.2% respectively. Genotypes KAT-DT-EE-02, KAT-DT-EE-04, KAT-DT-EE-05 and KAT-DT-E-06 recorded the lowest cultivar superiority () values between 0.20 and 0.26 on the cultivar superiority index demonstrating their high grain yield and wide adaptability to drought prone conditions. These identified genotypes are drought tolerant, high yielding and stable hence suitable candidates for deployment to farmers in semi-arid areas.

Key words

Drought tolerant, anthesis-silking interval, heritability, genotype-by-location interaction, genotypic stability

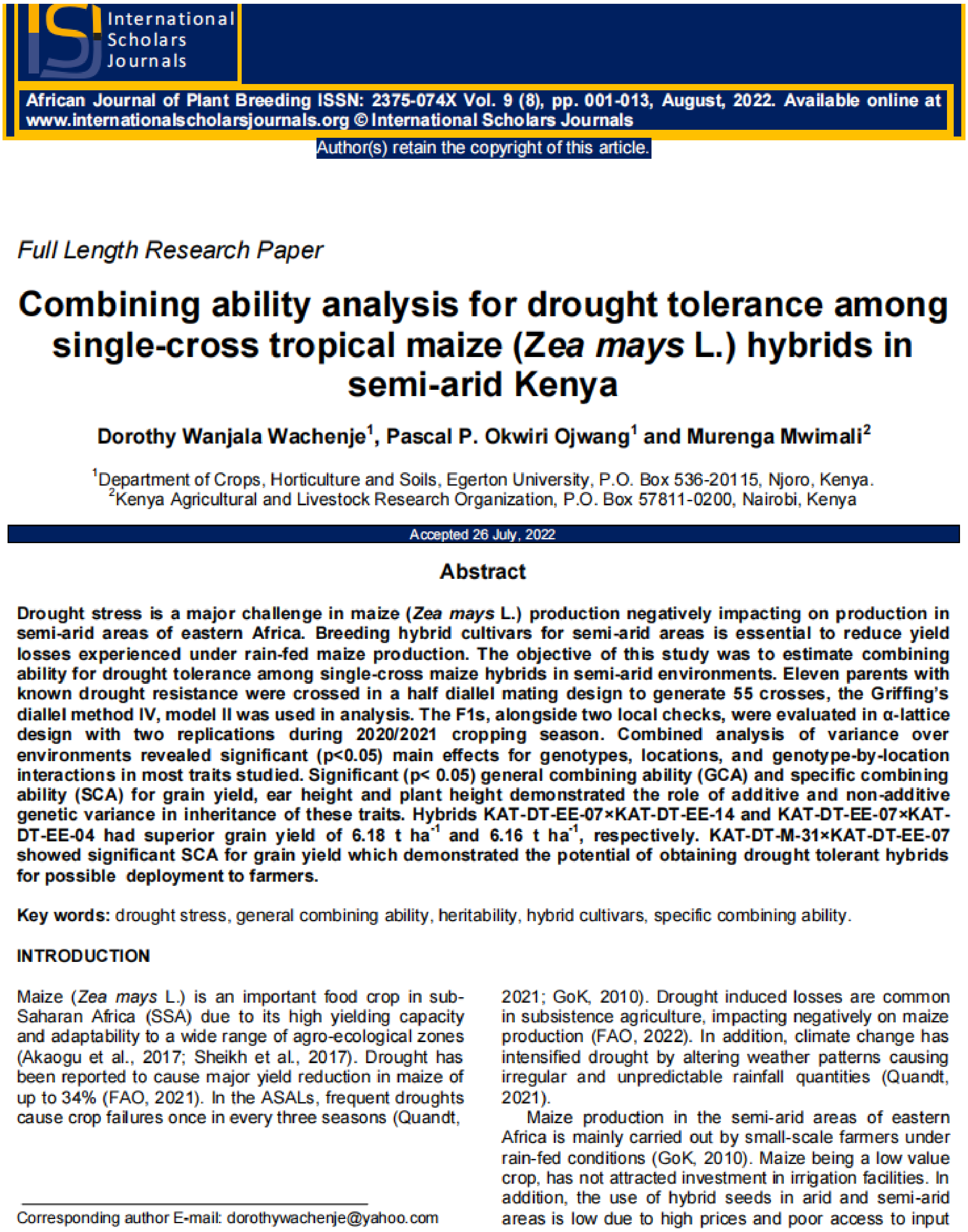
INTRODUCTION

Drought is a major constraint limiting maize production in sub-Saharan Africa (SSA) where cultivation is mainly under rain fed conditions (Shiferaw *et al*., 2011). Drought causes a significant negative impact on global food supply resulting in an estimated 15% yield loss annually (FAOSTAT, 2020). In the arid and semi-arid lands (ASALs), there is pronounced rainfall variability which is characterized by unpredictable onset and length of the growing season. As a consequence, terminal drought sets in because maize varieties planted in the ASALss are late maturing. In addition, the ASALs experience major droughts every five years causing total crop failure (Omoyo *et al*., 2015). Climate change effects of extreme natural events are becoming more frequent thereby aggravating drought stress on maize yield. Despite SSA recording the lowest maize yield in the world, the production in this region is bound to decline further partly due to the negative effects of climate change (Setimela *et al*., 2017).

Farming in Kenya is predominantly practised by small-scale farmers with limited access to irrigation technology exposing them to rainfall variability (Kalungu *et al*., 2013). In addition to this, farmers in the ASALs have limited access to suitable maize varieties prompting them to grow varieties recommended for medium to high potential areas (Muli *et al*., 2017). The widely cultivated open pollinated varieties are less adapted to drought conditions however, the basis of this choice is mainly due to their plasticity to survive drought hence assured yields despite having lower productivity compared to hybrid cultivars (Kutka, 2011). Selection of quality seed is a critical factor in successful maize cultivation (Zaidi *et al*., 2017). Resource poor farmers prefer drought tolerant maize varieties due to their limited capacity to access irrigation (Cairns *et al*., 2013).

[#]Corresponding author:dorothywachenje@yahoo.com

Appendix K: Abstract of a paper published from objective two



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Full Length Research Paper

Combining ability analysis for drought tolerance among single-cross tropical maize (*Zea mays* L.) hybrids in semi-arid Kenya

Dorothy Wanjala Wachenje[1], Pascal P. Okwiri Ojwang[1] and Murenga Mwimali[2]

[1]Department of Crops, Horticulture and Soils, Egerton University, P.O. Box 536-20115, Njoro, Kenya.
[2]Kenya Agricultural and Livestock Research Organization, P.O. Box 57811-0200, Nairobi, Kenya

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Abstract

Drought stress is a major challenge in maize (*Zea mays* L.) production negatively impacting on production in semi-arid areas of eastern Africa. Breeding hybrid cultivars for semi-arid areas is essential to reduce yield losses experienced under rain-fed maize production. The objective of this study was to estimate combining ability for drought tolerance among single-cross maize hybrids in semi-arid environments. Eleven parents with known drought resistance were crossed in a half diallel mating design to generate 55 crosses, the Griffing's diallel method IV, model II was used in analysis. The F1s, alongside two local checks, were evaluated in α-lattice design with two replications during 2020/2021 cropping season. Combined analysis of variance over environments revealed significant ($p<0.05$) main effects for genotypes, locations, and genotype-by-location interactions in most traits studied. Significant ($p< 0.05$) general combining ability (GCA) and specific combining ability (SCA) for grain yield, ear height and plant height demonstrated the role of additive and non-additive genetic variance in inheritance of these traits. Hybrids KAT-DT-EE-07×KAT-DT-EE-14 and KAT-DT-EE-07×KAT-DT-EE-04 had superior grain yield of 6.18 t ha^{-1} and 6.16 t ha^{-1}, respectively. KAT-DT-M-31×KAT-DT-EE-07 showed significant SCA for grain yield which demonstrated the potential of obtaining drought tolerant hybrids for possible deployment to farmers.

Key words: drought stress, general combining ability, heritability, hybrid cultivars, specific combining ability.

INTRODUCTION

Maize (*Zea mays* L.) is an important food crop in sub-Saharan Africa (SSA) due to its high yielding capacity and adaptability to a wide range of agro-ecological zones (Akaogu et al., 2017; Sheikh et al., 2017). Drought has been reported to cause major yield reduction in maize of up to 34% (FAO, 2021). In the ASALs, frequent droughts cause crop failures once in every three seasons (Quandt, 2021; GoK, 2010). Drought induced losses are common in subsistence agriculture, impacting negatively on maize production (FAO, 2022). In addition, climate change has intensified drought by altering weather patterns causing irregular and unpredictable rainfall quantities (Quandt, 2021).

Maize production in the semi-arid areas of eastern Africa is mainly carried out by small-scale farmers under rain-fed conditions (GoK, 2010). Maize being a low value crop, has not attracted investment in irrigation facilities. In addition, the use of hybrid seeds in arid and semi-arid areas is low due to high prices and poor access to input

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Corresponding author E-mail: dorothywachenje@yahoo.com