MAKERERE UNIVERSITY

SELECTION STRATEGY FOR DEVELOPING MAIZE INBRED LINES WITH DROUGHT AND DISEASE RESISTANCE IN UGANDA

BINAISSA U. LEVENE CASTIANO

BSc. Agro-Business- (Instituto Superior Politécnico de Manica)

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DECLARATION

I, Binaissa U. Levene Castiano, certify that this study is original and has not been submitted for any other degree award to any University before.

Signed ……. Date:……...
Castiano, Binaissa Uassaleia Levene

This thesis has been submitted on our approval as supervisors

Signed ……. Date:…….
Dr. Richard Edema
(BSc. (Agric) Hon, MSc. (Agric) MAK; PhD. (The Ohio State University)).
Makerere University, Kampala Uganda

Signed ……. Date:…….
Dr. Godfrey Asea
(BSc. (Agric) Hon, MSc. (Agric) MAK; PhD. (The Ohio State University)).
National Crop Resources Research Institute (NaCRRI), Namulonge, Uganda

DEDICATION

To my parents: May God protects their soul, and to my brothers and sisters and all collaborators who have made this work possible.

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ACRONYMS AND ABBREVIATIONS

AD:	Anthesis Date
ANOVA:	Analysis of Variance
ASC:	Specific Combining Ability
ASI:	Anthesis Silking Interval
CIMMYT:	Centro Internacional de Malhoramento de Maize y Trigo
CML:	CIMMYT Mexico Line
EH:	Ear Height
Envt:	Environment
ExMS:	Expected Mean Square
F2:	Self generation two
GCA	General Combining Ability
GxE:	Genotype Environment Interaction
GY:	Grain yield
KARI:	Kenya Agriculture Research Institute
KR:	Kernel Rows
MSD:	Maize Streak Disease
MSV:	Maize Streak Virus
NaCRRI:	National Crop Resource Research Institute
NARO:	National Research Organization
PG:	Predicted Gain
SC:	Single Cross
SD:	Silking Date
TLB:	Turcicum Leaf Blight
YLD:	Yield
σ^2a	Additive variance
σ^2e:	Error variance

$\boldsymbol{P}_{\mathbf{LBF2}}$= phenotypic value of TLB score at F_2 generation

$\boldsymbol{P}_{\mathbf{TLBF3}}$= phenotypic value of TLB score at F_3 generation

$\boldsymbol{P}_{\mathbf{TLBF4}}$= phenotypic value of TLB score at F_4 generation

$\boldsymbol{P}_{\mathbf{MSVF2}}$= phenotypic value of MSV score at F_2 generation

$\boldsymbol{P}_{\mathbf{MSVF3}}$= phenotypic value of MSV score at F_3 generation

$\boldsymbol{P_{MSVF4}}$= phenotypic value of MSV score at F_4 generation

$\boldsymbol{P_{ADF2}}$= phenotypic value of anthesis date at F_2 generation

$\boldsymbol{P_{ADF3}}$= phenotypic value of anthesis date at F_3 generation

$\boldsymbol{P_{ADF4}}$= phenotypic value of anthesis date at F_4 generation

$\boldsymbol{P_{SDF2}}$= phenotypic value of silking date at F_2 generation

$\boldsymbol{P_{SDF3}}$= phenotypic value of silking date at F_3 generation

P_{SDF4}= phenotypic value of silking date at F_4 generation

$\boldsymbol{P_{ASIF2}}$= phenotypic value of anthesis silking interval date at F_2 generation

$\boldsymbol{P_{ASIF3}}$= phenotypic value of anthesis silking interval date at F_3 generation

$\boldsymbol{P_{ASIF4}}$= phenotypic value of anthesis silking interval date at F_4 generation

$\boldsymbol{P_{KRF3}}$= phenotypic value of kernel row at F_3 generation

$\boldsymbol{P_{TCAD}}$= phenotypic value of anthesis date of testcross

$\boldsymbol{P_{TCSD}}$= phenotypic value of silking date testcross

$\boldsymbol{P_{TCASI}}$= phenotypic value of anthesis silking interval testcross

$\boldsymbol{P_{TCMSV}}$= phenotypic value of MSV testcross

$\boldsymbol{P_{TCTLB}}$= phenotypic value of TLB testcross

$\boldsymbol{P_{TCPH}}$= phenotypic value of plant height testcross

$\boldsymbol{P_{TCEH}}$= phenotypic value of ear height testcross

$\boldsymbol{P_{TCEPP}}$ = phenotypic value of ear per plant testcross

$\boldsymbol{P_{TCKR}}$= phenotypic value of kernel row testcross

$\boldsymbol{P_{TCYLD}}$= phenotypic value of yield testcross

ABSTRACT

Breeding for host plant resistance along with performance traits requires the use of an effective breeding method and selection strategy. This study of a maize population identified efficient selection indices and a selection strategy for maize lines that combines selecting for traits of primary interest such as anthesis-silking interval (as a proxy for drought tolerance), and resistance to both Turcicum leaf blight (TLB) and maize streak virus (MSV) with other characteristics that directly and indirectly influence grain yield. Such a selection strategy and related indices should contribute to reducing the time required for breeding, and saving resources for further development and testing.

Testcrosses were generated in season 2011B at Kasese, with single cross (SC) testers from heterotic groups A and B used as males, planted in multiple rows, and pollen-bulked. F_3 lines were used as females, and planted ear-to-row in single-row plots. These crosses were then tested in three locations (Serere, Namulonge and Bulindi), in order to evaluate the performance of families in their early-segregating generations.

Results for anthesis-silking-interval (ASI) showed a high frequency of F_2 plants falling within the range of -3 to 0 days (67.4%), while only 29.2% of F_3 families fell in that range. In the inbreds, partial dominance conditioned for low disease pressure of TLB was indicated by 90% of F_2 progeny and 81% of F_3 progeny scoring resistant. In the F_3 families, 63.4% showed resistance to MSV, suggesting both some effect of segregation and a high response of the genotypes to environment. And selection among F_2 and F_3 progeny of a biparental cross has contributed for improvement of the performance of lines.

Significant GxE terms occurred frequently, but the GxE variance components were usually lower in magnitude than the pooled error. Variance components for lines for yield (YLD), number of kernel rows (KR), ear per plant (EPP), Turcicum leaf blight (TLB), maize streak virus (MSV), silking date (SD) and anthesis silking interval (ASI) were larger than LxE interactions. Suggesting that early generation test-crossing could be a good strategy for developing hybrid maize with the desirable traits for yield, Turcicum leaf blight, maize streak virus, and drought tolerance.

Results showed high broad sense heritability (BSH) values of 71% for AD and 60% for SD. The relatively high heritability makes the across environment selection for earliness easier on

the basis of phenotype. Meanwhile, levels of heritability across locations were moderate for ASI (55%), MSV (46%) and TLB (59%), indicating the influence of environment on disease incidence and severity.

Nine lines have been identified as the best, based on a consistent ranking correlated with maximum vigour in the hybrids in all four of the indices proposed, using AD, SD, ASI, yield and resistance to TLB and MSV as key components in the selection indices. These nine lines are WL-429-33; WL-429-40, WL-429-49; WL-429-37; WL-429-57; WL-429-34; WL-429-4, WL-429-50 and WL-429-119. The strategy used for the present study was to utilize all the indices developed, applying them from inbred development up through the testcrosses, tracking the best and most consistent genotypes.

Recommendations emerging from this study include the use of effective blocking, more testing sites and careful attention to experimental precision to minimise random variation and error variance. Also, since the across-environment mean for total yield and cobs-per-plant indicated low heritability, which was probably due to little genetic variance among the parents used to derive the population, we recommends using diverse crosses to develop breeding populations, and then selecting for yield-per-plant in later generations.

In the present study we noted that selecting by the selection index in either the F_3 generation or with the F_3-testcrosses was the best strategy for identifying the desirable individuals, and may improve the breeder's consistency in selecting the most promising lines with the best potential for multi-trait combination hybrid (as for MSV and TLB resistance, drought tolerance and high yield). And also noted that the highest gains for selection ($\geq$5%) are obtained when the selection is done at the testcross level, especially for traits with a high level of heritability in early stages (such as for MSV, TLB or ASI).

In the determination of heterotic group, results led us to conclude that there is no clear evidence supporting these lines belonging to heterotic group B, since most of them had SCA estimates of >1 SE in only one environment (14 lines in Serere) and 1 SE is not a very strong criterion to distinguish them, since 16% of lines (about 10 lines) are expected to have SCA values exceeding 1 SE by chance. However, there was a strong Line x Tester x Environment interaction, indicating the sensitivity to environmental influences of the performance of a specific line with a specific tester.

CHAPTER ONE
INTRODUTION

1.1 Economic Importance of Maize

The government of Uganda has identified maize as one of the five non-traditional agricultural crops to promote for export. It ranks second in Uganda for acreage of land planted to crop production. Its revenue contribution has been low at about USD 457,991 in 2004 (Falk, 2008).

Maize provides income and partial food security for about 3 million Ugandan households (Nadal and Wise 2004). The crop is commonly grown by both small-scale farmers, who own 1 ha each, and medium-scale farmers with less than 3.0 ha (RATES, 2003; Falk, 2008). Maize has become the most heavily-traded commodity in the East African Community (EAC) and in the Common Market for Eastern and Southern Africa (COMESA). Demand for it is expected to continue rising due to its traditional use as both food for the world's growing population and feed for their animals (Falk, 2008). In processed form, maize can be used as source of ethanol for fuel and starch (Jéan, 2003). Maize can also be used for other applications, appearing in products as diverse as beer, ice cream, syrup, shoe polish, glue, fireworks, ink, batteries, cosmetics, aspirin and paint (Jéan, 2003).

The growth of the biofuel market has caused a strong increase in demand for products traditionally used as animal feeds (Brookes, 2006). Also the same author indicated that the demand for feed grain was expected to increase by 10% by 2011 in response to population growth, urbanization, rising incomes and associated levels of meat consumption, particularly in the developing countries of Latin America, North Africa, the Middle East and China. While the use of maize has increased by 4%, as food and by 7% as feed since 2000, the use of cereal crops for industrial purposes, such as biofuel production, has increased by more than 25% in these 10 years (Brookes, 2006). According to FAO (2007), most of the ethanol for bio-fuel is from maize.

1.2 Constraints Affecting Maize Production

Most maize in Africa is grown by small-scale farmers with limited resources; these farmers use diverse cropping systems and continuously face a number of biotic and abiotic threats (FAO, 2007). Because of increasing scarcity of arable land and a growing population, production of maize is spreading into several diverse areas, including those marginal for maize production

(Fischler & Wortmann, 1999). Such expansion of the production area will likely expose maize to increased risks, such as water shortage and competition from grazing animals (Fischler, & Wortmann, 1999). Therefore, the stability of the maize harvest in Africa will depend as much on reducing yield losses as well as maximizing yield potential, using additional resource inputs (FAO, 2007).

Regionally, diseases affect the production of maize. Those include seedling blightor seed rots (*Bacillus sabtilis*), ear rots (*Fusarium moniliform*) and foliar diseases *(E. turcicum; Puccina spp; Genus mastrevirus* (Smith, *et al.* 1997). Based on the severity of attack and economic loss to pathogens, the diseases incited by air-borne fungi probably contribute for biggest crop losses (Smith, *et al.* 1997).

Several studies have recorded the severity and distribution of high-impact diseases in the African continent, especially of turcicum leaf blight (TLB) in the highland tropics, and *Maize streak mastrevirus* (MSV) in the lowland tropics (CIMMYT, 1994). Research carried out in the Republic of South Africa showed a reduction in yield of 30-60% attributed to Gray Leaf Spot (GLS), depending on the level of susceptibility of the variety and environmental conditions (Smith, *et al.* 1997). A recent survey in Uganda and Kenya revealed that GLS, MSV and TLB, are the most important diseases in two key maize growing agro-ecologies, the mid-altitude and highland regions of eastern Africa (FAO, 2007).

Several alternatives have been suggested for the control and management of maize diseases, including crop rotation, pesticide application, and conventional tillage (FAO, 1999). Each of these practices must take into account the cost-benefit and feasibility of its use. For certain diseases, such as TLB, management is most effectively focused on protection by both limiting the source of primary inoculum through crop rotation and residue management, and by reducing the rate of disease development (Storey and Howland, 1967). For control of MSV, crop rotation, inter-cropping, and planting of resistant varieties is required.

However, the development of varieties with good agronomic characteristics and multiple resistance to foliar diseases is still a challenge in breeding program. Control of foliar diseases has

been identified as a top priority for improvement of the maize crop in sub-Saharan Africa (CIMMYT 2004).

1.3 Rationale and Justification of the Study

Cyclically, maize production is affected by several factors, such as drought, flooding, pests and diseases (CIMMYT 2004). Therefore, it is necessary to improve the tolerance of the crop to these stresses by using a diversity of genetic materials to combine different lines with genes of interest (CIMMYT 2004). Since the process of creating and selecting inbred lines capable of producing good hybrid requires much time and resources, the process should be made as efficient as possible by using the available germplasm under the local conditions.

For hybrids to be successful, the strategy should take into account essential characteristics important to the farmer, such as stable yield, drought tolerance, generally desirable agronomic traits and resistance to Turcicum Leaf Blight (TLB) and *Maize Streak-Virus* (MSV) (Gibson 2012). In Uganda, promising populations have been created by crossing exotic lines that have TLB & MSV resistance and drought tolerance with locally adapted inbred lines as a source of new improved lines (Asea 2011). An effective strategy depends on transmitting the essential characteristics from inbred parents into the hybrid, and evaluating the testcrosses for their potential as new inbreds.

Therefore, there is need to evaluate the process of developing the maize hybrid and testcrossing by comparing the information gained at early (F3) or later (F6) generations regarding genetic components of variance, correlation of inbred-hybrid performance, and presence of traits for resistance to MSV and TLB. Such an understanding will assist in developing an effective strategy for selecting inbred lines that will produce high-yielding, drought-tolerant and disease-resistant hybrids.

Information is also needed regarding the effectiveness of selecting for these traits based on inbred performance in early and sequential generations. This would include an evaluation of the effectiveness of improving maize by testcrossing at early generations under local conditions with simultaneous attention given to drought tolerance and resistance to TLB and MSV in populations

resulting from the exotic x adapted parents. Even the cumulative genetic gains in these specific crosses of CIMMYT x locally-adapted lines are unknown, as is their performance in early generation test-crossing for simultaneous improvement of multiple traits. The resulting hybrids have also not been characterized for resistance to these traits.

Breeding for host plant resistance requires the use of an effective breeding method and selection strategy. In this study an efficient selection index that combines the traits of interest is employed, in order to develop an effective strategy for selecting inbreds. Such an index can become very important in reducing the investment of time and resources and should also help to identify the potential for combining multiple traits such as drought tolerance and resistance to MSV and TLB in the CIMMYT x NARO selections (drought-tolerant and multiple-resistant, respectively). It could also be used to determine the degree to which the inbreds derived from a genetically diverse-source population correspond to the heterotic group assigned to that population.

The strategy of developing inbred maize by testcrossing at an early generation (as F_3 instead of F_6) can maximize resources and time needed to develop new hybrids. However, this approach is effective only if the genetic variance among testcrosses is sufficiently larger than the interaction between genotype x environment (GxE) or error variance, and shows adequate genetic gain. This method can be useful for identifying cross combinations with high genetic variation. Crosses identified on the basis of this approach are expected to include a relatively large number of superior recombinants with a minimum involvement of non-additive genetic effects, which are generally known to reduce the response to selection (Kostova *et al*. 2006).

1.4 Objectives

The overall goal of this study was to develop an effective selection strategy for inbreds that will produce high-yielding, drought-tolerant, and disease-resistant hybrids.

1.4.1 The specific objectives:

1-To determine inbred and testcross performance resulting from selection among F_2 and F_3 progeny of a biparental cross

a) To estimate the relative magnitude of line and line x environment variance components for traits of interest in testcrosses of F3 inbred lines.

b) To estimate the relationships between inbreds and their testcrosses for traits of interest.

2-To characterize and compare selection indices based on inbred and testcross performance for traits of interest.

3-To predict the expected genetic gain from selection for individual traits and from use of selection indices

4- To determine the degree to which inbred lines correspond to the heterotic group assigned to the source population.

1.5 Research Questions

1a- Is the genetic variance among inbreds generations and testcrosses progeny large enough compared to GxE and error variances for selection to be effective for developing superior hybrids?

1b-How beneficial is selection in each generation of inbreeding in obtaining superior testcrosses for various traits of importance?

2-To what extent do the inbreds with the best selection index correspond to the testcrosses with the best selection index?

3-How much gain is added by including a selection index for inbreds when using a selection index for the testcrosses?

4-Does the heterotic group of the lines correspond to that assigned to the source population from which were the inbreds were derived?

CHAPTER TWO

LITERATURE REVIEW

2.1 Worldwide Production of Maize

Maize was already grown in prehistoric times by inhabitants of Central America, such as the Mayans (Chahal and Gosal, 2002). In the early 16th century it was introduced to Europe, from where it then quickly spread to other regions in the world (Chahal and Gosal, 2002). One advantage of maize is that it can be produced and adapted to different agro-climatic regions. Maize (*Zea mays L)* is considered the number one cereal in the world. Its global production is higher than that of wheat or rice, maize is also a staple food for the people in African continent and used worldwide as a fodder crop for livestock (Anon, 2007).

The crop is classified as *Zea mays L,* of the family Gramineae and order Poales (FAO, 1990). Worldwide annual maize production stands at 590 million tons grown on 139 million hectares of land, with an average yield of 4,229 kg ha-1. Maize is known as "king of cereals" because of its high production potential and wide adaptability (Falk, 2008). Among the cereals grown in Africa, it is gaining significant importance because of growing demand for its diversified uses, including as human food, animal feed and industrial uses (Anon, 2007). In most parts of the world maize is used primarily as food for humans. The dry maize kernel contains about 77% starch, 2% sugar, 9% protein, 2% ash and 5% oil, which is low in linolenic acid (0.7%) and contains a high level of natural flavour (FAO, 1990).

The strong demand of maize as staple food in Uganda is complemented by its higher potential to become an important non-traditional crop for export (Falk, 2008)

2.2 Progress in Maize Improvement

The most significant achievement that stands out as a landmark in the history of biological science during the twentieth century is the discovery of the phenomenon of heterosis, accompanied by the development of the technology for breeding hybrids and the successful commercial exploitation of heterosis in maize (Bernardo, 2010). Since the crop is a highly cross-pollinated species, a number of genotypes are now available to maize growing farmers for

commercial cultivation, such as single crosses, three way crosses, double crosses, varietal hybrids, multiple hybrids, composites, synthetics, pools and populations (Bekavac *et al*. 2006).

The hybrid development program for maize involves developing and evaluating inbred lines, crossing selected inbreds with different testers, in order to assess their cross inbred performance, combining ability and nature of inheritance for various quantitative traits (Kempthorne, 1957).

In such a breeding program based on heterosis, the selection of inbreds to be used as parents is based on their morphological diversity with good combining ability, a consideration that is very important to producing superior hybrids (Kempthorne, 1957). The analysis of their general and specific combining abilities helped to identify parental inbreds with the potential for producing superior hybrids. According to Kempthorne (1957), the line × tester analysis is one of the simplest and most efficient methods of evaluating a large number of inbreds for their performance and combining ability as parents.

2.3 Characteristics of the key pathogens and traits considered in this study

2.3.1 Maize streak virus

Maize streak mastrevirus (MSV) is a major pathogen of maize throughout sub-Saharan Africa (CIMMYT, 1994). Although the levels of maize streak disease (MSD) are low in some years, devastating epidemics have occurred, often after drought periods or irregular early rains, and sometimes resulting in complete crop failure (CIMMYT, 1994). Maize streak virus was first observed in South Africa in 1901 and is now widely distributed throughout Africa south of the Sahara, from 0 to 2000 metres above sea level (CIMMYT, 1994). Streak disease is characterized by white chlorotic stripes, uniformly distributed across the leaf surface. In highly susceptible genotypes, the chlorotic streaks may coalesce to form large chlorotic and later necrotic leaf areas, though partially or highly resistant genotypes produce few or no streaks. Infection of seedlings leads to stunted plants that may die or produce poor ears, but infection of six to eight week old plants usually has little or no detrimental effect (CIMMYT, 1994).

MSV is a single stranded DNA Gemini-virus, obligatorily transmitted by leaf hoppers (*Cicadulina spp*.) and infecting a wide range of grass species. *Cicadulina mbila* is the most

important MSV vector (Bonga, 1992). In 1931 the first source of resistance was observed in cultivars Peruvian Yellow (P) and Arkells Hickory-H (Kempthorne, 1957). A single, incompletely dominant gene was reported to govern MSV resistance in P x H, a hybrid of the above two cultivars (Kempthorne, 1957).

Comprehensive screening activities were begun at IITA in 1975, leading to the identification of a resistant Tropical Zea Yellow population (TZY) that was derived from a cross between a CIMMYT Mexico line and an unknown source of yellow germplasm from East Africa (CIMMYT, 1994). A highly resistant inbred line, IB32, was developed from TZY and studied genetically (Diallo, 1999).

The generation means analysis of IB32 and four susceptible Corn Belt inbreds indicated quantitative inheritance of MSV resistance with relatively few genes involved. Rather simple inheritance of MSV resistance was also observed in other Mexican and Tanzanian germplasm (Diallo, 1999).

Various breeding methodologies have been applied at CIMMYT's maize research station near Harare, Zimbabwe, to create a wealth of germplasm with intermediate to high levels of streak resistance, though, in-depth studies on the genetic basis of resistance in this germplasm were not undertaken (Diallo, 1999).

Maize breeding programs designed to improve grain yield combined with tolerance to diseases usually require a good knowledge of the combining ability of the breeding materials to be used (Betran *et al*., 2003a). For effective selection for grain yield and other desirable traits, information is required on the magnitude of useful genetic variances in the population, especially regarding their combining ability and heterosis (Legasse *et al.*, 2009).

2.3.2 Turcicum leaf blight

Turcicum leaf blight (*Exserohilum turcicum*), also known as northern corn leaf blight in the USA, is one of the major diseases affecting maize in warm and humid parts of the world, including in Uganda (Adipala *et al.*, 1993). It is caused by the fungal pathogen *Exserohilum*

turcicum (synonym; Helminthosporium turcicum (Pass) and others. The disease also occurs whenever maize and sorghum are grown together (Murrithi, 2001). Hosts of *E. turcicum* include maize, sorghum, Johnson grass and other grass species (Hooker, 1963). It has particularly been noticed to cause a significant reduction in maize yield in most production areas (Adipala *et al*,. 1993).

The disease is considered a major limiting factor in maize producing regions of sub-Saharan Africa, especially in the humid mid-attitude and highland regions (Murrithi, 2001). It affects the foliage of maize, causing yield reductions associated with necrosis or chlorosis of leaves in the upper two-thirds of the canopy (Kyetere *et al.*, 1995). The disease can cause extensive defoliation during the grain filling period, resulting in yield losses of up to 50% or more (Murrithi. 2001). Yield losses may be minimal if the infection is delayed to 6-8 weeks after silking or until flowering. Turcicum leaf blight also predisposes plants to stalk rots caused by other pathogens (Gevers, 1975)**.**

2.3.2.1 Life cycle of leaf blight disease

Exserohilum Turcicum, the cause of leaf blight disease in maize, remains dormant during the dry period in residue of maize that was infected the previous season and in the subsequent growing season; the fungus sporulates on the residue (Adipala *et al.,* 1993). Conidia are wind-blown over long distances to settle on the leaves of maize and sorghum plants. Subsequently, conidial germination occurs 3-6 hours after inoculation (Murrithi. 2001). Germ tubes grow at an angle rather than parallel to the veins of the leaf, producing aspersoria from which a penetration peg develops, (Murrithi. 2001).

2.3.2.2 *Exserohilum turcicum* races

Five races of *E. turcicum* have been reported to overcome specific *Ht* resistance genes - namely races 0, 2, 2N, 23, and 23N, all of which occur in East Africa, though race 0 is the most prevalent (Adipala *et al.,* 1993). So far, among cultivated crops, the vast majority of *E. turcicum* races have been isolated from maize, but the same pathogen has been isolated from several species of grass crops (Adipala *et al*., 1993).

2.4 Genetics of resistance and heritability

The earliest sources of resistance to TLB were first found in popcorn in 1940 (Hooker, 1963). The *Ht1* gene identified from the popcorn cultivar, Ladyfinger, and field corn inbred GE440 was characterized by chlorotic lesions, reduced sporulation and small necrotic lesions (Hooker, 1963). Later, studies showed this reaction to be a type of resistance that was conditioned by a single gene called *Helminthosporium turcicum (Ht)*, the name of the pathogen at the time (Hooker, 1963). A gene-for-gene reaction was identified, and with the discovery of several new races, more *Ht* resistance loci have been reported (Carson *et al*. 2002).

The degree of resistance expressed by lines with the *Ht* gene is influenced by the level of partial resistance in the line (Paterniani *et al.,* 2000). Incorporation of the *Ht* gene into a background having partial resistance confers the most effective resistance to *E. turcicum*, displayed by reduced sporulation, and lessened number and size of lesions (Jensen *et al*., 1983). Polygenic or partial resistance is considered to be more durable, since single-gene resistance is vulnerable to the development of new races of the pathogen (Pernet *et al.*, 1999a). A combination of monogenic *Ht* resistance with partial resistance permits additive or complementary interallelic interactions that may enhance the overall level of resistance (Pernet *et al.*, 1999a and 1999b).

Quantitatively, partial resistance ranges from a high level of resistance with a few small lesions to a low level displaying many large sporulating lesions (Raymundo & Hooker, 1981). Whereas several quantitative genes have been found, break down of resistance is quite common (Raymundo and Hoolker 1981). The development of new races of the pathogen shortens durability of the *Ht*-based resistance (Adipala *et al.,* 1993). Durable resistance is characterised by a reduced number of lesions and a decrease in lesion size and degree of sporulation, typical of polygenic resistance (Carson *et al*., 2002).

Diverse sources of qualitative and quantitative resistance are available, but qualitative resistance (*Ht* genes) is often unstable. In the tropics especially, it is either overcome by new virulent races or it suffers from climatically sensitive expression. Quantitative resistance is expressed independently of the physical environment and has never succumbed to *Setosphaeria turcica* pathotypes in the field.

2.5 Anthesis-silking interval

Numerous studies have shown that maize kernel number and yield is a function of the rate of crop growth around flowering (Banziger *et al*., 2004). Environmental conditions that alter plant growth during this period affect specific aspects of flowering dynamics. The most widely observed effect is the temporal separation of male (anthesis) and female (silking) floral maturity, referred to as the anthesis-silking interval (Campos *et al*., 2004).

The relationship between final grain yield and the ASI has been described in numerous studies, and has attracted considerable attention in maize-breeding program (Bolaños & Edmeades, 1996; Banziger *et al*. 2004; Campos *et al*., 2004).

The relationship between plant growth and specific aspects of the flowering process is not yet completely resolved. Identifying the physiological mechanisms that regulate the visually observed changes in flowering dynamics has important implications for overcoming current limitations to grain yield in maize (Banziger *et al*. 2004).

Maize is a monoecious plant, with staminate (male) flowers borne on an apical inflorescence (commonly referred to as a tassel) and with pistillate (female) flowers produced on one or more lateral branches that develop into grain-bearing rachises, commonly referred to as ears (Borrás *et al*., 2007). At the individual plant level, anthesis is defined as the beginning of pollen shed from the tassel, and is visually determined when at least one anther has dehisced and is liberating pollen.

Appearance of the first pollen-receptive stigmas (commonly referred to as silks) from within the surrounding husks on the primary ear defines the silking date for each plant (Borrás *et al*. 2007). As such, both flowering descriptors are qualitative traits that define a change of state. At any point in time, a plant either has or has not reached these flowering stages, anthesis or silking (Campos *et al*. 2004).

When these flowering processes are considered at the population level, anthesis and silking dates are set when a pre-determined proportion of plants in the population reach the stage and in

general, anthesis or silking for a population is reported when 50% of the plants attain the stage (Borrás *et al*., 2007). This simplification reflects the fact that all plants in a population do not achieve anthesis or silking at the same time.

Rather, flowering throughout the population is recognized as a continuous, but finite process. Thus, for the population, floral anthesis is a quantitative process; for individual plants, it is a qualitative process (Campos *et al*., 2004).

Considering maize-flowering dynamics as a quantitative trait at the population level and as a qualitative trait at the plant level enabled us to identify and integrate key genotypic coefficients needed to quantify silking behaviour. These factors are

(i) the relationship between plant growth rate to ear growth rate;

(ii) the pattern of ear biomass accumulation during early growing stages; and

(iii) the amount of accumulated biomass an ear needs to accumulate to reach the silking stage.

A population-based approach that takes into account the plant-to-plant variability is used to understand time-to-silking in maize crops (Campos *et al*., 2000).

2.5.1 Heritability and genetic relationship with ASI

The genetic relationship between grain yield (GY) and anthesis-silking interval (ASI) in a diverse array of genotypes grown under drought at flowering is about -0.6, suggesting that ASI is a visual indicator of underlying processes affecting reproductive success (Derera *at al.*, 2008).

The broad sense heritability of ASI is typically 0.5 to 0.7, and several quantitative trait loci for the trait have been identified (Derera e*t al.*, 2008). Yield and grain number per plant show a dependence on the increase of dry weight per plant during the flowering period. Genetic variation for ASI may indicate differences in this relationship, and hence differences in partitioning of assimilate formed to the ear at flowering (Derera *et al.*, 2008).

2.6 Breeding for drought tolerance in maize

Water stress is a problem that affects more than 45% of the geographic area in the world, is a major constraint in maize production, and the most important contributor to yield reduction in

semiarid regions (Richards, 2006; Amjad Ali *et al.*, 2011). Improving drought resistance is therefore necessarily a major objective in plant breeding programs for rain fed agriculture in semi-arid regions (Tuberosa *et al*., 2005). Since knowledge of genetic behaviour and type of gene action controlling target traits is basic to designing an appropriate breeding procedure for genetic improvement (Richards, 2006).

The success of any selection or hybridization breeding program depends on precise estimates of genetic variation components for traits of interest, the estimate include additive, dominant and non-allelic interaction effects (Mohammad *et al*., 2009).

The genetic basis of drought resistance has received limited attention because it is a complex physiological phenomenon (Mohammad *et al*., 2009). Therefore, little information is available on the genetic architecture of drought-related characters that could provide practical information to breeders attempting to develop drought-tolerant varieties (Nadal and Wise, 2004). The potential for improving crop performance under drought stress cannot be achieved until we have identified genes or gene products that are responsible for desired characteristics of drought resistance at different stages of plant growth and development (Dudley and Johnson, 2009).

2.6.1 Physiology of drought tolerance in maize

Drought can be defined as the absence of adequate moisture necessary for normal plant growth and completion of its life cycle (Bekavac *et al.* 2006). The lack of adequate moisture leading to water stress is a common occurrence in rain fed areas, aggravated by infrequent rains or poor irrigation, (Bekavac *et al.* 2006).

Proline and quaternary ammonium compounds (as glycinebetaine, choline and prolinebetaine) are key osmolytes that contribute to osmotic adjustment (Duvick *et al*. 2004). In higher plants the oxygen toxicity is more serious under conditions of deficient water supply (Bekavac *et al.* 2006).

Water stress causes stomatal closure, which reduces the CO_2/O_2 ratio in leaves and inhibits photosynthesis (Moussa, 2006). These conditions increase the rate of reactive oxygen species

(ROS), like the superoxide radical (O_2^-), hydrogen peroxide (H_2O_2), and the hydroxyl radical ($OH^{\bullet}$), due to enhanced leakage of electrons to oxygen, particularly in the chloroplast and mitochondria (Bekavac *et al.* 2006).

The superoxide radicals and their dismutational product, hydrogen peroxide, can directly attack membrane lipids and inactivate enzymes (Moussa, 2006). The hydroxyl radical, one of the most reactive oxygen species, is responsible for oxygen toxicity *in vivo*, causing damage to DNA, protein, lipids, chlorophyll and almost every other organic constituent of the living cell (Duvick, 2004).

2.6.2 Effect of Drought on Maize

Water deficit, or drought, can affect maize development from the time of its establishment up to grain filling .The physiological responses are usually complex and unpredictable (Moreno *et al.,* 2005). Three critical stages that, under drought stress, can affect maize growth and yield have been identified:

1) Establishment of the crop;
2) Flowering; and
3) Mid- to-late grain filling.

When drought occurs during flowering or the grain filling stage, yield is most seriously affected (Banzinger *et al*., 2000). Under drought at flowering stage, the anthesis silking interval (ASI) is typically lengthened (Welcker *et al*., 2007).

The maize plant is highly sensitive to drought from 2 to 22 days after silking, with a peak at 7 days. At this time the number of kernels can be reduced by up to 45% of their potential and the ASI is lengthened (Bolaños & Edmeades, 1996).

Often, when drought affects photosynthesis shortly before flowering, the silk growth is delayed; increasing the anthesis silking interval (ASI) and a lack of pollination is observed (Banziger *et al.,* 2000). If the stress affects the plant during the period 12 to 16 days after silking, the kernel weight may fall to 51% of its potential weight. When drought occurs in the period just before

tassel emergence to the early stage of grain filling, yield may be reduced by up to 90% (Mosisa *et al*, 2001).

2.7 Multi-trait Selection

In practical maize breeding programs, selection of more than one trait is common (Hallauer, *et al.,* 2010). The trait of primary importance is yield, but several other traits are included if the genotype under development is to be competitive (Falconer, 1989).

Alternative methods that may be used in selecting for several traits are: a) Tandem selection, which emphasizes only one trait; b) Independent culling levels, which attributes an intensity for several traits in the same generation but in sequence for each trait, and c) Selection indices, a procedure that is used for selecting several traits simultaneously (Hallauer, *et al.,* 2010).

The focus of this study was on developing selection indices, based on an evaluation of inbreds and families in replicated trials. This required accuracy in the evaluation of several characteristics to allow selection to be efficient. Some quantitative traits, such as yield and plant or ear height, could be measured directly, but a metrical evaluation was not possible for some characters, such as disease resistance, or ear and plant aspect.
For these traits a scale (e.g. from 0 to 5) was commonly used, with the accuracy of the evaluation also depending on the breeder's experience and amount of compromise made for different traits (Hallauer *et al*, 2010).

Several authors have reported that use of a selection index would improve selection efficiency over selection based on only one trait (Laible & Dirks, 1968 cited by Hallauer *et al.* 2010). Young (1961) reported that the superiority of an index of selection increases as the number of traits under selection is increased, but is less effective when there is a great difference in the importance of various traits. In other words, its superiority was at a maximum when the traits considered were equally important. Gain from selection for any given trait is expected to decrease as additional traits are included in the index, so the choice of traits to include must be made carefully.

Since highly improved populations require better techniques for further improvement. a selection index may be useful when high precision parameter estimates that can enhance expected progress are available. The procedures for the use of a selection index were originally given by Smith (1936), Hazel (1943), Kempthorne (1957), and Brim *et al*., (1959). The phenotypic value of any individual can be represented by P = G + E for each trait (Falconer, 1989). When considering several traits, it is desirable to choose individuals with the best combination of these traits (Falconer, 1989).

The basis for such a selection is a index selection, which takes into account a combination of traits according to their relative weights. Thus each individual plant or line has a value (score) and selection is based on this value (Hallauer *et al.,* 2010).

2.7.1 Relationship between inbred and testcrosses

The difficulties of establishing a relationship between inbred lines and hybrid traits have been one of the major limitations of inbred and hybrid development program (Buckler *et al.*, 2009). Since it is expensive to conduct yield trials, information obtained about an inbred line that is indicative of its performance in a hybrid can be useful to eliminate the need for making crosses and conducting an extensive number of trials (Hallauer *et al*., 2010).

Hence, it is desirable to investigate possible ways to reduce testing of inbred lines in hybrids and to determine if the expression of traits in inbred lines is transmissible to their hybrids (Hallauer *et al*., 2010). Although some traits are relatively easy to improve genetically, such as flowering time and disease resistance, others, like grain yield and drought tolerance, have been challenging, seemingly related to the genetic complexity of traits (Buckler *et al.*, 2009).

Studies of relationship between inbred line traits and the same or different traits in their hybrids have been used to determine the effectiveness of selection towards hybrid performance, although studying the relation between performance of inbreds and their testcrosses is still challenging and difficult to predict (Hallauer, 2010).

Dudley & Johnson (2009) studied the relationship between F_2 lines from elite germplasm and compared the F_2 line with its testcrosses at the F_2 and F_5 generation for grain yield. A correlation coefficient of 0.14 was obtained between F_2 and F_5 testcrosses, compared to a 0.67 between F_2 and F_5 testcrosses.

2.8 Evaluation of testcrosses

One system for developing maize inbred lines involves visual selection among and within ear-per row progeny for several selfing generations (Hallauer, 1990). Testcross evaluation is delayed until the number of selections is greatly reduced and the lines are nearly homozygous (Hallauer, 1990).

A second system involves evaluation of testcrosses during the early generation of selfing. Lines that do not perform well are discarded early to allow expenditure of resources on the more promising lines (Hallauer, 1990). This procedure, called early generation testing, "relies on the assumption that combining ability of the lines is determined during early stage of selfing and does not change substantially with continued inbreeding" (Sprague, 1946).

Early testing will be effective if it allows identification of partially inbred lines that would eventually perform well in testcrosses at homozygosity (Sprague, 1946). One measure of the effectiveness of early testing is the relationship between the phenotypic testcross value of an S_n individual or line and the true genetic value (i.e., value in the absence of non-genetic effects) of the testcross of a directly descended individual or line at an advanced generation (Hallauer, 1990).

The final evaluation of inbred lines can be determined by hybrid and mean inbred performance (Hallauer1990). A significant correlation between yields of inter-crossed inbred lines and the same lines as top crosses (Hallauer, 1990). This author reasoned that the most valuable lines for use in double crosses, multiple crosses or synthetic varieties are those which on average produce the best hybrids when tested with wide range of germplasm (Hallauer, 1990). This study also

concluded that crossing with standard open pollinated varieties provides an efficient method for the preliminary testing of inbred lines for later use in other types of hybrid combinations.
The use of top crosses provides an efficient method for the preliminary evaluation of inbred lines and they are especially useful for determining general combining ability for a large number of lines (Hallauer, 1990).

A simple inexpensive performance test was designed by Jugenheimer (1962) for the preliminary screening of a large number of entries. Each three-way cross was planted in replicated, single-hill plots. Its performance was compared to that of the single-cross tester grown adjacent to it. The lines observed in the preliminary tests to be better could be grown in larger populations for additional selection within families, if seemingly desirable. The remaining material could also be evaluated in standard yield tests to identify the superior inbred lines and hybrids.

Vasal *et al*., (1999), who identified potential inbred lines in early generations that he used in modified single-cross hybrids of maize, suggested that the essential pre-requisite for commercial production of maize hybrids based on single crosses is the development of vigorous high-yielding inbred parents.

2.8.1 Estimation of genetic gain

Predicting genetic gain enables plant breeders to determine desirable breeding methods, and thus solidify plant breeding as a science (Duvick *et al*. 2004). Developing desirable selection strategies to enhance gains has resulted in significant increases in crop yields (Duvick *et al*. 2004). Genetic gain, or the response to selection, refers to the change in the population mean over the season due to selection, and can be generally predicted as:

$$\boldsymbol{P.G} = \frac{K * \sigma^2 a}{\sigma^2 a + \sigma^2 na + \frac{\sigma^2 gxe}{\#env} + \frac{\sigma^2 e}{\#envxrep}}$$

where $\boldsymbol{P.G}$ =Predicted Gain; K=Standard selection differential; $\sigma^2 a$=additive genetic variance, $\sigma^2 e$=error variance, *envt*=environment, $\sigma^2 gxe$=variance of genotype by environment and rep=number of replications (Holland *et al*. 2003).

Clearly defining selection and response units and their genetic relationships is critical to accurately predicting selection gain (Holland *et al.* 2003). The parameters for genetic relationships are naturally described through heritability, which was originally defined by Lush (1948) in the context of mass selection as "the proportion of the phenotypic variance among individuals in a population that is due to heritable genetic effects." Lush's definition is referred to as narrow sense heritability (h^2) and was based on his experience as an animal breeder.

In plant species, there is a vast diversity of modes of reproduction to derive selection and response units, and selection units are often families that are replicated within and across environments (Holland *et al*., 2003). This diversity leads to confusion when predicting gain, and for this reason. Holland (2004), suggested that plant breeders define heritability as "the fraction of the selection differential expected to be gained when selection is practiced on a defined reference unit." This definition interprets heritability in the context of estimating gain for an appropriate selection procedure, which enables accurate comparisons of different selection strategies.

2.9 Assignment of breeding materials into heterotic groups

The use of contrasting heterotic groups is crucial in breeding hybrid maize (Reif *et al*., 2003; Xingming *et al*., 2009). Selection must be based not only on agronomic aspects of the inbred parents per se, but also on attaining high heterosis in their crosses. This is achieved by using testers of a known heterotic group. Broadly speaking, there are two heterotic groups, A and B, to which inbred lines are assigned in maize breeding, though sometimes there can be more than two such classifications, depending on the differences in performance observed among varieties. China uses four heterotic groups for maize, A, B, A/B and C (Xingming *et al*., 2009).

Two major heterotic classification methods currently used around the world include the traditional method, which uses specific combining ability and some line-pedigree or field-yield information, and the molecular marker method, which uses genetic similarity (GS) and genetic distance (GD) to assign inbred lines to heterotic groups (Xingming *et al*., 2009).

CHAPTER THREE

MATERIALS AND METHOD

3.1 Experimental sites

This study was conducted in three experimental sites: the National Crops Resource Research Institute (NaCRRI)-at Namulonge in the Central region of Uganda; Bulindi-Hoima in the western region of Uganda; and the National Semi-Arid Resources Research Institute (NaSARRI) at Serere in the eastern region. Namulonge is considered a hot spot for Maize streak virus and Turcicum leaf blight and is a random drought environment, located at altitude 1159 (masl), 32^0 37″E. The coordinates of the Bulindi-Hoima site are: 01^0 24″N, 31′ 18″E, and it was selected because it generally produce a high yield. Serere selected for random drought testing, is located at 1^0 31′ 58″N, 33^0 28′ 49″E.

3.2 Germplasm Source

The parental materials were developed at the Uganda National Agricultural Research Organization (NARO) and the International Centre for Maize and Wheat Improvement (CIMMYT) The germplasm varied in resistance to Turcicum leaf blight (TLB), and to maize streak virus disease (MSV) and in drought tolerance (Table1).

Table 1: Source and characteristics of germplasm

Genetic material	Characteristics	Source
Parent 1 NARO	Adapted, weevil resistant	NARO
Parent 2 CIMMYT Pedgree	Drought tolerant, resistant to MSV, TLB WL-429-14/(CML442/CML197//TuxPSEQ) C1F2/P49-SR	
F2	Advanced material (Heterotic Group A)	NARO
Testers (Heterotic group A & heterotic group B)	Single Cross (SC) CML 202/CML395	NARO
Check- Longe 10H	Commercial hybrid- susceptible to drought	NARO
Check- Longe 5H	Commercial hybrid- MSV; TLB susceptible	NARO
Check- CML 202	TLB-susceptible inbred line	CIMMYT/NARO
Check- CML 312	MSV-susceptible inbred line	CIMMYT/NARO

ML=CIMMYT Mexico Line; NARO=National Crop Resource Research Institute; MSV= Maize Streak virus, TLB=Turcicum Leaf Blight

3.3 Population advancement and management

This study began with F_2 seed, which was planted and advanced to F_3 at NaCCRI in 2011A (first rainy season, beginning in March). Disease response and ASI data had been collected on the F_2 plants. The F_3 seeds were screened at NaCCRI for their reaction to Turcicum leaf blight (TLB) following artificial inoculation. For Maize streak virus (MSV), seedlings were first inoculated by viruliferous leafhoppers in cages in a screen house, transplanted into the field, and then scored for resistance to MSV at 4, 6 and 10 weeks after transplanting. In each F_3 row, plants that performed well were selfed.

Testcrossing was done at Kasese to provide an appropriate isolation by both distance and separation in time, planting 30 days later than farmers planted their maize, in season 2011B (second rainy season, beginning in September). To generate testcross (TC) the single cross (SC) testers were used as males, planted in multiple rows and pollen-bulked, while the F_3 lines were used as females, and planted ear-to-row in single-row-plots. In all generations data was recorded for Anthesis-Silking-Interval (ASI), Turcicum leaf blight (TLB), and plant height. Frequency distributions in the F_2 and F_3 generations were used to determine whether the traits are controlled by quantitative or qualitative genes. Narrow sense heritability was determined for the inbred generations using the parent-offspring regression method.

3.4 Inoculum preparation and management of TLB trails

A laminar flow hood was used to create an aseptic working environment. The fungus was placed on PDA medium and the plates put upside down to grow in the incubator at 22^{o}-25^{o} C (Figure 1). After five days, the fungus was ready for transfer from the base plate to a new plate. This was done by transferring small pieces of agar with the fungus and placing them onto a new plate. To prepare for inoculating the plants in the field the fungus was inoculated in sorghum seeds for ten days.

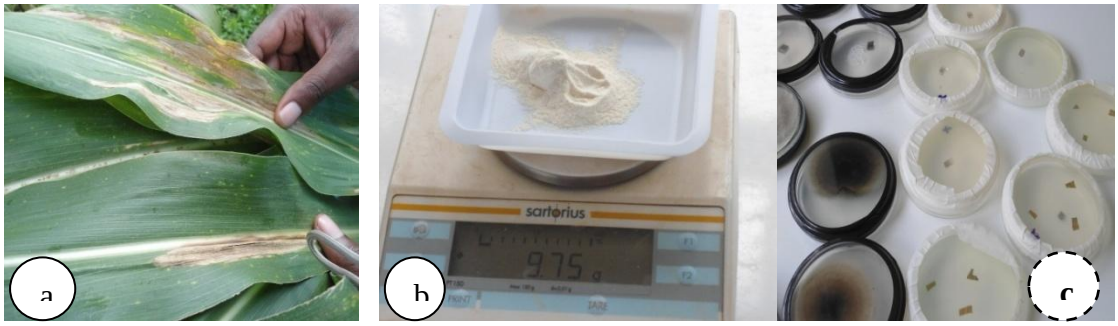


Figure 1: TLB Inoculum preparation

a =collection of TLB inoculum, b= PDA for medium preparation, c = Plates with small pieces of agar with the fungus growing

Maize plants were inoculated at the 4-6 leaf stage of growth in the field. Inoculations were done in the evening, placing 5-10 infected sorghum seeds into each maize whorl. Disease severity was assessed by visual symptoms, beginning two to three weeks after inoculation, and using a rating scale of 1 to 5 following CIMMYT's procedure. In this scale 1 to 1.5 is used to indicate no lesions, 1.6 to 2.5 few lesions and 2.6 to 5.0 for almost completely blighted leaves. The rating was based on an average of visual estimate of leaf area covered by the lesions per plant or family. Data for severity estimates per family was averaged for all plants in the row. Ratings of 1-1.5 were considering resistant, 1.6 to 2.5 intermediate and 2.6 to 5.0 susceptible.

3.5 Inoculation and assessment of maize streak virus disease

Standard procedures employed at the maize improvement program at NaCRRI-Namulonge were used to screen for MSV infection. The procedure used a high density population of viruliferous adults of the leafhoppers (*Cicadulina mbila*-Naude), as described by Storey & Howland (1967). Leafhoppers were given 48 hours for an Acquisition Access Period (AAP) on MSV-infected maize seedlings. Thereafter, the leafhoppers were given 48 hours (2 days) as an Inoculation Access Period (IAP) on maize seedlings at the 2-3 leaf stage (Figure 2). Seedlings were then transplanted to the field and scored for MSV disease at 4, 6 and 10 weeks after transplanting, on a rating scale of 1 to 5, following CIMMYT's procedures. In this scale 1= no symptom on

leaves; 1.5= very few streaks on leaves; 2= light streaking on old leaves, gradually decreasing on young leaves; 2.5= light streaking on old and young leaves; 3= moderate streaks on old and young leaves; 3.5=moderate streaks on old with young leaves with slight stunting; 4= severe streaking on 60% of leaf area, plants stunted; 4.5= severe streaking on 75% of leaf area, plants severely stunted; and 5= severe streaking on more than 75% of the leaf area where plants are severely stunted, dying or dead.

Figure 2: Maize streak virus inoculation in the screen house

a=maize plant with MSV (source of inoculum), b=cages with leafhoppers (vectors) and c=seedlings to be infected

3.5.1 Experimental design and layout of field trail

Border rows of other maize genotypes were planted around trials in all locations. Inbred lines CML 202 and 312 were included as checks when the F_4 inbreds were evaluated. For test cross trials, Longe 5 and Longe 10H were used as checks (Table 1). An alpha-lattice design of 8 blocks x 15 entries per block, with two replications was used. Spacing was 0.75 m between rows and 0.30 m between hills. Two seeds per hill were planted along the row, and thinned to one plant per hill three weeks after germination.

A termiticide (Chlorpyrifos, 480g/l), was applied to the soil at planting and after flowering to control termites that were problematic in all three sites. Other agronomic practices included weed control, application of 150kg/ha Di-Ammonium Phosphate (DAP) fertilizer at planting and 125 kg/ha of Urea 46% at seedling 45 days after planting and at flowering. Supplementary irrigation was supplied by sprinklers at NaCRRI in the dry season before flowering with two weeks interval. The alley effect was controlled at harvest by excluding one plant at each end of the plot.

Data was collected on a plot basis for: days to silking (SD) (from planting until 50% of plants showed silk emergence); and days to anthesis (AD) (number of days from planting to 50% of plants beginning to shed pollen). The anthesis-silking-interval (ASI) was calculated from the difference between the silking and anthesis dates (ASI = SD – AD).

TLB and MSV scores were recorded as the mean symptom rating for each entry per replication. MSV disease incidence was obtained by counting infected plants on each plot and calculated as according to the formula below:

$$Disease\ Incidence \quad DI \quad = \frac{Numberof\ MSV\ infected\ plants}{Plant\ stand\ count} \times 100$$

Data on plant height (in cm) was collected on six random plants per row by measuring the plant stalk from the ground level to the base of the last leaf sheath of the mature plant.
Ears per plant (EPP), was determined as the number of ears with at least one or more completely developed grain at harvest. Yield (t/ha) was obtained from shelled grain weight (GW) from each plot, adjusted to 12% grain moisture. Adjustment of yield per hectare was made according to the number of harvested plants per plot or area in m^2 accounting for grain moisture and fresh weight at harvest time. Shelling percentage was considered and 15%gi of moisture content after drying. Then yield was computed by converting the obtained yield from individual plot into hectare and considering a correction factor according to the formula suggested by CIMMYT, (1985).

$$\text{Yield ton/ha} = \frac{FW*10}{Area}\ x\ \frac{100-GM}{100-15}\ x\ S\%$$

Where: FW = fresh weight at harvest; GM = grain moisture; Area = plot area of each entry in m^2; S% = shelling percentage (0.8)

3.5.2 Assignment of heterotic group

Two testers (designated A and B) were used to discriminate between the heterotic groups of 58 lines that previously had been all assigned to heterotic group A, based on the parentage of the population. Each of the 58 lines were crossed with both testers (A and B), and the resulting test-

crosses were evaluated in the three locations for yield and other traits. The inbred that give SCA values greater than one standard error ($SCA>1SE_{SCA}$) for their testcross with tester A were tentatively assigned to heterotic group B. Legesse *et al*. (2009) state that an inbred is assigned to opposite heterotic group that of the tester if it shows a strong positive specific combining ability (SCA) effect for that crossing combination.

3.6 Statistical Methods for Data Analysis

The Field Book package (Bindiganavile *et al.,* 2007) was used for randomization of the 120 genotypes in the testcross trial. Analysis of variance for single environments was based on lattice design using the linear mixed model procedure GENSTAT 14th edition (Bindiganavile *et al.,* 2007). Genotypes were considered random effects (since they represented essentially random lines from the F_2 population. For testcrosses, testers were considered fixed effects and lines were considered random. Environments, replications and blocks within replication were also considered random effects in the analysis to calculate the ANOVA, and variance components Analysis was done for both individual environments and across environments. Skeleton ANOVAs are presented in Tables 2 & 3. The variance components derived from the ANOVA were used to calculate heritability and predicted gain.

Table 2: Skeleton ANOVA for genetic variances and components for single environments (2 Reps, 58 Lines, and 2 Testers)

Source of Variation	DF	Effect	MS	Ftest den	Fprob	ExpMS	Variance Components
Block/Rep	14	random		LEE		$\sigma^2 e+7.5\sigma^2_{B/Rep}$	$\sigma^2_{Blockep/Rep}=(MS_{block/Rep}- MS_{rep.})/7.5$
Line	57	random		LEE		$\sigma^2 e+2\ \sigma^2_{L}$	$\sigma^2_{Line}=(MS_{Line}- MS_{Lee.})/2$
Tester	1	fixed		L*T		$\sigma^2 e+2\sigma^2_{LxT}+116\sigma^2_{T}$	$\sigma^2_{T}=(MS_{Tester}- MS_{LxT})/116$
Line xTester	57			LEE		$\sigma^2 e+2\ \sigma^2_{LxT}$	$\sigma^2_{LxT}=(MS_{LxT}- MS_{Lee.})/2$
Lattice Eff. Error (LEE)	105					$\sigma^2 e$	σ^2_{Lee}

Note: the variance components were calculated based on entry means in individual environment

Table 3: Skeleton ANOVA for across environment analysis (3 Environments, 58 Lines, 2 Testers, based on testcross means averaged over 2 reps within each environment)

Source of Variation	Df	Effects	MS	Ftest den	Fp	ExpMS	Variance Component
Tester	1	Fixed		Composite[1]		$\sigma^2 e+\sigma^2_{LxTxE}+3\sigma^2_{LxT}+58\ \sigma^2_{TxE}+174\ \sigma^2_{T}$	$\sigma^2_{T}=(MS_{T}\ -MS_{TxE}-MS_{LxT}+MS_{LxTxE})/174$
Lines	57	Random		MS_{LxE}		$\sigma^2 e+2\ \sigma^2_{LxE}+3\ \sigma^2_{L}$	$\sigma^2_{Line}=(MS_{Line}-MS_{LxEnv})/6$
Line x Tester	57	Random		MS_{LxTxE}		$\sigma^2 e+3\ \sigma^2_{LxT}$	$\sigma^2_{LxT}=(MS_{LxT}-MS_{ExLxT})/3$
Tester x Envt	2	Random		MS_{LxTxE}		$\sigma^2 e+\sigma^2_{LxTxE}+58\ \sigma^2_{TxE}$	$\sigma^2_{ExT}=(MS_{TxE}-MS_{LxTxE})/58$
Line x Envt	114	Random		Error		$\sigma^2 e+2\ \sigma^2_{LxE}$	$\sigma^2_{LxE}=(MS_{LxEnv}-MS_{Pderror})/2$
Line x Tester x Envt	114			MS_{Error}		$\sigma^2 e+1\ \sigma^2_{LxTxE}$	$\sigma^2_{LxTxE}=MS_{LxTxE}-MS_{error}$
Pooled Error	3150					$\sigma^2 e$	$\sigma^2_{e'}$

The variance components estimates were based on entry means per location. The error mean square ($\sigma^2 e$) was divided by the number of reps (2). [1]Ftest den = (Tx Envt + LxT) - LxTxE

3.7 Estimation of narrow sense heritability (h^2) and gains

Narrow-sense heritability was calculated according to the following formula.

h^2 or NS-CGD=($\sigma^2_{GCAl} + \sigma^2_{GCAt}$)/($\sigma^2_{GCAl} + \sigma^2_{GCAt} + \sigma^2_{SCA} + \sigma^2_e$)

Where: h^2=Narrow sense heritabilityσ^2, $_{GCAl}$=variance of general combining ability for lines σ^2_{GCAt}=variance of general combining ability for testers, σ^2_{SCA}=variance of specific combining ability, σ^2a=additive genetic variance; σ_e^2= error variance, σ^2_n= non-additive genetic variance; env=environment, r=replication; σ^2_{GxE}=genotype x environment variance, env x rep=environment x rep, K=standard selection differential

3.7.1 Estimation of expected gain and Relationship

The expected gain in the testcross performance was calculated using the formula below suggested by Gibson (2012) (see explanation of symbols above).

$$\boldsymbol{P.G} = \frac{K * \sigma^2 a}{\sigma^2 a + \sigma^2 na + \frac{\sigma^2 gxe}{\#env} + \frac{\sigma^2 e}{\#envxrep}}$$

Individual predicted gain for F_2; F_3; F_4 generation and narrow-sense heritability was estimated using parent-offspring regression, considering "**r"** value as heritability. The gain for selection index of inbred lines at different generations and at the testcross level was obtained using the formula below, also suggested by Gibson (2012).

$$\mathbf{G_i = K*h^2*\sqrt{\sigma^2_{ph}}} \quad \text{and} \quad \mathbf{G_T = (\sigma^2 a *K)/ \sqrt{\sigma^2_{ph}}}$$

Where: G_i=gain for selection on inbreds; G_T=Gain for selection using testcrosses; K=Selection differential; σ^2ph=phenotypic variance; Σ BSH=sum of values of broad sense heritability of the trait over three environment including BSH across environment; h^2=narrow sense heritability of the trait averaged over three generations (F_2, F_3 and F_4).

3.7.2 Relationship between inbred and testcross performance

The phenotypic and genetic correlations among successive generation of inbreds and inbreds testcrosses were determined with Excel using the formulae below presented by Falconer (1989).

Phenotypic correlations (a)

$$rP = \frac{covP}{\sigma Px\sigma Py}$$

X and **Y**= the two characters under consideration**; rP**=phenotypic correlation; **cov**=covariance of the two characters X and Y, with subscripts P, and **σ**=variance and standard deviation, with subscripts P, and X or Y according to the character referred to Falconer, (1989).

3.8 Selection indices

The indices used for best prediction of individuals were constructed considering eleven (11) important traits. However the traits for resistance to MSV and TLB, grain yield silking date, anthesis date and anthesis silking interval were weighted most heavily in the index chosen. The indices were developed for three environments separated and combined using the principles and formulas suggested by Falconer (1989).

I (index) = $b_1P_1 + b_2P_2 + b_3P_3 + \ldots\ldots$

in this formula the ***b's*** are the factors by which each measurement is to be weighted and ***P's*** are phenotypic values.

3.8.1 Index constructed for inbreds

Indices were constructed using the sum of products, with each component in the index (phenotypic scores) given a specific multiplication factor according to researcher's judgment of its importance. In the inbred more weight was given to the traits of anthesis silking interval (ASI), Turcicum leaf blight (TLB) resistance and maize streak virus (MSV) resistance especially at the F3 and F4 generations, in which a whole plot was evaluated rather than single plants. The variability for a particular trait was assessed as the difference between the 75^{th} and the 25^{th} percentiles for entry means for that trait. This difference was then divided by the difference between the index value at the 75^{th} and 25^{th} percentile, with the result converted to percent by multiplying by 100. This criterion was

used to evaluate the effect of the trait multiplier on the resulting index for all the indices calculated in this study. Because this criterion does not account for correlations between traits, the sum of the values is greater than one, and the criterion does not estimate the direct contribution of a trait to the overall variability in the index. However, it does provide a convenient relative indication of the trait's contribution to the index. The inbred index that incorporated F_2, F_3 and F_4 generations was calculated as follows *(Prof. Paul Gibson, 2012. Personal communication).*

$$\mathbf{I_I=3*P_{TLBF2}+13*P_{TLBF3}+11*P_{TLBF4}+5*P_{MSVF2}+17*P_{MSVF3}+9*P_{MSVF4}+0.5*P_{ADF2}+1*P_{ADF3}+0.5*P_{ADF4}+1*P_{SDF2}+8*P_{SDF3}+3*P_{SDF4}+2*P_{ASIF2}+11*P_{ASIF3}+14*P_{ASIF4}+(-12)*P_{KRF3}}$$

In this index numerical values are multiplier (which may be increased or decreased depending on the weight of a trait) and $\boldsymbol{P_{\text{Trait-generation,}}}$ indicate the trait and the generation of measurement (adapted from Falconer, 1989). Traits abbreviations are listed in the list of abbreviation**.**

3.8.2 Test-cross Index

The following shows the index used for evaluating the testcrosses.

$$\mathbf{I_{TC}=0.5*P_{TCAD}+0.5*P_{TCSD}+10*P_{TCASI}+3*P_{TCMSV}+5*P_{TCTLB}+(-0.01)*P_{TCPH}+0.01*P_{TCEH}+(-8*P_{TCEPP})+(-1*P_{TCKR})+(-20*P_{TCYLD})}$$

In this index numerical values are multiplier (which may be increased or decreased depending on the weight of a trait) and $\boldsymbol{P_{\text{Trait-testcross,}}}$ indicate the trait measurement of testcross (adapted from Falconer, 1989).

3.8.3 Index including both test crosses and their corresponding inbred lines

The following gives the formula for the selection index used in this study (adapted from Falconer, 1989).

$$\mathbf{I_{(I+TC)}ndex=}3*P_{TLBF2}+10*P_{TLBF3}+13*P_{TLBF4}+3*P_{MSVF2}+10*P_{MSVF3}+9*P_{MSVF4}+0.1*P_{ADF2}+0.5*P_{ADF3}+0.75*P_{ADF4}+0.1*P_{SDF2}+0.75*P_{SDF3}+0.8*P_{SDF4}+3*P_{ASIF2}+6*P_{ASIF3}+9*P_{ASIF4}+9*P_{KRF3}+3*P_{TCAD}+2*P_{TCSD}+9*P_{TCASI}+8*P_{TCMSV}+9*P_{TCTLB}+0.1*P_{TCPH}+0.1*P_{TCEH}+(-12*P_{TCEPP})+(-2*P_{TCKR})+(-41*P_{TCYLD})$$

CHAPTER FOUR

RESULTS AND DISCUSSION

4.1 Inbred and Testcross Performance

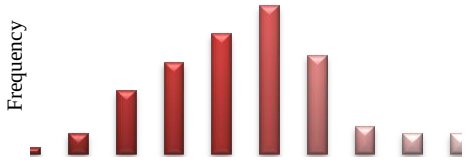
The mean value recorded for ASI was ranged from -3 to 3 days in F_2, and -3 to 6 days in F_3. A high frequency of 67.4% of F_2 individual plants fell within the range of -3 to 0 days and 29.2% of F_3 families in the range of -3 to 0 days of ASI.

Male and female flowering of F_2 individuals exhibited a range of 60 to 79 days. In the F_3, they exhibited a wide range of 60 to 89 days to flowering. A relatively large number of individuals (76.4% in $F_2$and 84% in F_3) were observed to be in the range of 70-79 days of flowering. In other words, we can say they exhibited moderate maturity, between early and late. About 6.7% of F_3 families had an elongated period before the onset of flowering, around 10 days beyond the mean.

High differences of ASI (-3 to 3 days at F_2 and -3 to 6 days at F_3) give a clear picture of segregating progeny. Due to irregular rainfall and drought a few days before flowering period in the F_3 generation in season 2011B (September-December), there was a strong response of genotypes to environmental conditions (figure 3). The anthesis-silking interval at generations F_2 and F_3 was normally distributed, suggesting quantitative inheritance controlled by several genes.

4 .1.1 Inbred line distributions

ASI in Days at F2 generation

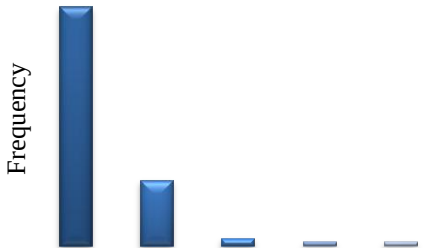


ASI in Days at F3 generation

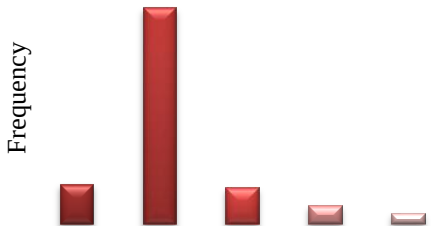
Figure 3: Frequency distribution of anthesis silking interval (ASI) of 89 inbred lines in F2 and F3 generations in the field at Namulonge-Uganda in 2011A (March-October) and 2011B (September – January) respectively.

Plant disease scores ranging from 1 to 2.5 (resistant) were observed in 90% of F_2 progeny and 81% of F_3 progeny, suggesting partial dominance conditioning resistance to TLB in the maize inbreds. Since the two generations were evaluated separately, no direct comparison is possible. However, both generations showed a high frequency of resistant progeny, though the small variation can be accounted for by environmental factors (figure 4).

In sorghum, disease severity of F_2 plants and F_3 families in the greenhouse were skewed towards resistant, suggesting quantitative inheritance with mainly additive effects, but with partial dominance toward resistance to TLB (Beshir e*t al.*, 2012). In the current study, especially in the F_3 generation, a normal distribution was observed; implying resistance was controlled by major genes. Probably this was influenced by environmental conditions and the genetic makeup of the crop. Clearly the distribution in our study argues against qualitative resistance, which is characterized by small lesions surrounded by a chlorotic halo, also referred to as Ht (*Helminthosporium turcicum*) type lesion. This resistance was first found on lady finger popcorn in the 1940's and later on regular maize genotypes (Hooker, 1963, Gevers, 1975; and Adipala *et al*., 1993).



TLB score 1-5 F2 generation



TLB score 1-5 F3 generation

Figure 4: Frequency distribution of disease score rating for turcicum leaf blight (TLB) of 89 inbred lines in F_2 and F_3 generations in the field at Namulonge- in 2011A (March-October) and 2011B (September–January) seasons, respectively.

Abut 63,4% of 89 F_3 families showed resistance to maize streak virus with a severity score of less than 2.5, and about 36.6% showed susceptibility to MSV. The distribution was continuous and normal, implying resistance is conditioned by multiple genes (figure 5). Asea (2005) noted that not even the resistant parent, CML202, nor any of the 410 $F_{2:3}$, or selected $F_{2:4}$ families were completely resistant to maize streak virus. This suggests that resistance provided by CML 202 conditions for only partial resistance to maize streak virus. In the present study, a high response at all score levels was a result of the effectiveness of inoculation in the screen house combined with environmental conditions following transplanting. There was low rainfall and high temperatures, known to be favorable conditions for MSV devolopment (Rose, 1978, cited by Asea, 2005).

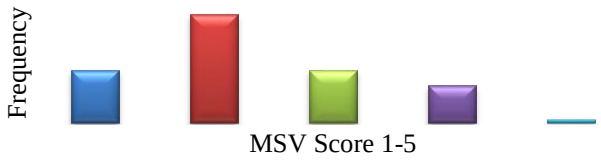


Figure 5: Frequency distribution of maize streak virus disease score rating of 58 inbred lines in F_3 generation, screened at Namulonge- 2012B (March-October)

4.1.2 Testcross performance in single locations

4.1.2.1 Namulonge

Analyses of variance for AD, SD, and ASI for the Namulonge location are presented in Table 4. Significant differences in testcross means were observed among lines, indicating genetic variability among lines within the population WL-429-14/(CML442/CML197//TuxPSEQ) C1 F2/P49-SR. Testcross means for AD showed that 38.7% of lines had dates ranging from 67 to 70 days, and 61.3% of the lines were considered late maturing (70-74 days to AD). Meanwhile, 34.8% of the lines (20) had a female flowering date (SD) ranging from 66 to 70 days, with the remainder (65.2%) ranging from 71 to 74 days. ASI ranged from -1.2 to 1.3 days, but about 20 lines (34.5%) ranged from -1.2 to 0 days. The negative ASI were observed

on lines WL-429-28, WL-429-113 and WL-429-70 (see Appendix 1). Tester A produced TC's with better ASI values, but some TC's with tester B also had good ASI values. ASI can help to identify drought tolerant and high yielding lines since ASI is an indicator of drought tolerance and has a strong relationship to yield (Welcker *at al*., 2007).

Testers also demonstrated highly significant differences (Table 4), with tester A showing a negative ASI of -0.10 days and tester B a positive ASI of 0.82 days. This indicates clearly that they were influenced by multiple genes because distributions were continous and normal without grouping plants into phenotypic classes. This finding is supported by Borrás, e*t al*. (2007), who reported the flowering process at the individual plant level as critical for evaluating the enviromental effects on maize phenology at the population level. This was particulary evident when plant-to-plant variability within the population was large, as is often the case in maize, especially under stressfull growing conditions.

In our study, differences for AD, SD and ASI among lines and between testers were observed, and were influenced by a short drought that occurred from one week before flowering until 6 days after the flowering period. The response of specific lines to stress during flowering is indicated by the ASI value. Namulonge was considered a hot spot for disease reaction, and high responses were observed on testcrosses, especially for MSV incidence. There was about 50% incidence of MSV on tester A and 47% on tester B, with a mean of 30.5 for testcrosses onto tester A and 23.7 for testcrosses onto tester B. Obviously tester B transmits more resistance. Both lines and testers showed highly significant differences ($P<0.001$) based on the measurement of incidence. The most resistant lines were lines 104, 82, 61, 28, 50, 119, 32, 75, 95, 19, 117, 76 and 96 with < 21% incidence. The interation beween effect of genotype and pathogen often inflences variations in the level of host resistance in genotypes when they are tested in either single or multi-locations (Carson e*t al.,* 2002).

Kyetere *et al*., (1999 cited by Asea 2005) identified a major QTL on the short arm of chromosome 1(1S - bin1.04) and designated it *msv1*. The same locus was identified by Welz *et al*., (1988) in a population derived from crossing CML202, (an MSV resistant inbred) with Lo951, (a susceptible inbred), using a different viral isolate.

Additional studies by Pernet (1999a and 1999b) using two other resistance sources, identified a major QTL in the same genomic location on chromosome 1S. He proposed that MSV

resistance was under the control of two genetic systems, one arising from a major gene on the short arm of chromosome1, and the other conditioned by minor genes on chromosomes 2, 3 and 10, that confer quantitative resistance. The consistent results of these studies, suggest that different sources of resistance likely contain the same resistance factor, *msv1* that accounts for the large phenotypic variance associated with differences of disease response among genotypes.

The TLB reaction was similar on both testcrosses from testers A & B with scores of 2.4 and 2.5, respectively. It is clear that the testers did not show a great contribution towards an improved TLB-resistant genotype. Though testcross means were significantly different ($P<0.05$) among lines, as were testers ($P<0.001$), line and tester interanction was not significant (Table 4).

Paternian *et al.* (2000) and Legesses *et al.* (2009) reported additive gene effects when they crossed inbred lines for foliar disease resistance and agronomic traits. In our study, results are confirming these findings, probably because the lines have more genetic variability and their contribution (GCA line) are more noticeble than LxT interaction, in especially for the treats such as MSV and TLB resistance, SD, ASI, EPP, KR and 100 grain weight.

Grain yield varied significantly among testcrosses only for testers. Non-significant differences were observed for lines and line by tester interactions, probably due to lack of genetic variability within the lines resulting from low genetic diversity for this trait in the parents. Also the interactions of line x tester were non-significant in most cases.

Table 4: Single environment analysis of variance of mean square and means for key traits and agronomic traits of testcrosses and 58 F3 lines with testers A and B, season 2012A (March-October) at Namulonge

		Namulonge-MS								
S. variation	Df	YLD	100 GW	KR	EPP	TLB score	MSV%	AD	SD	ASI
Lines	57	0.69	7.87***	0.59*	0.0090*	0.20***	125***	1.72***	1.58***	0.63*
Tester	1	13.4***	283***-	0.32	0.0005	0.20	1347***	24.6***	97.1[?]	24.9***
Line xTester	57	0.68	4.47	0.39	0.0053	0.08	38.6	0.79**	0.67	0.36
LEE	105	0.58	3.27	0.37	0.0055	0.07	55.5	0.41	0.55	0.39
Grand mean		6.78	39.2	13.8	1.08	2.47	27.1	70.4	70.7	0.36
CV %		11.3	4.6	4.4	6.87	10.7	27.5	0.90	1.1	173
Tester A Mean		6.44	37.7	13.8	1.08	2.43	30.5	69.9	69.8	-0.10
Minimum		4.80	32.9	12.4	0.88	1.74	15.1	66.7	66.4	-1.49
Maximum		7.38	44.2	15.9	1.32	3.04	50.0	72.9	72.3	1.71
Variance among TC's		0.33	6.14	0.59	0.007	0.09	75.7	1.46	1.22	0.38
Tester B Mean		7.12	40.8	13.9	1.08	2.51	23.7	70.8	71.7	0.82
Minimum		3.89	34.5	12.3	0.96	1.45	8.72	68.2	70.1	-0.94
Maximum		9.39	46.6	15.2	1.31	3.52	47.9	73.5	74.4	2.75
Variance among TC's		1.04 m	6.20	0.39	0.006	0.19	88.5	1.05	1.03	0.61.

*, **, *** indicates significance at 0.05, 0.01, and 0.001 probability levels, respectively. Namulonge-MS=Namulonge mean square; AD= Anthesis date; SD=Silking date; MSVi=Maize streak virus incedence; SD=Standard deviation; KR=Kernel rows; YLD=Yield tons per hectare; 100 GW= 100 Grain weight(g); TLB=Turciccum leaf bligth (1=none; 5=severy); LEE=Lattice effective error

However, the average yield and grain weight of testcrosses from tester B was significantly greater than those from tester A (Table 4).

Other agronomic traits, such as kernel-row-pe-cob showed significant differences among lines ($P<0.05$) and non-significant differences for tester and tester by line interaction (Table 4), were observed.

Table 5 : Single environment GCA and SCA mean squares and variance components for yield of testcrosses at Namulonge

Source of variation	Df	M.S	Var. Components
GCA_L	57	0.691	0.054
GCA_T	1	13.4***	0.110
SCA/Line*Tester	57	0.682	0.027
LEE	105	0.584	0.584
SE_{GCA-L}		0.382	
SE_{SCA}		0.541	

$h^2 = (GCA_L+GCA_T)/(GCA_L+GCA_T+SCA+\sigma^2_e)$

$h^2 = 0.21$

Baker's ratio = $(GCA_L+GCA_T)/(GCA_L+GCA_T+SCA)$

Baker's= 0.86

The general combining ability of lines (GCA_L) and of testers (GCA_T) being lower than the error variance automatically lowers the narrow sense heritability (h^2) (Table 5). The implication of this for a breeding strategy is that selection of inbred lines based on the F_3 testcross performance will be very difficult. Probably a reduction of the error variance and an increase of replications could compensate somewhat for the low heritability estimates. But Baker's ratio being high (0.86) helps to predict the performance of progeny resulting from the crosses.

However, lines WL-111, 113, 115, 25, 34, 43, 51, 56, 57, 68, 75, 77, 90 and 94 showed large and positive GCA's for yield (Appendix 3), suggesting that those lines could be used for improvement of yield traits.

Yield response is higher when two inbreds are crossed from different heterotic groups than within the same heterotic group (Reif *et al*., 2003). This emphasises that probably our lines were from heterotic group A/B,, so no great contribution of the testers was observed. Lack of significance of line x tester interation may indicate an A/B type of response.

Banzinger *et al*., (2000) indicate that selection based on grain yield alone is inefficient, suggesting that selection efficiency can be improved through the use of secondary traits of adaptive value, such as ASI.

4.1.2.2 Serere

Mean performance on AD, SD and ASI are presented in Appendix 1. ASI ranged from -0.5 to 2.3 days, with 10% of 58 evaluated testcrosses ranging from -0.5 to 0 days. However, only line WL-429-14-25, presented a negative ASI of -0.5 days. Though the rang of flowering dates and ASI were smoll the differences were highly significant (Table 6, $P<0.001$). Likewise highly sgnificant variation was revealed for means of the testcrosses for ASI. Under favourable growing condictions, silking dynamics for the two testers were nearly identical but, ASI was not. This would be expected since we assume that all plants had plant growth rates well above the minimum needed to suport ear growth (Borrás, e*t al*. 2007).

A very low (MSV) disease response was observed at Serere, but even so, the very small difference between testers was significant, and non-significant among lines (Table 6). The low disease pressure on that location probably was due to unfavourable condition such regular rains and absence of drought period improper for development of *Cicadulina* species. Non-significant among lines may was because of low disease pressure and low scores, so the lines means square was so closer to error mean square.

The TLB response was also low, with mean scores of 1.5 and 1.4 for testers A and B, respectively. Significant differences were observed among testcrosses due to lines (Table 6), with disease ranging from 0.93 to 2.4, the low scores are due to low disease pressure on this location. Turcicum leaf blight caused by *E. turcicum*, becomes a more serious disease when climatic conditions are cool with high relative humidity (Muriithi, 2001). Those conditions were not present at Serere site, resulting in a low TLB disease response.

Table 6: Single environment analysis of variance of mean square and means for key trait and agronomic traits of testcrosses of 58 F3 lines with testers A and B, season 2012A (March-October), at Serere

		Serere-MS								
Source of variation	Df	YLD	100 GW	KR	EPP	TLB	MSV%	AD	SD	ASI
Lines	57	0.87	8.01**	0.51	0.015*	0.11*	0.51	3.16***	3.73***	0.54***
Tester	1	4.72*	91.7***	1.30*	0.0002	0.20	3.22*	0.13	0.70	0.06
Line*Tester	57	1.05**	4.25	0.31	0.0095	0.08	0.51	2.10*	2.30	0.29
LEE	105	0.61	4.19	0.39	0.010	0.07	0.54	1.37	1.79	0.24
Grand mean		7.33	40.6	12.8	1.17	1.43	0.30	66.3	67.0	0.67
CV%		10.7	5.04	4.88	11.7	18.5	244	1.77	1.99	73.1
Tester A Mean		7.13	39.8	12.9	1.17	1.47	0.47	66.3	66.9	0.65
Minimum		5.00	35.8	11.8	0.95	0.98	0.58	62.3	63.1	-1.04
Maximum		9.27	46.3	14.2	1.44	2.43	3.29	70.2	70.6	2.89
Variance among TCs		0.73	6.32	0.32	0.012	0.11	0.77	2.35	2.67	0.49
Tester B Mean		7.53	41.5	12.7	1.17	1.39	0.13	66.4	67.1	0.69
Minimum		5.47	36.9	10.9	0.93	0.93	0.53	62.3	62.5	-0.03
Maximum		10.13	47.7	13.9	1.44	2.30	1.97	70.4	71.4	2.10
Variance among TCs		1.20	5.94	0.50	0.013	0.09	0.25	2.91	3.37	0.34

*, **, *** indicates significance at 0.05, 0.01, and 0.001 probability levels, respectively. Serere-MS=Serere mean square; AD= Anthesis date; SD=Silking date; MSVi=Maize streak virus incedence; SD=Standard deviation; KR=Kernel rows; YLD=Yield tons per hectar; 100 GW= 100 Grain weight; TLB=Turciccum leaf bligth; LEE=Lattice effective error

Serere was selected primarly as the location for testing drought tolerance, but the area received good rainfall without drought during the period of the experment (season 2012A March-October). The site did not provide information we desired regarding drought tolerance or segragation for disease resistance, but did yield well and reveal yield differences.

The testcross means for grain yield at this site varied significantly between tester and the tester by line interaction was significant (Table 6). Tester A had a mean yield of 7.13 t/ha (5 to 9.3 t/ha), And tester B mean yield of 7.53 t/ha (5.5 to 10.13 t/ha). It would seem that tester B is carries alleles for the desirable yield trait, as also noted in greater weight for 100 grains. A desirable cross is one in which the parents are genetically divergent and produce progeny with better performance (Legesse *et al*. 2009).

Table 7: Single environment GCA and SCA mean square and variance component for yield of testcrosses at Serere

Source of variation	df	S.S	M.S	Var. Components
GCA_L	57	49.66	0.871	0.132
GCA_T	1	4.73	4.728	0.030
SCA (LinexTester)	57	59.95	1.052	0.222
LEE	105	63.76	0.607	0.607
SE_{GCA-L}			0.389	
SE_{SCA}			0.551	

$h^2 = (GCA_L + GCA_T)/(GCA_L + GCA_T + SCA + \sigma^2 e)$

$h^2 = 0.16$

Baker's ratio = $(GCA_L + GCA_T)/(GCA_L + GCA_T + SCA)$

Baker's = 0.42

The highest GCA_L effects for yield were observed for inbred line WL-429-14-33 (at 1.2 t/ha), followed by WL-429-14-24 (1.1 t/ha) and WL-429-14-40 (0.95 t/ha). Unfortunately both narrow sense heritability and Baker's ratio were low, the contribution of the parents can not predict the performance of the offspring wey well, so selection for yield trait would be very difficult at an early stage. Once again, as mentionad earlier, to improve the narrow sense heritability (h^2) and Baker's ratio we must increase the number of repetitions and reduce error variance in the experiment and it necessary to apply more effort to breeding for the desired results (Welcker *et al.*, 2007).

4.1.2.3 Bulindi site

In the Bulindi site, the AD, SD, and ASI, varied significantly among lines and testers ($P<0.05$-0.001), though non-significant differences were observed for line by tester interactions (Table 8). In terms of performance, lines WL-429-14-28, 27, 50, 15 and 49 showed negative ASI's, ranging from -1.3 to -0.2 days. About 12% of the total lines showed ASI's of -1.3 to 0, and 88% had ASI's ranging from 0.3 to 2.5 days. The maize crop responds differently under variable conditions that alter the plant's growth. During this growth period, the most affected aspect is that of flowering dynamic, the most widely observed being the temporal separation of male (anthesis) and female (silking) floral maturity, (anthesis-silking interval) (Borrás *et al*., 2007).

In our study, the variation observed in AD, SD and ASI (Table 8) is probably due to the irregular rainfall, field variability and the shadow effect provided by trees around field experiment.

The mean performance for MSV incidence in the testrosses (TC) was moderate, with a grand mean of 9%. 0.12 to 29% for Tester A and 0.16 to 17% for Tester B (Table 8)

Lines that showed a high level of MSV resistance in Namulonge were also consistently resistant at Serere and Bulindi. Tester B transmitted more resistant to MSV than Tester B. Lines WL-429-14-17, WL-429-14-82, WL-429-14-71, WL-429-14-56 and WL-429-14-36 were indentified to have the highest resistance to MSV. Analyses of variance showed significant differences for testcross means among lines and testers ($P<0.05$).

Kyetere *et al*., (1995; 1999 cited by Asea 2005) identified a major QTL on the short arm of chromosome 1(1S - bin1.04) and designated it *msv1*. The same locus was identified by Welz *et al*., (1988) in a population derived from crossing CML202, (an MSV resistant inbred) with Lo951, (a susceptible inbred), using a different viral isolate.

Additional studies by Pernet (1999a and 1999b) using two other resistance sources, identified a major QTL in the same genomic location on chromosome 1S. He proposed that MSV resistance was under the control of two genetic systems, one arising from a major gene on the short arm of chromosome1, and the other conditioned by minor genes on chromosomes 2, 3 and 10, that confer quantitative resistance. The consistent results of these studies, suggest that different sources of resistance likely contain the same resistance factor, *msv1* that accounts for the large phenotypic variance associated with differences of disease response among genotypes.

The reaction to Turcicum leaf blight (TLB) was also moderate among the testcrosses in Bulindi, with a mean score of 2.1 for each tester, but with significant difference among lines (Table 8). Although lines showed significant differences, the "lines" mans square was not that much bigger than the error mean square.

The mean yield in the Bulindi site, yield was 3-8 t/ha for tester A, and 2-9 t/ha for tester B. Non-significant differences were observed, among lines, testers, and line by tester interactions. This would indicate field variability that was not effectively controlled by lattice blocking leading to a large expermental error. Also non-significant differences were observed for traits such as kernel row and 100 grain weight for tester and line x tester interaction. However, significant differences were observed for testcross means among lines for kernel row and grain weight (Table 8).

Table 8: Single environment analysis of variance of mean square and means for key trait and agronomic traits of testcrosses of 58 F_3 lines with testers A and B, season 2012A (March-October), at Bulindi

		Bulindi-MS							
S. Variation	Df	YLD	100 GW	KR	EPP	TLB	MSV%	AD	SD	ASI
Lines	57	2.47	7.12**	0.56*	0.017	0.22**	31.3*	6.07*	8.77**	1.07**
Tester	1	0.85	11.9	0.31	0.082*	0.04	646.***	39.3**	121***	22.5**
Line*Tester	57	1.66	4.09	0.39	0.019	0.15	14.8	4.48	6.68	0.61
LEE	105	2.03	4.15	0.33	0.020	0.13	20.3	4.50	4.97	0.56
Grand mean		5.74	35.7	12.8	0.94	2.12	9.61	70.9	71.9	1.00
CV%		24.8	5.71	4.49	15.0	17.0	46.9	2.99	3.10	74.8
Tester A Mean		5.82	35.4	12.8	0.96	2.11	11.9	70.4	70.9	0.56
Minimum		3.16	31.3	11.1	0.62	1.35	0.12	66.5	66.0	-2.00
Maximum		8.31	43.2	14.8	1.30	4.16	23.8	77.5	79.5	2.48
Variance among TCs		1.48	4.90	0.56	0.018	0.20	27.5	5.45	8.04	0.83
Tester B Mean		5.65	36.0	12.7	0.91	2.14	7.25	71.5	73.0	1.44
Minimum		2.70	30.8	11.1	0.58	1.40	0.16	67.5	68.5	-1.01
Maximum		9.27	41.4	14.2	1.29	3.43	17.6	77.0	80.5	3.50
Variance among TCs		2.65	6.31	0.38	0.018	0.16	18.6	5.10	7.41	0.86

*, **, *** indicates significance at 0.05, 0.01, and 0.001 probability levels, respectively. Bulindi-MS=Bulindi mean square; AD= Anthesis date; SD=Silking date; MSVi=Maize streak virus incedence; SD=Standard deviation; KR=Kernel rows; YLD=Yield tons per hectare; 100 GW= 100 Grain weight; TLB=Turciccum leaf bligth; LEE=Lattice effective error

Table 9: Single environment GCA and SCA mean square and variance component for yield of testcrosses at Bulindi

Source of variation	d.f.	S.S	M.S	Var. Components
GCA_L	57	140.8	2.471	0.208
GCA_T	1	0.86	0.860	-0.01
SCA	57	94.60	1.660	-0.20
LEE	105	213.0	2.028	2.03
SE_{GCA-L}			0.712	
SE_{SCA}			1.007	

$h^2 = (GCA_L+GCA_T)/(GCA_L+GCA_T+SCA+\sigma^2e)$

$h^2 = 0.098$

Baker's ratio = $(GCA_L+GCA_T)/(GCA_L+GCA_T+SCA)$

Baker's ratio = 1

Bulindi was the location were highest error variance was observed, almost equalling the GCA_L mean square, and greater than the GCA_T and SCA mean squares which give negative estimate of their respective variance components (Table 9). Low and negative GCA's and high error values resulted in a low heritability of 0.098, suggesting that selection based on testcross means would not be effective at an early stage of inbreeding. Baker's ratio was 1.00, since the variance component for SCA was negative and therefore considered to be zero.

At Bulindi, 17 lines (29%) of the 58 exhibited a large positive GCA for yield (Appendix 3), and the best combinations were from crosses between lines with tester B. Therefore tester B can tentatively be best option for producing high yielding hybrids.

4.1.3 Testcross performance averaged across locations

Analysis of means for testcross performance among lines in each location showed significant differences for most of the traits studied. The combined analysis also revealed significant differences for locations, line and line x environment (LxE) interactions (Table 10). The presence of significant LxE showed the inconsistency of performance of genotypes across enviroments for most traits except 100 grain weight and anthesis date.This suggest that there

was field variability and ineffective blocking that may have contributed to the large error mean square at Bulindi. Mosisa *et al.,* (2001) noted that large pooled error associated with high error on a single location can have a negative influence on identifying differences. The results fo this experiment also showed that factors other than elevation and rainfall distribution during the growing period had a great impact on the performance of the maize genotypes.

Findings of Mosisa *et al.,* (2001), conform to our results. For example, Serere had low mean square for yield, the lines were significant differences becaus of a low error mean square .In contrast Bulindi environment showed high yield which lead to large mean square for yield but non-significance differences were observed because of the large error mean squere. This latter could be attributed to irregular rainfall that occurred during vegetative growth there and field variability, leading to increased error thus making it difficult to identify differences in genotypes.

Significant differences were observerd on environment by tester (TxE), in traits such yield, 100 grain weight, anthesis date (AD), silking date (SD) and anthesis-silking-interval (ASI) (Table 10). Line, tester and environment (LxTxE) interaction was significant for yield, grain weight (100 GW), ear per plant (EPP), turcicum leaf blight (TLB), silking date (SD) and anthesis silking interval (ASI) while AD and MSV incidence were non-significant. Non-significance observed for MSV incidence across location probably was due to low mean squere of LxTxE which was closer to error mean squere (pooled error) used as F-test for the across locations analysis (Figure 6).

Significant differences was observed for Line x Tester interaction for traints as turcicum leaf blight (TLB), maize streak virus incidence (MSV), anthesis date (AD), silking date (SD), and Anthesis silking interval (ASI). This indicate that the lines used in the present study were diverse and the difference were present in the progeny.

Kyetere *et al*., (1995; 1999 cited by Asea 2005) identified a major QTL on the short arm of chromosome 1(1S - bin1.04) and designated it *msv1*. The same locus was identified by Welz *et al*., (1988) in a population derived from crossing CML202, (an MSV resistant inbred) with Lo951, (a susceptible inbred), using a different viral isolate.

Derera *et al*. (2008) studying the type of gene action controlling yield traits under drought stress and non-drought conditions a observed highly significant GxE interaction for yield under non-drought conditions.

Legasse *et al*. (2009) found non-significant differences when investigating the cross of six (6) testers and twenty six (26) inbred lines for improve yield and Turcicum leaf blight resistance. Xingiming *et al*. (2001) suggested that non-significance of GxE interaction is an indication that the genotypes should be quite stable in their response in the different location.

Peiris and Hallauer, (2005), in studying tripple test-crosses in maize revealed significant mean squares due to diversity in the parents (both lines and testers), crosses and parents versus crosses indicating that lines used in his study were diverse Significant differences were observed in all traits except number of krnel rows (KR).

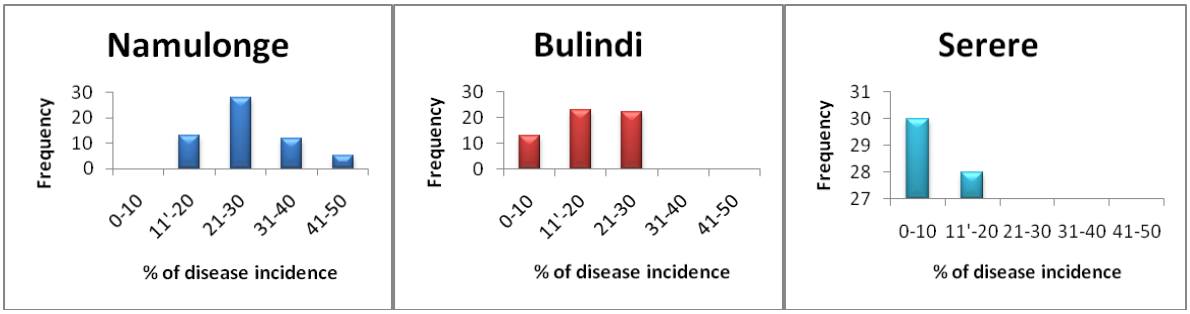


Figure 6: Maize streak virus disease incidence at three different testing sites (testcross average for the 58 F_3 lines)

Table 10: Mean square and means from multi-location analysis of variance for key trait and agronomic traits of testcrosses of 58 F_3 line with testers A and B, in Uganda season 2012A (March-October). Mean squares are on an entry mean within environment basis.

Source of variation	Df	YLD t/ha	100 GW_g	KR	EPP	TLB	MSV%[1]	AD	SD	ASI
Tester	1	7.03	297	0.42	0.025	0.01	1930	44.7	156	33.1
Line	57	1.39	16.2***	0.74*	0.014	0.29***	109***	6.89***	7.83***	1.18***
Line.xTester	57	1.14	5.58*	0.3	0.014	0.14*	33.4*	2.94*	4.09*	0.54*
Tester*Envt	2	6.36**	44.7***	0.76	0.028[?]	0.21	63.6	9.63*	30.9***	7.15***
Line x Envt	114	1.27***	3.38	0.46***	0.012***	0.12***	47.3***	2.03	3.13***	0.53***
Line x Tester x Envt	114	1.20***	3.61***	0.40***	0.010***	0.08***	20.1	2.22	2.78***	0.36***
Pooled Error	315	0.54	1.93	0.18	0.006	0.04	18.9	1.05	1.22	0.20
Grand mean		6.39	38.5	13.2	1.06	2.01	18.7	69.3	69.9	0.68
CV%		11.5	3.6	3.21	7.3	9.95	23.4	2.05	1.58	65.7
Tester A Mean		6.25	37.6	13.2	1.07	2	21.3	68.9	69.3	0.37
Standard deviation		1.24	2.98	0.81	0.14	0.54	11.7	2.52	2.6	0.82
Variance		1.53	8.88	0.66	0.02	0.29	138	6.37	6.77	0.67
Tester B Mean		6.53	39.5	13.1	1.05	2.01	15.5	69.6	70.6	0.99
Standard deviation		1.7	3.47	0.84	0.15	0.6	11.0	2.87	3.21	0.84
Variance		2.87	12	0.71	0.02	0.36	121	8.23	10.3	0.70
SEM Line		0.46	0.75	0.27	0.046	0.14	3.44	0.58	0.72	0.29
SEM Tester		0.19	0.51	0.06	0.0014	0.039	0.74	0.24	0.43	0.20
SEM Line*Tester		0.63	1.09	0.36	0.058	0.167	3.17	0.86	0.96	0.35
LSD Line		1.29	2.1	0.77	0.13	0.39	8.13	1.63	2.02	0.83
LSD Tester		1.16	3.08	0.4	0.08	0.21	13.3	1.43	2.57	1.23
LSD Line*Tester		1.86	3.36	1.06	0.17	0.52	11.6.	2.42	3.02	1.24

*,- **, *** indicates significance at 0.05, 0.01, and 0.001 probability levels, respectively. AD-=Anthesis date mean square; SD-=Silking date mean square; ASI-=Anthesis silking interval mean square; MSV%=Maize streak virus incedence mean square;TLB=Turciccum leaf bligth; 100 GWg=100 grain weigth in grams; EH=Ear higth; Cob/plt=Cob per plant; KR=Kernel row; YLD=Yield; Envt*Line=Environment, line interaction; Envt*Tester=Environment tester interaction; Line xTester x Envt=Line, Tester, Environment interaction; LSD=Least significant differences; SED=Standard errors of differences; CV%=Coeficient of variation in percentage.

[1]analysis was done considaring two locations ony (Namulonge and Bulindi, because Serere disease pressure was low df=1 and df=57 for lines

4.1.4 Relative magnitude of lines and lines x environment variance components

Estimation of variance components was based on analysis of expected mean squares. In general, error variance was relatively higher in magnitude than Genotype x Environment interaction (GxE), revealing unpredictable performance of GxE. Although significant GxE terms were usually lower than the pooled error. However, not always; yield (YLD), number of kernel rows (KR), ear per plant (EPP), Turcicum leaf blight (TLB), maize streak virus (MSV), silking date (SD) and anthesis silking interval (ASI) line variance components was larger than LxE interaction. Also yield, KR, and SD LxTxE interaction variance component was larger than error (Table 10).

Table 11: Multi-location variance component for key trait and agronomic traits of testcrosses of 58 F3 line with testers A and B, in Uganda season 2012A (March-October). Entry mean per environment basis.

Source of var.	YLD	100 GW	KR	EPP	TLB	MSV%[a]	EH	AD	SD	ASI
Tester (GCA_T)	0.004	1.44	-0.001	0.0000	-0.001	16.1	41.0	0.197	0.716	0.148
Line (GCA_L)	0.019	2.14	0.047	0.0003	0.029	15.6	33.9	0.809	0.783	0.107
LinexTester (SCA)	-0.018	0.66	-0.034	0.0014	0.018	6.64	20.0	0.241	0.435	0.058
Tester*Envt (GCA_TxEnvt)	0.089	0.71	0.006	0.003	0.002	0.75	8.00	0.128	0.486	0.117
Line*Envt (GCA_LxEnvt)	0.369	0.72	0.138	0.00035	0.037	14.2	10.5	0.005	0.954	0.166
L*T*E (SCAxEnvt)	0.660	1.68	0.217	0.0041	0.039	0.56	11.0	0.193	1.562	0.163
Pooled Error'	0.541	1.94	0.181	0.0060	0.045	18.9	20.7	1.05	1.218	0.20
SE_{GCA-L}	0.46	0.49	0.21	0.014	0.110	3.44	1.32	0.038	0.445	0.235
SE_{SCA}	0.63	1.09	0.36	0.058	0.167	3.17	1.91	0.86	0.0.96	0.34
Vph	0.23	2.71	0.123	0.002	1.28	27.4	40.84	1.15	1.30	0.20
BSH_{acr}	0.08	0.79	0.38	0.11	0.60	0.57	0.83	0.71	0.60	0.55
h^2	0.03	0.52	0.14	0.02	0.22	0.44	0.59	0.31	0.37	0.38
Backer's	1.0	0.84	1.0	0.13	0.60	0.83	0.79	0.81	0.78	0.81

ExTxL=Environment, Tester, Line interaction; $BSH_{acr=}$Broad Sense Heritability across location; AD = anthesis date, SD silking date, ASI = anthesis silking interval, TLB = turcicum leaf blight; MSV=Maize streak virus incedence; Plt H=Plant higth; Ear H=Ear higth; EPP=ear per plant; KR=Kernel rows; YLD=Yield; 100 GW=100 Grain weigth.

[a] analysis was done considering two environments, (Namulonge and Bulindi) because Serere disease presure was low, (df=1)

Interestingly, lines had a large variance component than the error variance for traits such as 100 GW, MSV% and SD. A negative contribution (-2.40) of lines was observed for plant height (PH) result not showed. The overall comparisons of variance components suggest that lines were significantly different from each other.

Broad sense heritability (BSH) on an, entry mean within each environment was considered reasonably good at 0.45 for AD and 0.43 for SD, was also good on the basis of means across locations. The BSH were 0.71 for AD and 0.60% for SD and for traits such as ASI (0.55), MSV (0.57), 100 GW (0.79), and TLB (0.60). This suggests that the selection can be done easily at an early stage since a high portion of the phenotypic variability for ASI, MSV, 100 GW and TLB across locations was accounted for by genetics. Since error was reduced by increasing the number of observations (n) or replications across locations the heritability of these traits was increased.

Richard *et al*. (2006) suggested that increasing the number of testing locations, improving field uniformity and high quality data in each location are keys to improving selection.

Mohammed's finding (2009) that broad sense heritability (H) was intermediate for yield (0.48) suggested that environmental effects had an important role in the variation observed for the trait. Narrow sense heritability (h^2) was moderately low (0.27), indicating that selection for high yield will require effort. During calculation of the variance components, negative values of GCA and SCA effects were replaced by zero.

There was a moderate BSH for kernel rows (0.38) and a low BSH for ears per plant (0.11), and yield (0.08), on a mean basis across environments, and also very low narrow sense heritability (h^2) and Baker's ratio (Table 11). This is probably a result of lack of genetic variance among parents used to derive this population or inbreds. Since the breeding strategy for selecting for those traits will be very difficult in the F_3 generation, selection could be more efficiently done at a later stage F_5 or F_6-testcrosses.

Very low narrow sense heritability and non-significant values for GCA and SCA, was found in the across site analysis of yield. Line x environment interaction (LxE) and error variance had larger variance components than lines, suggesting that effective identification of promising lines can be done more successfully in later generations.

Otherwise selection among inbred lines should focus on the size of GCA effects, with the choice of test environments taking into account the magnitude of narrow sense heritability or NS-CGD in those environments. The high error variance at Bulindi and the sizeable GxE effect in the across-site analysis reduced reliability of selection.

Richard *et al*., (2006) suggested that increasing the number of testing locations, improving field uniformity and high quality data in each location are keys to improving selection.

Summarizing the analysis of line by environment (LxE) means for test-cross performance across locations showed high significant differences ($P<0.001$) for almost all the key traits such as yield, Turcicum leaf blight, maize streak virus and anthesis-silking interval. The presence of significance LxE interaction shows the inconsistency of performance of genotypes across environments. The error variance component was relatively higher in magnitude than other variance components for most traits except for MSV, SD and ASI where the Lx E component was larger than the LxTxL interaction. The low magnitude of variance components in the LxE interaction suggests that there was field variability and ineffective blocking that may have greater contribution to the large error in particular at Bulindi.

4.1.5 Determination of the relationship of selected traits between inbreds of different generations and inbred-F_3 testcrosses

In hybrid breeding programs, testcross evaluation of lines can be done during the early stages of selfing or delayed until the lines are near homozygosity. In this section, the usefulness of early testing is evalueted by comparin phenotypic correlations between inbreds at different generations of selfing and performance of F_3-testcrosses for selected traits.

The results of regression analysis are presented in Table 12. Differences were observed in the correlation coefficient for both magnitude and direction for the ASI trait at different generations. This was the only significant correlation and had a moderate correlation to the anthesis silking interval in generations F_2 to F_3 ($r=0.36$, $b=0.60$), indicating that reduction of one unit of anthesis silking interval in the F_2 would be associated with 0.36 days of ASI

difference in the F_3 generation and also the level of heritability is verry good (0.60). Significant correlation of ASI between F_3 and TCA (r = 0.33, b = 0.08), suggesting that decrease of one unit of anthesis silking interval would be associated with 0.33 days of difference in ASI, though the heribability value is verry low in $F_{3:}$TCA but the relationship is still good.

Turcicum leaf blight exhibited significant correlations with r values of 0.28 for F_3TCA, 0.26 F4:TCA, 0.26 for F_4TCB and b values of 0.15 for $F_{3:}$TCA, 0.14 for $F_{4:}$TCA and 0.18 for $F_{4:}$TCB implying that increase one unit of turcicum leaf blight resistance in the F_3 and F_4 generations resistance of test-crosses increases in 0.15 in the avarege. Moderate and significant correlation of maize streak virus was observed in $F_{4:}$TCB (r = 0.23, b = 0.68), implying that improvement of meize streak virus (MSV) resistance in F4 would be associated with 0.68 level of resistance of MSV in TCB.

Positive and highly significant associations were noted for kernel rows from the F_3 generation and tescrosses (Table 12). For correlaction between traits maize streak virus, Turcicum leaf blight and number of ear per plant exhibited positive associations with grain yield with significant for turcicum leaf blight and the ear per plant at probability levels of 0.05 and 0.01 respectively.

Parent-offspring (PO) regression estimates of heritability ("b") were high for ASI in the $F_{2:3}$ generation (60% F_2 plants to F_3 rows) and for MSV resistance in the F_4 to testcross (68%). Moderate heritablity ("b") was shown for TLB, in $F_{3:4}$, and F_4TCA and TCB and also for kernel rows number for $F_{3:}$TCA and F_3:TCB.

In correlation between traits significant and moderate relationship between ear per plant and yield (r = 0.34 and b = 0.32) reveals that increases of one ear per plant would result in a 3.2 kg/ha yield increase. In another important association observed between maize streak virus disease (MSV) and yield, we noted that in this experiment increases of one unit of MSV disease incidince yield decreases in 30 kg/ha. Also significant difference was revealed bettween TLB-MSV (r = 0.30, b = 5), suggesting that presence of TLB infection would be associated with MSV disease incidence.

Bernardo (1990) noted that the probability of correctly retaining lines that are genetically superior in testcrosses at homozygosity is higher in later selfing generations than in earlier, or the probability increases as heritability increases so does the probability of retention of the best genotype. The level of heritability desireable to consider retaining a genetically superior individual is at least 0.60, even in the early selfing generations. Jesen *et al*., (1983) attested that the phenotypic correlation between the F_1 and F_4 testcrosses in maize for grain yield, when crossed to different testers was about 0.67, with a heritability of 0.80.

In this study, the results contradict the findings of Bernardo, (1990) and Jesen *et al*., (1983), because our levels of heritabilities were very low in $F_{3:}$TC's except the heritability in F_4:TCB for maize streak virus suggesting that the results could have been influenced by enviromental effects.

Table 12: Regression of inbred generation F_2 on F_3, on F_4 and of inbred generations with F_3 testcrosses from both heterotic Groups (A and B) (n=58), [a] regression between traits in testcross was done at testcross avaraged tacross 3 locations

		Parent - offspring regression		Correlation/regression between traits of TC's[a] (n=58)		
Trait	Generations	r	b	Traits	R	b
ASI	$F_{2:3}$	0.36**	0.60	EPP-YLD	0.34**	0.321
	$F_{3:4}$	-0.03	-0.018	MSV-ASI	0.07	-1.28
	F_3:TCA	0.33*	0.08			
	$F_{3:}$TCB	0.18	0.06	TLB-ASI	0.04	19.21
	F4:TCA	-0.17	-0.07	MSV-YLD	-0.13	-0.032
	F4:TCB	-0.018	-0.009	TLB-MSV	0.30*	5.00
TLB	$F_{2:3}$	-0.052	-0.030			
	$F_{3:4}$	0.252	0.252			
	$F_{3:}$TCB	-0.112	-0.051			
	$F_{3:}$TCA	0.28*	0.150			
	F_4:TCA	0.26*	0.140			
	F_4:TCB	0.26*	0.176			
MSV	$F_{2:3}$	0.055	0.111			
	$F_{3:4}$	0.068	0.048			
	$F_{3:}$TCB	0.111	0.030			
	$F_{3:}$TCA	0.019	0.007			
	$F_{4:}$TCB	0.23*	0.680			
KR	$F_{3:}$TCA	0.39***	0.18			
	$F_{3:}$TCB	0.33***	0.13			

*, **, *** indicates significance at 0.05, 0.01, and 0.001 probability levels, respectively. r^2=Coefficient of determination; r=Correlation coeficient; b=Regression coeficient; $F_{2:3}$=Regression of F_3 on F_2; $F_{3:4}$=Regression of F_4 on F_3; $F_{4:}$TCB=Regression of testcross with tester B on F4; $F_{4:}$TCA=Regression of testcross with tester A on F4 genetation, for traits as MSV=Maize streak virus, TLB=Turciccum-- leaf bligth,

4.2 Selection indices

Five indices of selection were developed: 1) inbred performance of $F_{2:3}$; 2) inbred performance $F_{2:3:4;}$ 3) performance of test-cross B across environment. 4) combination of mean of both testers (A and B) across enviroments, and 5) combination of inbreds generations and their testcrosses.

4.2.1 Inbreds only indices

Indices for the inbreds were developed with more weight given to Turcicum leaf blight (TLB) score, maize streak virus (MSV) incidence and anthesis silking interval (ASI) because of the expected inbred-hybrid correlation for these traits and their importance in the resulting hybrids, also resistance to TLB and MSV, along with drought tolerance are priority traits for selection. The ASI was used as an indicator of drought tolerance and productivity, since ASI has a strong relationship to yield especially under drought or nitrogen stress. High multipliers were used for traits in the F_3 and F_4 generations order for them to have more contribution in the percent of index difference. The indexes were created such that the lowest scores indicated the most desirable lines to select, (see Tables 13 and 14, Appendix 1).

The index value from these two indices revealed that four (4) inbred lines (WL-429-10; WL-429-78; WL-429-85 and WL-429-4) scored consistently in the top 10 lines (Tables 13 and 14). This probably indicates that even if these lines continued to be selfed there would be little change because they were already stable. Also, they were four (4) inbred lines that consistently performed poorly, ranking in the 10 lowest (WL-429-14-90; WL-429-14-2; WL-429-14-28; and WL-429-14-24).

Table 13: Selection index values of the 10 best and 10 worst out of 58 inbreds, based on key traits in only the F_2 and F_3 lines. Smaller index values indicate superior performance

		Traits	TLB F2	TLB F3	MSV F2	MSV F3	AD, F2	AD, F3	SD, F2	SD F3	ASI, F2	ASI F3	F3 KR
		Multiplier	5	39	5	21	0.5	1	0.5	4	2	8	33
		Percent of index[b]	2	29	3	30	1	8	2	35	6	29	78
Rank	Index	Line											
1	1722	WL-429-78	1.0	2.5	1.5	2.1	67.0	75.0	66.0	75.3	-1.0	0.3	12.0
2	1735	WL-429-10	1.0	2.5	2.0	1.5	67.0	86.0	66.0	80.0	-1.0	-3.0	11.3
3	1741	WL-429-49	1.0	1.5	2.0	2.4	68.0	77.0	66.0	76.0	-2.0	-1.0	10.3
4	1743	WL-429-56	1.0	2.0	2.0	2.1	67.0	66.2	68.0	69.6	1.0	3.4	11.3
5	1752	WL-429-96	1.0	2.3	2.0	2.8	68.0	80.5	67.0	79.5	-1.0	-1.0	10.0
6	1757	WL-429-40	1.0	1.9	1.0	1.3	70.0	67.6	73.0	67.2	3.0	-0.4	10.0
7	1757	WL-429-50	1.3	2.4	2.0	1.7	68.0	70.6	68.0	71.2	0.0	0.6	11.3
8	1760	WL-429-85	1.0	2.2	2.0	1.0	69.0	71.2	68.0	69.8	-1.0	-1.4	10.7
9	1763	WL-429-32	1.0	3.4	2.0	2.4	68.0	76.6	66.0	77.6	-2.0	1.0	11.3
10	1763	WL-429-4	1.3	3.0	2.0	2.3	68.0	73.0	70.0	72.0	2.0	-1.0	10.3
49	1863	WL-429-90	1.5	2.2	1.5	2.6	72.0	73.8	73.0	79.4	1	5.6	13.0
50	1866	WL-429-2	1	2.3	2	4.2	72.0	76.6	73.0	80.6	1	4	10.0
51	1874	WL-429-33	1	1.5	2	2.6	74.0	68.0	72.1	67.5	-2	-0.5	11.3
52	1874	WL-429-108	1.3	1.9	2	2.6	73.0	76.8	74.0	77.2	1	0.4	10.7
53	1878	WL-429-28	1	2.9	2	3.6	74.0	71.8	71.4	68.5	-3	-3.25	11.3
54	1879	WL-429-17	1.8	2.3	2	1.7	74.0	74.4	72.3	75.6	-2	1.2	10.7
55	1891	WL-429-109	1.3	1.7	2	2.8	73.0	72.2	74.0	72.6	1	0.4	13.3
56	1897	WL-429-30	2.0	2.4	2	1.9	74.0	74.2	74.0	75	0	0.8	11.7
57	1903	WL-429-24	1.5	3.2	2	3.4	73.0	72	74.2	73.8	1	1.8	13.0
58	1947	WL-429-36	1.0	3.1	2	3.3	76.0	76.3	74.1	75.75	-2	-0.5	12.7
Mean	1821		1.2	2.2	1.8	2.6	70.9	73.5	70.7	74.4	-0.2	1.0	11.5

[b] calculation of this percentage is explained in section 3.8.1. Trait abbreviations are in the list of abbreviations,
TLB,F_2=Turcicum leaf blight score at F_2 generation; MSV,F_3=Maize streak virus score at F_3 generation;
AD,F_2=Anthesis date at F_2 generation; SD,F_2=Silking date at F_3 generation; ASI,F_2=Anthesis silking interval F_2 generation

Table 14: Selection index values and trait scores of the 10 best and 10 worst lines of 58 inbreds based on key traits of F_2, F_3 and F_4 lines. The low indexes values indicate superior performance.

			Traits	TLB F2	TLB F3	TLB F4	MSV F2	MSV F3	MSV F4	AD F2	AD F3	AD F4	SD F2	SD F3	SD F4	AS F2	ASI F3	ASI, F4	F3 K.R
			Multiplier	3	13	11	5	17	9	0.5	1	1	0.5	1	8	3	11	14	12
			% of index[b]	1.2	10.5	11.9	2.9	26.0	11.1	1.5	8.5	7.7	2.1	9.4	58.7	9.3	43.7	21.6	30.9
$F_{2,3}$ Rank	Rank	Index	Line																
1	1	780	WL-429-78	1.0	2.5	2.0	1.5	2.1	1.5	67.0	75.0	66.0	66.0	75.3	66.0	-1.0	0.3	0.0	12.0
19	2	804	WL-429-119	1.0	2.2	1.0	1.0	2.8	1.0	71.0	69.4	67.0	71.0	72.0	67.0	0.0	2.6	0.0	12.0
11	3	807	WL-429-34	1.0	2.2	2.3	2.0	2.0	1.0	69.0	77.0	73.0	66.0	77.0	71.0	-3.0	0.0	-2.0	10.7
2	4	813	WL-429-10	1.0	2.5	1.3	2.0	1.5	1.3	67.0	86.0	74.0	66.0	80.0	75.0	-1.0	-6.0	1.0	11.3
12	5	825	WL-429-105	1.0	2.2	1.5	1.0	2.3	1.0	70.0	71.8	69.0	69.0	73.4	70.0	-1.0	1.6	1.0	12.3
8	6	831	WL-429-85	1.0	2.2	1.9	2.0	1.0	1.0	69.0	71.2	73.0	68.0	69.8	74.0	-1.0	-1.4	1.0	10.7
31	7	833	WL-429-71	1.0	2.0	1.2	2.0	2.2	1.0	71.0	69.8	75.0	70.0	70.2	75.0	-1.0	0.4	0.0	12.7
34	8	837	WL-429-94	1.0	2.4	1.3	1.0	2.7	2.1	72.0	74.8	74.0	72.0	77.8	72.0	0.0	3.0	-2.0	13.3
10	9	839	WL-429-4	1.3	3.0	2.5	2.0	2.3	1.0	68.0	73.0	72.0	70.0	72.0	71.0	2.0	-1.0	-1.0	10.3
53	10	847	WL-429-28	1.0	2.9	1.3	2.0	3.6	1.0	74.0	71.8	78.0	71.0	68.5	77.0	-3.0	-3.3	-1.0	11.3
48	49	951	WL-429-57	1.5	2.3	1.5	2.0	2.3	1.0	73.0	75.6	84.0	71.0	77.2	83.0	-2.0	1.6	-1.0	10.7
22	50	951	WL-429-15	1.0	3.3	1.8	2.0	2.3	1.0	70.0	70.0	79.0	69.0	72.4	80.0	-1.0	2.4	1.0	11.7
40	51	952	WL-429-102	1.5	2.2	1.0	2.0	1.8	3.0	72.0	84.3	73.0	72.0	86.0	75.0	0.0	1.7	2.0	10.0
46	52	954	WL-429-101	1.3	1.8	1.0	2.0	3.0	1.0	72.0	78.4	77.0	72.0	81.2	78.0	0.0	2.8	1.0	11.0
57	53	955	WL-429-24	1.5	3.2	2.0	2.0	3.4	1.0	73.0	72.0	78.0	74.0	73.8	79.0	1.0	1.8	1.0	13.0
36	54	957	WL-429-89	1.3	1.8	2.0	1.0	2.4	1.5	73.0	77.0	77.0	74.0	82.6	76.0	1.0	5.6	-1.0	10.0
49	55	964	WL-429-90	1.5	2.2	1.5	1.5	2.6	2.0	72.0	73.8	79.0	73.0	79.4	79.0	1.0	5.6	0.0	13.0
47	56	973	WL-429-51	1.0	1.9	2.0	2.0	2.1	1.8	72.0	75.8	80.0	74.0	79.0	80.0	2.0	3.2	0.0	10.7
24	57	1020	WL-429-44	1.0	2.8	1.7	2.0	3.9	2.2	69.0	71.0	77.0	70.0	77.3	78.0	1.0	6.3	1.0	11.7

50	58	1114	WL-429-2	1.0	2.3	2.0	2.0	4.2	2.0	72.0	76.6	82.0	73.0	80.6	85.0	1.0	4.0	3.0	10.0
	Mean	893		1.2	2.2	1.6	1.8	2.6	1.4	70.9	73.5	75.7	70.7	74.4	76.1	-0.2	1.0	0.4	11.5

[b] calculation of this percentage is explained in section 3.8.1. Trait abbreviations are in the list of abbreviations, TLB,F_2=Turcicum leaf blight score at F_2 generation; MSV,F_3=Maize streak virus score at F_3 generation; AD,F_2=Anthesis date at F_2 generation; SD,F_2=Silking date at F_3 generation; ASI,F_2=Anthesis silking interval at F_2 generation; KR, F3=F3 generation kernel rows

4.2.1.1 Relationship between $F_{2:3}$ indices and $F_{2:3:4}$ indices

As indicated in figure 7 below there is a moderate and significant relationship between the index values of $F_{2:3}$ and those of the $F_{2:3:4}$ lines, implying that if selection is done effectively in the F_3 using index values, the lines will continue to improve significantly in their index ranking into the next generation.

The regression line and correlation coefficient suggest that effective selection in $F_{2:3}$ will significantly improve the index values of the $F_{2:3:4}$ lines by 0.40 units for every unit of improvement in the $F_{2:3}$ index. It appears that selection can be done effectively in the F_3 generation resulting in improved performance in the F_4.

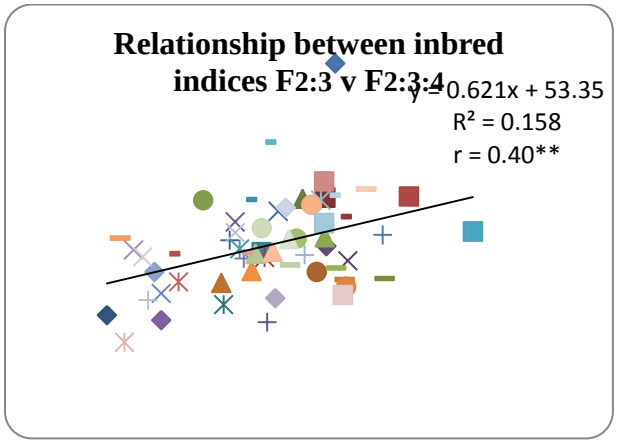


Figure 7: Relationship between two indices developed with the $F_{2:3}$ and $F_{2:3:4}$ generations

4.2.2 Indices involving testcrosses only

The indices for lines x tester B (Test cross B) in individual location and across locations gave more weight to yield followed by MSV%, anthesis silking interval (ASI), Turcicum leaf blight (TLB), 100 grain weight , SD, AD, EPP, PH and EH.

When using this approach, three test-crosses were consistently in the top 10 of the index values (WL-429-14-40, WL-429-14-57 and WL-429-14-25; tables 15 and 16), in each of the three environments suggesting that those test-crosses were stable across environments. Another four lines WL-429-14-96; WL-429-14-40; WL-429-14-71 and WL-429-14-32; were ranked in the

best 10 of the inbred lines.. Ranking consistently among the bottom 10 of in the indices for both inbred and testcrosses were the lines WL-429-14-2, WL-429-14-30, WL-429-14-95 and WL-429-14-89.

Bekavac *et al.*, (2006) suggest that consistency of the top ranking for certain lines calls the attention of breeder to these as, probable sources for breeding, since such frequency is a kind of genotypic response that is expressed in the phenotypic value. This kind of selection index would probably be the most practical selection approach for parallel improvement in multi-traits in a recurrent selection program.

Table 15: Across location selection index values of the 10 best and 10 worst lines with tester B (n=58, low index values are best)

			Traits	AD	SD	ASI	MSV%	MSVs	TLB	KR	EPP	E. H	PH	GW	YLD
			Multiplier	2	2	10	6	9	13	12	19	0.1	0.1	2	35
			Percent of index	5.4	5.8	15.6	51.9	3.8	9.7	8.4	2.7	1.6	1.8	8.8	69.4
Rank	Rank $F_{2:3:4}$	Index	Lines												
1	21	27	WL-43	68.2	68.3	0.5	10.5	1.6	1.7	13.2	1.1	100	210	42.5	8.2
2	12	30	WL-40	67.7	68.8	1.1	6.0	1.3	1.8	12.9	1.0	98	205	38.9	7.1
3	20	31	WL-104	70.3	70.2	0.5	4.7	1.2	2.3	12.3	1.1	95	211	38.7	7.5
4	23	36	WL-96	68.5	68.9	0.8	6.8	1.3	1.7	13.2	1.1	95	214	41.2	7.3
5	55	37	WL-90	68.5	71.2	0.9	5.1	1.3	2.0	13.2	1.1	102	209	39.3	7.2
6	25	42	WL-32	67.8	68.5	0.9	6.8	1.5	2.4	13.4	1.1	102	208	40.6	7.3
7	49	43	WL-57	70.4	71.8	1.0	7.8	1.3	1.9	13.5	1.1	115	225	41.9	7.7
8	37	43	WL-25	67.7	68.8	0.5	8.3	1.3	1.7	13.1	1.0	96	219	39.1	7.2
9	30	46	WL-56	67.7	68.8	1.3	8.8	1.3	1.9	13.6	1.0	99	203	44.7	7.6
10	7	50	WL-71	66.6	68.4	1.0	3.9	1.0	2.0	13.1	1.1	90	209	40.2	6.3
49	27	129	WL-68	68.8	70.5	1.2	12.3	1.6	1.8	13.1	1.1	98	194	38.6	5.8
50	54	134	WL-89	71.5	71.1	0.9	11.0	1.7	2.2	12.5	1.0	93	206	41.7	6.2
51	26	134	WL-52	69.1	71.5	1.0	11.2	1.5	2.1	12.5	0.9	92	195	39.7	5.9
52	36	135	WL-49	68.1	71.1	0.2	19.3	1.8	1.9	13.1	1.1	95	195	38.4	6.6
53	44	137	WL-108	72.5	71.1	0.4	14.9	1.3	1.9	12.9	1.0	91	208	38.2	6.1
54	14	140	WL-109	70.0	70.3	0.7	15.9	1.6	2.0	13.6	1.1	95	198	38.7	5.9
55	34	142	WL-95	67.4	72.0	1.8	10.2	1.5	2.8	13.0	1.0	86	204	36.9	5.5
56	38	153	WL-30	68.5	72.6	1.0	18.1	1.7	2.1	13.0	1.1	87	202	36.7	6.2
57	3	159	WL-34	68.4	72.9	1.0	11.5	1.7	2.2	12.2	1.1	101	194	39.1	5.4
58	58	174	WL-2	69.2	73.2	1.5	18.8	2.1	2.0	12.8	1.1	105	207	38.9	6.2
Mean		94		68.9	70.6	1.0	10.4	1.5	2.0	13.1	1.1	96.0	204	39.5	6.5

AD=anthesis date, SD silking date, ASI= anthesis silking interval, TLB=Turcicum leaf blight sevearty; MSV=maize streak virus incidence;

P. H=plant higth; Ear H=ear higth; EPP=ear per plant; KR=kernel rows; YLD=Yield; 100 GW=100 grain weight

Table 16: Combined across site selection index values of the 10 best and 10 worst test crosses with both testers (n=58, low index values are best)

			Traits	AD	SD	ASI	MSV	MSV%	TLB	P.H	E.H	EPP	KR	YLD
			Multiplier	0.5	0.5	10	3	3	5	0.01	0.01	8	1	20
			Percent of index	4	4	32	0	11	7	1	0.46	5	3	89
Rank	$F_{2:3:4}$ Rank	Index	Lines											
1	18	-113	WL-33	67.2	67.6	0.5	1.0	0.2	1.15	232	115	1.31	13	8.5
2	39	-111	WL-77	66.7	66.8	0.0	1.1	0.9	1.37	222	113	1.34	13	8.3
3	12	-110	WL40	64.7	65.1	0.3	1.0	0.2	1.37	214	101	1.1	12	8.3
4	53	-108	WL-24	65.7	66.6	0.8	1.0	0.1	1.4	223	106	1.2	13	8.4
5	13	-107	WL-6	68.5	68.6	0.1	1.0	-0.3	1.71	229	111	1.26	13	8.1
6	17	-107	WL-37	66.3	66.3	0.0	1.0	0.8	1.08	194	88.4	1.18	12	8.1
7	56	-106	WL-51	64.9	65.3	0.5	1.0	0.1	1.33	210	93	1.26	13	8.1
8	49	-106	WL-57	66.8	67.3	0.9	1.0	-0.2	1.11	232	109	1.32	13	8.3
9	37	-104	WL-25	64.7	64.1	-0.5	1.0	1.0	1.23	208	99.4	1.2	12	7.6
10	16	-103	WL-50	64.0	64.4	0.3	1.0	-0.1	1.77	212	107	1.04	12	8.0
49	41	-68	WL-82	66.4	67.6	1.2	1.0	0.4	1.38	218	104	1.09	13	6.8
50	42	-66	WL-75	67.1	68.5	1.5	1.0	0.0	1.49	210	97.6	1.04	13	6.8
51	5	-63	WL-105	67.5	68.1	0.5	1.0	0.8	1.97	207	88.3	1.12	14	6.4
52	29	-63	WL-76	66.4	67.8	1.3	1.0	0.7	1.25	191	82.1	1.13	13	6.6
53	15	-62	WL-106	68.7	69.8	1.0	1.0	0.0	1.49	192	85.3	1.06	13	6.5
54	32	-61	WL-110	66.7	67.57	0.8	1.0	0.0	1.25	201	95.9	1.16	12	6.2
55	45	-59	WL-115	68.2	69.15	0.98	1.0	0.8	1.77	211	98.4	1.27	13	6.4
56	48	-58	WL-17	68.8	70.49	1.92	1.0	-0.2	1.81	203	90.1	1.06	12	6.9
57	34	-47	WL-95	68.1	69	0.97	1.0	0.1	1.89	195	91.2	1.16	13	5.7
58	22	-38	WL-117	65.2	67.66	2.32	1.1	1.1	1.55	186	79.8	1.2	13	5.9

AD =anthesis date, SD silking date, ASI = anthesis silking interval, TLB = Turcicum leaf blight; MSV=Maize streak virus incidence;

P. H=plant higth; E.H=ear higth; EPP=ear per plant; KR=kernel rows; YLD=Yield; 100 GW=100 grain weight

4.2.3 Relationship between inbred only indices and testcross only indices

Only a weak non significant relationship was observed between index values of testcross B and the index of testcross means across environments (Figure 8).

The low relationship between these two selection indices probably is due to difference in performance of the line with both testers across site, error variability in scoring level and also inconsistency of genotypes across environments.

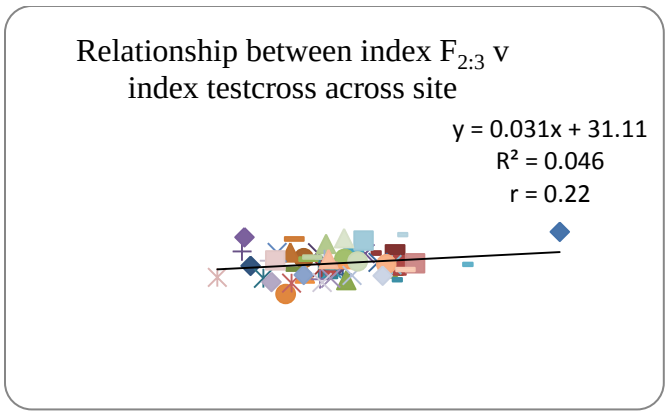


Figure 8 : Relationship between selection index values for $F_{2:3}$ and selection index value for testcrosses means, across locations

4.2.4 Spearman's correlation coefficient (rho)

Analysis based on Spearman's rank correlation is shown in Table 17. A strong and significant correlation (ρ=0.93) was observed between the indices for $F_{2:3}$ and F_4 also moderate but highly significant correlation (ρ=0.22) in the $F_{2:3}$ and F_4 values, implying that improving the effectiveness of the selection index in $F_{2:3}$ improve the index selection in $F_{2:4,}$ and in the F_4. A much weaker, but still significant relationship was also fund between the selection indices for the $F_{3:4}$ and that for testcrosses across locations, including F_3 values and test crosses (TC) values. Unfortunately the $F_{2:4}$ index was not correlated with the testcross index across locations, suggesting that an improvement of the $F_{2:4}$ index does not result in any changes in the index selection for testcrosses across locations.

Table 17: Spearman's rank correlation between the various indices (n = 58)

Item	$F_{2:3}$ Index v $F_{2:4}$ Index	$F_{2:3}$ Index v Testcross across loc. Index	$F_{2:4}$ Index v Testcross across loc. Index	$F_{2:3}$ Index v F_4 Values	F_3 values v TC values
Σd_j^2	2356	23978	26044	25506	30552
ρ(rho)	0.93***	0.26*	0.20 ^{ns}	0.22***	0.06*

*, *** indicates significance at 0.05 and 0.001 probability levels; ^{ns} = non significante; Σd_j^2= sum of differences between two ranks; ρ (rho) = Spearman's correlation coefficient

4.2.4 Combined inbred and testcross indices.

Five different methods of creating a selection index to generate effective selection criteria indicated that inbred lines and their testcrosses differed in performance in each index developed. In most indices nine lines were observed to be consistently ranked in the top 10 of the indices, well as in the combined inbred and testcross indices (Tables 14; 15; 16;17 and 18). These nine lines were WL-429-14-33; WL-429-14-40, WL-429-14-49; WL-429-14-37; WL-429-14-57; WL-429-14-34; WL-429-14-4, WL-429-14-50 and WL-429-14-119 .Meanwhile nine lines were noted consistently poor in performance (Tables 14; 15; 16;17 and 18 and Appendices 1 and 2). These lines were WL-429-14-44; WL-429-14-106; WL-429-14-15; WL-429-14-90; WL-429-14-2; WL-429-14-75; WL-429-14-110; WL-429-14-17 and WL-429-14-95.

Effective selection can use either the $F_{2:3}$ generation selection indices or the combined inbred and testcross indices, because most of the lines that appear in the combined inbred and testcross indices are consistently present in other single selection indices, and we are sure that these hybrids will perform better in single and across enviroment trials. Using the selection index for the combined means of inbred and testcross indices is the best way to capture the most promising individuals in the F_3 testcross.

Bernardo (1990), states that when the breeder selects 50 out of 100 lines based on their testcross performance, at least 30 of the 50 lines selected are expected to be superior at homozygosity. Thus, early testing should be effective in discriminating between lines with above and below average performance. Probability of capture desired individual in early generations are low if strong selection pressure is applied (α=10%). If the test-cross heritability is equal to 0.50, and the breeder selects 10 of 100 lines based on testcross performance, only 3 of the 10 lines selected are expected to be superior (i.e.; in the top 10%) at homozygosity.

In our study heritability of traits was more than 0.50 at F_3-testcross especially for traits such as resistance to Turcicum leaf blight (0.65), anthesis date (0.83), silking date (0.65), anthesis silking interval (0.60), and 100 grain weight (0.84). This suggests that for these traits selection can be done at an early stage. However for traits with low heritability values, as for yield, ear per plant and (less so for) maize streak virus (MSV), serious selection should wait until a later stage.

Hallauer, 1990 cited by Bernardo (2010), state that late testing during inbred development for hybrid cultivars involves selection for easily scored traits, such as plant type and leaf disease resistance, during the early selfing generations. Testcross evaluation, which is more expensive than per se selection, is delayed until the families are near-homozygous and are greatly reduced in number. In contrast assumes that the testcross performance of a family is determined during the early selfing generation and does not change substantially with continued inbreeding.

Table 18: Combined selection index of inbred and testcross for identifying 10 best and 10 worst lines (n = 58, low index values are best)

	Traits	TLB F2	TLB F3	TLB F4	MSV F2	MSV F3	MSV F4	ASI F2	ASI F3	ASI F4	F3 K.R	TC s AD	SD	ASI	MSV%	TLB	E.H	EPP	KR	YLD
	Multiplier	5	10	10	3	10	9	3	6	9	-9	3	2	9	8	19	0.1	12	2	41
Percent of index		3	10	13	2	18	13	11	29	17	28	10	7	12	12	11	2	3	3	72
Index	Lines																			
391	WL-33	1.0	1.5	1.0	2.0	2.6	1.0	-2.0	-0.5	0.0	11.3	67.2	67.6	0.5	0.2	1.2	115	1.3	13.0	8.50
396	WL-40	1.0	1.9	2.1	1.0	1.3	1.5	3.0	-0.4	1.0	10.0	64.6	65.1	0.3	0.2	1.4	101	1.1	12.2	8.28
420	WL-49	1.0	1.5	1.8	2.0	2.4	1.0	-2.0	-1.0	1.0	10.3	65.8	66.0	0.2	1.0	1.2	96	1.3	13.1	7.92
422	WL-37	1.0	2.1	1.3	2.0	2.2	1.0	-2.0	-1.8	2.0	12.3	66.3	66.3	0.0	0.8	1.1	88	1.2	12.2	8.07
424	WL-57	1.5	2.3	1.5	2.0	2.3	1.0	-2.0	1.6	-1.0	10.7	66.8	67.3	0.9	-0.2	1.1	109	1.3	13.3	8.27
431	WL-34	1.0	2.2	2.3	2.0	2.0	1.0	-3.0	0.0	-2.0	10.7	65.7	66.8	1.0	0.1	1.1	107	1.3	12.3	7.20
434	WL-4	1.3	3.0	2.5	2.0	2.3	1.0	2.0	-1.0	-1.0	10.3	65.1	65.9	0.8	0.1	1.3	99	1.2	12.7	7.58
440	WL-50	1.3	2.4	2.0	2.0	1.7	2.0	0.0	0.6	1.0	11.3	64.0	64.4	0.3	0.0	1.8	107	1.0	12.5	8.02
444	WL-70	1.5	2.4	1.0	2.0	2.1	1.0	-1.0	0.2	0.0	11.0	66.8	67.1	0.4	1.0	1.4	89	1.1	12.5	7.68
445	WL-119	1.0	2.2	1.0	1.0	2.8	1.0	0.0	2.6	0.0	12.0	67.1	67.5	0.6	0.0	1.3	97	1.2	13.0	7.71
523	WL-44	1.0	2.8	1.7	2.0	3.9	2.2	1.0	6.3	1.0	11.7	65.5	65.9	0.5	1.3	1.6	94	1.2	12.7	6.14
525	WL-106	1.5	1.7	1.6	2.0	1.5	1.3	-1.0	2.2	0.0	12.7	68.7	69.8	1.0	0.0	1.5	85	1.1	12.7	6.50
527	WL-105	1.0	2.2	1.5	1.0	2.3	1.0	-1.0	1.6	1.0	12.3	67.5	68.1	0.5	0.8	2.0	88	1.1	14.0	6.35
533	WL-90	1.5	2.2	1.5	1.5	2.6	2.0	1.0	5.6	0.0	13.0	66.6	67.4	0.7	1.7	1.1	106	1.1	13.3	7.58
545	WL-75	1.0	1.6	1.5	2.0	2.6	1.0	0.0	3.8	1.0	13.0	67.1	68.5	1.5	0.0	1.5	98	1.0	13.2	6.81
547	WL-110	1.0	1.8	1.0	2.0	3.1	1.0	0.0	1.2	1.0	13.3	66.7	67.6	0.8	0.0	1.3	96	1.2	12.2	6.15
553	WL-15	1.3	1.5	1.5	1.5	3.2	1.5	1.0	2.4	0.0	12.0	68.2	69.2	1.0	0.8	1.8	98	1.3	13.2	6.37
571	WL-2	1.0	2.3	2.0	2.0	4.2	2.0	1.0	4.0	3.0	10.0	68.2	68.7	0.5	0.6	1.4	109	1.2	12.3	7.23
574	WL-17	1.3	1.8	1.0	2.0	3.3	1.0	0.0	0.2	3.0	13.3	65.2	67.7	2.3	1.1	1.6	80	1.2	13.2	5.89
579	WL-95	1.5	1.5	3.2	2.0	2.4	1.3	1.0	1.0	0.0	12.3	68.1	69.0	1.0	0.1	1.9	91	1.2	12.6	5.73
Mean		1.2	2.2	1.6	1.8	2.6	1.4	-0.21	0.97	0.4	11.5	66.4	67.1	0.7	0.30	1.4	97.1	1.2	12.8	7.3

TLB,F_2=Turcicum leaf blight score at F_2 generation; MSV,F_3=maize streak virus score at F_3 generation; AD,F_2=anthesis date at F_2 generation; SD,F_2=silking date at F_3 generation; ASI,F_2=anthesis silking interval at F_2 generation; KR, F_3=F3 generation kernel rows

4.3 Predicted genetic gain

4.3.1 Gain for individual traits from inbred values at different generations and from testcross performance

Different gains are obtained when selection is done at different generations. On these lines (CIMMYT x NARO) if selection is done at F_2, instead of F_3 or at F_3 instead of F_4, the gains obtained in selection are noticeably different (Table 19).

From the results of overall analysis presented in Table 19, we noted that with same selection intensity (i=20), better gains on these materials are obtained when the lines are selected in the F_3 generation than in the F_2 or F_4 generations. Generally if selection is done at F_3, we have the chance to improve the flowering date by reducing approximately 0.15 units in the anthesis date (AD), 0.41 units in the silking date (SD), and 0.06 days in the anthesis silking interval (ASI). Also, we gain the opportunity for increase scores for resistance to MSV by 0.04 units and to TLB by 0.17 units (Table 19). This implies that the higher gain observed in the F_3 generation is probably due to a high response of genotypes to the environmental factor. Selecting in F_3 or F_4 generation is more reliable than in the F_2 generation, because in the F_2 we are dealing with single plant data with a very small chance of gauging individuals accurately, and at F_2 the level of heterozygosity is still high.

Table 19: Gain for selection in 58 inbred lines at F_2, F_3 and F_4 (k=1.40, i=20%)

Generations	Components	AD	SD	ASI	MSV	TLB
	Means	70.9	70.7	-0.21	1.78	1.18
	σ^2Ph	4.01	5.37	1.75	0.15	0.07
F2 Generation	h^2	0.09	0.05	0.60	0.11	0.03
	Gain	-0.25	-0.17	-1.11	0.06	0.01
	Means	73.45	74.42	0.969	2.595	2.212
	σ^2Ph	16.33	19.38	4.84	0.62	0.22
F3 Generation	h^2	0.03	0.07	0.02	0.04	0.25
	Gain	-0.15	-0.41	-0.06	0.04	0.17
	Means	75.72	76.12	0.397	1.416	1.645
	σ^2Ph	13.01	12.49	1.401	0.303	0.223
F4 Generation	h^2	0.09	0.150	0.009	0.030	0.077
	Gain	-0.45	-0.74	-0.01	0.02	0.05

In the test crosses more gain was obtained when selection was done based in the performance either of tester A or tester B, though tester B performed better especially for the traits of MSV incidence, yield and quite good gain for MSV severity (Table 20). Apparently, slightly higher gain can be obtained if selection is done with more attention given to performance of testcrosses from tester A.

Peiris and Hallauer (2005), state that selection response depends on the relative importance of different types of genetic variance and the frequencies of allele that affect genetic variance. In an additive genetic model with equal allele frequency in the initial population, genotypic mean of hybrid response are expected to improve continuously for a number of cycles of selection.

Table 20: Expected gain from selection in 58 inbred lines when test crossed with two testers A and B (i=20% K=1.40)

Generations	Comp	AD	SD	ASI	MSV	MSV%	TLB	YLD
	Means	69.2	69.6	0.37	1.76	14.3	2.00	6.25
Tester A	σ^2Ph	1.15	1.30	0.23	0.04	27.5	0.06	0.61
	h^2	0.70	0.60	0.48	0.40	0.57	0.48	0.03
	σ^2a	0.81	0.78	0.11	0.016	15.6	0.029	0.019
	Gain	-1.05	-0.96	-0.32	0.11	4.17	0.17	0.03
	Means	69.6	70.6	1.00	1.49	10.4	2.01	6.53
Tester B	σ^2Ph	1.56	2.03	0.34	0.05	25.1	0.08	0.32
	h^2	0.52	0.38	0.32	0.41	0.62	0.36	0.06
	σ^2a	0.81	0.78	0.11	0.47	15.6	0.029	0.019
	Gain	-0.91	-0.77	-0.26	0.10	4.35	0.14	0.04

AD=anthesis date; SD=silking date; ASI=snthesis silking interval; MSVi=maize streak virus incedence; MSVs=maize streak virus score; TLB=Turcicum leaf bligth, YLD=yield; σ^2Ph =phenotipic variance; σ^2a=additive variance; K=selection differential; PG=predicted gain

4.3.2 Gain for selection index values

For each index developed we noted that the ranking of the genotypes were variable. The expected gain based in the $F_{2:3}$ index was 20 units and 31 units for the $F_{2:4}$ index. The selection of desired lines can be done effectively when based on the performance of test-crosses with tester

B, because the gain of 6.4% in improvement of genotypes is slightly higher than the gain for individual testers A or test-crosses of both testers across locations (Table 21).

Table 21: Gain obtained for 58 lines, using different indices at different stages (i=20; K=1.40)

Generations	$F_{2:3}$	$F_{2:4}$	TA	TB	TCs across loc.
Mean indices	1357	897	88	59	-85
Variance of index values (phenotypic)	1285	3136	82	65	48
h^2/ (Average of NSH or BSH for all traits)	0.40	0.40	0.31	0.34	0.43
Gain in index value units	-20	-31	-3.9	-3.8	-4.2
Gain in index value in %	1.5%	3.5%	4.4%	6.4%	4.9%

h^2= Narrow sense heritability; BSH=Broad sense heritability.

The overall results suggest the benefits of selecting in the $F_{2:3}$ generation based on the inbred only index before test crossing, because the best lines then are likely to perform well consistently in subsequent generations. If the breeder decides to make his selection at the testcross level, combining the inbred and testcross indices provide the best option. Our findings revealed that nine lines of the 58 consistently ranked in the top 10 in the all indices, suggesting that these lines there were already stable at that early stage. These top-ranking line were WL-429-14-33; WL-429-14-40, WL-429-14-49; WL-429-14-37; WL-429-14-57; WL-429-14-34; WL-429-14-4, WL-429-14-50 and WL-429-14-119.

When a breeder selects 50 out of 100 lines, for example, based on testcross performance, at least 30 of the 50 lines selected are expected to be superior at homozygosity. Thus, early testing should effectively discriminate between lines with above or below average performance. In the testcrosses heritability is 0.50 the probability of obtaining the best lines at early generations is low if strong selection pressure has been applied. If the breeder selects 10 lines out of 100, based on testcross performance, only 3 of the 10 selections are expected to be superior at homozygosity (Bernardo, 1990).

Hallauer and Miranda, (1981) suggested that at an early stage the heritability of maize grain yield usually is less than 0.30. For traits such as this with low heritability, selfing for three or more generations prior to testcrossing may be desirable to increase the likelihood of retaining lines that perform well at complete homozygosity.

Bernardo (2010), suggest that selection during the early generation is desirable because it permits a greater expenditure of resources on the family that are most promising. An increase of number of environment or replication reduces means variance and increases narrow sense heritability and selection for quantitative traits at any early stage can therefore be effective if each family is grown in extensive performance tests.

4.4 Assignment of heterotic groups

The SCA values were evaluated for each location and across locations. Based on this criterion, 29 lines (50%) had some indication of belonging to heterotic group B based on SCA value for at least one location (Table 22). The number of lines expected to have |SCA values| > 1 SE due to random chance is 16% or about 10 in each location. Therefore there is little overall evidence of and lines clearly belonging to heterotic group B, but there was considerable interaction of lines with environments. This interaction was noted in the highly significant line x tester x environment mean square in Table 10.There is no clearly evidence that the lines belongs heterotic group B since most of them had SCA>1 SE in only one environment and 1SE is not a very strong criterion, these lines which showed SCA>1 SE was by random chance and a strong effect of Line x Tester x Environment interaction. There would be many more that had a stronger SCA in favour of group A.

Table 22: Values of specific combining ability (SCA) of lines crossed with tester A. (Lines with |SCA| > SE_{SCA} were tentatively assigned to heterotic group B)

Locations	Namulonge	Serere	Bulindi	Across Location
SE_{SCA}	0.54	0.55	1.01	0.63
Lines/SCA values	SCA	SCA	SCA	SCA
WL-429-14-10		0.56	1.10	
WL-429-14-101			1.29	
WL-429-14-108	0.74			
WL-429-14-109	0.61	1.12		
WL-429-14-111		0.83		
WL-429-14-115		0.97		
WL-429-14-117		0.57		
WL-429-14-118	0.79			
WL-429-14-119			1.59	
WL-429-14-15		0.73	1.10	
WL-429-14-2		1.24		
WL-429-14-24	1.16			
WL-429-14-26			1.85	
WL-429-14-27	0.56			
WL-429-14-30		1.39		
WL-429-14-33	0.99			
WL-429-14-34		0.86	1.36	0.73
WL-429-14-4	0.95			
WL-429-14-41	1.77			0.82
WL-429-14-49		0.59		
WL-429-14-50			1.43	
WL-429-14-52			1.77	
WL-429-14-61		1.12	1.20	0.85
WL-429-14-68			1.42	
WL-429-14-71	0.58			
WL-429-14-76		0.79		
WL-429-14-78		0.71		
WL-429-14-93			1.23	
WL-429-14-94		1.39		
Number of lines	9	14	11	3

CHAPTER FIVE

CONCLUSIONS AND RECOMMENDATIONS

5.1 Overall Conclusions

There is growing interest to develop maize inbred lines that give high-yielding hybrids with drought tolerance and multiple disease resistance, especially to maize streak virus and *Turcicum* leaf blight. To improve efficiency of selection, a selection index that employs these traits was assessed for use in the development an effective strategy to easily identify inbred lines for further development and testing. In the present study 58 F_3 lines from a cross of a CIMMYT drought-tolerant line x a locally bred (NARO) multiple-resistant inbred were evaluated. These lines were each crossed with two CIMMYT testers (A & B), giving 116 testcrosses that were evaluated for yield and related traits in three locations that represented a drought-prone location, a disease hotspot, and an optimal site. Both inbred lines and testcrosses were evaluated for disease resistance (to MSV and TLB) and for drought tolerance, using the anthesis-silking interval as indicators of drought tolerance in the genotype, combined with early silking for drought avoidance.

From this study, genotypes resistant to MSV and TLB were identified, with segregation patterns suggesting that resistance to both pathogens is controlled by quantitative genes. Usually, partial resistance is more difficult to transfer than qualitative resistance due to the multi-genes nature of resistance in the host and the strong influence of the environment on its response (Cai *et al*. 2003). In this study significant differences among lines were consistently observed in two sites (Namulonge and Bulindi) as well as across all three locations. The level of heritability was sufficiently high to expect that selecting inbred lines with good levels of resistance would be possible.

Tester B was superior to Tester A for transmitting resistance to maize streak virus, while lines with superior resistance to Turcicum leaf blight transmitted that resistance to testcrosses from both testers.

Significant differences were observed among ASI values among testcrosses for both in individual and combined environments, confirming that the inbred lines were diverse and that significant differences were present in the progeny. However, there was a significant line x environment interaction, indicating that ASI is more strongly expressed under drought condition. This has been reported by Borrás, *et al.* (2007), who showed that maize genotypes respond differently to variable conditions that alter plant growth during this period, with changes in ASI being the most widely observed.

The error variance component was relatively higher in magnitude than G x E interactions in some of the traits. However line variance components for yield, number of kernel rows, resistance to *Turcicum* leaf blight and maize streak virus, anthesis silking interval and ears per plant were larger than for L x E interaction. For several traits (anthesis date, silking date, anthesis-silking interval, *Turcicum* leaf blight resistance, ear height and 100 grain weight) the broad sense heritability (BSH) was reasonable high $\geq$ 55% on an entry mean basis across locations. This suggests that selection for those traits could be easily achieved at an early stage and desired alleles captured.

Grain yield for entry mean across locations in the F_3 testcrosses had a very low heritability (0.08), probably due to low heritability of this trait in single locations associated with instability of genotype across locations and the high error variance observed at Bulindi. Apparently, selection for yield gains in this population will be difficult, and probably would be more effective in later generation testcrosses (e.g., F_5 or F_6 testcross). Alternatively, increasing the number of replications or testing locations to reduce error variability and increasing field uniformity would be a good strategy for improving the level of heritability.

Selection indices were developed based on five key traits in the inbred generations and eleven traits in the F_3-testcrosses. Using the resulting indices in both the F_3 generation and F_3-testcrosses provided the best strategy for developing and capturing desirable individuals, and therefore could improve the breeder's ability to consistently identify and select the most promising lines with potential for hybrids combining many traits (as for resistance to MSV and TLB, drought tolerance and high yields). The use of selection indices can reveal the overall value

of selected genotypes with greater accuracy and less physical effort, though it requires much critical thinking about the relative importance of the traits. Using this approach, the following lines have been identified as already stable at an early stage and consistent in the indices and that could, therefore, be considered the best sources for a breeder to use for improving hybrid production were: WL-429-14-33; WL-429-14-40, WL-429-14-49; WL-429-14-37; WL-429-14-57; WL-429-14-34; WL-429-14-4, WL-429-14-50 and WL-429-14-119.

The overall performance of the inbred lines was considered good because some improvement was noted from one generation to the next. However, in the F_2 generation, a relatively large number of individuals (67.4%) exhibited an ASI of -3 to 0 days, and in the F_3 29.2% of the individuals had an ASI ranging from -3 to 6 days. The high difference in ASI gives a clear picture of the progeny segregating and a strong response of genotypes to environmental conditions.

For resistance to TLB disease, both generations showed a high frequency of resistant progeny, 90% of individuals in the F_2 and 81% in the F_3, suggesting partial dominance conditioning for resistance to TLB in the inbred lines. For MSV, 63.4% of the F_3 families showed resistance with a severity score of less than 2.5, with a distribution that was continuous and normal, implying resistance is conditioned by multiple genes (Figure 5).

The performance of testcrosses at Namulonge showed significant differences in testcross means among lines for anthesis date (AD), silking date (SD) and anthesis-silking-interval (ASI), indicating genetic variability among lines within the population: WL-429-14/(CML442/CML197//TuxPSEQ)C1F2/P49-SR. About 20 lines (34.5%) had ASI's ranging from -1.2 to 0 days (see Appendix 1). ASI is an indicator of drought tolerance and can, therefore help to identify drought tolerant and high yielding lines. It is likely that these 20 lines will transmit some level of drought resistance and high yield to their hybrids.

High disease responses were observed in the testcrosses, with 21.3% incidence of MSV on tester A and 15.5% on tester B, and means of 30.5% for testcrosses onto tester A and 23.7% onto tester B at Namulonge. This suggests that tester B transmits more resistance and would be a better

candidate for generating MSV resistant hybrids. The 13 lines with < 21% incidence can be used as lines resistant to MSV for hybrid improvement.

Testers did not provide a greater contribution towards an improved TLB-resistant genotype, suggesting that a different tester could be used for improvement of TLB-resistance hybrid, since the lines themselves are resistant to TLB. Fourteen lines showed large and positive GCA's for yield (Appendix 3), suggesting that those lines could be used for improvement of yield traits. Generally, there was high response to disease and random short drought observed at Namulonge during the experiment. Namulonge is the best location for selecting disease-resistant and drought-tolerant genotypes.

At the Serere site a very low percentage of testcrosses showed an ASI ranging from -0.5 to 0 days (10%). Though the range of ASI was small, the differences were highly significant. The disease response to MSV and TLB was also low there, probably due to unfavourable conditions, such as regular rains without a drought period that would initiate development of the *Cicadulina* species, as well as the absence of cool conditions with high humidity that is favourable to development of *E. Turcicum.* Due to these conditions the site did not provide the information we desired regarding drought tolerance or segregation for disease resistance.

However, the Serere site did yield well, and revealed significant differences in yield between testers and in line x tester interactions. Tester B performed better, with a mean yield of 7.53 t/ha, while tester A yielded 7.13 t/ha. It would seem that tester B carries alleles for the desirable yield traits and 100 grain weight, suggesting that crossing tester B rather than Tester A with lines from this population would produce progeny with better performance. The lines with highest GCA effects for yield were inbred lines WL-429-14-33 (1.2 t/ha), followed by WL-429-14-24 (1.1 t/ha) and WL-429-14-40 (0.95 t/ha), and should be useful for futher testing in order to obtain the highest yeilding hybrids. Unfortunately, the narrow sense heritability for yield was low (0.16), so selection for yield traits would be very difficult at an early stage**.**

Because of its favourable weather conditions during the period of testing, Serere was the best site for gaining reliable information about the yield potential of the genotypes.

Variable condititions and inrregular rainfall observed during the growth period in the Bulindi had affected the flowering dynamic.

In this site moderate MSV incidence was observed with significant differences among lines. Interestingly, lines that showed a high level of MSV resistnce in Namulonge were also consistently resistant in Bulindi. These lines were 429-14-17, WL-429-14-82, WL-429-14-71, WL-429-14-56 and WL-429-14-36. This consistency suggests that these lines may have different sources of resistance that likely contain the same resistance factor that accounts for the large phenotypic variances associated with differences of disease response among genotypes. Turcicum leaf blight severity was also moderate among testcrosses in Bulundi, with a mean score of 2.1 for each tester.

The mean yield in Bulundi was 5.82 for tester A and 5.65 for tester B, but this location did not provide reliable information regarding the yield potential among testcrosses, due to the field variability, which was not effectivly controlled by lattice blocking and so resulted in a large experimental error. This factor underscores the need for significant improvement in uniformity so that expermnetal error can be reduced in order to detect differences among the genotypes.

The combined results across locations also revealed significant line x environment interactions (LxE) for traits such as yield, kernel rows, ears per plant, resistance to *Turcicum* leaf blight and maize streak virus, SD, AD, and ASI. The presence of significance L x T interactions implies inconsistency in performance of the genotypes across environments.

5.2 Recommendations

Further testing and selection is needed, especially for those traits that showed low heritability.
The study recommend that testing and selection at F_3 could be done efficiently for traits that showed high heritability such as: maize streak virus and *Turcicum* leaf blight resistant, anthesis silking interval and grain weight.

Serious effort towards improving experimental uniformity is encouraged, and the use of more testing locations or an increased number of replications to reduce error variability. Evaluation of drought tolerance was under natural conditions, therefore, subject to random occurrence of drought. Due to unpredictable weather, the degree of water stress observed at the expected drought site (Serere) did not occur, and while some drought occurred at Namulonge, the duration and severity was not enough to provide precision in identifying drought-tolerant genotypes. Further testing is needed, and if possible, an irrigated site with dependable drought stress should be used to create the desired timing and severity of drought.

Because of their performance and consistency in the selection indices constructed, lines WL-429-14-33. WL-429-14-40, WL-429-14-49, WL-429-14-37, WL-429-14-57, WL-429-14-34, WL-429-14-4, WL-429-14-50 and WL-429-14-119 could be used as reliable sources for resistance to both Turcicum leaf blight (TLB) and maize streak virus (MSV), as well as for producing high-yielding hybrids.

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APPENDICES

Appendix 1: Selection index values of 58 inbred lines based on key traits of F_2, F_3 and F_4 lines. The low indexes values are superior

		Traits	TLB F2	TLB F3	TLB F4	MSV F2	MSV F3	MSV F4	AD F2	AD F3	AD F4	SD F2	SD F3	SD F4	ASI F2	ASI F3	ASI F4	F3 K.R
	Index	Multiplier	3	13	11	5	17	9	0.5	1	1	0.5	1	8	3	11	14	-12
	897	Mean	1.2	2.2	1.6	1.8	2.6	1.4	70.9	73.5	75.7	70.7	74.4	76.1	-0.2	1.0	0.4	11.5
	864	25% percentile	1.0	1.9	1.3	1.6	2.1	1.0	70.0	70.6	73.0	69.3	71.2	74.0	-1.0	-0.5	0.0	10.7
	929	75% percentile	1.3	2.4	2.0	2.0	3.1	1.8	72.0	76.1	78.0	72.0	77.3	78.8	1.0	2.1	1.0	12.3
	65	Difference	0.3	0.5	0.7	0.4	1.0	0.8	2.0	5.5	5.0	2.8	6.1	4.8	2.0	2.6	1.0	1.7
	Difference*multiplier		0.8	6.8	7.7	1.9	16.9	7.2	1.0	5.5	5.0	1.4	6.1	38.0	6.0	28.3	14.0	-20.0
	Percent of index diff.		1	11	12	3	26	11	2	8	8	2	9	59	9	44	22	31
Rank	Index	Lines																
1	780	WL-429-78	1.0	2.5	2.0	1.5	2.1	1.5	67.0	75.0	66.0	66.0	75.3	66.0	-1.0	0.3	0.0	12.0
2	804	WL-429-119	1.0	2.2	1.0	1.0	2.8	1.0	71.0	69.4	67.0	71.0	72.0	67.0	0.0	2.6	0.0	12.0
3	807	WL-429-34	1.0	2.2	2.3	2.0	2.0	1.0	69.0	77.0	73.0	66.0	77.0	71.0	-3.0	0.0	-2.0	10.7
4	813	WL-429-10	1.0	2.5	1.3	2.0	1.5	1.3	67.0	86.0	74.0	66.0	80.0	75.0	-1.0	-6.0	1.0	11.3
5	825	WL-429-105	1.0	2.2	1.5	1.0	2.3	1.0	70.0	71.8	69.0	69.0	73.4	70.0	-1.0	1.6	1.0	12.3
6	831	WL-429-85	1.0	2.2	1.9	2.0	1.0	1.0	69.0	71.2	73.0	68.0	69.8	74.0	-1.0	-1.4	1.0	10.7
7	833	WL-429-71	1.0	2.0	1.2	2.0	2.2	1.0	71.0	69.8	75.0	70.0	70.2	75.0	-1.0	0.4	0.0	12.7
8	837	WL-429-94	1.0	2.4	1.3	1.0	2.7	2.1	72.0	74.8	74.0	72.0	77.8	72.0	0.0	3.0	-2.0	13.3
9	839	WL-429-4	1.3	3.0	2.5	2.0	2.3	1.0	68.0	73.0	72.0	70.0	72.0	71.0	2.0	-1.0	-1.0	10.3
10	847	WL-429-28	1.0	2.9	1.3	2.0	3.6	1.0	74.0	71.8	78.0	71.0	68.5	77.0	-3.0	-3.3	-1.0	11.3
11	851	WL-429-13	1.0	2.4	1.4	1.0	2.3	1.0	71.0	71.0	73.0	71.0	71.2	73.0	0.0	0.2	0.0	10.3

12	853	WL-429-40	1.0	1.9	2.1	1.0	1.3	1.5	70.0	67.6	72.0	73.0	67.2	73.0	3.0	-0.4	1.0	10.0
13	855	WL-429-7	1.8	2.3	1.5	2.0	1.7	2.0	74.0	74.4	79.0	72.0	75.6	76.0	-2.0	1.2	-3.0	10.7
14	857	WL-429-109	1.3	1.7	1.5	2.0	2.8	1.3	73.0	72.2	78.0	74.0	72.6	77.0	1.0	0.4	-1.0	13.3
15	864	WL-429-106	1.5	1.7	1.6	2.0	1.5	1.3	72.0	73.0	76.0	71.0	75.2	76.0	-1.0	2.2	0.0	12.7
16	864	WL-429-50	1.3	2.4	2.0	2.0	1.7	2.0	68.0	70.6	72.0	68.0	71.2	73.0	0.0	0.6	1.0	11.3
17	866	WL-429-37	1.0	2.1	1.3	2.0	2.2	1.0	71.0	70.8	76.0	69.0	69.0	78.0	-2.0	-1.8	2.0	12.3
18	869	WL-429-33	1.0	1.5	1.0	2.0	2.6	1.0	74.0	68.0	79.0	72.0	67.5	79.0	-2.0	-0.5	0.0	11.3
19	873	WL-429-70	1.5	2.4	1.0	2.0	2.1	1.0	72.0	74.6	76.0	71.0	74.8	76.0	-1.0	0.2	0.0	11.0
20	878	WL-429-104	1.0	2.1	1.3	1.0	1.8	2.5	74.0	78.8	72.0	74.0	77.8	74.0	0.0	-1.0	2.0	11.3
21	880	WL-429-43	1.0	2.1	2.0	1.0	4.1	2.8	70.0	70.2	75.0	71.0	70.6	74.0	1.0	0.4	-1.0	12.0
22	882	WL-429-117	1.3	1.8	1.0	2.0	3.3	1.0	70.0	67.0	73.0	70.0	67.2	76.0	0.0	0.2	3.0	13.3
23	882	WL-429-96	1.0	2.3	1.0	2.0	2.8	1.0	68.0	80.5	73.0	67.0	79.5	74.0	-1.0	-1.0	1.0	10.0
24	885	WL-429-61	1.0	2.5	1.5	2.0	3.2	1.0	71.0	68.2	71.0	71.0	70.0	73.0	0.0	1.8	2.0	12.7
25	886	WL-429-32	1.0	3.4	1.8	2.0	2.4	1.0	68.0	76.6	72.0	66.0	77.6	73.0	-2.0	1.0	1.0	11.3
26	886	WL-429-52	1.0	2.4	2.0	2.0	1.6	1.0	71.0	71.8	77.0	72.0	73.4	76.0	1.0	1.6	-1.0	10.3
27	888	WL-429-68	1.0	3.0	3.0	2.0	4.0	1.0	71.0	72.4	72.0	68.0	70.6	73.0	-3.0	-1.8	1.0	10.7
28	888	WL-429-111	1.0	1.9	1.5	1.0	2.6	2.1	71.0	74.0	81.0	72.0	73.2	80.0	1.0	-0.8	-1.0	12.0
29	889	WL-429-76	1.0	1.6	1.3	2.0	3.0	1.0	71.0	70.0	73.0	71.0	72.3	74.0	0.0	2.3	1.0	11.3
30	891	WL-429-56	1.0	2.0	1.7	2.0	2.1	1.2	67.0	66.2	73.0	68.0	69.6	74.0	1.0	3.4	1.0	11.3
31	892	WL-429-27	1.5	2.5	1.3	1.0	1.3	2.0	71.0	69.8	77.0	70.0	71.2	78.0	-1.0	1.4	1.0	12.0
32	895	WL-429-110	1.0	1.8	1.0	2.0	3.1	1.0	71.0	77.4	76.0	71.0	78.6	77.0	0.0	1.2	1.0	13.3
33	902	WL-429-107	1.3	1.9	1.6	2.0	2.8	1.1	69.0	74.4	75.0	70.0	75.6	76.0	1.0	1.2	1.0	12.0
34	904	WL-429-95	1.5	1.5	3.2	2.0	2.4	1.3	71.0	70.8	78.0	72.0	71.8	78.0	1.0	1.0	0.0	12.3
35	904	WL-429-41	1.3	1.9	1.8	2.0	2.8	1.5	71.0	72.4	77.0	72.0	73.8	77.0	1.0	1.4	0.0	12.0
36	905	WL-429-49	1.0	1.5	1.8	2.0	2.4	1.0	68.0	77.0	78.0	66.0	76.0	79.0	-2.0	-1.0	1.0	10.3
37	906	WL-429-25	1.0	2.0	1.5	1.5	4.8	1.3	72.0	70.4	78.0	71.0	69.0	79.0	-1.0	-1.4	1.0	13.0

38	909	WL-429-30	2.0	2.4	2.0	2.0	1.9	1.5	74.0	74.2	78.0	74.0	75.0	78.0	0.0	0.8	0.0	11.7
39	912	WL-429-77	1.5	2.5	1.3	2.0	2.1	1.8	69.0	75.8	80.0	68.0	77.2	80.0	-1.0	1.4	0.0	13.0
40	913	WL-429-36	1.0	3.1	1.8	2.0	3.0	1.0	76.0	76.3	82.0	74.0	75.8	81.0	-2.0	-0.5	-1.0	12.7
41	917	WL-429-82	1.0	2.4	2.0	2.0	3.2	1.0	71.0	73.8	77.0	71.0	75.3	76.0	0.0	1.5	-1.0	10.0
42	923	WL-429-75	1.0	1.6	1.5	2.0	2.6	1.0	71.0	76.4	76.0	71.0	80.2	77.0	0.0	3.8	1.0	13.0
43	924	WL-429-26	1.0	2.3	1.8	2.0	3.8	3.0	70.0	72.6	75.0	71.0	71.2	76.0	1.0	-1.4	1.0	10.7
44	931	WL-429-108	1.3	1.9	1.5	2.0	2.6	1.2	73.0	76.8	77.0	74.0	77.2	78.0	1.0	0.4	1.0	10.7
45	937	WL-429-115	1.3	1.5	1.5	1.5	3.2	1.5	71.0	67.2	81.0	72.0	69.6	81.0	1.0	2.4	0.0	12.0
46	941	WL-429-93	2.3	1.9	1.7	1.5	3.3	2.0	72.0	68.8	78.0	71.0	70.2	79.0	-1.0	1.4	1.0	11.3
47	945	WL-429-60	1.3	2.8	2.5	2.0	3.1	1.0	72.0	74.7	77.0	73.0	72.7	79.0	1.0	-2.0	2.0	11.0
48	950	WL-429-18	1.0	1.6	1.3	2.0	3.4	1.8	68.0	79.6	72.0	68.0	84.8	73.0	0.0	5.2	1.0	11.0
49	951	WL-429-57	1.5	2.3	1.5	2.0	2.3	1.0	73.0	75.6	84.0	71.0	77.2	83.0	-2.0	1.6	-1.0	10.7
50	951	WL-429-15	1.0	3.3	1.8	2.0	2.3	1.0	70.0	70.0	79.0	69.0	72.4	80.0	-1.0	2.4	1.0	11.7
51	952	WL-429-02	1.5	2.2	1.0	2.0	1.8	3.0	72.0	84.3	73.0	72.0	86.0	75.0	0.0	1.7	2.0	10.0
52	954	WL-429-101	1.3	1.8	1.0	2.0	3.0	1.0	72.0	78.4	77.0	72.0	81.2	78.0	0.0	2.8	1.0	11.0
53	955	WL-429-24	1.5	3.2	2.0	2.0	3.4	1.0	73.0	72.0	78.0	74.0	73.8	79.0	1.0	1.8	1.0	13.0
54	957	WL-429-89	1.3	1.8	2.0	1.0	2.4	1.5	73.0	77.0	77.0	74.0	82.6	76.0	1.0	5.6	-1.0	10.0
55	964	WL-429-90	1.5	2.2	1.5	1.5	2.6	2.0	72.0	73.8	79.0	73.0	79.4	79.0	1.0	5.6	0.0	13.0
56	973	WL-429-51	1.0	1.9	2.0	2.0	2.1	1.8	72.0	75.8	80.0	74.0	79.0	80.0	2.0	3.2	0.0	10.7
57	1020	WL-429-44	1.0	2.8	1.7	2.0	3.9	2.2	69.0	71.0	77.0	70.0	77.3	78.0	1.0	6.3	1.0	11.7
58	1114	WL-429-2	1.0	2.3	2.0	2.0	4.2	2.0	72.0	76.6	82.0	73.0	80.6	85.0	1.0	4.0	3.0	10.0

Abbreviations of the traits a presented in the list of abbreviations

Appendix 2: Combined Selection Index of inbred and test cross for identifying best lines (n=58, low index values are best)

	Traits	TLB F2	TLB F3	TLB F4	MSV F2	MSV F3	MSV F4	SD F3	SD F4	ASI, F2	ASI F3	ASI F4	F3 KR	TCs AD	SD	ASI	MSV%	TLB	E.H	EPP	KR	YLD
Index	Multiplier	5	10	10	3	10	9	0.8	0.75	3	6	9	9	3	2	9	8	19	0.1	-12	-2	-41
481	Mean	1.2	2.2	1.6	1.8	2.6	1.4	74.4	76.1	-0.2	1.0	0.4	11.5	66.4	67.0	0.7	0.3	1.4	97.1	1.2	12.8	7.3
451	25% percentile	1.0	1.9	1.3	1.6	2.1	1.0	71.2	74.0	-1.0	-0.5	0.0	10.7	65.5	66.0	0.3	0.0	1.3	91.2	1.1	12.5	6.8
505	75% percentile	1.3	2.4	2.0	2.0	3.1	1.8	77.3	78.8	1.0	2.1	1.0	12.3	67.2	67.9	1.0	0.7	1.6	101	1.2	13.2	7.8
54	Difference	0.3	0.5	0.7	0.4	1.0	0.8	6.1	4.8	2.0	2.6	1.0	1.7	1.8	1.9	0.7	0.8	0.3	9.9	0.1	0.7	0.9
Difference*multiplier		1.3	5.3	7.0	1.1	9.9	7.2	4.6	3.6	6.0	15.5	9.0	15.0	5.3	3.8	6.2	6.2	5.9	1.0	-1.5	-1.4	-38.6
Percent of index diff.		3	10	13	2	18	13	9	7	11	29	17	28	10	7	12	12	11	2	-3	-3	72
Index	Lines																					
391	WL-429-33	1.0	1.5	1.0	2.0	2.6	1.0	67.5	79.0	-2.0	-0.5	0.0	11.3	67.2	67.6	0.5	0.2	1.2	115	1.3	13.0	8.5
396	WL-429-40	1.0	1.9	2.1	1.0	1.3	1.5	67.2	73.0	3.0	-0.4	1.0	10.0	64.6	65.1	0.3	0.2	1.4	101	1.1	12.2	8.3
420	WL-429-49	1.0	1.5	1.8	2.0	2.4	1.0	76.0	79.0	-2.0	-1.0	1.0	10.3	65.8	66.0	0.2	1.0	1.2	96	1.3	13.1	7.9
422	WL-429-37	1.0	2.1	1.3	2.0	2.2	1.0	69.0	78.0	-2.0	-1.8	2.0	12.3	66.3	66.3	0.0	0.8	1.1	88	1.2	12.2	8.1
424	WL-429-57	1.5	2.3	1.5	2.0	2.3	1.0	77.2	83.0	-2.0	1.6	-1.0	10.7	66.8	67.3	0.9	-0.2	1.1	109	1.3	13.3	8.3
431	WL-429-34	1.0	2.2	2.3	2.0	2.0	1.0	77.0	71.0	-3.0	0.0	-2.0	10.7	65.7	66.8	1.0	0.1	1.1	107	1.3	12.3	7.2
434	WL-429-4	1.3	3.0	2.5	2.0	2.3	1.0	72.0	71.0	2.0	-1.0	-1.0	10.3	65.1	65.9	0.8	0.1	1.3	99	1.2	12.7	7.6
440	WL-429-50	1.3	2.4	2.0	2.0	1.7	2.0	71.2	73.0	0.0	0.6	1.0	11.3	64.0	64.4	0.3	0.0	1.8	107	1.0	12.5	8.0
444	WL-429-70	1.5	2.4	1.0	2.0	2.1	1.0	74.8	76.0	-1.0	0.2	0.0	11.0	66.8	67.1	0.4	1.0	1.4	89	1.1	12.5	7.7
445	249 -119	1.0	2.2	1.0	1.0	2.8	1.0	72.0	67.0	0.0	2.6	0.0	12.0	67.1	67.5	0.6	0.0	1.3	97	1.2	13.0	7.7
446	WL-429-52	1.0	2.4	2.0	2.0	1.6	1.0	73.4	76.0	1.0	1.6	-1.0	10.3	66.3	66.6	0.3	-0.3	1.9	92	1.1	12.1	7.6
446	WL-429-10	1.0	2.5	1.3	2.0	1.5	1.3	80.0	75.0	-1.0	-6.0	1.0	11.3	65.4	66.1	0.8	-0.2	1.2	91	1.1	13.1	6.8

447	WL-429-85	1.0	2.2	1.9	2.0	1.0	1.0	69.8	74.0	-1.0	-1.4	1.0	10.7	65.6	66.0	0.3	-0.3	1.3	103	1.1	13.0	6.7
449	WL-429-78	1.0	2.5	2.0	1.5	2.1	1.5	75.3	66.0	-1.0	0.3	0.0	12.0	67.6	68.1	0.5	0.1	1.6	96	1.3	12.7	7.7
450	WL-429-96	1.0	2.3	1.0	2.0	2.8	1.0	79.5	74.0	-1.0	-1.0	1.0	10.0	66.1	66.3	0.2	0.2	1.3	98	1.2	13.1	7.2
453	WL-429-94	1.0	2.4	1.3	1.0	2.7	2.1	77.8	72.0	0.0	3.0	-2.0	13.3	64.8	66.4	1.5	0.0	1.2	99	1.0	13.3	8.1
453	WL-429-51	1.0	1.9	2.0	2.0	2.1	1.8	79.0	80.0	2.0	3.2	0.0	10.7	64.9	65.3	0.5	0.1	1.3	93	1.3	12.6	8.1
460	WL-429-32	1.0	3.4	1.8	2.0	2.4	1.0	77.6	73.0	-2.0	1.0	1.0	11.3	64.1	64.9	0.6	-0.1	1.6	104	1.1	13.2	7.7
460	WL-429-77	1.5	2.5	1.3	2.0	2.1	1.8	77.2	80.0	-1.0	1.4	0.0	13.0	66.7	66.8	0.0	0.9	1.4	113	1.3	12.7	8.3
460	WL-429-36	1.0	3.1	1.8	2.0	3.0	1.0	75.8	81.0	-2.0	-0.5	-1.0	12.7	68.5	68.6	0.1	-0.3	1.7	111	1.3	13.4	8.1
461	WL-429-71	1.0	2.0	1.2	2.0	2.2	1.0	70.2	75.0	-1.0	0.4	0.0	12.7	64.1	65.1	1.0	-0.2	1.4	90	1.2	12.9	7.0
461	WL-429-26	1.0	2.3	1.8	2.0	3.8	3.0	71.2	76.0	1.0	-1.4	1.0	10.7	65.2	66.4	1.1	1.0	1.3	103	1.2	12.7	8.2
466	WL-429-25	1.0	2.0	1.5	1.5	4.8	1.3	69.0	79.0	-1.0	-1.4	1.0	13.0	64.7	64.1	-0.5	1.1	1.2	99	1.2	12.4	7.6
470	WL-429-28	1.0	2.9	1.3	2.0	3.6	1.0	68.5	77.0	-3.0	-3.3	-1.0	11.3	67.2	67.5	0.3	1.0	1.1	92	1.3	13.9	6.4
471	WL429-104	1.0	2.1	1.3	1.0	1.8	2.5	77.8	74.0	0.0	-1.0	2.0	11.3	67.9	68.2	0.3	-0.2	1.8	95	1.2	11.5	7.7
472	WL429-113	1.0	2.4	1.4	1.0	2.3	1.0	71.2	73.0	0.0	0.2	0.0	10.3	67.4	67.9	0.7	0.0	1.4	90	1.1	11.6	6.7
472	WL-429-60	1.3	2.8	2.5	2.0	3.1	1.0	72.7	79.0	1.0	-2.0	2.0	11.0	66.0	66.0	0.0	0.0	2.0	101	1.1	13.3	7.9
473	WL-429-43	1.0	2.1	2.0	1.0	4.1	2.8	70.6	74.0	1.0	0.4	-1.0	12.0	65.7	66.3	0.7	0.3	1.6	92	1.1	13.4	7.8
477	WL429-109	1.3	1.7	1.5	2.0	2.8	1.3	72.6	77.0	1.0	0.4	-1.0	13.3	67.0	67.8	0.8	-0.2	1.5	97	1.3	13.0	7.4
477	WL429-102	1.5	2.2	1.0	2.0	1.8	3.0	86.0	75.0	0.0	1.7	2.0	10.0	66.7	66.6	0.0	0.0	1.3	96	1.1	13.0	7.6
478	WL-429-68	1.0	3.0	3.0	2.0	4.0	1.0	70.6	73.0	-3.0	-1.8	1.0	10.7	65.5	65.9	0.5	0.1	1.3	99	1.1	12.9	7.0
479	WL429-111	1.0	1.9	1.5	1.0	2.6	2.1	73.2	80.0	1.0	-0.8	-1.0	12.0	66.6	66.9	0.3	0.1	1.2	100	1.4	12.8	6.8
483	WL-429-24	1.5	3.2	2.0	2.0	3.4	1.0	73.8	79.0	1.0	1.8	1.0	13.0	65.7	66.6	0.8	0.1	1.4	106	1.2	13.3	8.4
491	WL429-108	1.3	1.9	1.5	2.0	2.6	1.2	77.2	78.0	1.0	0.4	1.0	10.7	68.1	68.7	0.5	1.1	1.5	91	1.1	12.9	7.4
491	WL-429-17	1.8	2.3	1.5	2.0	1.7	2.0	75.6	76.0	-2.0	1.2	-3.0	10.7	68.8	70.5	1.9	-0.2	1.8	90	1.1	11.9	6.9
492	WL-429-93	2.3	1.9	1.7	1.5	3.3	2.0	70.2	79.0	-1.0	1.4	1.0	11.3	64.4	65.8	1.5	0.7	1.2	91	1.1	12.9	7.4
494	WL429-107	1.3	1.9	1.6	2.0	2.8	1.1	75.6	76.0	1.0	1.2	1.0	12.0	67.0	67.5	0.3	0.0	1.5	96	1.1	12.1	7.3
497	WL-429-27	1.5	2.5	1.3	1.0	1.3	2.0	71.2	78.0	-1.0	1.4	1.0	12.0	65.7	66.1	0.5	0.1	1.6	91	1.1	12.6	6.8
497	WL-429-82	1.0	2.4	2.0	2.0	3.2	1.0	75.3	76.0	0.0	1.5	-1.0	10.0	66.4	67.6	1.2	0.4	1.4	104	1.1	13.0	6.8
500	WL-429-41	1.3	1.9	1.8	2.0	2.8	1.5	73.8	77.0	1.0	1.4	0.0	12.0	67.7	68.9	1.1	0.1	1.6	98	1.1	12.8	7.4

502	WL-429-15	1.0	3.3	1.8	2.0	2.3	1.0	72.4	80.0	-1.0	2.4	1.0	11.7	66.6	66.6	0.2	0.1	1.6	85	1.3	12.5	7.1
502	WL-429-56	1.0	2.0	1.7	2.0	2.1	1.2	69.6	74.0	1.0	3.4	1.0	11.3	65.6	66.8	1.2	-0.1	1.4	95	1.0	13.0	6.8
504	WL-429-89	1.3	1.8	2.0	1.0	2.4	1.5	82.6	76.0	1.0	5.6	-1.0	10.0	67.8	68.0	0.2	0.9	1.4	90	1.2	12.1	7.2
505	WL-429-30	2.0	2.4	2.0	2.0	1.9	1.5	75.0	78.0	0.0	0.8	0.0	11.7	67.3	67.9	0.5	1.6	1.4	97	1.2	12.8	7.2
506	WL429-118	1.0	1.6	1.3	2.0	3.4	1.8	84.8	73.0	0.0	5.2	1.0	11.0	65.3	65.9	0.7	-0.3	1.2	97	1.1	13.3	7.2
506	WL429-101	1.3	1.8	1.0	2.0	3.0	1.0	81.2	78.0	0.0	2.8	1.0	11.0	67.8	69.7	1.8	-0.1	1.4	121	1.2	13.7	7.5
512	WL-429-76	1.0	1.6	1.3	2.0	3.0	1.0	72.3	74.0	0.0	2.3	1.0	11.3	66.4	67.8	1.3	0.7	1.3	82	1.1	13.2	6.6
516	WL-429-61	1.0	2.5	1.5	2.0	3.2	1.0	70.0	73.0	0.0	1.8	2.0	12.7	64.7	65.3	0.7	0.1	1.5	91	1.2	12.5	6.7
523	WL429-44	1.0	2.8	1.7	2.0	3.9	2.2	77.3	78.0	1.0	6.3	1.0	11.7	65.5	65.9	0.5	1.3	1.6	94	1.2	12.7	8.1
525	WL429-106	1.5	1.7	1.6	2.0	1.5	1.3	75.2	76.0	-1.0	2.2	0.0	12.7	68.7	69.8	1.0	0.0	1.5	85	1.1	12.7	6.5
527	WL429-105	1.0	2.2	1.5	1.0	2.3	1.0	73.4	70.0	-1.0	1.6	1.0	12.3	67.5	68.1	0.5	0.8	2.0	88	1.1	14.0	6.4
533	WL-429-90	1.5	2.2	1.5	1.5	2.6	2.0	79.4	79.0	1.0	5.6	0.0	13.0	66.6	67.4	0.7	1.7	1.1	106	1.1	13.3	7.6
545	WL-429-75	1.0	1.6	1.5	2.0	2.6	1.0	80.2	77.0	0.0	3.8	1.0	13.0	67.1	68.5	1.5	0.0	1.5	98	1.0	13.2	6.8
547	WL429-110	1.0	1.8	1.0	2.0	3.1	1.0	78.6	77.0	0.0	1.2	1.0	13.3	66.7	67.6	0.8	0.0	1.3	96	1.2	12.2	6.2
553	WL429-115	1.3	1.5	1.5	1.5	3.2	1.5	69.6	81.0	1.0	2.4	0.0	12.0	68.2	69.2	1.0	0.8	1.8	98	1.3	13.2	6.4
571	WL-429-2	1.0	2.3	2.0	2.0	4.2	2.0	80.6	85.0	1.0	4.0	3.0	10.0	68.2	68.7	0.5	0.6	1.4	109	1.2	12.3	7.2
574	WL429-117	1.3	1.8	1.0	2.0	3.3	1.0	67.2	76.0	0.0	0.2	3.0	13.3	65.2	67.7	2.3	1.1	1.6	80	1.2	13.2	5.9
579	WL-429-95	1.5	1.5	3.2	2.0	2.4	1.3	71.8	78.0	1.0	1.0	0.0	12.3	68.1	69.0	1.0	0.1	1.9	91	1.2	12.6	5.7

Appendix: 3 Specific and general combining ability (SCA & GCA) for yield of 58 lines with 2 testers A and B in 3 locations

Locations	Namulonge			Serere			Bulindi			Across Locations		
Lines	SCA Tester A	SCA Tester B	GCA	SCA Tester A	SCA Tester B	GCA	SCA Tester A	SCA Tester B	GCA	SCA Tester A	SCA Tester B	GCA
WL-429-10	-0.70	0.70	-0.93	0.56	-0.56	-0.57	1.10	-1.10	-0.73	0.32	-0.32	-0.63
WL-429-101	-0.48	0.48	0.09	-0.03	0.03	0.19	1.27	-1.27	1.22	0.25	-0.25	0.22
WL-429-102	0.43	-0.43	0.23	-0.13	0.13	0.27	-0.42	0.42	1.20	-0.04	0.04	0.66
WL-429-104	0.34	-0.34	0.30	0.31	-0.31	0.36	-1.01	1.01	1.41	-0.12	0.12	0.70
WL-429-105	0.32	-0.32	-0.56	-0.37	0.37	-0.97	0.08	-0.08	-2.75	0.01	-0.01	-1.35
WL-429-106	-0.16	0.16	0.24	0.35	-0.35	-0.83	-0.42	0.42	1.70	-0.08	0.08	0.56
WL-429-107	-0.11	0.11	-0.17	0.15	-0.15	-0.01	1.02	-1.02	0.18	0.35	-0.35	-0.08
WL-429-108	0.74	-0.74	-1.17	-0.89	0.89	0.08	-0.54	0.54	-1.60	-0.23	0.23	-0.80
WL-429-109	0.61	-0.61	-0.68	1.12	-1.12	0.09	-0.76	0.76	-0.78	0.32	-0.32	-0.37
WL-429-110	0.20	-0.20	-0.23	0.17	-0.17	-1.18	0.04	-0.04	0.08	0.14	-0.14	-0.29
WL-429-111	-0.74	0.74	0.40	0.83	-0.83	-0.50	-0.90	0.90	-0.47	-0.27	0.27	-0.09
WL-429-113	-0.72	0.72	0.59	-0.23	0.23	-0.63	-1.27	1.27	-0.15	-0.74	0.74	0.01
WL-429-115	-0.67	0.67	1.60	0.92	-0.92	-0.95	0.42	-0.42	-0.75	0.22	-0.22	-0.04
WL-429-117	-0.22	0.22	-0.82	0.57	-0.57	-1.44	0.31	-0.31	-0.20	0.22	-0.22	-0.75
WL-429-118	0.79	-0.79	0.00	0.18	-0.18	-0.13	-0.05	0.05	-0.08	0.30	-0.30	-0.08
WL-429-119	-0.35	0.35	0.06	-0.49	0.49	0.38	1.16	-1.16	-1.15	0.11	-0.11	-0.09
WL-429-15	-0.65	0.65	-0.68	0.73	-0.73	-0.21	1.10	-1.10	0.00	0.40	-0.40	-0.32
WL-429-17	-1.47	1.47	0.23	-0.46	0.46	-0.47	-0.33	0.33	1.36	-0.75	0.75	0.18
WL-429-2	-0.63	0.63	0.00	1.24	-1.24	-0.10	0.38	-0.38	0.21	0.33	-0.33	0.11
WL-429-24	1.63	-1.63	-1.17	-0.53	0.53	1.10	0.06	-0.06	-0.29	0.39	-0.39	-0.19
WL-429-25	-0.23	0.23	0.41	-0.43	0.43	0.29	0.14	-0.14	0.28	-0.18	0.18	0.48
WL-429-26	-0.27	0.27	-0.15	-0.87	0.87	0.83	1.85	-1.85	0.58	0.24	-0.24	0.24
WL-429-27	0.58	-0.58	0.14	0.29	-0.29	-0.51	-1.48	1.48	-0.29	-0.21	0.21	-0.15
WL-429-28	0.30	-0.30	-0.13	-1.21	1.21	-0.92	-1.70	1.70	1.22	-0.87	0.87	-0.17
WL-429-30	0.34	-0.34	-0.28	1.39	-1.39	-0.15	-0.17	0.17	0.86	0.52	-0.52	0.10

WL-429-32	-0.39	0.39	-0.01	-1.08	1.08	0.33	-0.47	0.47	0.22	-0.65	0.65	0.21
WL-429-33	0.99	-0.99	-0.51	0.34	-0.34	1.17	0.06	-0.06	1.11	0.46	-0.46	0.56
WL-429-34	-0.04	0.04	0.52	0.86	-0.86	-0.12	1.36	-1.36	-1.59	0.73	-0.73	-0.41
WL-429-36	-0.62	0.62	-0.04	-0.87	0.87	0.79	0.22	-0.22	-0.76	-0.42	0.42	-0.19
WL-429-37	-0.28	0.28	0.31	-1.16	1.16	0.74	0.66	-0.66	-0.01	-0.26	0.26	0.37
WL-429-4	0.95	-0.95	-0.03	-0.61	0.61	0.25	-0.09	0.09	-2.25	0.08	-0.08	-0.63
WL-429-40	-0.09	0.09	0.32	0.18	-0.18	0.95	-0.49	0.49	0.04	-0.13	0.13	0.49
WL429-41	1.77	-1.77	-1.46	-0.09	0.09	0.09	0.76	-0.76	-0.35	0.82	-0.82	-0.51
WL-429-43	-0.85	0.85	0.41	-0.79	0.79	0.45	-1.07	1.07	0.73	-0.90	0.90	0.50
WL-429-44	-0.18	0.18	0.28	0.48	-0.48	0.81	-1.35	1.35	-0.48	-0.35	0.35	0.41
WL-429-49	0.23	-0.23	-0.57	0.60	-0.60	0.60	0.16	-0.16	1.55	0.33	-0.33	0.54
WL-429-50	0.08	-0.08	-1.04	0.09	-0.09	0.69	1.42	-1.42	0.87	0.53	-0.53	0.04
WL-429-51	0.42	-0.42	0.52	-1.42	1.42	0.79	-0.58	0.58	0.94	-0.53	0.53	0.73
WL-429-52	0.02	-0.02	0.30	0.05	-0.05	0.27	1.78	-1.78	-0.71	0.62	-0.62	-0.21
WL-429-56	0.07	-0.07	0.42	-0.54	0.54	-0.50	-1.29	1.29	1.94	-0.59	0.59	0.59
WL-429-57	-0.08	0.08	1.02	-1.66	1.66	0.94	-0.54	0.54	-1.00	-0.76	0.76	0.19
WL-429-60	-0.06	0.06	0.02	-0.27	0.27	0.61	-0.61	0.61	0.13	-0.31	0.31	0.16
WL-429-61	0.24	-0.24	-0.46	1.13	-1.13	-0.59	1.20	-1.20	-0.54	0.86	-0.86	-0.58
WL-429-68	0.07	-0.07	0.72	-0.33	0.33	-0.32	1.42	-1.42	-1.43	0.39	-0.39	-0.52
WL-429-70	-0.17	0.17	0.32	-0.81	0.81	0.36	0.16	-0.16	-0.34	-0.28	0.28	0.03
WL-429-71	0.58	-0.58	-0.35	-0.58	0.58	-0.34	0.30	-0.30	0.10	0.10	-0.10	-0.10
WL-429-75	-0.79	0.79	1.05	0.18	-0.18	-0.51	0.31	-0.31	-2.57	-0.10	0.10	-0.62
WL-429-76	-0.02	0.02	0.32	0.79	-0.79	-0.78	-0.16	0.16	0.05	0.20	-0.20	-0.07
WL-429-77	-0.38	0.38	0.59	0.57	-0.57	0.97	-1.10	1.10	1.09	-0.31	0.31	0.88
WL-429-78	-0.19	0.19	0.13	0.71	-0.71	0.39	0.00	0.00	1.87	0.17	-0.17	0.78
WL-429-82	0.15	-0.15	-0.27	-0.10	0.10	-0.53	-0.84	0.84	0.20	-0.26	0.26	-0.05
WL-429-85	0.02	-0.02	-0.58	-0.56	0.56	-0.59	0.01	-0.01	-1.83	-0.18	0.18	-0.94
WL-429-89	0.30	-0.30	0.05	-0.47	0.47	-0.15	0.04	-0.04	-1.11	-0.04	0.04	-0.38
WL-429-90	0.12	-0.12	0.46	0.40	-0.40	0.25	-0.81	0.81	1.87	-0.10	0.10	0.79
WL-429-93	-0.16	0.16	-0.37	-0.49	0.49	0.07	1.24	-1.24	0.28	0.20	-0.20	0.03
WL-429-94	-0.79	0.79	0.93	1.39	-1.39	0.76	-0.43	0.43	-0.62	0.05	-0.05	0.31

WL-429-95	0.10	-0.10	0.02	0.46	-0.46	-1.60	0.82	-0.82	-0.03	0.46	-0.46	-0.46
WL429-96	0.22	-0.22	-0.48	0.46	-0.46	-0.18	-2.06	2.06	1.56	-0.46	0.46	0.24

SCA=specific combining ability, GCA=general combining ability