

1/ DETERMINATION OF COMBINING ABILITIES FOR
GRAIN YIELD AND GREY LEAF SPOT RESISTANCE
AMONG SELECTED MAIZE INBRED LINES//

BY

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DECLARATION

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DEDICATION

To my dear husband Benjamin and my son David for their ceaseless efforts and support through out the course.

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ABSTRACT

Maize is a staple food crop for about 90% of Kenyans. Its production by smallholder farmers often plays a vital role in food security and alleviating poverty. Grey Leaf Spot (GLS) caused by *Cercospora zea maydis* significantly reduces maize yields in farmers' fields. This study was carried out at three sites (KARI-Kiboko, Kabete Field Station and KARI-Kakamega) in 2006 to determine the combining abilities for yield, GLS resistance and other traits among seven selected maize inbred lines CML 204, CML 312, CML 373, CML 384, TZMI 102, TZMI 711 and TZMI 712. Griffing's method one and model one of diallel analysis was used for data analysis using the SAS program.

Significant differences were noted for most traits indicating that the good entries obtained in this work could be used as suitable testers in future breeding efforts. Different lines performed differently across the different sites; CML 373 with 3.16T_{Ha}⁻¹ and 2.83T_{Ha}⁻¹ was the highest yielder in KARI-Kiboko and KARI-Kakamega respectively whereas TZMI 711 with 8.43T_{Ha}⁻¹ was the highest yielder in Kabete Field Station. However, CML 384 was the most stable highest yielding entry across environments implying that it had a high frequency of yield improvement genes. CML 373 and TZMI 711 had high GLS resistance. CML 373 and TZMI 711, which had high frequency of GLS resistance genes, could be used as male and female in hybrid combinations to impart GLS disease resistance in the elite maize germplasm. Non significant correlations were noted for GLS disease resistance and other diseases. The resistance genes in TZMI 711 and CML 373 should be pyramided into one good line to develop multiple disease resistant lines, for future development of open pollinated varieties and hybrids.

CHAPTER I

INTRODUCTION

1.1 General Introduction

Maize was introduced to Africa in the sixteenth century (Miracle, 1966). Since then, production has expanded and the crop has become a major staple food in eastern and southern Africa owing to its high yield potential and readily available market. Maize provides 50% of calories in the diets of people in southern Africa, 30% in eastern Africa and 15% in west and central Africa (Pswarayi and Vivek, 2004). It is estimated that the global demand for maize will increase by 50% from 558 million tonnes in 1995 to 837 million tonnes by 2020 overtaking the demand for rice and wheat. In addition, maize demand in the developing countries is projected to increase from 282 million tonnes in 1995 to 504 million tonnes in 2020 (Pingali and Pandey, 2001). Despite the importance of maize in Sub Saharan Africa (SSA), farmers realize low yields. The low maize yields in SSA could be attributed to abiotic, biotic and socio-economic factors (Simmons, 2003).

Among the biotic factors that constrain maize production, Turcicum leaf blight, maize streak virus (MSV) and grey leaf spot (GLS) have been ranked as high research priorities in SSA by the International Maize and Wheat Improvement Center (CIMMYT), International Institute of Tropical Agriculture (IITA) and other national maize research programmes in the region (Generation Challenge Program, 2006). The significance of these diseases varies with location and they are most important when infection occurs at seedling or grain filling stages of crop growth.

Grey leaf spot (GLS) is a fungal disease caused by *Cercospora zeae maydis* (Tehon and Daniels, 1925) and is considered a major threat to maize production in Kenya and the world at large (Menkir and Ayodele, 2005). The disease was first described in the U.S.A in 1925 on maize grown in Alexander County (Clement *et al.*, 2000; Lipps *et al.*, 1998). In Africa, the disease was first reported in 1990 in South Africa. The disease has spread to many other places like Zimbabwe, Zambia, Cameroon, Kenya and Uganda. In Kenya, the disease was first reported in 1995 by visiting South African researchers. It is present in all the major maize growing areas of Rift valley, Western and Central Kenya (Ward *et al.*, 1999).

1.2 Problem statement and justification

Grey leaf spot (GLS) caused by *Cercospora zeae-maydis* (Tehon and Daniels, 1925) poses a serious problem to maize production in SSA. The pathogen causes intense water loss from the plant thereby leading to severe blighting of the leaves and reduced photosynthesis. This eventually leads to undersized ears, low grain yield and premature death of maize plants. Severe blighting of the upper eight or nine leaves that contribute 75-90% of the photosynthates for grain fill may lead to stalk weakening or even infectious stalk rot diseases leading to premature stalk death and lodging (Lipps *et al.*, 1998; Ward *et al.*, 1999). GLS has been rigorous in recurrence and distribution and has led to economic yield losses: over 60% in western Kenya (Odongo *et al.*, 2000), 10 - 60% in Tanzania (Kuwite, 2004) and up to 60% in South Africa (Vivek *et al.*, 2001).

One approach to combat GLS would be to apply chemical fungicides. However, the application of fungicides is not economical for maize production (Ward *et al.*, 1997;

Derera *et al.*, 2008) since the resource poor small scale farmers lack the financial means to apply fungicides and other management options to control the disease. Moreover, the farmers obtain low yields and most of them own small parcels of land. This is exacerbated by the fact that most farmers in the rural areas are women and children since most men move to urban areas to supplement the family income leading to low yields.

GLS infection could be reduced through conventional resistance breeding. In Kenya, Kakamega synthetic I and II, KH634A, H614, SC Duma 41, and SC Simba 61 were reported to have some tolerance to GLS (Kinyua, 2006). Nevertheless, a large proportion of Kenyan germplasm ranges from moderate to high susceptibility to GLS (Wang *et al.*, 1998). Since GLS is rapidly spreading in the region, it demands a quick and effective control strategy. More sources of GLS resistance should be identified and utilized in breeding programmes and hence, this study was undertaken.

1.3 Main objective

To contribute towards increased maize production in Kenya through identification and utilization of new sources of resistance to GLS in maize breeding

1.4 Specific objectives

1. Identify potential heterotic inbred lines with high GLS resistance and grain yield
2. Determine genotype and environment effects on GLS and grain yield
3. To investigate the phenotypic correlations among the traits of economic significance

1.5 Null hypotheses

1. There are no heterotic parents among the inbred lines resistant to GLS
2. Genotype and environment interactions of GLS are non significant
3. There were negative correlations among the traits of economic importance

CHAPTER 2

LITERATURE REVIEW

2.1 Maize

Maize (*Zea mays L.*) is a monoecious, cross-pollinated plant with separate male (tassel) and female (ear) organs located at the top and half way on the plant respectively. Its populations include mixtures of genotypes that depend on particular combination of the two gametes that unite in a zygote. The ear and tassel are distinguished in variations of race, populations, hybrids and inbred lines. Tassels vary in length, number and spacing of tassel branches, compactness, colour, ease of pollen shed and amount of pollen shed. The ear varies in placement on plant, length, diameter, kernel row number, ear number and kernel colour (Hallauer and Miranda, 1981).

Maize is grown globally on 140 million hectares (ha) with an annual production of 600 million tonnes (Paliwal *et al.*, 2000). In eastern and southern Africa, only 15 million ha are used for maize production giving an annual production of 15 million metric tons that is way below the required yield (Simmons, 2003). It is the staple food for 90% of Kenyans (annual production 2.6 million tonnes). The production of a staple food crop by smallholder farmers often plays a vital role in alleviating poverty through income generation and contributes positively to the local and national economy.

2.2 GREY LEAF SPOT

2.2.1 Introduction

Grey leaf spot (GLS), caused by *Cercospora zeae-maydis* (Tehon and Daniels, 1925) is recognized as one of the most yield-limiting diseases of maize worldwide through

reduction of functional photosynthetic area as stated by Sprague and Eberhart (1977). Stromberg (2000) and Menkir and Ayodele (2005). The yield components most affected by the disease include number of kernels per ear and kernel size. The yield losses vary depending with the stage of the plant infection, disease severity, hybrid's susceptibility and yield potential, and the ability of leaf blighting to predispose hybrids to stalk rots.

The conservation tillage and continuous maize cultivation has increased the GLS intensity favouring its distribution and severity (Ayers *et al.*, 1984; Donahue *et al.*, 1991; de Nazareno *et al.*, 1993; Gevers *et al.*, 1994). The leaves of susceptible maize hybrids may become severely blighted prior to physiological maturity affecting radiation interception, production and translocation of photosynthate to developing kernels. Additional losses are incurred when photosynthates are diverted from the stalks to the roots, which then predispose the tissues to stalk and root rots resulting in stalk lodging (Ward *et al.*, 1999).

GLS symptoms comprise greyish black water soaked pinpoint spots surrounded by a yellow or chlorotic halo that turns tan later in the season (Rane and Ruhl, 2002). The early symptoms are easily observed when the leaf is held against the light. In about 7 days, the mature lesions elongate into the typical long and narrow rectangular lesions that run parallel to the leaf veins. Lesions may band together and blight the whole leaf at high disease pressure. Severe blighting of leaves and leaf sheaths leads to stalk deterioration and severe lodging and premature death of leaves. This ultimately reduces the amount of photosynthates (sugars) vital for ear fill (Ward *et al.*, 1999).



Plate 1. Maize leaf showing typical grey leaf spot lesions

To manage GLS, the canopies of dense populations provide more of a protection to wind-borne spores as opposed to open canopies (Caldwell, 2002). The tillage operations that bury debris also help to manage GLS whereas crop rotation with other cereals is a feasible strategy since the host specific pathogen does not survive beyond a year in infected maize debris. The removal of weeds increases airflow and dries up the canopy faster therefore reducing the environment favourable for infection (Coates and White, 1994; Gevers *et al.*, 1994). Other cultural practices like timely harvesting of maize help to reduce the levels of GLS related stalk lodging. The regular scouting of the fields helps to detect and assess grey leaf spot severity vital in making production choices. Practising early planting can also reduce the amount of fungal inoculum available at earlier stages of plant maturity. The economical use of fungicides until physiological maturity is common in

commercial maize production and this tends to delay leaf blighting, especially during grain fill (Ward *et al.*, 1999).

Maize is the only crop known to be attacked by *Cercospora zeae-maydis*. This pathogen is a poor competitor in the soil and survives on infested maize debris that is its source of primary inoculum (Stromberg, 1986; de Nazareno *et al.*, 1992). *Cercospora zeae-maydis* over winters in the debris of previously diseased maize remains after several days of high relative humidity before developing into mature lesions on leaves. The conidia for secondary spread are produced from two to four weeks after initial leaf infection. The germinating spores produce appresoria over stomata before penetrating the host tissue. Conidiophores emerge through stomata on the leaf surfaces and give rise to conidia. Primary infections usually develop on the lower maize leaves and when lesions mature, conidia are wind-dispersed to infect upper leaves.

Unlike most fungi, *C. zeae-maydis* is highly weather dependent. GLS can remain dormant during unfavourable environmental conditions (hot, dry weather) and resume rapid development as soon as favourable weather conditions return. GLS is most severe in warm (20-28⁰C) and prolonged humid conditions when there is enough free moisture on the leaves vital for disease development. Under prolonged favourable conditions and a closed canopy, developing lesions coalesce ensuing into extensive blighting and necrotic leaf tissue. With further blighting on the leaf sheath, yield losses in excess of 40 % could occur (Asea *et al.*, 2005).

GLS is influenced by plant maturity since initial symptoms do not appear until anthesis. Though under favourable environmental conditions, (>90% RH; 22-30⁰C or monoculture

maize), GLS may occur before tasseling. The lower (older) leaves are usually the sites of initial infection. After about 2 weeks, the resulting lesions generate a new crop of spores that infect the middle and upper leaves. Vulnerability to GLS increases as plants mature explaining its late season appearance in many affected areas (Lipps *et al.*, 1998).

2.2.2 Breeding for GLS Resistance

Host plant resistance remains the most viable option for managing GLS (Coates and White, 1994; Ward *et al.*, 1999). Resistance to GLS has been evaluated using natural and artificial inoculation and several sources of resistance identified. For efficient utilization of the sources of resistance in breeding programmes, it is important to understand the nature of gene action present in each source. The diallel and generation mean analyses have been conducted using various sources of resistance (Coates, 1989; Elwinger *et al.*, 1990; Donahue *et al.*, 1991; Bubeck *et al.*, 1993), qualitative (dominance), and quantitative (additive) type of inheritance identified. The qualitative type of resistance has been associated with chlorotic lesions (Freppon *et al.*, 1994). The quantitative type of resistance has been associated with the size and number of lesions, latent period and sporulation.

In South Africa, maize germplasm with either quantitative or qualitative GLS resistance have been identified (Gevers and Lake, 1994; Ward *et al.*, 1997; Caldwell, 2002; Menkir and Ayodele, 2005). The lesions of moderately resistant maize lines take long to appear (longer incubation period) and sporulation may be delayed (longer latent period) and vice versa (Stromberg, 1986). The diallel analyses indicate that both GCA and SCA gene actions are important and thus, variations among hybrids for grey leaf spot are associated

with both additive and non-additive effects with the latter showing predominance (Vasal *et al.*, 1992; Martinez *et al.*, 1993; Nass *et al.*, 2000; Iken and Olakojo, 2002 and Derera *et al.*, 2008). Coates (1989), using the generation mean analyses also noted that additive genes controlled GLS resistance. Bubeck *et al.*, (1993) and Saghai *et al.*, (1993) identified QTLs associated with GLS resistance and reported that GLS inheritance was associated with additive, dominance and epistatic effects.

2.2.3 Inoculum Preparation and Inoculation

To prepare the inoculum, portions of leaves with *Cercospora zeae maydis* are usually collected and incubated in petri dishes lined with filter paper and placed under high relative humidity for 3 days to allow for sporulation. A blend of freshly clarified V8 agar (350ml of V8 vegetable juice, 20g of agar and 3g of Calcium carbonate to clarify the agar) and 0.25g/L of streptomycin sulfate (to amend the mixture and control bacterial contaminants) is prepared and then shaken to suspend the calcium carbonate (Coates and White, 1994; Freppon *et al.*, 1996). The blend is then autoclaved at 121⁰C for 20 minutes and then cooled. The cold blend is dispensed in sterilized glass plates under very sterile conditions and the plates tightly sealed by use of cling foil to avoid further contamination. Single conidia from the conidiophores are then picked with a sterile glass needle and placed in the blend and streaking done to prepare the stock cultures which are then grown for 5 days at 28⁰C with 12 hour darkness and 12 hour fluorescent light. The stock cultures are then blended in deionized water. The resultant suspension is diluted with water and 0.2 ml/l of Tween 20 added which is a surfactant (Coates and White, 1998). This solution is then sieved through cheesecloth to obtain the fungal spores.

Asea *et al.*, (2005) highlighted four methods that may be used during the inoculation of the plants;

- i. Applying the conidial suspension by puncturing the leaves within the whorl severally
- ii. Spraying conidial suspension on the leaves
- iii. Colonized agar may be placed into lateral slits in leaves
- iv. The colonized agar may be placed into the whorls

The inoculation methods often affect incubation period, lesion length, percentage leaf area affected and sporulation of *Cercospora zae-maydis* on young maize. High level of moisture is usually maintained on the leaf canopy to promote disease development and this is achieved after 96 hours of incubation (Coates and White, 1994).

2.3. HETEROSIS AND GRAIN YIELD

Tropical maize hybrid development started in the 1940s with variable sustainability and adoption (Vasal *et al.*, 1999). The hybrid maize development in Kenya started in the 1950's (Wanyama *et al.*, 2006). This is because the hybrids show superior or increased strength in their grain yield performance and vigor (heterosis) as opposed to their parents or inbred lines (East, 1908 and Shull, 1908; Ford, 1964). The heterosis between parental inbred lines has augmented the efficiency of hybrid breeding programs since the hybrids have better yields than open pollinated varieties, greater uniformity and incorporate favourable qualitative traits adaptable to varied environments. The exploitation of heterosis as a method of plant breeding helps in the development of cultivars with high yielding potential (Deepa and Ananda, 2001). This heterosis has been described as the

increase in vigor and productivity in hybrids (Wricke and Weber, 1986; Hill *et al.*, 1997). Shull (1914) also described it as the stimulation of heterozygosis. Heterosis has also been defined as the difference in value of the hybrid and the mean value of the two parents (Falconer and Mackay, 1996). Shull (1948) also defined heterosis as the genetic expression of the beneficial effects of hybridization.

Heterosis was hypothesized to be under the influence of additive and dominant gene effects (Sprague, 1983) and vary with the level of gene frequency (Makumbi, 2005). Two hypotheses have been put forward to explain the genetic basis of heterosis; general dominance and the over dominance hypothesis. General dominance also called dominance complementation involves several non-interacting loci (Wricke and Weber, 1986) and this attributes the higher yields of the hybrids to the suppression of the deleterious genes in one parent by the dominant alleles in the other parent (Ford, 1965). Epistasis of the harmful genes over the beneficial genes may also lead to this heterosis. Heterosis in wheat occurred due to linkage and interaction of alleles thus dominance complementation was in operation (Pickett and Galwey, 1997). The work by Bingham *et al.*, (1994); Husband and Schemske (1997) have substantiated this hypothesis. They suggested that the additional copies of each gene found in polyploids, depress inbreeding. On the other hand, the over dominance hypothesis assumes that the hybrid is superior to either parent at key loci (Crow, 1998). The genes with pleiotropic effects in the hybrid contribute many good traits thus complementing those of the inbreds leading to increased yields in the subsequent hybrids. Upon combination at a particular locus, favourable dominant alleles accumulate in the F1 (hybrid). Thus, the beneficial effects remain dominant while the deleterious ones stay recessive through selection that modifies and

optimizes genes' action. Xiao *et al.*, (1995) opposed the overdominance theory for heterosis while dealing with a cross between two subspecies of rice. This was due to lack of correlation between the traits and overall genome heterozygosity. He discovered that the hybrids were not superior to both parents in analysis of quantitative trait loci but some F8 inbred lines were actually superior to the F1 for all traits evaluated.

Betran *et al.*, (2003) distinguished two types of heterosis found in plant breeding. The best or high parent heterosis is expressed as the percentage of the difference between the better parent and the mean of the two parents. The mid parent heterosis is the percentage of the difference between the average of the parents to the value of the hybrid.

- i. High Parent Heterosis, $HPH = (F1-HP)/HP * 100$
- ii. Mid Parent Heterosis, $MPH = (F1-MP)/ MP* 100$

Where $MP = (P_i + P_j)/2$, P_i is yield of inbred line i; P_j is yield of inbred line j. F1 is yield of hybrid.

Maize has been found to be a unique plant in much of the heterosis breeding experiments aimed at yield improvement due to its domestication and genome size doubling by retrotransposon. Heterosis in maize was found to be highly correlated with grain production (Makumbi, 2005). This is because the greater light interception with the increased leaf sizes influences the amount of dry matter accumulated at maturity favouring the partitioning of the accumulated dry matter to the grain (Tollenaar, 2004). Work by Moll *et al.*, (1962) revealed that the heterosis in maize yield among maize hybrids was dependent on the genetic divergence of the source population. Thus,

increased genetic diversity was associated with high heterosis (Tulu, 2001). The interactions between genotype and environment affect the level of heterosis. Betran *et al.*, (2003) stated that the environment influences the parental inbreds and hybrids because of the degree of inbreeding of the parental lines. Similarly, work done on sorghum hybrid grown on sites with differential water supply revealed the importance of characterizing specific good single cross hybrid lines for each specific environment (Chapman *et al.*, 1999). On sesame, heterosis coupled with high SCA effects was found to be suitable criteria in the selection of the best cross combinations in the improvement of seed yield and capsules per plant (Solanki and Gupta, 2001).

2.4 Combining Abilities

Since the per se performance of a line does not always indicate that its crosses will be superior, the genetic diversity of the parents involved, nature and extent of gene action controlling the inheritance of the traits needs to be established (Betran *et al.*, 2003). Thus, the combining ability of an inbred line is the ultimate factor that determines the future usefulness of the line for further breeding (Vasal *et al.*, 1992; Martinez *et al.*, 1993; Iken and Olakojo, 2002). Both narrow and broad based genetic populations have been used in the combining ability analysis (Sanghi *et al.*, 1983). The combining ability analysis when used among homozygous lines reveals the genetic structure of natural populations (Bebhardt, 1990). It has also been used to study the yield characters and heterotic groups for inbred lines with the aim of developing new hybrids with good quality, high yields and multiple disease tolerance (Xingming *et al.*, 2001).

There are two types of combining abilities: general and specific combining ability (Sprague and Tatum, 1942).

- The general combining ability (GCA) is the average performance of a line in hybrid combinations (Jugenheimer, 1985). The GCA is also the difference between the mean performance of the progeny of a given male and the mean of the progeny from all the males (Kearsey and Pooni, 1996). It reflects how well male genes combine with those of females in the population thus helping to identify good hybrids for use as commercial varieties. It also indicates parents that contain matching complementary alleles that can be recombined in later generations by selection. When one scores inbred lines themselves, lines with highest GCA are those with highest mean score (Kearsey and Pooni, 1996). The lines with the most number of trait enhancing alleles are used to initiate a breeding program (Xingming *et al.*, 2001). General combining ability is an important factor during the development of high yielding synthetics (Makumbi, 2005). General combining ability is associated with additive genetic action (Falconer and Mackay, 1996).
- The specific combining ability (SCA) is the individual performance of an inbred line in a single specific combination (Jugenheimer, 1985). The SCA deals with certain hybrid combinations that is either better or poorer than would be expected on the average performance of parent inbred line included (Wricke and Weber, 1986). Sprague and Tatum (1942) assumed that SCA was associated with dominance, epistasis and genotype by environment interaction.

The combining ability has been used to study the inheritance of various quantitative characters in maize and other crops (Venkateswarlu and Singh, 1982; Dua and Yadava, 1983; Rao, 1983; Nass *et al.*, 2000; Ortiz, 2001). High GCA and SCA variances for grain yield obtained in many studies imply that both additive and non additive gene actions play a pivotal role in the inheritance of maize yield characters (Varghese *et al.*, 1976; Iken and Olakojo., 2002; Verma, 2001; Derera *et al.*, 2007; Derera *et al.*, 2008). Betrán *et al.* (2003) reported significant GCA and GCA x environment interaction effects for grain yield under stress and nonstress environments. CMMYT has used the GCA and SCA effects to establish the heterotic patterns of its maize populations and pools (Vasal *et al.*, 1992). Vasal *et al.* (1992) also stated that the new synthetics developed from inbred lines show less inbreeding depression thus they are promising sources of new superior inbred lines. The identification of single crosses with high and positive general combining ability (GCA) effects for grain yield could be potential parents in the development of various hybrids, including three-way, double-cross and double top cross hybrids. Most high general combiners produce genotypes with high SCA. Nevertheless, on other crops other than maize, pearl millet genotypes with low GCA effects for various traits produced genotypes with high SCA estimates. This implied that the parents involved were genetically diverse (Bhatnagar and Mehrotra, 1980). In this case, there is need to screen many genotypes and the selection of the suitable parents done to produce desirable genotypes. Solanki and Gupta (2001) working on sesame noted that the promising parents involved in crosses were medium by high, high by low and medium by low general combiners for seed yield and its component characters. This signified the presence of non fixable non additive types of gene action. The study concluded that non

conventional breeding methods like biparental mating and /or diallel selective mating, which accumulate favourable genes in homozygous state, and / or helps in breaking the linkage blocks could be used in the further improvement of the breeding materials.

2.5 Diallel Analysis

Diallel crosses have been popular and efficient breeding strategies in the concentration of favourable genes in maize genotypes (Ojulong *et al.*, 1996). The diallel cross involves crossing a set of genotypes in all possible combinations (Hill *et al.*, 1997). This type of crossing gives the largest number of cross combinations from which selection can be made thus, enabling the identification of superior cultivars especially in uncharacterised germplasm (Gevers *et al.*, 1994). Diallel crosses have also been used to assess the combining ability (the GCA and SCA effects) of inbred lines and crosses for different traits and their implications in breeding (Griffing, 1956; Malhotra *et al.*, 1980). Diallel crosses also enable a breeder to predict progeny performance from parental performance (Ojulong *et al.*, 1996). Crossing among genotypes is conducted in either a complete or a partial diallel. The complete diallel involves taking a set of 'n' genotypes, selfing and intercrossing them in all combinations including reciprocals to produce N^2 Full Sib (FS) families. On the other hand, the partial diallel involves sampling of crosses produced by many inbred lines and helps maintain the efficiency of diallels (Varghese *et al.*, 1976) because of its high efficiency in the estimation of GCA effects (Singh and Hinkelmann, 1998).

The evaluation of diallel cross data has been used to test the significance of general combining ability (GCA) and the specific combining ability (SCA) of lines and crosses

(Elwinger *et al.*, 1990; Ulrich *et al.*, 1990; Donahue *et al.*, 1991; Nass *et al.*, 2000). Pairs of parental lines that yield heterotic crosses have also been identified by use of the diallel analysis. These analyses have been found to be pivotal in the development of appropriate hybrids (Vega and Chapman, 2006). The diallel analysis has also been used to evaluate GLS resistance and its inheritance among maize germplasm (Coates and White, 1998). In a diallel cross, three sets of materials are usually involved; parents, F1 crosses and reciprocals.

Griffing (1956) highlighted four methods of analyzing data from a diallel mating design depending on the breeding material involved. This method also called Griffing's method shows the significance of the combining ability analysis (Singh and Chaudhary, 1977):

- i) Parents (n), $n(n-1)/2$ F1's and reciprocals,
- ii) Parents and F1's only,
- iii) F1's and reciprocals
- iv) F1's only.

Griffing (1956) also pinpointed two models while using the Griffing's method.

- i. Eisenhart's model I (fixed effect) is used where the experimental population is the population about which inferences can be drawn. The estimates from the analysis apply to those genotypes alone: thus, genotypic effects are constant (Hill *et al.*, 1997). GCA and SCA mean squares are tested against the error mean square.
- ii. Model II (random effect). The parents are assumed to be unselected from some reference population thus inferences are made about the parameters of that

population (Hill *et al.*, 1997). In this model, GCA mean square is tested against the SCA mean squares, which is in turn tested against the error mean squares.

Several authors have used the Griffing's methods (Griffing, 1956) to estimate GCA and SCA effects for various traits (Verma, 2001; Vivek *et al.*, 2001; Pswarayi and Vivek, 2004; Makumbi, 2005). Ojulong *et al.*, (1996) who used the Griffing's method 2, model 1, noted that northern leaf blight resistance could be incorporated in the Uganda germplasm using recurrent selection.

2.6 GENOTYPE AND ENVIRONMENT INTERACTION (GXE)

The maize genotype has different kinds of gene actions that interact differently in the inheritance of the various plant attributes. On one hand, maize grows on a wide range of environmental conditions in terms of water balance, solar radiation, and temperatures (Hill *et al.*, 1997). The different responses of these maize germplasm to these varied AEZ is called genotype by environment interaction (GXE) and it often hampers the identification of high yielding and stable maize hybrids (Dudley and Moll, 1969; Epinat-Le Signor *et al.*, 2001). The GXE interaction variance can be controlled by increasing number of environments. Argillier *et al.*, (1994) stated that GXE interaction for grain yield was influenced by variations in vegetative or flowering traits of maize. This implies that delayed silking greatly lowers the grain yield thus favouring the early maize germplasm in some environments. The GXE interactions are thus a function of the environmental, genotypic, morphological, phenological, and physiological traits of the varieties. (Nachit *et al.*, 1992; Epinat-Le Signor *et al.*, 2001). Thus, the establishment of the specific factors responsible for GXE interaction is a prerequisite for the efficient

selection of superior maize varieties. Genotype by environment interaction could be used to identify potential candidates for promising hybrid combinations (Nass *et al.*, 2000). On the other hand, the stability (antonym for GXE) of maize varieties “the response of crosses across several environments” is a very crucial factor because it increases the farmers’ acceptability of the new varieties (Jong and Brewbaker, 2005). The good maize genotypes tend to utilize the resources in higher performing environments to produce above average maize varieties in all the environments.

Many GXE interaction studies involving diallel crosses have been carried out in maize. The GXE interaction analysis has been performed using different methods. They include: stability analysis following additive main effects and multiplicative interaction model (AMMI) , principal component analysis and linear regression analysis, Analysis of Variance (ANOVA) that consider heterosis, GCA and SCA (Gauch and Zobel, 1988; Nachit *et al.*,1992; Yan and Hunt, 1998; Vargas *et al.*,1999; Tulu, 2001). ANOVA for GXE interaction reported significantly differences at $P < 0.01$ for all traits measured except grain yield (Tulu, 2001) while Makumbi (2005) obtained significant GXE interaction for all traits involved. The highly significant environment by hybrid interaction obtained by Derera *et al.*. (2007) indicated that hybrid selection across sites was inconsistent. Further work by Menkir and Ayodele (2005) showed highly significant GXE interaction and significant rank correlations for GLS resistance across sites. This implied that the differences in the GLS scores between inbred lines and their hybrids led to the genotype x environment interactions (Carson *et al.*, 2002). Linear trends have been used in GXE interaction analysis (Sprague and Eberhart, 1977; Jong and Brewbaker, 2005). The diallel analysis done by Sprague and Eberhart (1977) and Jong and

Brewbaker (2005) showed that $G \times E$ interactions could be interpreted from the linear response of the highly significant GCA effects to the environment as opposed to less significant SCA \times E thus a breeder could select for stable inbred lines across temporal environments. From these findings, it can be deduced that $G \times E$ interaction has an additive and a non additive genetic component. Kang and Gorman (1989) found out that none of the environmental factors involved in his study influenced the interaction for maize grain yield. John *et al.*, (2001) studied twenty-five sesame genotypes and assessed them for genotype by environment interaction by AMMI. The AMMI analysis reported that the mean squares for genotypes, seasons (environments) and $G \times E$ interactions were highly significant implying the performance of genotypes was different over seasons.

2.7 Correlations among Traits

When characters are associated with the performance, easy and efficient identification of the inbred lines can be done by selection of a highly correlated trait. In the study of Patil *et al.*, (1969) grain yield was significant and positively correlated with plant height and days to maturity and plant height under drought conditions (Makumbi, 2005). Delayed silking under drought leads to less assimilate partitioning into growing ears around anthesis thus resulting in lowered ear growth rates, increased ear abortion and plants that are more barren. Edmeades *et al.*, (1996) noted that the capability of a genotype to produce an ear under stress is the most important characteristic exhibiting drought tolerance. Pearson's phenotypic correlations conducted among four drought environments for yield ranking of eighty hybrids displayed strong significant correlation with yield under drought (Derera *et al.*, 2007). Betrán *et al.*, (2003) reported that

correlation between midparent and hybrids were significant at ten environments and non-significant for two environments.

Vivek *et al.*, (2001) noted that correlations between GCA effects for disease resistance were non-significant implying the possibility of gene pyramiding. Menkir and Ayodele (2005) while working on maize germplasm reported significantly different correlation between GLS score and other agronomic traits; plant aspect ($r = 0.92$, $P < 0.0001$), ear aspect ($r = 0.52$, $P = 0.006$) and grain yield ($r = 0.64$, $P < 0.0004$). Pearson correlations between all environment/rating period combinations for GLS ranged from 0.33 to 0.92 at $P < 0.01$ (Clements *et al.*, 2000). Stuber *et al.*, (1966) reported an association between plant and ear height and days to tassel.

CHAPTER 3

MATERIALS AND METHODS

3.1 Introduction

Seven inbred lines were used for preliminary evaluation of GLS resistance in three sites, KARI-Kiboko, University of Nairobi's Kabete Field Station and KARI-Kakamega (Generation Challenge Program, 2006). Inbred lines CML 204, CML 312, CML 373 and CML 384 from CIMMYT, TZMI 102, TZMI 711 and TZMI 712 from IITA were used in this study.

3.2 Inbred lines

3.2.1 CIMMYT Maize Lines

i. CML 204

The pedigree of this inbred line is pedigree is [7794]-SELF-4-1-S9-1-4-7-4-5-BB. It is adapted in the mid altitude and semitropical areas of Africa. It is a long late maturing inbred line. It has white grains and a dent texture. It belongs to heterotic group B and has good tolerance to MSV and rust (Pswarayi and Vivek, 2004).

ii. CML 312

Its source germplasm is P500 with a pedigree of S89500F2-2-2-1-1-B*5. This is a tall intermediate maturing inbred line with white semi flint kernels adapted to subtropical areas. It is susceptible to rust and ear rot. It belongs to heterotic group A and has been reported to have good general combining abilities with many inbreds making it one of the best A testers. It has good resistance to GLS and turcicum (Pswarayi and Vivek, 2004).

iii. CML 373

The source germplasm of this inbred line is P43SR with a pedigree of P43SR-41-1-2-1-B-8-1-BBB. It has white flint textured kernels with intermediate maturity. It is a tall inbred adapted to the subtropical areas and is susceptible to rust, turcicum and ear rot. It belongs to heterotic group A (Pswarayi and Vivek, 2004).

iv. CML 384

This is a flint textured, white grained inbred line. Its source population is P502 with a pedigree of P502C1#-771-2-2-1-3-B. It is a tall late maturing inbred line with good resistance to ear rot and rust. It falls in heterotic group B. It has been reported to have tolerance and resistance to GLS and turcicum (Pswarayi and Vivek, 2004).

3.2.2 IITA Inbred Lines

i. TZMI 711

The TZMI 711 inbred line was derived from a cross between a maize variety grown in Tanzania, called National-1 Variety and an IITA MSV-resistant population, TZSR (Menkir and Adepoju, 2005). The TZSR was developed through intercrossing four populations namely TZB, TZPB, POP 21, and POP 22. Based on its combining ability effects and mean grain yields, TZMI 711 was assigned to the TZMI 102 heterotic group.

ii. TZMI 712

TZMI 712 was selected from a cross between a mid-altitude inbred line TZMI 501 from IITA and an inbred line ZSR 923 S4 bulk, from CIMMYT. TZMI 712 was assigned to the TZMI 102 heterotic group based on its combining ability effects and mean grain

yields of the lines in crosses with the two inbred testers, TZMI 102 and TZMI 407 (Menkir and Adepoju, 2005).

iii. TZMI 102

TZMI 102 was a parent of the best single-cross hybrid marketed in Plateau State of Nigeria as '8535-23' and which forms testcrosses (Menkir and Adepoju, 2005). Its pedigree is CamInb.TCSel1-13-1-1-1-B.

3.3 Site description

3.3.1 KARI-Kiboko

This is a KARI sub centre used for dry land research in Makueni District, Eastern Province, Kenya and is located 187 km east of Nairobi. It lies at an altitude 993m Above Sea Level (ASL) and latitude of 2^o 15' south and Longitude 37^o 45'E. It is classified under agro-ecological zone 5. The mean annual rainfall is 548mm. The long-term annual average rainfall is 615mm with a bimodal distribution (Mwacharo *et al.*, 2004). The short rains are more reliable and fall in October to January with a seasonal mean of 328 mm. The long rains fall from March to June with a seasonal mean of 233mm. It has annual mean maximum temperature of 30.6^o C, annual mean minimum temperature of 17.4^o C and overall annual mean temperature of 24^o C (Appendix 1). The soils are of rhodic ferrasols to ferric luvisol on the old peneplain and eutric fluvisol at the bottom of the river valley (<http://www.kari.org>, 2008). This site has conditions unfavourable for *Cercospora zae maydis* infection and spread thus KARI- Kiboko site was used to identify potential losses from the GLS disease.

3.3.2 Kabete Field Station

This is found at the University of Nairobi, Faculty of Agriculture located in upper Kabete Campus, 11 kilometers North West of Nairobi (Jaetzold and Schmidt, 1983). It lies at longitude 36° 44' East and latitude 1°15' South with an altitude of 1820m above sea level. It falls in Agro Ecological Zone 3, with bimodal rainfall pattern whose annual average is 1000 mm. The long rains fall from March to June while short rains occur from October to December. The site has annual temperature ranging from 16-23°C. Soils are well-drained, very deep, dark reddish brown, friable clay with acid humic top soil. The average daily soil temperature is 18°C. The daily sunshine hours are approximately 6.5 to 7.1 hours. This area is prone to GLS explaining the basis upon which this site was selected for this study.

3.3.3 KARI-Kakamega

This is a KARI Research Centre located near Kakamega town in Western Province is about 450 km west of Nairobi. It falls in Agro-ecological zone 2 with an altitude of 1585 m above sea level (ASL), latitude 0° 17'N, longitude 34° 46'E and receives a mean annual rainfall of 1995 mm. The average temperature is 20.3 °C. It has two cropping seasons with long rains falling in March to July and short rains in August to November. The soils are deep, friable, Basaltic loam, fertile and well drained (<http://www.kari.org>, 2008). KARI- Kakamega has conditions favourable for *Cercospora zea maydis* infection and thus this site was chosen as a GLS hot spot in this study.

3.4 Activities

3.4.1 Nursery management and pollination

The nursery was set up at Kiboko to generate the diallel crosses and multiply the seed population. The seeds were sown on 16th January 2006. Seven parents were sown in 13 rows each to allow for crossing with each line and have a self of each resulting to ninety-one rows. The seven parents were crossed in all possible combinations (diallel). After three weeks, weeding was done and buldock applied at the rate of 6 kg ha⁻¹ to protect the crop from maize stalk borer. Topdressing with CAN at the rate of 60kg N ha⁻¹ was applied as a split with half applied at planting and the rest at about 10th leaf. Supplementary irrigation was also done whenever needed. During flowering, hand pollination was done on the developing ears by covering the silks with silk bags (Jugenheimer, 1985). After silk emergence, appropriate tassels were bagged and on the following day, pollination was done to the desired plants generating 42 single cross hybrids. At maturity, ears from various crosses were harvested, shelled, labeled and packaged.

3.4.2 Field Evaluation

The single crosses generated through the diallel crosses at Kiboko in season one were evaluated at KARI-Kiboko, Kabete Field Station and KARI-Kakamega. Rows of 5m long with three replicates were planted. Fifty entries that included 42 hybrids, seven parents and a commercial checks were planted at a spacing of 0.75m X 0.25m. The experimental design was randomized complete block design with three replicates. At Kakamega, the plot sizes were reduced due to space limitation to 14 hills. Between replicates, a metre path was left to allow for easy movement during data taking. Two seeds per hill were sown and later thinned to one plant per hill. At Kiboko, the seeds were sown on 22nd June

2006, Kabete on 15th September, 2006 and in Kakamega on 6th October 2006. In Kabete Field Station, the plants were inoculated. The inoculum was prepared according to Coates and White (1994) methodology. Portions of leaves with *Cercospora zea maydis* (Tehon and Daniels, 1925) were collected from Kabete Field Station during the long rains season of 2006 and incubated in petri dishes lined with filter paper and placed under high relative humidity for 3 days to allow for sporulation. A blend of freshly clarified V8 agar and 0.25g/L of streptomycin sulfate was prepared (Coates and White, 1994; Freppon *et al.*, 1996). The blend was then autoclaved at 121^oC for 20 minutes and then cooled. The cold blend was dispensed in sterilized glass plates under very sterile conditions and the plates tightly sealed by use of cling foil to avoid contamination. Single conidia from the conidiophores were then picked with a sterile glass needle and placed in the blend and streaking done to prepare the stock cultures which were then grown for 5 days at 28^oC with 12 hour darkness and 12 hour fluorescent light. The stock cultures were then blended in deionized water. The resultant suspension was diluted with water and 0.2 ml/l of Tween 20 added (Coates and White, 1998). This solution was then sieved through cheesecloth to obtain the fungal spores. The inoculum was then applied on the plants by spraying the conidial suspension on the leaves according to Asea *et al.*, (2005) method. High levels of moisture were maintained on the leaf canopy by covering the inoculated leaves with polythene bags for three days to promote disease development.

3.4.3 Data collection of the single cross evaluation

The data collected during the evaluation of the single crosses was days to mid silking and mid pollen shed which implies the number of days from sowing to when 50% of the plants have silked and shed pollen respectively. Stem (SL) and root lodge (RL) data was

recorded as the number of plants lodged at the stem and root respectively and was observed two weeks before harvest. The ear height (EH) was recorded as the height from the ground to the node bearing the uppermost ear while the plant height (PH) was recorded as the height from the soil level to the node of the flag leaf. The ear aspect (EA) was noted as the overall appeal of harvested ears based on a 1 to 5 scale, where: 1 = clean, uniform, large, and well-filled ears and 5 = rotten, variable, small, and partially filled ears. The ear rot count (DE) was the number of rotten ears per plot. On the grain yield, the ears per plot were weighed and this was recorded as the field weight. The moisture content was then determined from a seed sample of ten randomly selected cobs. In Kabete field station and KARI Kiboko, only one row represented a plot with a size of 0.75mX 0.25m while in KARI Kakamega, there were two rows per plot with a plot size of 2 (0.75mX 0.25m). The harvested cobs were then adjusted to 13% moisture content while assuming an 80% shelling percentage.

3.5 Disease assessment

The diseases were scored under natural infestation apart from GLS in Kabete field station. GLS, northern corn blight, ear rot and maize streak virus infection were assessed by observing the disease symptoms and giving phenotypic scores based on the disease severity (DI).

3.5.1 Grey Leaf Spot

The rectangular GLS lesions were used to determine disease incidence at a scale of 1-5 (Saghai *et al.*, 1993), where:

1 =no symptoms. 2= moderate lesion below leaves subtending the ear, 3= heavy lesion development on and below the leaf subtending the ear with a few lesions above it. 4= severe lesion development on all but uppermost leaves may have few lesions and 5= all leaves dead

3.5.2 Leaf Blight (LB).

For Leaf Blight (LB), the long or small, elliptical, brownish, necrotic lesions were assessed as suggested Elliot and Jenkins (1946), where;

0.5= very slight infection, one or two restricted lesions on the lower leaves, 1= slight infection, a few scattered lesions on the lower leaves, 2= light infection, moderate number of lesions on lower leaves, 3= moderate infection, abundant lesions on lower leaves and few on middle leaves, 4= heavy infection, lesions abundant on all leaves, and extending to upper leaves and 5= very heavy infection, lesions abundant on all leaves, plants may be prematurely killed.

3.5.3 Maize streak virus (MSV)

Maize streak virus (MSV) was evaluated by counting the number of infected stems per plot (frequency of diseased plants observed in a particular plot)

3.5.4 Ear rot -The numbers of rotten ears were counted and recorded.

3.6. Grain Yield Evaluation

The ears per row were harvested at physiological maturity and their moisture content and field weights recorded.

3.7 Data Analysis

Data statistical analysis (means, correlation, least significant differences) of all parameters recorded was done using the SAS program (SAS, 1996).

3.7.1 Analysis of variance (ANOVA)

Analysis of Variance was carried using ProcGLM function of the SAS program. The GXE interaction was estimated and significance levels determined.

3.7.2 Combining Ability Analysis

Griffing's (1956) method I involving parents, F1's and reciprocals was used with a standard combining ability model (model 1). The inclusion of reciprocal crosses enabled detection of maternal effects within the crosses (Gevers *et al.*, 1994).

The statistical model was $Y_{ij} = m + g_i + g_j + s_{ij} + r_{ij} + 1/bc \sum \sum e_{ijkl}$.

Where: $i, j = 1, 2, \dots, n$, $k = 1, 2, \dots, b$ and $l = 1, 2, \dots, c$.

$Y_{ij} = 1/bc \sum \sum Y_{ijkl}$ = mean of ixj^{th} genotype over k and l .

g_i = GCA effect of i^{th} parent, g_j = GCA effect of j^{th} parent,

s_{ij} is the interaction (SCA effect), r_{ij} is the reciprocal effect and $1/bc \sum \sum Y_{ijkl}$ is mean error effect .

Estimation of sum of squares

Sum of squares (SS) due to GCA = $1/2n \sum (Y_{i.} + Y_{.j})^2 - 2/n^2 Y^2 ..$

SS due to SCA = $1/2 \sum \sum Y_{ij} (Y_{ij} + Y_{ji}) - 1/2n \sum (Y_{i.} + Y_{.j})^2 + 1/n^2 Y^2 ..$

Sum of squares due to reciprocals = $1/2 \sum \sum (Y_{ij} - Y_{ji})^2$ (Singh and Chaudhary, 1977).

3.7.3 Grain Yield

The formula below was used to give a standardized grain yield data in tonnes per hectare.

$$GY (T\text{ha}^{-1}) = (\text{field weight, Kg /Plot size}) * (100 - \text{MC} / 87) * (0.80) * 10$$

Where; MC is moisture content, 0.8=80% that is the estimated shelling percentage.

3.7.4 Phenotypic correlations among traits

Pearson correlation coefficients for grain yield, grey leaf spot, maize streak virus, leaf blight, ear rot, ear height, plant height, days to flowering, were generated using SAS (SAS, 1996) program.

CHAPTER 4

RESULTS AND DISCUSSION

4.1 General means at specific sites

4.1.1 KARI-Kiboko

There were significant differences ($P < 0.05$) for all traits measured except for MSV (Table 1). The parental means showed the breeding potential for the characters involved and could easily be used to discriminate poor lines in future breeding efforts. This site was used to expose potential losses due to the GLS disease.

The inbred line CML 373 which was the highest yielding parent with 3.16THa^{-1} had the most number of crosses with high yields. This implies that CML 373 contains many favourable genes that lead to improved grain yields. This inbred line CML 373 had resistance to MSV. It also had good husk cover crucial for ear rot resistance (Table 1). Thus, it could be used in the improvement of elite maize germplasm for use in the dry land areas. TZMI 711 was the least yielding parent implying that it had a low frequency of yield genes. Conclusively, no parent out yielded the check, H614D. The earliest maturing parent, TZMI 102 and the highest yielding parent, CML 373 produced the highest yielding hybrid TZMI 102/CML 373 with 11.01Tha^{-1} . TZMI 102/CML 373 out yielded the local check, H614D (4.63Tha^{-1}) by over 100%. TZMI 102 and CML 312 had a high frequency of earliness genes since they produced many early and high yielding hybrids. Pswarayi and Vivek (2004) working on early maturing maize germplasm stated that CML 312 crosses were intermediate in maturity.

Table 1 Mean values for grain yield and the other traits

Cross	GY	GLS	Blight	MSV
CML204 Self	1.59	1.2	2.5	1.64
CML204/CML312	10.23	1.07	2.6	1.52
CML204/CML373	9.01	1	2.6	1.7
CML204/CML384	8.7	1	2.6	1.61
CML204/TZMI102	7.8	1.06	2.6	2.09
CML204/TZMI711	7.48	1	2.7	1.93
CML204/TZMI712	8.1	1.06	3.4	1.96
CML373 Self	3.16	1	2.6	1.31
CML373/CML204	9.3	1	2.8	1.29
CML373/CML312	10.67	1	2.5	1.52
CML373/CML384	10.35	1	2.6	1.4
CML373/TZMI102	9.76	1.07	2.8	2.12
CML373/TZMI711	7.5	1.06	2.7	1.49
CML373/TZMI712	9.47	1.07	2.4	1.58
CML312 Self	1.69	1	2.6	1.4
CML312/CML204	9.84	1.12	2.7	1.53
CML312/CML373	9.96	1	2.5	1.45
CML312/CML384	7.9	1	2.6	1.89
CML312/TZMI102	8.46	1.07	2.6	1.24
CML312/TZMI711	8.91	1	2.6	1.13
CML312/TZMI712	8.55	1.04	2.4	1.26
CML 384 Self	1.7	1.07	2	1.37
CML384/CML204	8.14	1	2.7	1.4
CML384/CML373	10.52	1	2.7	1.42
CML384/CML312	7.73	1	2.5	1.14
CML384/TZMI102	8.19	1.05	2.5	1.94
CML384/TZMI711	7.22	1.15	2.5	1.44
CML384/TZMI712	7.86	1.07	2.4	1.86
TZMI 102 Self	1.64	1.95	2.2	2.95
TZMI102/CML204	7.66	1.21	2.5	2.04
TZMI102/CML373	11.01	1.13	2.7	2.26

recorded in KARI-Kiboko, 2006

DE	DTMF	DFFF	EH	PH
0.33	81.33	84	85	163.33
0	72	73.67	124.44	230
0	76	78.33	114.44	214.44
1.33	77	79	111.67	202.22
0.67	73.33	76.33	122.22	231.67
1	74.33	77.67	112.22	197.22
0	73.67	77	105.56	207.78
0.33	80.67	86	80.56	178.89
0	74.67	78	112.78	208.89
0	72.33	75	93.89	199.44
0.67	75.67	78	102.22	201.11
1	74	77	98.89	183.44
0.67	74	77.67	99.44	188.89
0	76.33	79	98.89	200
0.67	78.33	81.33	77.22	186.11
0.33	73.33	75.67	123.89	223.89
0	72	75.33	91.67	202.78
0.33	74.67	76	102.22	200
0.33	71.67	73.67	100	206.11
0	71.67	75.33	91.11	185.56
0.33	72.33	74.67	86.11	192.78
3.67	81.33	83.33	80.56	151.11
1.67	77	79.33	111.11	201.67
0.67	74.33	77	93.33	192.22
0	73.33	75	93.89	195
1	74	76	106.67	206.67
1	73.33	76.67	96.67	189.44
1.67	76	77	91.11	186.11
2	76.67	79.33	78.89	165.56
0	74	77.33	125.56	231.67
0	74.33	77	101.67	207.78

Cross	GY	GLS	Blight	MSV	DE	DTMF	DTEF	EH	PH
TZMI102/CML312	8.57	1.07	2.5	1.36	0	70.33	72.33	101.11	207.22
TZMI102/CML384	8.6	1.13	2.4	1.76	0.33	72.67	75.33	106.11	205
TZMI102/TZMI711	7	1.06	2.6	1.72	0.33	74.33	77.33	100.56	190
TZMI 02/TZMI 712	6.23	1.38	2.3	1.99	1.67	75.33	77.33	81.67	182.22
TZMI 711 Self	1.34	1.05	2.4	1.69	0.67	79	83	56.67	104.44
TZMI711/CML204	7.26	1	2.7	1.63	0.33	75.67	78	108.33	197.22
TZMI711/CML373	7.59	1.12	2.6	1.72	0	75	78.67	97.78	193.89
TZMI711/CML312	8.81	1.07	2.6	1.13	1	71.67	74.67	96.67	189.44
TZMI 711/CML384	6.73	1.07	2.6	1.66	0.33	72.67	75.33	94.44	176.67
TZMI 11/TZMI 102	6.51	1.23	2.6	2.21	0	76	77.33	91.67	183.89
TZMI 11/TZMI 712	4.92	1	2.4	1.9	0.33	78.33	79.67	67.22	138.33
TZMI 712 Self	1.95	1	2.4	1.77	1	83	87	53.33	117.78
TZMI712/CML204	7.2	1	2.6	2.55	0.33	76	78	103.89	205
TZMI712/CML373	7.8	1	2.3	1.67	1	77	78.67	89.44	190.56
TZMI712/CML312	8.46	1	2.2	1.15	0.67	72.67	74.67	94.44	201.11
TZMI712/CML384	7.91	1	2.3	1.55	1.33	76.33	78.33	89.44	187.22
TZMI 12/TZMI 102	6.13	1	2.2	1.49	0.33	77	78.67	83.89	186.67
TZMI 12/TZMI 711	5.74	1	2.7	1.48	0	78.67	81.33	73.33	150.56
CHECK	4.63	1.05	2.6	2.87	0.33	77	78	127.22	225.56
F	<.001	<.001	0.2	<.001	<.001	<.001	<.001	<.001	<.001
Lsd.	1.29	0.15	0.5	2.491	1.3	2.12	2.54	11.09	15.7
C.V%	10.9	8.5	0.3	1.255	135.2	1.7	2	7.1	5.1

Where; F= significance level, C.V%= percentage of coefficient of variation, Lsd= least square difference; GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DTEF= days to female flowering, PH= plant height, EH= ear height, MSV = maize streak virus, Blight= Southern corn leaf blight

These early maturing entries are ideal for intercropping since they have lesser time to compete for moisture, light, and nutrients as opposed to the later maturing varieties. Epinat-Le Signor *et al.*, (2001) also found flowering earliness desirable in areas with restricted water supply. TZMI 102/CML 373 had no rotten ears, no lodging and had good husk cover. Thus, TZMI 102/CML 373 could be ideal for release in areas with unreliable little rainfall like dry lands of Kenya. Since TZMI102/CML 373 was a tall plant (207.78cm) with high ear placement of 101.67cm, three way and double crosses with TZMI 711 (shortest entry with plant height of 104.4cm) could help reduce the plant height.

Other high yielding hybrids were CML 373 / CML 312, CML 384 / CML373, CML373 / CML384, CML 204 / CML312, CML 312 / CML373, CML 312 / CML 204 and CML 373 / TZMI 102 with grain yields ranging from 9.76 THa⁻¹ to 10.67 THa⁻¹. Among these higher yielders, CML 204 / CML312, CML 312 / CML373 and CML 373 / CML 312 (with either CML 312 being a male or a female) were the earliest entries with 72 days each in KARI Kiboko. The high yielders in KARI Kiboko reveal the potential of these specific hybrid combinations for grain yield and could be used to develop synthetics and composites. . These high yielding hybrids could be improved further for release to farmers who grow early maturing maize varieties. Due to recurrent drought in dry lands of Kenya, these early entries could help avert food shortages.

The high yielders in Kiboko reveal the potential of these specific hybrid combinations for grain yield. These good entries with other good agronomic traits (TZMI 102/CML. 373, CML 204 / CML312, CML 312 / CML.373 and CML 373 / CML 312) could be used to

develop synthetics and composites for future release in the Arid and Semi-Arid Lands (ASAL) of Kenya that have varied amounts of rainfall. These high yielding hybrids could be bred further for release to farmers who grow early maturing maize varieties that can grow during the off seasons. Due to recurrent drought in most dry land areas, these early entries could help avert famine related aftermaths in most areas of SSA.

4.1.2 Kabete Field Station

Significant differences ($P < 0.05$) were noted for all traits except MSV, Northern corn leaf blight (NCLB) (Table 2). Grain yields in Kabete were generally higher than the other sites due to better climatic conditions and long growth periods (Appendix 1). The longer growth periods favoured high yields and this supports finding by Paliwal *et al.*, (2000) statement that late maturing genotypes produce high yields. There is also genotype by environment interaction for grain yield. The highest yielding inbred line was TZMI 711 with 8.43THa^{-1} whereas CML 373 with 3.24THa^{-1} had the least yields. CML 373 was found to be immune to GLS with score 1 followed by TZMI 711 with score 2.2. TZMI 102 and CML 204 were highly susceptible to GLS with scores 4 and 4.5 respectively. TZMI 711 contained high frequency of yield alleles while TZMI 711 and CML 373 could be useful sources of GLS resistant genes. TZMI 711 and CML 373 were also resistant to ear rot, MSV and blight implying they could be good multiple disease resistant lines. The good lines could be used in development of many disease resistant hybrids.

Table 2. Mean values for grain yield and the other traits recorded in Kabete Field Station, 2006

Cross	GY	GLS	blight	MSV	DE	DTFF	DTMF	EH	PH
CML204 Self	3.3	4.5	1.7	1.3	2.3	92.7	91.3	143	253.8
CML204/CML312	19.9	2.8	1.7	1	2	90.3	89.3	118.3	241.3
CML204/CML373	15.6	2.2	1.7	1	3	92.3	91	148.3	258.5
CML204/CML384	18.3	2.8	2	1.2	7.3	88.7	85.7	122.8	230.8
CML204/TZMI 102	14.8	4.2	1.7	1.2	3	91.7	90.3	104.7	221.7
CML204/TZMI 711	15.9	2.3	1.7	1.4	10.3	92.3	90.7	111	229.2
CML204/TZMI 712	13.7	1.7	1.9	1	2	92	90	106.5	224.2
CML373 Self	3.2	1	1.7	1.2	5	95.7	94	111.3	222.7
CML373/CML204	18.8	3	1.7	1	8.7	89.3	86	126	240.8
CML373/CML312	13.6	1.5	1.7	1.2	2.3	88.7	87	102	207.3
CML373/CML384	19.3	1.7	1.7	1	6	91.3	90.3	129.2	249.8
CML373/TZMI 102	17.8	3	1.7	1	11.3	91	89.3	122.5	233.2
CML373/TZMI 711	14.5	1.5	1.7	1	5.3	93.3	90.7	114.3	225.2
CML373/TZMI 712	13.6	1.5	2	1.2	2	91.3	89.3	103.2	216.7
CML312 Self	4.6	2.8	1.7	1	8.7	94.3	93	106.5	211.2
CML312/CML204	20	2.3	1.9	1.2	7.3	89.7	88.3	114	219.5
CML312/CML373	15.3	1.5	1.9	1.2	3	89.3	86.3	108.7	223.3
CML312/CML384	18.7	2.7	1.7	1.2	13.3	89.3	88.3	136.8	253.8
CML312/TZMI 102	17.8	2.3	1.7	1	9.7	88	86	130.2	236.3
CML312/TZMI 711	15.7	1.5	1.7	1	6	91.7	89.3	110	211.8
CML312/TZMI 712	14.9	1.7	1.9	1.2	15.7	89.3	87.3	112.2	223.5
CML 384 Self	6.9	3.2	1.7	1	3.7	99.7	100	93.7	173.2
CML384/CML204	17.3	3.5	2	1	2.7	91.3	90	101.8	211.8
CML384/CML373	19.7	1.7	1.9	1	4.7	92.7	91.7	109.7	214.7
CML384/CML312	16.5	1.8	1.7	1	7.3	89	89	72.7	178.7
CML384/TZMI 102	17.5	3.3	1.7	1	8	88.3	86.7	115.3	226
CML384/TZMI 711	18.9	1.8	1.9	1	6	91.7	90.3	88.7	176.7
CML384/TZMI 712	19.3	2.3	1.7	1	4.7	90.3	89.3	94.7	180.2
TZMI 102 Self	5.4	4	1.7	1	4.7	95.3	93.7	94.3	186

Cross	GY	GLS	blight	MSV	DE	DTFF	DTMF	EH	PH
TZMI 102/CML204	15.9	3.5	1.7	1	10.3	90.7	89	78.8	170.8
TZMI 102/CML373	17.2	2.8	1.7	1.1	8	90.3	88	82.7	175.5
TZMI 102/CML312	16.1	3.3	2.2	1	8.7	88.7	87.7	62.7	130.7
TZMI 102/CML384	15.4	3.3	1.9	1	5.7	91.7	90	80.7	161.2
TZMI 102/TZMI 711	14.1	1.7	1.7	1	3	91.3	90	79.8	155.2
TZMI 102/TZMI 712	10	2	1.7	1.2	1	96.3	94.7	100.3	212.8
TZMI 711 Self	8.4	2.2	1.7	1	2.3	98.7	97	107	217.5
TZMI 711/CML204	15.4	2	1.9	1.4	11.7	94.7	93.3	125	244.8
TZMI 711/CML373	14.9	1.5	1.7	1	5.3	94	92.3	115.5	227.3
TZMI 711/CML312	13.5	1.5	1.7	1	12	91.3	89.3	108.8	228.5
TZMI 711/CML384	20.1	1.7	2	1	3	93.3	92.3	112.7	218.7
TZMI 711/TZMI 102	16.9	1.5	1.7	1	15	94.7	93.3	102.3	211.5
TZMI 711/TZMI 712	11.3	1.5	1.7	1.4	7	95.7	93.7	110.5	217.8
TZMI 712 Self	3.7	2.5	1.7	1.3	11.3	99	96.7	114	228.5
TZMI 712/CML204	14.1	1.7	1.9	1	6.3	93.7	91.7	86.8	188.4
TZMI 712/CML373	14.2	1.5	1.9	1	6.7	92	91	125.5	224.2
TZMI 712/CML312	14.4	1.5	1.7	1	2.7	91.7	90.3	145.2	254.3
TZMI 712/CML384	18.6	2.3	1.7	1	15	92.7	91.7	106	207.7
TZMI 712/TZMI 102	12	2.2	1.9	1	12	93.3	92.3	125.7	239.7
TZMI 712/TZMI 711	11.7	1.5	1.7	1.9	5.3	95.3	94	114.2	212.3
CHECK	17.3	2.7	1.7	1.5	3.7	87	84	124.3	241.8
F Value	<.001	<.001	0.5	0.4	<.001	<.001	<.001	<.001	<.001
lsd	4	0.8	0.4	0.5	5.8	3.2	3.5	15.8	24.1
cv%	16.9	22.7	13.4	28	53.6	2.2	2.4	9	6.9

Where; F= significance level, C.V%= percentage of coefficient of variation. Lsd= least square difference and G mean= grand mean; GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering. DTFF= days to female flowering, PH= plant height, EH= ear height. MSV = maize streak virus. Blight= northern corn leaf blight.

CML 384 and TZMI 711, which had a high frequency of yield improvement alleles, produced the highest yielding hybrid TZMI 711 / CML 384 with high GLS resistance of 1.7. TZMI 711 / CML 384 had good husk cover and was highly prolific with two ears per plant, and showed resistance to ear rot, MSV, root and stem lodging. Other high yielding and GLS resistant hybrids from the parents CML 384, CML 373 and TZMI 711 were CML 384 / CML 373, CML 373 / CML 384, CML384 / TZMI 711, TZMI 711 / TZMI 102 and CML 384 / CML 312.

These high yielding and GLS resistant hybrids also had other good agronomic traits as opposed to the local check, H513 that had GLS score of 2.7. They could be improved further to develop open pollinated varieties and synthetics for use in GLS endemic areas.

4.1.3 KARI-Kakamega

This was a hot spot for GLS and other foliar diseases. High temperatures and drought at flowering (Appendix 1) coupled with diseases adversely lowered the maize yields in this site. This site had the lowest yields as opposed to other sites suggesting the presence of genotype by environment interaction for grey leaf resistance and grain yield performance. All the traits measured were significantly different ($P < 0.05$) among the entries except MSV and root lodging (Table 3).

The inbred line CML 373 with a GLS score of 1 had the highest yield of 2.8THa^{-1} while TZMI 102 with a GLS score of 3.75 had the lowest grain yield of 0.092THa^{-1} implying that this disease adversely reduced the grain yield. TZMI 711 was highly resistant to GLS with a score of 1.5.

Table 3. Mean values for grain yield and the other traits recorded in KARI-Kakamega, 2006

Cross	GY	GLS	blight	MSV	DE	DTFF	DTMF	EH	PH
CML204 Self	0.486	4	2.75	1	1	96	93	77.75	153.8
CML204/CML312	3.982	3.25	3	1	1.5	79.5	79	122	236.8
CML204/CML373	3.807	3	2.5	0	2	81.5	79.5	93.5	205.8
CML204/CML384	4.021	4.25	2.5	1.5	1.5	81.5	81.5	119	223.8
CML204/TZMI 102	2.069	3.5	2.75	1	4	86	87	106.25	205.5
CML204/TZMI 711	2.708	2	2.5	0.5	0	89	87	90.75	183
CML204/TZMI 712	3.482	3	2.5	0.5	4	81	80.5	95.25	203.8
CML373 Self	2.831	1	2.5	0	1.5	96.5	94.5	58	133.8
CML373/CML204	2.201	3	2.5	0	1	82	80.5	83	189.2
CML373/CML312	3.925	2.25	2.75	0.5	2	79	78	81.5	192.2
CML373/CML384	4.13	2.25	2.5	1	2.5	81.5	80.5	87	187.8
CML373/TZMI 102	2.763	3.25	2.75	1	8	84.5	81	93	195.8
CML373/TZMI 711	3.399	1.5	3	1	2	81.5	79.5	81.25	177.8
CML373/TZMI 712	1.986	1.5	2.75	0	1	89	85	70.5	156
CML312 Self	0.123	2.75	3.75	0	0	94.5	92.5	62.5	164
CML312/CML204	4.245	3.5	3.5	2	2.5	78.5	78.5	122	238.5
CML312/CML373	3.091	2.25	2.5	1.5	2.5	79	77.5	89	202.5
CML312/CML384	3.708	3.5	3	2	2	79	79	99.5	209.5
CML312/TZMI 102	3.73	3.5	2.75	0	2.5	79	77.5	98.75	202.8
CML312/TZMI 711	2.857	2.5	2.5	2	0	79	77.5	96.5	202.8
CML312/TZMI 712	3.099	2.25	2.75	0.5	0	81.5	82	86.5	188.5
CML 384 Self	1.006	2.75	2.75	5	11.5	97	96.5	71.25	131.2
CML384/CML204	2.803	4	2.5	0.5	1.5	87.5	86.5	103.75	202.8
CML384/CML373	3.558	1.75	2.5	1	1.5	88	86	90.5	193.2
CML384/CML312	3.317	3.5	3	2	2.5	79	81.5	103	208.8
CML384/TZMI 102	3.165	4	3	0	6	81	82	102.75	200.5
CML384/TZMI 711	4.771	2.25	2.5	1	4	80	79	92.25	187.8
CML384/TZMI 712	1.946	3	2.5	0.5	2.5	88	88.5	75.5	168
TZMI 102 Self	0.092	3.75	3	0.5	0.5	91	89.5	49.25	99.5

Cross	GY	GLS	blight	MSV	DE	DTFF	DTMF	EH	PH
TZMI 102/CML204	1.889	4	2.75	0	3	85.5	80.5	114.5	215.5
TZMI 102/CML373	3.379	3.5	2.25	1.5	1.5	80.5	78.5	89	189.5
TZMI 102/CML312	5.105	4	3	0	4	77	75.5	110.25	231
TZMI 102/CML384	3.406	4	2.5	0	3	79.5	80.5	111.5	221.8
TZMI 102/TZMI 711	1.869	2.5	2.5	0	3.5	86.5	81	79.75	168.8
TZMI 102/TZMI 712	1.419	3	2.75	1	5.5	82	82.5	75.42	148.2
TZMI 711 Self	0.176	1.5	2.25	0	2	96	94	35.94	72.2
TZMI 711/CML204	3.655	2.5	2.5	0	1	87	88	99.25	195.8
TZMI 711/CML373	2.148	1.75	2.75	1	2.5	87.5	80.5	63	152.5
TZMI 711/CML312	2.903	2	2.5	1	2	82	81	81	175.8
TZMI 711/CML384	4.362	1.75	2.5	0.5	3.5	89	87.5	92.75	185.5
TZMI 711/TZMI 102	1.93	2.75	2.75	1.5	6	84	80	102.75	159.8
TZMI 711/TZMI 712	2.407	1.5	2.75	1	5	91	90	63	142.5
TZMI 712 Self	0.34	3.5	2.5	0	2	97.5	95.5	42.75	108.8
TZMI 712/CML204	2.484	2.5	2.5	0	4	87	86	93	196.8
TZMI 712/CML373	2.312	1.5	2.5	0.5	3	88.5	90.5	73	165.8
TZMI 712/CML312	2.241	2.5	2.75	0.5	1.5	81	81	85.5	196.5
TZMI 712/CML384	3.38	3.25	2.5	1	6.5	80.5	81	87.25	188
TZMI 712/TZMI 102	1.22	2.5	2.75	0	3	88	88.5	59.5	150.2
TZMI 712/TZMI 711	2.118	1.5	2.5	0	1.5	84.5	81.5	69.5	142.8
CHECK	3.435	3.5	2.75	1.5	2	80	80	123.75	224.5
F	<.001	<.001	0.012	0.063	<.001	<.001	<.001	<.001	<.001
lsd	1.3524	0.7883	0.5649	2.01	3.874	8.372	7.626	17.809	30.33
C.V%	24.8	14.1	10.5	129.9	70.1	4.9	4.5	10.2	8.3

Where; F= significance level, C.V%= percentage of coefficient of variation, Lsd= least square difference; GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DTFF= days to female flowering, PH= plant height, EH= ear height, MSV = maize streak virus, Blight= Southern corn leaf blight

The highest yielding single cross hybrid TZMI 102 / CML 312 with 5.105THa^{-1} had severe GLS infection with a score of 4. TZMI 102 / CML 312 which took the least days, 75.5 and 77 days to 50 % tasseling and silking respectively escaped severe GLS attack during grain filling period. Its parents, TZMI 102 and CML 312 were also earlier than the other parents thus, TZMI 102 / CML 312 competed more effectively for plant resources out yielding the other entries. Early maturing genotypes exhibit increased susceptibility to GLS than late maturing materials (Verma, 2001). The early maturing plants also suffered less damage from lodging than late maturing ones. Among the high yielding single cross hybrids, TZMI 711 / CML 384 had the highest GLS resistance (GLS score of 1.75). CML 384 / TZMI 711, CML 373 / CML 384 and CML 373 / CML 312 with high grain yields had moderate GLS resistance of 2.25 each. TZMI 711 / CML 384 was also highly prolific with two ears per cob. TZMI 711 / CML 384, CML 384 / TZMI 711, CML 373 / CML 384 and CML 373 / CML 312 were resistant to MSV, blight and ear rot. In this study, the GLS resistant hybrids were also very late maturing (87.5 -96.5 days). This further supports the fact that late maturing genotypes show decreased susceptibility to GLS (Verma, 2001). The inbred line TZMI 711 produced crosses that showed delayed senescence and which were also resistant to GLS in this study. Verma (2001) highlighted a stay green trait that has been contemplated to boost GLS resistance. However, research into this finding is indispensable. In this site, when CML 373 was crossed with TZMI 711, the hybrids TZMI 711 / CML 373 and CML 373 / TZMI 711 were highly resistant to GLS with scores of 1.8 and 1.5 respectively. This implies that TZMI 711 and CML 373 could be used as both male and female in hybrid combinations in this site. CML 204 and TZMI 102 had very high GLS scores of 4 and 3.75 respectively while CML 204 / CML

384 was the most susceptible entry to GLS with a score of 4.25 suggesting that the genes for susceptibility may be in CML 204.

4.2 General means across sites

All the traits measured showed significant differences ($P < 0.05$) among the entries implying that the genotypes involved in these study could be used as testers (Table 4). The components of variance due to genotype by environment were significantly different ($P < 0.05$) for all traits measured. Earlier studies by Epinat-Le Signor *et al.*, (2001); Betran *et al.*, (2003) and Derera *et al.*, (2007) have reported significantly different genotype by environment interaction. These results obtained in this study show that the best entries performed differently across environments. It was also noted that GXE interaction was small in comparison to the genotype effect.

Across the sites, CML 384 was the highest yielding parent with 2.971THa^{-1} followed by CML 373 with 2.539THa^{-1} while CML 312 and CML 204 had the lowest grain yields of 1.6 and 1.7 respectively. This implies that CML 384 and CML 373 had many stable yield favouring alleles as opposed to the other inbred lines. The inbred line CML 373 (GLS score of 1) was immune to GLS while TZMI 711 was highly resistant to GLS with score of 1.5. Thus, CML 373 could be an excellent source of grain yield and GLS resistance genes. CML 384 could be an excellent source of grain yield genes.

Table 4 ANOVA for grain yield and other traits recorded across 3 sites, 2006

Source	DF	GY	GLS	DTMF	DTFF	PH	EH	MSV	Blight	DE
ENV	2	3275.92**	77.42**	6200.27**	5408.49**	30161.83**	14010.57**	41.1**	69.46**	829.86**
REP (ENV)	3	40.38**	1.01**	29.99**	29.33*	454.75**	227.69**	0.35	0.04	5.49
Entry	96	43.66**	2.05**	71.79**	79.94**	4961.91**	1782.64**	0.78**	0.07*	15.65**
ENV*Entry	48	10.93**	0.59**	11.71**	10.95*	303.97**	130.21**	0.75**	0.07*	14.52**
G.M		8.16	2.08	83.29	85.10	195.57	97.27	0.86	1.99	3.13
CV		18.42	16.46	3.17	3.33	5.48	7.39	73.67	10.90	72.03

Where; GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DTFF= days to female flowering, PH= plant height, EH= ear height, MSV = maize streak virus, Blight= northern corn leaf blight, RL= root lodge, SL= stem lodge, DE= diseased ears, C.V%= percentage of coefficient of variation and G.M= grand mean

Table 5. Grain Yield and Associated Traits across sites

Cross	GY	GLS	Blight	MSV	DE	DTMF	DTFF	PH	EH
CML312/CML204	11.33	2.48	2.79	1.00	5.00	79.67	81.00	235.92	125.28
CML384/CML373	11.31	1.50	2.39	1.00	4.00	83.67	85.50	200.56	98.50
CML204/CML312	10.93	2.25	2.46	1.00	2.00	80.33	81.17	238.47	125.86
TZMI 102/CML373	10.73	2.57	2.27	1.00	6.00	80.33	82.83	209.31	102.36
CML373/CML384	10.65	1.58	2.34	1.00	4.00	82.50	84.00	203.70	99.67
TZMI 711/CML384	10.57	1.54	2.39	1.00	3.00	84.17	86.00	191.67	100.03
CML204/CML384	10.17	2.75	2.41	1.00	2.00	81.83	83.50	231.72	128.47
CML373/CML204	10.08	2.33	2.39	0.00	2.00	80.50	83.33	220.14	116.03
CML312/TZMI 102	10.06	2.45	2.38	0.00	2.00	78.17	80.00	214.89	104.72
CML384/TZMI 711	10.06	1.80	2.40	1.00	3.00	81.17	83.00	196.00	99.07
TZMI 712/CML384	9.93	2.25	2.18	1.00	3.00	82.83	83.67	197.47	93.53
CML384/CML204	9.68	3.00	2.49	0.00	4.00	85.00	86.33	214.64	112.97
TZMI 102/CML312	9.65	2.75	2.76	0.00	2.00	77.67	79.17	228.75	111.17
CML373/TZMI 102	9.65	2.45	2.46	2.00	7.00	81.17	84.00	198.11	103.00
CML204/CML373	9.62	2.17	2.33	1.00	6.00	82.17	84.00	216.25	108.33
CML384/TZMI 712	9.60	2.29	2.28	2.00	3.00	84.67	85.17	187.03	90.53
CML373/CML312	9.59	1.58	2.38	1.00	2.00	79.17	81.17	202.89	93.28
CML312/CML384	9.51	2.42	2.50	2.00	1.00	80.83	81.50	210.86	101.81
CML312/TZMI 711	9.49	1.67	2.31	1.00	0.00	79.50	82.17	203.03	97.33
CML384/CML312	9.39	2.17	2.44	1.00	2.00	81.33	80.67	213.14	106.81
CML384/TZMI 102	9.36	3.08	2.46	1.00	5.00	81.17	82.00	210.83	109.53
TZMI 711/CML312	9.33	1.54	2.35	0.00	3.00	79.83	82.00	199.20	97.61
TZMI 102/CML384	9.30	3.03	2.28	1.00	3.00	81.50	82.17	222.03	114.31
CML312/CML373	9.17	1.58	2.39	1.00	1.00	78.67	81.33	159.00	93.97
TZMI 711/CML204	9.06	1.92	2.39	0.00	2.00	85.50	86.33	204.75	110.81
CML204/TZMI 712	8.75	1.95	2.45	1.00	5.00	81.50	83.67	214.39	103.78
TZMI 102/CML204	8.67	2.99	2.43	1.00	3.00	81.17	84.50	229.78	122.36
CML204/TZMI 711	8.56	1.83	2.34	1.00	3.00	84.00	86.33	207.14	112.31
CML312/TZMI 712	8.55	1.67	2.44	0.00	1.00	80.50	82.17	200.06	93.64

Cross	GY	GLS	Blight	MSV	DE	DTMF	DTFF	PH	EH
CML373/TZMI 711	8.54	1.33	2.49	1.00	3.00	81.83	84.33	194.39	98.67
TZMI 711/CML373	8.31	1.45	2.41	1.00	2.00	83.00	86.83	186.69	90.33
CML373/TZMI 712	8.19	1.37	2.50	1.00	5.00	84.00	86.83	186.42	90.86
CML204/TZMI 102	8.17	2.95	2.33	1.00	6.00	83.33	84.33	230.33	120.44
TZMI 712/CML312	8.16	1.67	2.28	0.00	2.00	82.00	83.00	207.58	98.33
TZMI 102/TZMI 711	8.12	1.78	2.28	1.00	3.00	82.00	85.17	193.22	98.92
TZMI 711/TZMI 102	7.96	1.84	2.35	1.00	5.00	83.33	85.50	191.22	102.83
TZMI 712/CML373	7.93	1.33	2.33	1.00	7.00	86.33	86.67	189.56	87.56
TZMI 712/CML204	7.72	1.75	2.38	1.00	4.00	84.83	86.33	212.67	78.92
TZMI 712/TZMI 102	6.99	1.92	2.38	1.00	3.00	86.17	86.67	179.33	78.25
TZMI 102/TZMI 712	6.95	2.24	2.29	2.00	6.00	83.50	84.50	176.67	83.31
TZMI 712/TZMI 711	6.61	1.33	2.38	0.00	2.00	85.17	87.50	159.00	104.39
TZMI 711/TZMI 712	6.25	1.33	2.38	1.00	4.00	87.17	88.50	152.17	73.75
CML 384 Self	2.97	2.37	2.19	2.00	5.00	92.50	93.33	147.17	77.64
CML373 Self	2.54	1.00	2.33	0.00	4.00	90.00	93.33	163.41	72.56
TZMI 102 Self	2.20	3.31	2.33	2.00	2.00	86.67	88.67	148.50	73.39
TZMI 711 Self	1.87	1.36	2.14	0.00	1.00	90.50	93.00	97.75	49.54
TZMI 712 Self	1.76	2.50	2.24	1.00	3.00	91.00	93.83	119.36	52.97
CML204 Self	1.65	3.20	2.39	1.00	2.00	89.33	91.83	162.00	86.17
CML312 Self	1.56	2.25	2.75	0.00	3.00	88.00	90.17	176.08	70.42
F value	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001
lsd	3.09	0.73	0.55	2.00	4.00	5.40	5.74	21.14	14.60
C.V%	19.30	16.46	11.60	123.00	71.60	3.17	3.33	5.48	7.40

F= significance level, C.V%= percentage of coefficient of variation, Lsd= least square difference: GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DTFF= days to female flowering, PH= plant height, EH= ear height, MSV = maize streak virus, Blight= corn leaf blight, DE= diseased ears

The highest yielding hybrid across sites was CML 312 / CML 204 with 11.33T_{Ha}⁻¹ and a GLS score of 2.5 (Table 5). This hybrid showed resistance to MSV. This hybrid had early flowering and longer grain filling period making it escape severe GLS attack and this could have led to its high yields across sites. Thus, CML 312 / CML 204 could be improved further for release to farmers in GLS non-endemic areas. It could also be used to develop hybrids, open pollinated varieties and synthetics for use in areas of varied climatic conditions. Other hybrids that showed superior yield performance and GLS resistance were CML 384 /CML 373, CML 373 / CML 384, TZMI 711/ CML 384 and CML 384/ TZMI 711 (Table 5). In this study, CML 384 was a common parent in all these good crosses and this supports the fact that CML 384 has a high frequency of yield improving alleles. CML 384 /CML 373, CML 373 / CML 384, TZMI 711/ CML 384 and CML 384/ TZMI 711 also had either CML 373 and / or TZMI 711 as one of the parent suggesting that these two inbred lines are good sources of GLS resistance genes. In addition, TZMI 711 produced crosses with GLS scores ranging from 1.3-1.9 even with the susceptible parents (CML 204 and TZMI 102) as opposed to CML 373 whose crosses had GLS scores ranging from 1.5-2.6. Thus, TZMI 711 could be contemplated to have stable genes for GLS resistance. TZMI 711 could also be used as both male and female in hybrid combinations during further breeding work. CML 384 /CML 373, CML 373/ CML 384, TZMI 711/ CML 384 and CML 384/ TZMI 711, which had superior yield performance, were among the late maturing entries since they took more than 80 days to flower. This supports the statement by Verma (2001) that late maturing maize lines are usually more resistant to GLS than early maturing lines. They also had resistance to ear rot an important trait for commercial seed production.

4.3 COMBINING ABILITIES

4.3.1 Combining abilities at specific sites at KARI-Kiboko

In this site, all traits showed significant differences for GCA and SCA except ear rot implying the presence of both additive and non-additive gene actions (Table 6). The relative significance of GCA to SCA variances indicated that the GCA of the inbred lines contributed much of the genetic variability noted among the single cross hybrids except for the grain yield trait. Thus, the response of hybrids to the various agronomic traits could be predicted based on the GCA of the parents (Verma, 2001). CML 373 had the highest positive GCA for grain yield followed by CML 312 (Table 7). In further breeding work, recurrent selection could be done in early generations to get superior genotypes due to the significance of the additive gene action. In this study, none of the parents showed good GCA for all the traits implying that these inbred lines were genetically diverse. The SCA showed preponderance in conditioning the inheritance of the grain yield trait and this implied that cross combinations would be efficient in breeding the materials for improved yields. This also showed that the GCA alone could not give a complete prediction of hybrids' yield performance. There were some promising single cross hybrids with desirable SCA for grain yield in KARI Kiboko.

CML 373 / TZMI 102 had the highest positive SCA for grain yield of 2.45 and it involved the best combiner for yield, CML 373 and a good combiner for maturity, TZMI 102. This hybrid CML 373 / TZMI 102 also had good combining ability for ear rot resistance (Table 8). The second good combiner for grain yield was CML 312 / TZMI 711 with good combining ability for maturity. In this site, the good combiners for grain yield also had good combining ability for maturity.

Table 6. Combining Ability Analyses for grain yield and other Traits recorded in Kiboko, 2006

Source	GY	GLS	DTMF	DTFE	PH	EH	MSV	blight	DE	
GCA	6	14.86**	0.17**	38.84**	46.06**	4682.42**	2147.64**	11.73**	0.22n	0.54ns
SCA	21	27.04**	0.04**	22.34**	27.97**	1549.51**	528.53**	3.06ns	0.09ns	0.67ns
MAT	5	0.57ns	0.03*	5.27*	4.05ns	115.85ns	40.596ns	3.99ns	0.07ns	0.25ns
Error	48	0.69	0.01	1.73	2.64	61.36	38.398	2.11	0.1	0.51
C.V		11.18	8.95	1.75	2.09	4.098	6.49	90.13	8.63	170.95
Mean		7.425	1.08	75.11	77.69	191.14	95.44	1.61	3.73	0.42

Significance levels, **=P<0.01 and *=P<0.05; GCA= general combining ability, SCA= specific combining ability, GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DTFE= days to female flowering, PH= plant height, EH= ear height. MSV = maize streak virus, Blight= Southern corn leaf blight, DE= diseased ears

Table 7. GCA Estimates for grain yield and other Traits recorded in Kiboko, 2006

Parent	GY	GLS	DTMF	DTFE	PH	EH	MSV	blight	DE
CML 204	0.108	-0.021	0.39	0.41	15.88**	15.33**	-0.14	0.11	0.01
CML 373	1.213**	-0.04*	0.46	1.16**	4.99**	0.98	-0.39	0.07	-0.2
CML 312	0.418**	-0.05**	-1.97**	-2.16**	9.39**	1.28	-0.75**	0.06	-0.03
CML 384	0.089	-0.03	0.57*	0.06	-0.66	1.64	0.13	-0.06	0.22
TZMI 102	-0.13	0.17**	-0.97**	-1.19**	4.94**	1.16	1.21**	-0.08	-0.09
TZMI 711	-1.025**	-0.008	-0.15	0.23	-20.13**	-7.94**	-0.39	0.03	-0.03
TZMI 712	-0.67**	-0.022	1.67**	1.48**	-14.41**	-12.46**	0.35	-0.12*	0.117

Significance levels, **=P<0.01 and *=P<0.05; GCA= general combining ability, SCA= specific combining ability, GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DTFE= days to female flowering, PH= plant height, EH= ear height. MSV = maize streak virus, Blight= Southern corn leaf blight, DE= diseased ears

Table 8. SCA estimates for agronomic traits in KARI-Kiboko

Cross	GY	DTMF	DFFF	GLS	PH	EH	MSV	DE
CML204/CML373	0.55	-0.45	-1.27	-0.01	2.56	2.41	-0.19	-0.22
CML204/CML312	1.52**	-1.28*	-1.94**	0.08	9.41**	13.77**	0.07	-0.15
CML204/CML384	1.37**	0.93	0.83	-0.02	-0.94	-0.75	-0.19	0.35
CML204/TZMI 102	0.79*	-1.53*	-0.66	-0.06	18.45**	7.64**	-0.18	-0.08
CML204/TZMI 711	0.81*	-1.10	-1.09	-0.04	12.69**	6.33*	0.01	0.10
CML373/CML312	1.27**	-1.10	-1.19	0.01	-6.37	-5.21	0.28	-0.19
CML373/CML384	1.81**	-1.38*	-1.66*	0.00	2.02	-0.57	-0.01	0.31
CML373/TZMI 102	2.45**	-0.60	-0.66	-0.05	-14.33**	0.32	0.18	-0.12
CML373/TZMI 711	0.12	-0.67	-1.09	0.02	17.73**	11.51**	-0.01	0.06
CML312/CML384	-0.45	0.29	-0.34	0.00	1.38	3.30	0.39	-0.62
CML312/TZMI 102	0.58	-1.42*	-1.59*	-0.14**	0.36	0.44	-0.50**	-0.05
CML312/TZMI 711	2.23**	-1.74**	-1.27	0.03	7.92*	4.13	-0.29	0.38
CML384/TZMI 102	1.15**	-0.95	-0.80	-0.17**	9.99**	4.25	-0.07	-0.30
CML384/TZMI 711	0.56	-2.53**	-1.73*	0.09*	10.90**	4.61	0.14	0.38
TZMI 102/TZMI 711	0.58	0.75	0.26	-0.06	13.21**	6.33*	-0.02	-0.30
CML204/TZMI 712	1.07**	-2.17**	-1.84*	0.01	18.22**	9.19**	0.40*	-0.55
CML373/TZMI 712	0.61	-0.24	-1.09	0.04	12.85**	7.28**	0.02	0.17
CML312/TZMI 712	1.29**	-2.06**	-1.77*	-0.01	12.21**	6.57*	-0.30	-0.01
CML384/TZMI 712	1.45**	-1.10	-1.48*	0.03	11.44**	6.21*	-0.04	0.73*
TZMI 102/TZMI 712	-0.01	0.43	-0.23	0.01	5.83	-0.39	-0.29	0.56
TZMI 711/TZMI 712	-4.10**	3.04**	4.83**	-0.03	-43.97**	-18.84**	0.04	-0.65

Significance levels, **=P<0.01 and *=P<0.05; GCA= general combining ability, SCA= specific combining ability, GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DFFF= days to female flowering, PH= plant height, EH= ear height, MSV = maize streak virus, Blight= northern corn leaf blight, RL= root lodge, SL= stem lodge, DE= diseased ears

This implies that during future breeding work, the good combiners for various traits could produce transgressive segregants that could lead to new populations if the additive gene action in the good combiner and the non-additive gene action in the hybrid complement each other to maximize the good traits. To exploit both the additive and non additive gene actions revealed in this study among the breeding materials involved, reciprocal recurrent selections could be used in further breeding work

4.3.2 Kabete Field Station

All traits measured had significantly different SCA and GCA among the entries (Table 9). With regard to GCA: SCA ratio, GCA had greatest effects on GLS, bare tips, root lodging, ear rot, days to maturity, plant and ear height. In this site, SCA showed preponderance with regard to grain yield as opposed to the site KARI Kiboko. This suggests the presence of quantifiable genotype by environment interaction for grain yield. Work done by Verma (2001) and Menkir and Ayodele (2005) reported significant GCA in the inheritance of GLS. In this site, the inbred CML 384 had the highest positive GCA for grain yield followed by CML 312 while TZMI 712 and TZMI 102 had the lowest GCA for grain yield (Table 10). On disease resistance, TZMI 711 and CML 373 had the highest negative GCA for GLS whereas CML 204 and TZMI 102 had the highest positive GCA for GLS. The parents TZMI 711, CML 312 and CML 373 had the most number of trait enhancing alleles. All these parents were good combiners for GLS, ear rot and ear height. There was no single parent with high GCA for all the traits measured and this further reveals that these inbred lines are genetically diverse.

TABLE 9. Combining ability Analyses for grain yield and other Traits recorded in Kabete Field Station, 2006

Source	GLS	GY	RL	SL	DE	msv	blight	DTMF	DFFF	PH	EH	
GCA	6	11.24**	36.22**	15.47**	0.71*	125.14**	0.31	0.02	65.37**	65.87**	5445.2**	2822.9**
SCA	21	1.25**	97.88**	10.33**	0.74**	41.43**	0.28*	0.07	33.71**	28.71**	3511.7**	1372.7**
REC	21	0.26	2.10	0.47	0.07	25.27*	0.14	0.05	8.24*	5.35	178.8	167.6*
MAT	5	0.07	2.59	0.05	0.01	6.71	0.08	0.01	10.33	5.15	238.8	254.3*
Error	48	0.26	4.29	1.69	0.30	12.76	0.13	0.073	4.57	3.89	222.4	100.0
C.V		22.71	14.53	239.17	354.27	53.11	277.19	15.40	2.35	2.13	6.96	8.46
Mean		2.28	14.25	0.54	0.15	6.72	0.13	1.76	90.66	92.23	214.22	118.13

Significance levels, **=P<0.01 and *=P<0.05; GCA= general combining ability, SCA= specific combining ability, .GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DFFF= days to female flowering, PH= plant height, EH= ear height. MSV = maize streak virus, Blight= northern corn leaf blight, RL= root lodge, SL= stem lodge, DE= diseased ears

Table 10.GCA Estimates for grain yield and other Traits recorded in Kabete Field Station, 2006

Parent	GLS	GY	RL	SL	DE	MSV	blight	DTMF	DFFF	PH	EH
CML 204	0.64**	0.41	0.24	0.10	1.84**	-0.09	0.008	-0.80**	-0.66*	16.42**	14.14**
CML 373	-0.47**	-0.25	-0.49**	-0.10	1.84**	0.08	-0.01	-0.59	-0.309	0.30	-0.63
CML 312	-0.12	0.40	-0.32	-0.13	-2.32**	-0.02	0.02	-1.78**	-1.83**	7.13**	-0.72
CML 384	0.24**	1.96**	0.31	0.057	-1.87**	0.18**	-0.01	0.42	-0.11	-0.17	1.44
TZMI 102	0.65**	-0.62	1.14**	0.20*	0.77	-0.06	-0.01	-0.33	-0.33	3.82	2.07
TZMI 711	-0.54**	-0.01	-0.40*	-0.13	-1.01*	0.01	-0.05	1.714**	1.80**	-8.12**	-2.52
TZMI 712	-0.40**	-1.88**	-0.47*	0.01	0.74	-0.09	0.04	1.38**	1.45**	-19.40**	-13.8**

Significance levels, **=P<0.01 and *=P<0.05. GCA= general combining ability, SCA= specific combining ability, GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DFFF= days to female flowering, PH= plant height, EH= ear height. MSV = maize streak virus, Blight= northern corn leaf blight, RL= root lodge, SL= stem lodge, DE= diseased ears

Table 11. SCA estimates for agronomic traits in Kubete Field Station

Cross	GLS	GY	DE	DTMF	DFFF	PH	EH	MSV	blight
CML204/CML373	0.13	3.08**	-1.08	-0.76	-0.43	10.04	8.68*	-0.11	-0.05
CML204/CML312	-0.22	5.11**	2.58*	0.76	0.26	9.54	6.47	-0.11	-0.01
CML204/CML384	0.00	0.67	0.63	-2.45**	-1.45*	16.52**	11.84**	0.24	0.14**
CML204/TZMI102	0.25	0.72	1.66	0.14	-0.07	12.85*	7.60*	-0.09	-0.05
CML204/TZMI711	-0.22	1.43	0.61	0.43	0.12	7.72	7.39*	-0.04	0.01
CML373/CML312	-0.18	0.00	-4.24**	-1.62*	-1.10	-4.42	-3.84	-0.02	0.02
CML373/CML384	-0.38*	3.03**	0.47	0.50	0.19	4.30	2.98	0.51**	-0.01
CML373/TZMI102	0.44*	3.27**	1.49	-1.07	-0.93	12.81*	7.57*	0.01	-0.03
CML373/TZMI711	0.23	1.00	-2.22	-0.29	-0.07	6.84	4.26	-0.11	-0.02
CML312/CML384	-0.15	0.68	0.97	-0.64	-1.12	2.22	0.47**	-0.16	-0.07
CML312/TZMI102	0.02	2.54**	-2.34	-1.71*	-1.74*	16.39**	12.78	0.51**	0.13*
CML312/TZMI711	-0.11	2.30*	0.28	-1.26	-0.71	7.67	4.06	-0.11	-0.03
CML384/TZMI102	0.15	0.08	0.70	-2.43**	-1.79*	11.19*	7.50*	-0.14	-0.01
CML384/TZMI711	-0.23	3.66**	0.32	-1.48	-1.43*	9.56	5.66	0.08	0.11*
TZMI102/TZMI711	-0.81**	1.95*	1.85	-0.38	-0.71	8.65	3.02	-0.09	-0.02
CML204/TZMI 712	-0.86	1.02	2.35	-0.40	-0.19	17.25**	3.55	0.15	0.04
CML373/TZMI 712	0.09	1.59	5.68**	-1.29	-1.71*	14.45**	10.02**	-0.09	0.12*
CML312/TZMI 712	-0.17	1.56	-2.49	-1.43	-1.36	18.45**	14.43**	0.08	0.00
CML384/TZMI 712	0.21	3.77**	-3.10*	-1.98*	-2.07**	14.93**	5.89	-0.06	-0.08
TZMI 02/TZMI712	-0.45*	-0.22	-1.08	1.78*	1.48*	-16.69**	-12.86**	-0.06	0.01
TZMI711/TZMI712	1.02**	-7.46**	0.44	3.24**	3.86**	-44.8**	-21.75**	0.01	-0.06

Significance levels, **=P<0.01 and *=P<0.05; GCA= general combining ability, SCA= specific combining ability. GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DFFF= days to female flowering. PH= plant height, EH= ear height. MSV = maize streak virus, Blight= northern corn leaf blight, DE= diseased ears

CML 204 /CML 312 had the highest positive SCA for grain yield of 5.1 (Table 11). On the other hand, CML373/ CML384 and CML 384 / TZMI 711 had the highest combining ability for both GLS resistance and grain yield performance. CML373 /CML384 and CML 384 / TZMI 711 involved a good combiner for GLS (TZMI 711 or CML 373) and the good combiner for yield, CML 384. The involvement of two good combiners to produce a hybrid with good SCA contradicts Dua and Yadava's (1983) findings that additive-by-additive interaction rarely occurs. CML 373 / CML 384, which showed early maturity, had good husk cover and was resistant to root lodge and bird damage (data not shown). CML 384 / TZMI 711 showed resistance to stem lodging and root lodging. Thus, CML 373 / CML 384 and CML 384 / TZMI 711 were the promising hybrids in this site. It was also noted that CML 384 and 204 (best grain yielders) produced crosses with positive SCA for yield even when crossed with the poorest yield combiner (TZMI 712). CML 204 / TZMI 712, TZMI 102 / TZMI 711 and TZMI 102 / TZMI 712 had the highest SCA for GLS. These were crosses between poor combiners for GLS, CML 204 (0.65) and TZMI 102 (0.66) and good combiners for GLS, TZMI 712 (-0.4) and TZMI 711 (-0.54). Thus, if the additive gene action in CML 384 and 204 for grain yield; TZMI 711 and TZMI 712 for GLS and the non additive gene action in the good crosses complement each other to favour GLS resistance and improved yields, it is possible to develop populations with transgressive segregation with regard to yield performance and GLS resistance. However, CML 373 / TZMI 711 that involved good combiners for GLS had a low SCA for GLS. Thus, efficient breeding methods should first accumulate favourable genes in homozygous state while breaking the linkage blocks (Solanki and Gupta, 2001) to help reduce grain yield losses associated with GLS.

4.3.3 KARI-Kakamega

Kakamega site is a hot spot for diseases and has environmental conditions that favour grey leaf spot disease development under field conditions (Ininda *et al.*, 2007). There was severe GLS infection in this site and this was shown by the high combining ability values for grey leaf spot. All the traits studied had significantly different GCA and SCA effects among the entries except root lodging (Table 12). Based on GCA: SCA ratios, GCA played a significant role in all traits except days to maturity and root lodging. In this site, GCA predominantly influenced the grain yield performance as opposed to Kiboko and Kabete environments suggesting that genotype by environment interaction for grain was present. Menkir and Ayodele (2005) reported that GCA was more important in conditioning the GLS resistance but the SCA was more important than GCA with reference to grain yield. The parents CML 384, CML 373 and CML 312 had positive GCA for grain yield (Table 13) while the parents TZMI 711, CML 312, TZMI 712 had desirable negative GCA for GLS. Only CML 312 combined high grain yield (GCA of 0.3) with high GLS resistance (GCA of -0.6) as opposed to the other parents. CML 204 / TZMI 712, CML 384 / TZMI 711, CML 204 / TZMI 711 and CML 373 / TZMI 712 were the promising hybrids with positive SCA for grain yield (Table 14) and good SCA for GLS. These good hybrids involved one good combiner for grain yield (CML 384, CML 373, CML 312 and CML 204) and a good combiner for GLS (TZMI 711, CML 312 and TZMI 712). In this site, CML 373 had undesirable GCA for GLS as opposed to the other sites suggesting the presence of genotype by environment interaction for GLS resistance. Thus, the GLS resistance in CML 373 is unstable and it could only be used in GLS resistant backgrounds.

Table 12. Combining ability analyses for grain yield and other traits recorded in KARI-Kakamega, 2006

Source	GY	GLS	DTMF	DFFF	PH	EH	MSV	blight	RL	SL	DE
GCA	6 4.94**	8.93**	84.46**	90.97**	8087.56**	2765.36**	3.79**	0.54**	1.00ns	185.69**	24.42**
SCA	21 4.80**	0.59**	91.90**	100.61**	2961.05**	855.67**	1.98*	0.14*	1.52ns	44.01**	9.24**
GCA: SCA	1.02	14.9	0.91	0.90	2.73	3.231	1.91	3.72	0.65	4.218	2.643
MAT	5 0.27ns	0.02ns	16.58ns	15.68ns	120.71ns	10.03ns	0.61ns	0.06ns	1.47ns	7.81ns	4.61ns
Error	48 0.46	0.15	14.58	17.6	230.25	79.70	0.91	0.07	1.12	12.45	3.79
C.V	25.21	14.29	4.56	4.93	8.39	10.34	126.76	10.41	247.44	113.41	70.40
Mean	2.69	2.7	83.75	85	180.66	86.33	0.75	2.68	0.42	3.112	2.76

Significance levels, **=P<0.01 and *=P<0.05, ns= non significant; GCA= general combining ability, SCA= specific combining ability, GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DFFF= days to female flowering, PH= plant height, EH= ear height, MSV = maize streak virus, Blight= northern corn leaf blight, RL= root lodge, SL= stem lodge, DE= diseased ears

Table 13. GCA estimates for grain yield and other traits recorded in KARI-Kakamega, 2006

Parent	GY	GLS	DTMF	DFFF	PH	EH	MSV	blight	RL	SL	DE
CML 204	0.04ns	0.55**	0.56ns	0.57ns	19.65**	13.50**	-0.11ns	-0.005ns	0.07ns	1.38*	-0.76*
CML 373	0.33**	0.12ns	-2.82**	-3.39**	20.30**	6.55**	0.17ns	0.28**	-0.21ns	-1.50*	-1.12**
CML 312	0.33**	-0.58**	-0.46ns	0.39ns	-3.83ns	-7.03**	-0.11ns	-0.09ns	-0.14ns	-2.64**	-0.44ns
CML 384	0.49**	0.30**	0.99ns	-0.10ns	7.88**	7.04**	0.74**	-0.04ns	-0.07ns	-0.75ns	1.52**
TZMI 102	-0.40**	0.66**	-1.36*	-1.03ns	-2.93ns	2.37ns	-0.25ns	0.06ns	0.35ns	5.10**	0.87*
TZMI 711	-0.16ns	-0.80**	0.56ns	1.64*	-22.16**	-8.93**	-0.07ns	-0.13*	-0.07ns	-0.18ns	-0.26ns
TZMI 712	-0.63**	-0.26**	2.53**	1.92*	-18.91**	-13.51**	-0.36ns	-0.07ns	0.07ns	-1.39*	0.19ns

Significance levels, **=P<0.01 and *=P<0.05, ns= non significant; GCA= general combining ability, SCA= specific combining ability, GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DFFF= days to female flowering, PH= plant height, EH= ear height, MSV = maize streak virus, Blight= northern corn leaf blight, RL= root lodge, SL= stem lodge, DE= diseased ears

Table 1.4. SCA estimates for agronomic traits in KARI-Kukamega

Cross	GY	GLS	DTMF	DFFF	PH	EH	MSV	blight	RL	SL	DE
CML204/CML373	1.04**	-0.07	-2.75	-3.18	17.00*	15.60**	0.68	0.29*	-0.04	-1.00	1.12
CML204/CML312	-0.06	0.27	-3.85*	-4.21*	1.01	-4.56	-0.53	-0.08	-0.36	-1.60	-0.06
CML204/CML384	0.19	0.49**	-1.32	-0.96	5.04	4.50	-0.39	-0.14	0.07	-3.00	-2.02
CML204/TZMI 102	-0.36	-0.24	0.79	1.21	13.11	8.161*	0.11	0.01	-0.86	7.65**	0.62
CML204/TZMI 711	0.61*	-0.27	2.61	0.79	11.22	4.09	-0.32	-0.05	-0.18	-1.32	-1.24
CML373/CML312	0.15	-0.06	-2.71	-3.00	0.25	-0.61	0.18	-0.25*	0.18	1.04	1.05
CML373/CML384	-0.01	0.30	-1.67	-2.50	0.27	1.32	0.33	0.08	0.11	0.90	-0.91
CML373/TZMI 102	1.79**	0.19	-3.07	-2.57	18.84**	9.23*	-0.67	-0.16	-0.57	-0.71	0.73
CML373/TZMI 711	0.01	0.16	-2.25	-2.75	10.45	4.79	0.65	-0.33**	-0.14	-1.17	-0.38
CML312/CML384	0.33	-0.49**	-1.03	-0.54	5.78	2.41	-0.39	-0.05	0.04	0.54	-1.84*
CML312/TZMI 102	0.45	0.53**	-2.17	-1.86	18.73**	9.32*	0.86*	-0.16	-0.14	-4.07*	1.55
CML312/TZMI 711	-0.09	0.25	-3.85*	-2.54	10.46	1.75	0.43	0.42**	-0.21	-0.28	0.19
CML384/TZMI 102	0.50	0.27	-2.14	-3.61	25.50**	11.38**	-1.25**	0.04	-0.21	5.79**	-0.66
CML384/TZMI 711	1.54**	-0.27	-2.07	-2.04	20.24**	8.06*	-0.67	-0.01	-0.29	-1.67	-0.27
TZMI 102/TZMI711	-0.24	0.00	-2.46	-0.36	8.68	11.47**	0.33	0.01	1.04	4.47**	1.37
CML204/TZMI 712	0.89**	-0.31	-3.60*	-3.50	18.84**	7.80	-0.03	-0.10	-0.57	-1.35	1.80*
CML373/TZMI 712	0.28	-0.25	-1.96	-2.29	10.45	6.63	-0.07	-0.14	-0.04	1.04	-1.09
CML312/TZMI 712	-0.24	-0.41*	1.93	1.43	2.96	5.96	-0.03	0.11	-0.36	2.18	-0.52
CML384/TZMI 712	0.12	0.32	-2.53	-2.57	8.36	1.52	-0.39	-0.07	-0.43	-0.96	0.02
TZMI 102/TZMI712	-0.34	-0.41*	0.58	-0.89	-9.57	-7.73	0.36	0.08	1.39**	-4.32**	0.41
TZMI 711/TZMI712	-1.08*	1.27**	6.69**	8.6**	-34.09**	-16.55**	-0.03	-0.03	-0.07	0.68	-1.16

Significance levels. **=P<0.01 and *=P<0.05; GCA= general combining ability, SCA= specific combining ability; GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DFFF= days to female flowering, PH= plant height, EH= ear height, MSV = maize streak virus, Blight= northern corn leaf blight, RL= root lodge, SL= stem lodge, DE= diseased ears

4.4 Combining ability analysis across sites

There were significant differences for GCA for all the traits studied across the sites (Table 15). All the traits showed significant SCA effects for all traits except leaf blight. These results validate the findings from the specific locations. The significant GCA indicates the evidence of additive gene action and thus these materials could be improved through recurrent selection. Manh (1977), Thompson *et al.* (1987) and Huff *et al.* (1988) reported that additive gene action was important in the inheritance of GLS resistance.

The GCA: SCA ratio (Table 16) indicated the importance of additive gene action in the inheritance of all the agronomic characters except grain yield. Results from Kabete field station and KARI Kiboko showed that SCA was important with respect to grain yield. The GCA by environment interaction was significantly different for GLS, grain yield, days to maturity, root lodging and ear rot. Significant GCA x environment effects suggests that different parental lines for hybrids could be selected at specific environment. It also implies that the GCA effects of the parents were influenced by the environmental variability. CML 384 and CML 373 had the highest positive GCA effects for grain yield while TZMI 711 and CML 373 had the highest negative GCA values for GLS across sites (Table 17). CML 373 and CML 312 were also found to be good combiners for yield (positive GCA) and GLS resistance (negative GCA on 1-5 scale where, 1=immune, 5=susceptible). Across the sites, no parent had high GCA for all the characters measured thus the parents involved were genetically diverse. Considering the GCA X E: SCA by E, the GCA contributed much of the environmental variation noted among the traits except for plant height, ear height, stem and root lodging.

Table 15. Combining ability Analyses for grain yield and other traits recorded across 3 sites, 2006

Source	DF	GY	GLS	DTMF	DTFF	PH	EH	MSV	Blight	RL	SL	DE
GCA	6	34.6**	13.4**	147.9**	162.27**	15611.9**	6341.96**	1.68**	0.25**	7.9**	67.9**	42.4**
SCA	21	89.1**	0.78**	112.04**	125.39**	6720.8**	2180.09**	0.97**	0.05	39.92**	14.2**	13.98**
GCA: SCA		0.388	17.2	1.320	1.294	2.3	2.9	1.7	4.19	5.05	4.8	3.04
GCA*E	6	17.84**	4.4**	16.97*	14.82	190.97	76.05	0.65	0.05	14.8**	0.56	56.8**
SCA*E	21	13.81**	0.52**	4.32	3.8	349.4**	153.15**	0.44	0.03	24.15**	0.9083	15.99**
MAT	5	0.3188	0.1061	15.15	7.95	200.67	75.77	0.46	0.039	0.3464	3.4857	5.3131

Table 16. GCA Estimates for grain yield and other traits recorded across 3 sites, 2006

Parent	GY	GLS	DTMF	DTFF	PH	EH	MSV	Blight	RL	SL	DE
CML 204	0.13	0.40**	0.18	0.24	17.30**	14.398**	-0.07	0.02	0.12	0.56**	0.20
CML 373	0.56**	-0.398**	-0.19	0.45	0.25	-2.44**	-0.03	-0.02	-0.095	-0.97**	0.64**
CML 312	0.33*	-0.03	-2.31**	-2.54**	12.55**	2.06**	-0.03	0.11**	-0.36**	-0.61**	-1.1**
CML 384	0.79**	0.21**	0.69*	-0.07	2.57*	3.48**	0.31**	-0.03	0.32**	-0.11	0.097
TZMI 102	-0.35*	0.549**	-0.94**	-0.93**	3.11**	2.58**	-0.003	0.004	0.45**	1.72**	0.66**
TZMI 711	-0.46**	-0.51**	0.83**	1.32**	-18.86**	-7.297**	-0.05	-0.05*	-0.29**	-0.099	-0.8**
TZMI 712	-1.03**	-0.22**	1.76**	1.51**	-16.9**	-12.79**	-0.12	-0.04	-0.15	-0.49*	0.37

Significance levels, **= $P < 0.01$ and *= $P < 0.05$; GCA= general combining ability, SCA= specific combining ability, GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DTFF= days to female flowering, PH= plant height, EH= ear height. MSV = maize streak virus, Blight= corn leaf blight, RL= root lodge, SL= stem lodge, DE= diseased ears

Table 17. SCA estimates for agronomic traits across sites

Cross	GY	GLS	DTMF	DFFF	PH	EH	MSV	Blight	RL	SL	DE
CML204/CML373	1.05**	0.16	-1.94**	-2.11**	5.07	2.95	-0.33*	-0.04	-0.90*	-0.59	-0.48
CML204/CML312	2.62**	-0.09	-1.15	-1.70*	11.77**	11.84**	0.20	0.08	-0.56*	-0.45	1.47*
CML204/CML384	0.79*	0.18**	-0.73	-0.34	7.74**	5.58**	-0.23	0.02	-1.15**	-1.03*	-0.51
CML204/TZMI 102	0.35	-0.05	-0.27	0.02	14.08**	7.149**	-0.07	-0.02	-1.37**	2.38**	0.34
CML204/TZMI 711	1.004**	-0.10	0.46	-0.31	11.93**	7.18**	-0.15	-0.01	-0.63*	-0.46	-0.17
CML373/CML312	0.33	-0.07	-1.87**	-1.75*	-3.57	-3.27	0.12	-0.10	-0.35	0.41	-1.29*
CML373/CML384	1.58**	-0.36**	-0.70	-0.72	3.73	0.77	0.10	0.00	-1.02**	0.07	-0.20
CML373/TZMI 102	1.82**	0.29	-1.40*	-1.19	4.78	5.26**	0.25	-0.02	-1.07**	-1.43**	1.65**
CML373/TZMI 711	0.20	0.21*	-1.51*	-1.28	13.58**	6.96**	0.04	0.13*	-0.50	-0.10	-0.69
CML312/CML384	0.13	0.03	-0.58	-1.39	1.31	1.50	0.09	0.01	-0.59*	0.30	-0.42
CML312/TZMI 102	1.60**	0.01	-2.12**	-2.04**	10.59**	6.03**	-0.29	0.02	-0.98**	-0.28	-0.89
CML312/TZMI 711	1.57**	0.06	-2.14**	-1.79*	11.85**	5.44**	0.05	-0.12*	-0.24	-0.38	0.34
CML384/TZMI 102	0.54	0.23**	-1.69**	-2.00**	15.18**	8.58**	-0.57**	0.02	0.26	1.88**	-0.13
CML384/TZMI 711	1.98**	-0.12	-2.14**	-1.84*	14.55**	6.09**	-0.15	0.06	-0.92**	-0.71	0.36
TZMI 102/TZMI711	0.73	-0.30 **	-0.51	-0.14	12.40**	8.32**	0.05	-0.01	-0.46	1.46**	0.88
CML204/TZMI712	0.96*	-0.42**	-2.06**	-1.84*	17.58**	5.20**	0.09	0.01	-0.76**	-0.57	0.88
CML373/TZMI 712	0.42	-0.12	0.31	-0.30	9.09**	7.16**	-0.09	0.07	-0.63*	0.71	1.77**
CML312/TZMI 712	1.01**	-0.17	-1.48*	-1.48*	12.62**	9.44**	-0.18	-0.08	-0.29	0.35	-1.19*
CML384/TZMI 712	1.74**	0.19*	-1.98**	-2.11**	11.03**	4.07*	-0.18	-0.05	-1.05**	-0.57	-0.93
TZMI 102/TZMI712	0.33	-0.32**	0.73	-0.09	-3.75	-6.29**	-0.02	0.02	-0.43	-1.57**	0.43
TZMI 711/TZMI712	-4.35**	0.85**	4.19**	5.72**	-42.36**	-18.73**	0.31	-0.03	3.43**	0.81	-0.87

Significance levels, **= $P < 0.01$ and *= $P < 0.05$; GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DFFF= days to female flowering, PH= plant height, EH= ear height. MSV = maize streak virus, Blight= northern corn leaf blight, RL= root lodge, SL= stem lodge, DE= diseased ears

significant positive correlation with plant ($r= 0.62$) and ear height (0.56) respectively. This corroborates with findings by Ali and Naidu (1982) and Jugenheimer (1985) who stated that taller hybrids usually had higher yields than short ones. Days to flowering were significantly and negatively correlated with plant height and this was due to decreased maize growth after flowering.

4.5.2 Kabete Field Station

Grain yield was weakly and positively correlated with MSV ($r= 0.12$), bird damage ($r= 0.11$), plant height ($r= 0.73^{**}$), ear height (0.6^{**}) (Table 19). Plants were highly vigorous and showed resistance to MSV and northern corn leaf blight. The high yielding genotypes in this site were very tall. Grain yield was also negatively correlated with GLS, ear rot, DTMF, DTFF, root and stem lodging. The negative correlation between grain yield and the days to flowering is unusual and this may be attributed to some late crosses that gave low yields whereas exceptionally early ones gave very high yields. However, this was an advantage since the entries that took long in the field had longer grain-filling period due to more light interception (Muchow *et al.* 1990). GLS had negative correlation with grain yield, MSV, blight, bare tips, DTMF and DTFF. The non-significant negative correlation for resistance to GLS, MSV and blight indicates that it is possible to pyramid resistance into one good line to develop multiple disease resistant hybrids. GLS also had positive correlations with ear rot, plant height, ear height, root and stem lodging. The non significant positive correlations of GLS with ear rot implies that these two diseases could be evaluated further using artificial disease infections or by use of hot spots.

Table 18. Correlations among selected traits recorded in KARI-Kiboko, 2006

Trait	MSV	blight	GLS	DTMF	DTFF	PH	EH	DE	RL	SL	GY
MSV	1.00	-0.25**	0.3**	0.136	0.060	0.044	0.090	0.132	0.24**	0.152	-0.130
Blight		1.000	-0.022	-0.196*	-0.159	0.2*	0.198*	-0.26**	-0.002	0.029	0.26**
GLS			1.000	-0.021	-0.014	-0.1	-0.112	0.2**	0.393**	0.21**	-0.26**
DTMF				1.000	0.94**	-0.6**	-0.47**	0.22**	0.076	0.071	-0.7**
DTFF					1.000	-0.6**	-0.49**	0.195*	0.055	0.026	-0.69**
PH						1.000	0.89**	-0.25**	-0.029	0.077	0.62**
EH							1.000	-0.19*	-0.038	0.122	0.56**
DE								1.000	0.011	-0.015	-0.30**
GY											1.000

Table 19. Correlations among selected traits recorded in Kabete Field Station, 2006

Trait	GY	GLS	MSV	blight	DE	DTMF	DTFF	PH	EH	RL	SL
GY	1.0	-0.07	0.12	0.14	-0.03	-0.5**	-0.6**	0.73**	0.64**	-0.34**	-0.25**
GLS		1.00	-0.15	-0.1	0.03	-0.1	-0.13	0.17*	0.26**	0.5**	0.33**
MSV			1.00	0.3**	-0.05	-0.06	-0.06	0.06	0.03	-0.08	-0.02
Blight				1.0	0.01	-0.06	-0.05	0.11	0.11	-0.097	-0.07
DE					1.0	0.04	0.05	0.09	0.06	-0.098	-0.09
DTMF						1.0	0.96**	-0.68**	-0.55**	0.10	0.07
DTFF							1.0	-0.7**	-0.56**	0.095	0.112
PH								1.0	0.91**	-0.12*	-0.2*
EH									1.0	-0.08	-0.08
RL										1.0	0.37**
SL											1.0

Significance levels, **= $P < 0.01$ and *= $P < 0.05$, GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DTFF= days to female flowering, PH= plant height, EH= ear height, MSV = maize streak virus, Blight= northern corn leaf blight, RL= root lodge, SL= stem lodge, DE= diseased ears

4.5.3 KARI-Kakamega

Kakamega was hot spot for the diseases and this provided a suitable environment for quick visual identification and the distinguishing of the GLS resistant entries from the susceptible ones. Grain yield had negative correlations with DTMF ($r = -0.62^{**}$), DTFF ($r = -0.67^{**}$), blight ($r = -0.08$), root lodging ($r = -0.2^*$), stem lodging ($r = -0.07^{**}$) (Table 20). There was premature death of plants due to severe disease infection leading to severe stem and root lodging that led to declined yields. Grain yield also had significant and positive correlations with plant (0.72**) and ear height (0.64**). Ear rot, MSV, root lodge, stem lodge and southern leaf blight had positive correlations with GLS (Table 15). This was due to sink-induced susceptibility (Hohls *et al.*, 1995). Thus, these diseases could easily be evaluated under inoculation or in hot spots. Days to maturity were significantly and negatively correlated with GLS and this bolsters Bubeck *et al.*, (1993) assertion that early maturing genotypes usually have high GLS severity.

Table 20. Correlations among selected traits recorded in KARI-Kakamega, 2006

Trait	DTMF	DTFF	GLS	blight	MSV	PH	EH	RL	SL	GY
DTMF	1	0.93**	-0.26**	-0.03	0.01	-0.64**	-0.59**	0.14	-0.13	-0.62**
DTFF		1	-0.32**	-0.06	-0.04	-0.70**	-0.66**	0.19	-0.09	-0.67**
GLS			1	0.20*	0.03	0.43**	0.53**	0.1	0.38**	0.09
blight				1	0.01	0.14	0.14	0.13	0.09	-0.08
MSV					1	0.04	0.13	-0.02	-0.09	0.01
PH						1	0.90**	-0.13	0.16	0.72**
EH							1	-0.11	0.31**	0.64**
RL								1	0.04	-0.20*
SL									1	-0.07
DE										0.02
GY										1

Significance levels, **=P<0.01 and *=P<0.05, GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DTFF= days to female flowering, PH= plant height, EH= ear height. MSV = maize streak virus, Blight= northern corn leaf blight, RL= root lodge. SL= stem lodge

4.6 Phenotypic correlations among selected traits across locations

Across the sites, grain yield had significantly different negative correlations with root lodge and stem lodge (Table 21). Grain yield also had non-significant negative correlations with GLS ($r=-0.07$) and blight ($r= -0.18$). The lack of significance implies that GLS and blight infection did not significantly lower the mean yields of all entries across sites. Some of the entries showed tolerance to GLS and blight especially in Kabete field station. Due to genotype by environment interaction for grain yield and grey leaf spot resistance, different entries performed differently across the different sites. Grain yield also had significantly different positive correlations with days to male flowering ($r= 0.22$), days to mid silking ($r= 0.22$), plant height ($r= 0.67$), ear height ($r = 0.66$) and ear rot ($r= 0.32$). Jugenheimer (1985) stated that grain yield among hybrids have a significant and positive correlation with maturity. Findings by Sanghi *et al.*, (1983) have also associated high yields with late maturity. However, some of the early hybrids in KARI Kakamega and KARI Kiboko produced the highest yields due to the GXE interaction that favoured the early maize germplasm. Most hybrids in Kabete field station had two ears per plant that could have led to the high yields as opposed to KARI Kiboko and KARI Kakamega.

GLS showed significant negative correlations with MSV (-0.23) and blight (-0.49). It also showed significant positive correlations with days to flowering (DTMF= 0.36 , DTFF= 0.31), plant height and ear height. Maturity had a negative correlation with GLS severity.

Table 21. Correlations among selected traits across locations, 2006

Trait	GY	MSV	GLS	DTMF	DFFF	PH	EH	blight	DE	RL	SL
GY	1	-0.18**	-0.077	0.22**	0.22**	0.66**	0.66**	-0.40**	0.32**	-0.12*	-0.29**
MSV		1	-0.23**	-0.36**	-0.37**	-0.12*	-0.09	0.42**	-0.22**	-0.035	-0.05
GLS			1	0.36**	0.31**	0.17**	0.18**	-0.49**	0.35**	0.36**	0.37**
DTMF				1	0.98**	-0.1	-0.06	-0.78**	0.49**	0.20**	-0.035
DFFF					1	-0.13*	-0.09	-0.76**	0.47**	0.201**	-0.04
PH						1	0.92**	-0.21**	0.22**	-0.103	-0.047
EH							1	-0.20**	0.23**	-0.045	0.011
Blight								1	-0.56**	-0.16**	0.006
DE									1	0.083	0.03
RL										1	0.055
SL											1

Significance levels, **= $P < 0.01$ and *= $P < 0.05$, ns= non significant; .GY= grain yield, GLS = grey leaf spot, DTMF= days to male flowering, DFFF= days to female flowering, PH= plant height, EH= ear height, MSV = maize streak virus. Blight= leaf blight, RL= root lodge, SL= stem lodge, DE= diseased ears

CHAPTER 5

CONCLUSIONS AND RECOMMENDATIONS

1. There were genotypes with stable genes for grain yield and GLS resistance.
 - The parent CML 384 had the highest mean grain yield and the highest GCA for grain yield; CML 373 and TZMI 711, which had the least mean GLS score and highest negative GCA effects for GLS, were immune and highly resistant to GLS respectively. The three entries; TZMI 711, CML 373 and CML 384 produced high yielding and GLS resistant hybrids namely; CML 373 / CML 384, TZMI 711/ CML 384 and CML 384/ TZMI 711.
 - These traits exhibited dominance in their inheritance and thus the good entries identified need subjection to more AEZ in more hybrid combinations to identify favourable donor lines with other desirable traits for introgression into elite maize germplasm.
 - The single cross hybrids could be used as heterozygous testers in recurrent selection for SCA to produce highly resistant and GLS resistant synthetics.
 - TZMI 711 and CML 373, which combined well with other inbred lines for GLS resistance, could be used as both male and female in hybrid combinations.
 - These lines TZMI 711 and CML 373 were excellent sources of both grain yield and GLS resistance genes in high and mid altitude AEZ respectively.
2. Some genotype by environment interaction was noted in this study. Therefore, different parental lines should be selected for the different AEZ.
 - CML 373 had the highest mean and highest positive GCA for grain yield in KARI-Kiboko. In Kabete Field Station, TZMI 711 had the highest mean yield

while CML 384 had the highest GCA effect for grain yield. In KARI- Kakamega, CML 373 had the highest mean yield for grain yield while CML 384 had the highest positive GCA for grain yield. On GLS resistance, TZMI 711 had the highest negative GCA for GLS in Kabete Field Station and in KARI-Kakamega. In addition, TZMI 102/CML 373, CML 312 / CML373 and CML 373 / CML 312 had superior yield performance in KARI-Kiboko. The hybrids with high GLS resistance and superior yield performance were; CML 384 / CML 373, CML 373 / CML 384 and CML 384 / TZMI 711 in Kabete Field Station and TZMI 711 / CML 384 and CML 384 / TZMI 711 in KARI-Kakamega.

- This implies that the inbred lines were good sources of GLS resistance genes and other desirable agronomic characters in the various environments; thus, the GCA of these inbred lines contributed much of the genetic variation for the various traits among the single cross hybrids at each AEZ. Hence, breeders should use recurrent and back cross recovery program to develop high yielding and GLS resistant hybrid parents, open pollinated varieties and synthetics to exploit this revealed additive gene action.
 - On the other hand, the genetic variability for grain yield was attributable to the SCA effects; thus, the maintenance of superior entries in heterozygous state and having more hybrid combinations would ensure the exploitation of the non-additive gene action.
3. Non significant correlations were noted for disease resistance especially GLS, blight, ear rot and MSV signifying that the resistance genes in the good entries should be pyramided into the two good lines (CML 373 and TZMI 711) to develop multiple

disease resistant lines which could be used for future development of disease resistant hybrids for the different AEZ.

Recommendations for future work

- The production of other elite synthetics and inbred lines from the good entries obtained in this research is required to bridge the gap between research and farmers' yields in SSA.
- More research on the stay green trait in TZMI 711 and its introgression into the susceptible but high yielding maize germplasm
- CML 373, which was immune to GLS, was susceptible to *Phaeosphaeria* leaf spot disease (PLS). More research to establish the association between PLS and GLS is important
- TZMI 102 and CML 204 should be grown as susceptible checks in areas where GLS has not been established locally to help identify areas prone to this fast spreading disease causing pathogen *Cercospora zeaе maydis* and counter the GLS aftermaths in SSA
- Further multi-location evaluation of these breeding materials in more locations and seasons to affirm the stability of GLS disease resistance since this disease is new and is spreading very fast.
- Additional work to identify the quantitative trait loci (QTLs) associated with GLS resistance in TZMI 711 and CML 373 through Marker Assisted Selection (MAS) and DNA finger printing.

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APPENDIX

Appendix 1. Weather Conditions at the Various Sites

KARI-Kiboko weather conditions 2006

Month	Total Rainfall	Temperature (°C)	
		Max	Min
January	12.4	32.4	19.19
February	6	32.88	18.77
March	85.7	33.21	20.23
April	205.8	30.95	18.82
May	44	30.18	17.68
June	0	28.95	14.88
July	0	27.74	14.1
August	0	29.65	15.21
September	5.4	30	15.12
October	1.5	31.53	19.16
November	157.5	29.25	18.38
December	150	28	19

Source: Kiboko meteorological department, 2006.

Kabete Field Station Weather Conditions 2006

Month	Total Rainfall (mm)	Temperature (°C)	
		Max	Min
January	15	25.2	13.7
February	25.9	26.5	14.3
March	204.9	25.2	15.1
April	276.4	22.3	14.9
May	220.5	22.6	14
June	7.3	22.2	12.4
July	5.9	19.9	12
August	37.2	22.9	11.5
September	25.4	22.7	12.4
October	87.4	24.8	14
November	348	22	14.7
December	246	22.9	14.6

Source: Kabete meteorological department, 2006.

KARI-Kakamega weather conditions

Month	Rainfall	Temperature °C	
		Maximum	Minimum
October, 2006	114.9	28.1	14.5
November, 2006	291.7	26.1	15
December, 2006	194.3	26	15.2
January, 2007	27.4	28.1	14.3

Source: Kakamega meteorological department, 2006/2007