

**ASSESSED LINE BY TESTER ANALYSIS OF MAIZE INBREDS FOR
NORTHERN LEAF BLIGHT AND OTHER YIELD COMPONENTS IN
SELECTED COUNTIES, KENYA**

FERISTA WANJIKU NDUNG’U (BSC. AGRICULTURE)

A143/CE/25908/2014

**A THESIS SUBMITTED IN PARTIAL FULFILLMENT OF THE
REQUIREMENT FOR THE AWARD OF A DEGREE IN MASTER OF
SCIENCE IN PLANT BREEDING IN THE SCHOOL OF AGRICULTURE AND
ENTERPRISE DEVELOPMENT, KENYATTA UNIVERSITY.**

JANUARY, 2021

DECLARATION

I declare that this thesis is my original work and has not been presented in part or in whole for any awards in any other institution.

Signature..... Date.....

Ferista Wanjiku Ndung’u A143/CE/25908/2014

Department of Agricultural Science and Technology

Supervisors

We confirm that the work reported in this thesis was carried out under our supervision and has been submitted with our approval.

Signature..... Date.....

Dr. Wilson M. Thagana

Department of Agricultural Science and Technology

Kenyatta University

Signature..... Date.....

Dr. David K. Ndung’u

Chief Officer-Agriculture

Kiambu County Government

DEDICATION

I dedicate this manuscript to my daughters Brielle and Britney. You are my greatest source of inspiration.

ACKNOWLEDGEMENTS

I wish to express my sincere appreciation to my supervisors Dr. Wilson M. Thagana and Dr. David K. Ndung'u for their skillful, ever inspiring guidance, patience, unwavering support and kind supervision from the inception of my studies in MSc. Plant Breeding.

I am highly indebted to my mentor Mr. Sudhakar for believing in me, his supportive criticism and guidance all through.

I am grateful to Don White the managing director of Agventure Limited for the positivity he has had in me, moral support and always granting me time to accomplish on all areas regarding my research work.

I would also love to express my sincere gratitude to my parents John Ndungu and Jane Ndungu, my siblings Grace, Samuel and Esther for their encouragement in the entire journey. To my dear husband Joseph, I highly appreciate you for your support and above all for always being there.

Above all, I am grateful to the Almighty for being my guide, my source of strength and for enabling me go through my studies to successful completion.

TABLE OF CONTENTS

DECLARATION	ii
DEDICATION	iii
ACKNOWLEDGEMENTS	iv
LIST OF TABLES.....	viii
LIST OF FIGURES.....	ix
LIST OF ABBREVIATIONS AND ACRONYMS.....	x
ABSTRACT	xi
CHAPTER ONE.....	1
INTRODUCTION	1
1.1 Background Information.....	1
1.2 Management Strategies.....	5
1.3 Line by Tester Design.....	5
1.4 Statement of the problem.....	6
1.5 Justification and Significance of the Study.....	6
1.6 Significance of the Study.....	7
1.7.0 Objectives	7
1.7.1 General Objective.....	7
1.7.2 Specific objectives.....	7
1.8 Hypotheses.....	8
1.9 Conceptual Framework.....	9
CHAPTER TWO.....	10
LITERATURE REVIEW	10
2.1 Maize Yield Components	10
2.2 Genotype by Environment Interactions	12
2.3 Maize Diseases	12
2.4 History of the pathogen.....	15
2.5 Description.....	17
2.6 Genetics of Resistance to <i>E. turcicum</i>	17

2.7.0 Combining Ability analysis	18
2.7.1 General combining Ability.....	19
2.7.2 Specific Combining Ability	19
2.8 Testers.....	20
2.9 Heterotic Classification.....	20
CHAPTER THREE.....	25
MATERIALS AND METHODS.....	25
3.1 Experimental site	25
3.2 Experimental Designs and management.....	25
3.3 Experimental Materials.....	26
3.4.1 Methods	27
3.4.2 Data Collection	27
3.5 Data Analysis	28
3.5.1 Analysis of Variance	28
CHAPTER FOUR	30
RESULTS.....	30
4.1 Kakamega	30
4.1.1 General Combining Ability Analysis.....	30
4.1.2 Specific Combining Ability Analysis	33
4.1.3 Heterotic Classification.....	36
4.1.4 Yield of the Crosses	37
4.2 Embu.....	39
4.2.1 General Combining Ability Analysis.....	39
4.2.2 Specific Combining Ability Analysis	42
4.2.3 Heterotic Classification.....	44
4.2.4 Yield of the Crosses	46
4.3 Muranga	47
4.3.1 General Combining ability Analysis.....	47
4.3.2 Specific Combining Ability Analysis	49

4.3.3 Heterotic Classification	54
4.4.4 Yield of the Crosses (Muranga)	55
4.4: Across Sites Analysis	57
4.4.1: Yield of the Crosses across the Locations	57
CHAPTER FIVE	59
DISCUSSION.....	59
CHAPTER SIX.....	61
Conclusion and Recommendation	61
6.1 Conclusion	61
6.2 Recommendations.....	63
REFERENCES	64
APPENDICES.....	79
Appendix I: NACOSTI Research License	79

LIST OF TABLES

Table 3.1 Stock ID and Pedigree of the Lines Used in the Study	26
Table 4.1: General Combining Ability Estimates for Northern Leaf Blight in Kakamega	30
Table 4.2: General Combining Ability Estimates of the Lines for Days to Anthesis and Days to Silking in Kakamega	32
Table 4.3: Specific combining ability Estimates of the crosses with Tester A for Grain Weight	33
Table 4.4: Specific Combining Ability Estimates of the Crosses with Tester B for Grain Weight	34
Table 4.5: Specific Combining Ability Effects of the Crosses to Northern Leaf Blight in Kakamega	35
Table 4.6: Heterotic Classification of the Lines using the SCA for Grain Weight in Kakamega	36
Table 4.7: Yield of the Crosses in Kakamega	38
Table 4.8: General Combining Ability Estimates of the Lines to Northern Leaf Blight in Embu	39
Table 4.9: General Combining Ability Estimates of the lines for Days to Anthesis (AD) and Days to Silking (SD) in Embu	40
Table 4.10: Specific Combining Ability Estimates of Tester A Crosses for Grain Weight in Embu	42
Table 4.11: Specific combining ability Estimates of Tester B Crosses for Grain Weight in Embu	43
Table 4.12: Heterotic classification of the Lines using the Specific Combining Ability for Grain Weight in Embu	45
Table 4.13: Yield of the Crosses in Embu	46
Table 4.14: General Combining Ability Estimates for Northern Leaf Blight in Muranga	47
Table 4.15: General Combining Ability of the lines for Days to Anthesis and Days to Silking in Muranga	48
Table 4.16: Specific Combining Ability Estimates of the Crosses with Tester A for Grain Weight in Muranga	50
Table 4.17: Specific Combining Ability Estimates of the Crosses with Tester B for Grain Weight in Muranga	51
Table 4.18: Specific combining ability Effects of the Crosses to Northern Leaf Blight in Muranga	52
Table 4.19: Heterotic Classification of the Lines in Muranga	54
Table 4.20: Yield of the Crosses in Muranga	56
Table 4.21: Across sites Yield in mt/ha	58

LIST OF FIGURES

Figure 1.1: Conceptual Framework of the Study..... 8

LIST OF ABBREVIATIONS AND ACRONYMS

AD	Days to 50% Anthesis
ANOVA	Analysis of Variance
CIMMYT	International Maize and Wheat Improvement Center
DAP	Diammonium Phosphate
EA	Ear aspect
EH	Ear Height
FW	Field Weight
GCA	General combining Ability
GD	Genetic Distance
GLS	Gray Leaf Spot
GS	Genetic Similarity
GW	Grain Weight
LxT	Line by Tester
MLND	Maize Lethal Necrosis Disease
Mt	Metric tonnes
NE	Number of Ears
NLB	Northern Leaf Blight
NPT	National Performance Trials
PH	Plant Height
SCA	Specific Combining Ability
SD	Days to 50% Silking
TLB	Turcicum Leaf Blight

ABSTRACT

Northern Leaf Blight (NLB) also known as Turcicum Leaf Blight (TLB) is a foliar disease of maize caused by *Exserohilum turcicum*. It is a great challenge in many maize production regions worldwide. It has a growing season characteristic of high humidity and moderate temperatures ranging from 17-27⁰C. The disease can result to great yield losses in maize ranging at 40-70% in the case where there is disease presence 2-3 weeks after the crop silks. The main aim of this study was to assess the combining ability of the maize lines to NLB and other yield related traits, to determine the heterotic orientation of the lines and to establish the yield potential of the crosses across different environments. The lines were introductions and the study was aimed to determine the performance of the lines prior to further development. Forty nine lines used in the study were obtained from a segregating population in the F₄ were crossed to two CIMMYT testers Tester A (CML312/CML442) and Tester B (CML395/CML444). The 98 crosses were planted in 3 mid-altitude agro-ecological zones of Kenya (Kakamega, Muranga and Embu). The heterotic orientation was determined for the lines and that differed across the 3 sites. The 3 sites were treated as independent environments due to genotype x environment interactions. Data was analyzed using REML, META-R and AGD-R tools. The results indicated significant GCA and SCA of some of the lines to NLB and different yield related traits including AD (days to anthesis) and SD (days to silking). The lines expressing significant GCA and SCA for NLB tolerance and high yield, the lines are recommended for further testing and development of NLB tolerant and high yielding maize hybrids in the mid-altitude agro-ecological zones of Kenya. The lines will recommended for use in breeding following further segregation hence could be used to develop hybrids that could be further subjected to trialing to obtain hybrids that are resistant to NLB, early maturing and high yielding. For the lines that could not be classified to their heterotic groups using Tester A and Tester B, these could be subjected to further tests with different testers in order to determine their heterotic groups and the knowledge could later be used in development of crosses.

CHAPTER ONE

INTRODUCTION

1.1 Background Information

Maize (*Zea mays*) is an important cereal crop in Kenya. Maize is ranked third as an important food in Kenya after wheat and rice (Khalili *et al.*, 2013). It has very high nutrient content and is one of the sources for fiber and calories. Maize was domesticated about ten thousand years ago in Mexico by an indigenous people. Maize total production area is 2.1 million ha of Kenya's 5.3 million ha of all crops harvested area (FAOSTAT 2015). Shortage of maize in the country often results in famine amongst the urban and rural poor. Future boost to maize production will depend mostly on yield improvement and not increase in area as most arable land in Kenya is already being cultivated. Different varieties of maize are grown under prevailing conditions determined by the ecological zones.

Kenya depends almost entirely on the agriculture sector for food hence due to variance in climate therefore the country is not totally food-sufficient every year. With maize as the country's main staple food hence a very crucial crop in both value and land area. An estimate of 90% of the maize being grown is in small land areas of below 5 hectares Nyoro *et al.*, 2004. Severe droughts in Kenya mainly results to maize failure causing food inadequacy as maize is a great source of nutrient for most people.

In Kenya, there are two growing seasons which range from 4-5 months in the lowlands and the mid-altitude ecology while the western highlands and the Rift Valley has a range of 8 months. Maize Breeders in the country having taken this into account hence develop lines for the arid areas which are characterized by early maturity and drought tolerance. Developed varieties have been bred for the medium altitudes and the cool highlands that have the longer growing seasons of about 8 months (Gebrekidan *et al.*, 1992).

In Kenya maize diseases that are of importance in are; rusts caused by *P.sorghii* and *P.polysora*; leaf blight caused by *E.turcicum*, *B.maydis*, *Phaesophaeria maydis* leaf spot, maize streak virus, Gray leaf Spot (GLS) and Maize Lethal Necrosis Disease (MLND). The implementation of sound breeding for these diseases in maize improvement is of importance in the country.

Breeders should have adequate knowledge on nature of the parental material and their combining ability, the characteristics and potential in hybrid development and performance in order to start up a breeding program with the goal to achieve maize production levels that are high. The information assists breeders in selection of suitable parental lines by defining the gene action types that are involved in the control of quantitative traits. The combining ability concept was defined by Sprague and Tatum (1942) to give two expressions, general combining ability (GCA) and specific combining ability (SCA) these are genetic parameters with great effect in choosing the next stage of the breeding program. Studies on combining abilities are of importance in the classification of parent lines into various heterotic groups.

Line by Tester method Kempthorne (1957) has been used mostly in derivation of information on the heritability of suitable traits from parents to progenies hence a performance comparison of lines in hybrids developed. This method is used in evaluation and selection of good hybrid combinations and provides information on the mode of gene action controlling different traits (Murenga *et al.*, 2015). Kempthorne (1957) developed line by tester analysis design which has been implemented widely by breeders worldwide to generate data that can be applied on GCA and SCA impact on parental lines and their hybrids. This method has been applied continually been in maize studies on quantitative genetics by a number of workers (Joshi *et al.*, 2002, Sharma *et al.*, 2004). This method could hence be utilized to give information on categorization of parent lines to their differing heterotic groups and also to check on the gene action types that are involved to express yield and the related traits.

Testers are used for identifying genotypes that are superior to use in breeding programs and hence choose heterotic relativity of genotypes. The purpose of line x tester testing is

estimation of combining ability of pure lines in a variety development program and selection of breeding values of genotypes for population improvement. Kempthorne (1957) defined a method of statistical analysis of the line x tester for testing GCA and SCA of inbred lines. The line by tester analysis design is used in breeding of both self-pollinated plants and cross pollinated plants and estimation of suitable parents and crosses. Sharma (2004) also reported that line by tester analysis is a good method with efficiency of speed that is achievable.

Northern leaf blight also known as Turcicum Leaf Blight (TLB) disease is caused by *Helminthosporium turcicum* (*Exserohilum Turcicum*). It is an important disease that affects photosynthesis with severe reduction in grain yield. Due to the fundamental relationship between photosynthesis and yield, there is considerable interest to study photosynthesis in respect to the incidence of *E.turcicum* in maize. Infected leaves show a progressive reduction in the leaf surface area as the disease severity increases. Disease symptoms appear on the leaves at any stage of the plant growth and mostly at or after anthesis. The disease can reduce the grain yield of maize by 40-70%.

The symptoms of NLB are recognized easily. Early symptoms comprise of oval, water-soaked spots on the leaves while the mature symptoms are characteristic cigar shaped lesions which are 3-15 cm long. These lesions are elliptical and tan in colour hence they develop distinct dark areas associated with fungus sporulation as they mature. Appearance of these lesions is on the lower plant leaves and spread to the upper leaves and plant sheaths with the crop maturity. If the infection is severe, the lesions merge causing blight to the whole leaf. The lesions differ depending on the tolerance or resistance levels of the host plant. As the lesions develop, classic symptoms of NLB are observed; long, oblong (cigar shaped) tan or grayish lesions. These lesions produce black or olive green fungal spores under high humidity conditions. These spores would be visualized by use of a hand lens.

Identification of *E.turcicum* is confirmed examination of the conidia by use of a microscope in the mature NLB lesions. There are several physiological races of

E.turcicum that have pathogen effects on maize. These races differ depending on their pathogenicity to different maize types with differing levels of resistance. A number of genes causing resistance to NLB are identified and are: Ht1, Ht 2, Ht 3 and Ht N. A different Race 0 of *E.turcicum* is avirulent to all Ht genotypes while race 23 is only virulent on Ht 2 and Ht 3 genotypes.

NLB is a disease of importance of maize in areas of high humidity in the country. These areas are characteristic of temperatures ranging at 17-27⁰ C with extensive durations of dew and wetness in the leaves. The NLB pathogen occurs mostly in regions where minimal tillage is practiced as the pathogen dwells in crop debris that cover the soil surface. In farmlands with high Nitrogen application, NLB highly occurs.

Apart from maize, *E.turcicum* also affects sorghum, Johnson grass, gama grass, teosinte and Sudan grass.

Disease symptoms may vary with hybrid susceptibility. Partially resistant hybrids produce fewer and smaller lesions and fewer fungal spores. Hybrids with race specific resistance tend to be smaller and yellow and do not produce spores. The lesions may also appear on the husks and leaf sheaths of susceptible hybrids.

When the conditions seem suitable for earlier onset of the disease, the productivity is reduced. NLB lesions minimize the leaf surface area of plants hence limiting photosynthesis. The earlier the lesions develop and the more they are in number, the greater the loss of the leaf photosynthetic area. When the lesions reach the flag leaf or beyond at 2 weeks prior to tasseling, yield losses happen. Yield losses may be less if the lesions do not appear on the upper leaves until later in the season. NLB lesions can cause stalk rots development hence lodging.

E.turcicum in the affected crop remains as mycelium and chlamydospores. At the start of the following season, the fungus in crop refuse begins to sporulate as a response to high temperatures and increased humid conditions. The conidia are disbursed through the wind of rainfall and cover the maize recently planted. Their germination takes place

at temperatures of between 17- 27⁰C under long wet conditions (6-18 hours) therefore affecting the host. The second phase of the disease occurs when the conidia is spread in the crop and to the rest of the crops within the field through wind or rainfall.

1.2 Management Strategies

Host plant resistance is one of the efficient ways in the disease control. The identified genes of resistance to NLB are introduced to most commercial varieties hence offering great resistance. Management of the disease would be termed successful through the use of qualitative resistance and would be dependent on the pathogen race that is present. Restriction of the lesion growth and spore formation would be made available by use of quantitative resistance.

Zero-tillage or minimal tillage lands planted with susceptible varieties have a greater risk in NLB occurrence though the climatic conditions play a role in the disease occurrence. Strategy is hence of importance in fields that show risk of the disease occurrence.

Crop rotation of maize with different family crops assists in minimizing the disease. The inoculum levels at the beginning of a season can be reduced through reduction of refuse.

Use of fungicides in the control of NLB is only effective if applied at the right crop stage. The application should be done immediately the lesions are seen. In the seasons that are cool and dry. The application of fungicides is not economical.

1.3 Line by Tester Design

This mating scheme has been used widely in breeding programs to evaluate on the potential of parents which could be either inbred lines or crosses with wide genetic base (Bernardo, 2002). Testers are used to identify superior genotypes and to determine the heterotic orientation of genotypes in breeding programs.

The purpose of the Line by Tester design is to estimate combining abilities of lines. It is also used to evaluate breeding values for improvement of populations (Bernardo, 2002).

The method is used in both self-pollinated and cross-pollinated plants to estimate suitability of parents and crosses, their SCA and GCA.

Line by tester design has been used widely in maize breeding (Sharma *et al.*, 2000). Makumbi *et al.*, (2005) evaluated the yield potential of 19 maize varieties in stress and non-stress environments using the LxT analysis. Significant differences for yield and days to 50% AD were found between the synthetic hybrids that had parental synthetics. Nature of gene action and combining ability for yield and protein in maize was studied through L x T design and it revealed action on non-additive gene action (Shanthi *et al.*, 2002).

1.4 Statement of the problem

The maize crop is affected by a number of diseases one of which is Northern leaf blight. It is an important disease that affects photosynthesis with severe reduction in grain yield. Due to the fundamental relationship between photosynthesis and yield, there is considerable interest to study photosynthesis in respect to the incidence of *E.turcicum* in maize. Infected leaves show a progressive reduction in surface area as the disease severity increases. Disease symptoms appear on the leaves at any stage of the plant growth and mostly at or after anthesis. The disease can reduce the grain yield of maize by 40-70%.

Major disease constraint and unknown heterotic patterns for maize collections and introductions is quite a challenge on maize productivity and breeding in Kenya. Maize introductions could have some traits of value that can be useful if the genetic base is broadened and their heterotic groups classified to make them useful in the breeding programmes in Kenya.

1.5 Justification and Significance of the Study

Major disease constraint and unknown heterotic patterns for maize collections and introductions is quite a challenge on maize productivity and breeding in Kenya. Introductions could have some traits of value that can be useful if the genetic base is

broadened and their heterotic groups classified to make them useful in breeding programmes in the country.

The study was conducted in Kakamega, Embu and Muranga counties of Kenya that are mid altitude agro-ecological zones with mean temperatures of 14-27⁰C, 12-27⁰C and 21-35⁰C respectively. The NLB disease is prevalent in maize growing areas with temperatures ranging at 17-27⁰C with extensive durations of dew and wetness hence the selected counties were suitable to allow for evaluation of the disease.

1.6 Significance of the Study

Lines with negative and significant GCA for NLB and with established heterotic groups could be crossed across the heterotic groups to develop NLB tolerant and resistant hybrids. The developed hybrids could be evaluated in the NPT trials for screening and release of NLB tolerant hybrids to the farmers in NLB prone areas. The high yielding testcrosses could be advanced to the NPT for evaluation and release and avail yield competitive varieties for the farmers.

1.7.0 Objectives

1.7.1 General Objective

To estimate the combining abilities of the inbred lines to NLB and other yield related traits under different agro-ecological environments.

1.7.2 Specific objectives

1. To estimate the GCA and SCA effects of the inbred lines to NLB and other yield related traits
2. To determine the heterotic orientation of the inbred lines.
3. To evaluate on the performance of the testcross to NLB and other yield related traits

1.8 Hypotheses

1. There is no significance in the GCA and SCA estimates of the inbred lines for NLB and other yield related traits.
2. There is no difference in the heterotic orientation of the inbred lines
3. There is no yield difference for the testcrosses in the different environments.

1.9 Conceptual Framework

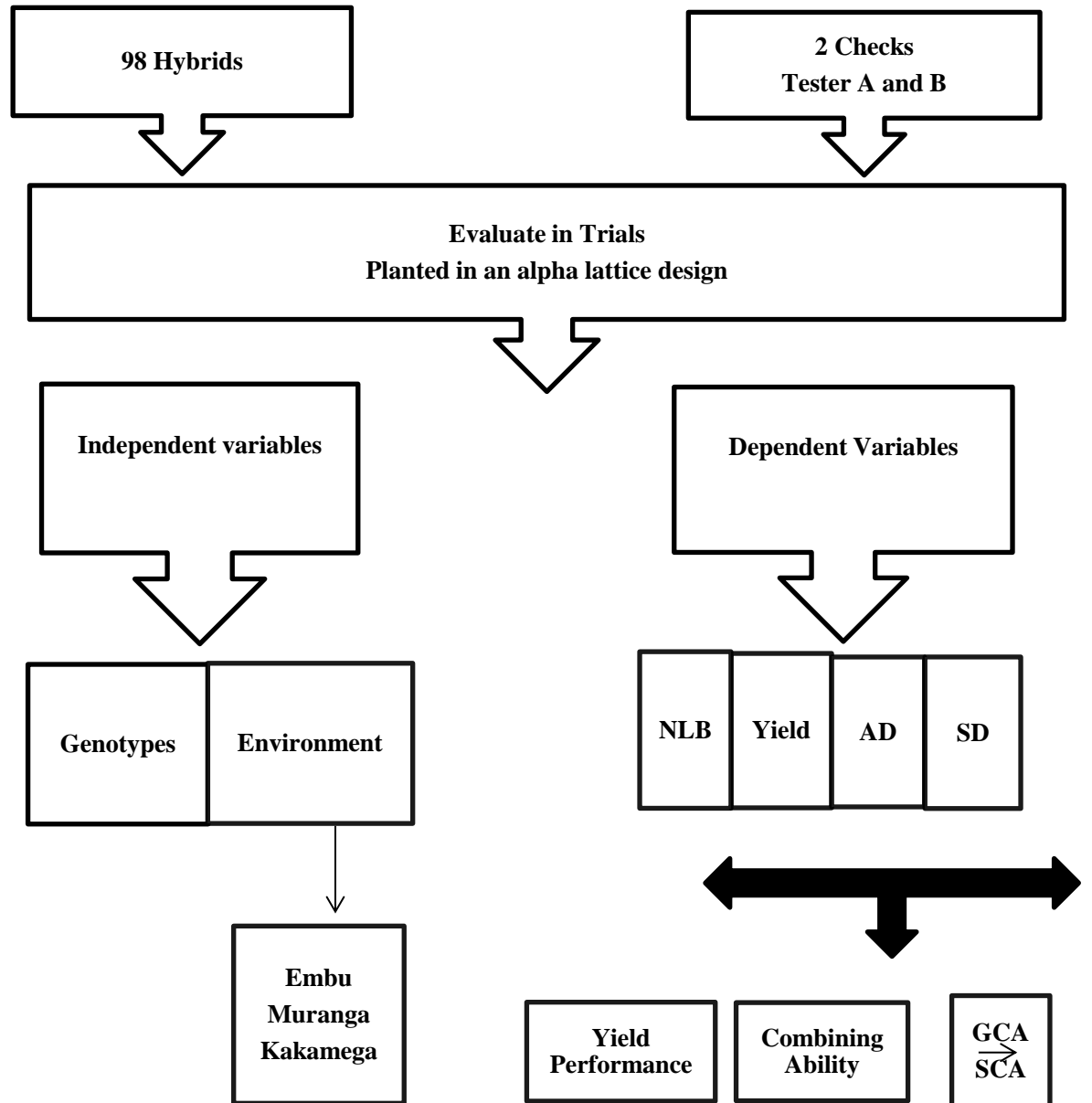


Figure 1.1: Conceptual Framework of the Study

CHAPTER TWO

LITERATURE REVIEW

2.1 Maize Yield Components

Globally, maize is a cereal of importance grown under very diversified environments unlike all other crop. It is ranked third as a food of importance across the world right after wheat and rice and therefore provides around 15-19% of calories required in third world countries (Shakoor *et al.*, 2007). Expansion of maize growing is due to its range of plasticity. Maize productivity characteristic is affected by a number of genes which are in action with the environment (Bocanski *et al.*, 2009).

Maize is a staple to over 85% of the Kenyan population. Individual consumption ranges at 98-100 kilograms that is an estimate of 2700 thousand (mt) metric tonnes annually (Nyoro *et al.*, 2004). Small scale growers account for seventy percent (70%) of the total production. The other thirty percent (30%) is from large scale growers (Export processing zone Authority, 2005).

Most of the crop is grown for subsistence by the small scale growers who then retain some 58% for household use from the total output (Mbithi, 2000).

With the annual consumption requirement annually, deficits have to be acquired through importation. Unsuitable weather conditions are mostly said to be the cause for low yields in some years. Average yields have however been at a constant mean of 2 tonnes per hectare which is below the 6 tonnes per hectare which should be the potential. This has been attributed to inadequate uptake of technology which includes planting of high yielding hybrid seed maize, lack of fertilizer use to avoid incurring high input costs and lack of credit (Republic of Kenya, 2004; Kangethe, 2004).

Lack of credit impacts inadequate capital hence farmers cannot afford to procure inputs which include certified seed, fertilizers and pesticides. Kenya incurs higher costs of production than other maize growing regions of other countries. This hence impacts

negatively the maize surplus due to cheaper imports from other countries like Uganda (Nyoro *et al.*, 2004).

Maize yield is determined highly by the growth and development of the crop, photosynthesis and the efficiency of the photosynthate partitioning into grain. Yield is also as a result of interaction between genotype, environment and management. The environmental factors of importance are water, temperature and solar radiation. The factors vary with the different growing seasons and cannot be controlled by the growers.

Maize growth could be Sub-divided into two growth stages, the vegetative growth and the reproductive growth stages. The vegetative stage growth occurs between seedling emergence and vegetative growth stage. After the maize crop reaches physiological maturity, environmental stress does not affect yield. Factors such as lodging, stalk breakage and ear dropping can damage the plant and decrease the harvestable yield.

Yield comprises of physical elements that are a correlation to the produced grain directly. These components are inter-linked and have compensating effects. The primary components which are the first order yield traits (ear numbers, number of kernels, kernel weight) effects directly impact on the final yield and also the yield components whose effects are indirect that may develop later (Fageria *et al.*, 1980).

Yield levels have a multiplying impact on the end product of a number of factors that are known as the yield components (Zeeshan *et al.*, 2013). The components are heritable with reduced environment changes and selection on the basis of the components is better unlike selection on the basis of yield. Assessing parent lines under the yield component performance basis could be useful in selecting highly performing parents for development of high yielding varieties (Bocanski *et al.*, 2009). With good characterization of physiological characters and the connection with maize yield and the components, genetic variance could be utilized to improve and increase diversity of germplasm (Alake *et al.*, 2008; Al-Tabbal *et al.*, 2012).

2.2 Genotype by Environment Interactions

Genotype by Environment interactions in maize breeding are challenging as they are an indication of failure in genotypes consistent response across different environmental conditions. On the basis of diverse biotic and abiotic factors, Africa's maize production environments vary. Africa is variable. This hence results in GxE interactions that are complex for important traits disease resistance and yield (Vivek *et al.*, 2010; Sibiya *et al.*, 2012).

Identification of stable genotypes for wide range of environments is the best way in minimizing GxE interactions. Presence of the interactions could also be exploited by selection of superior genotypes to suit specific environments (Alwala *et al.*, 2010).

When variations caused by hybrid by environment are partitioned into GCA x E and SCA x E, both the components are mostly of importance for yield and other agronomic traits (Badu-Apraku and Oyekunle 2012) It is an indication that the GCA of the parent lines and SCA of the hybrids change with environments. Apart from identifying crosses that are high yielding, it is of importance to identify parent lines which possess stability for GCA effects for adjustment of environmental variations and not only for high (Dehghanpour, 2013).

2.3 Maize Diseases

Maize is prone to many diseases caused by fungus, bacteria, viruses and nematodes leading to massive damage. These diseases include but are not limited to seedling blights, stalk rots, foliar diseases, downy mildews and ear rots. Among the fungal diseases is NLB which is caused by *E.turcicum* Leonard and Suggs. (Synonyms: *Helminthosprium turcicum*. It is one foliar disease of importance and it causes great grain and fodder reduction of up to 40-70%.

Northern leaf blight is a potential foliar disease of importance in regions where there is temperature drop in the night and with high humidity. The NLB disease highly affects the maize crop at all growth stages. Yield losses are higher if it arises at the onset of flowering and grain filling stages. NLB injures or kills the leaf tissues once in contact

and therefore reduces the photosynthetic area hence hindering the manufacture of food. If a sizeable area of the leaf is killed, the yield and vigour are greatly reduced. Starch formation is reduced when most of the green leaf area tissues are dead hence grain kernels seem chaff. The leaves with blight are hence not of good quality to utilize as fodder due to the deteriorated nutrition value. .

E.turcicum is the causative pathogen of NLB that was first reported in Passerini on maize in Italy in 1876. In the USA, it was first detected at New Jersey in the year 1878. This was later followed by an outbreak of NLB in Connecticut in 1889. It is favoured by low temperatures and humid conditions (Ullstrup, 1970).

The lesion length adds up with the increase in length of dew periods. Severity of the disease epidemics are dependent on the environment and the pathogen which trigger the pathogen to grow and enhance sporulation on maize as reported by Levy (1989). There has been effective control of the disease through use of Ht gene which has dominance (Smith and Kinsey, 1980, Turner and Johnson, 1980).

Combination of Ht 1 and Ht 3 genes never resulted in lower disease levels for each of Ht 1 or Ht 3. Dunn and Numm (1970) reported on gene dosage effects for the Ht gene while Hooker and Perkins (1980) reported on gene dosage effects for Ht 2 gene.

Combining Ht and Ht2 or Ht3 could offer resistance from races 1, 2 and 3 Kinsey (1980). Great levels of mild resistance by use of the Ht genes present a unique approach in minimizing crop defoliation from NLB. This also reduces the high productivity effect that is linked to Ht genes resistance in susceptible germplasm Pataky (1994).

Isolates gathered from different regions proved to be different in pathogen attacks as shown in infection differentials, spore formation and size of the lesions with isolates from a similar region proved to be variants especially under zero till regime reported by Levy (1991). Yield losses dropped significantly when the disease attack went up to the higher leaves (Pataky, 1992). Plants with no defoliation on third lower parts had no significant yield losses (Levy *et al.*, 1990).

Durrishahwar *et al.*, (2008) used a scale of 1-5 in his study with ranges from 0-100 as the percentage diseased leaf area and noticed that visual assessments may be of value in some situations. Large 1965 reported that disease assessments in trials and variety productivity performance to assist in estimation of production and quality reduction.

Adipala *et al.*, (1993) used a (zero) 0,0.5,1,5,10.25,50 and 75% severity scale to evaluate of maize NLB where a total of 20 plants were obtained through sampling along cardinal geography points. Farms that were selected and site chosen where 5 plants were visually examined each to the north, South, East and West hence assessed for disease severity.

Disease severity rating depending on leaf area affected by lesions was done at a scale range of 0-5 (Muiru *et al.*, 2007). Durrishahwar *et al.*, (2008) visualized NLB as follows: 0.5-very slight infection (one or two restricted lesions on the lower leaves), 2-light infection (a few number of lesions on the lower leaves), 3-moderate infection (abundant lesions on lower leaves and few on middle leaves), 4-heavy infection (lesions abundant on all leaves and extending to upper leaves), 5-very heavy infection (lesions abundant on all leaves hence plants may be prematurely killed).

Pataky (1992) used a ratio of 2-90% to study resistance and susceptibility of corn. This was generated using DISTRAN which is a program founded by Tomerlin and Howell (1988). The analysis was based entirely on the flag leaf, top and bottom leaves that caused 33-40% of the total leaf surface area.

Susceptible maize had uniformity in yield loss against those with the Ht genes. Pedersen *et al.*, (1986) used a scale of 1-9 that was taken up from Perkins and Hooker (1981) for analysis on resistance levels of NLB through inoculation of pure lines B37, B37Ht1, B37Ht2 and Oh43Ht3 within plots under a controlled greenhouse environment. Some inbred lines distinguished to be resistant in the controlled environment and with susceptibility under varying conditions and regions as a result of differing temperatures lighting and humidity.

Manwiller *et al.*, (1985) scored maize behavior to NLB in Muguga though he did not subject them to the disease conditions. Nicholson and Warren (1975) applied the rate of 0-5 for disease pressure and area of tissue affected by the lesions.

Gaunt (1995) suggested use of remote sensing, imaging and positioning hardware in providing new techniques to assess disease levels. Nutter and Forrest (1995) gave the report that use of technology in assessing disease severity and training could be efficient in terms of accuracy and prediction during visual scores.

Maize is a cross pollinated crop hence the trait has been used extensively in the development of hybrids. It is a highly allogamous crop and it has been successfully exploited for the production of hybrids. Parent evaluation is of importance to develop varieties. Line by Tester analysis has been used broadly to evaluate pure lines through crossing them to testers (Kempthorne, 1957). The importance of an inbred line in hybrid development programs relies mostly on the suitability in creating combination by use of different lines to create hybrids that are better performing in terms of yield and resistance to disease pathogens. Plant breeders utilize combining ability to run the program suitably. Use of hybrid vigor and evaluation of parent lines on the value of CA is important in breeding to allow creation of successful programs. Line by tester design is utilized to analyze pure lines often. Through the L x T a number of lines ranging around 50% are ridden of (Singh and Chaudhary, 1979). The technique helps in cutting down the number of lines to a small number than can easily be managed for hybrid crosses.

2.4 History of the pathogen

Northern leaf blight was detected first in Perma Italy in 1876. Pammel *et al.*, (1910), Dreschler stated it to be similar to *Trichometasphaeria turcica* (Luttrell). Further, Leonard and Suggs (1974) renamed the perfect stage as *Setosphaeria turcica* (Luttrell) Leonard and Suggs and described the conidial stage as *E.turcicum* (Pass.) Leonard and Suggs in which the conidial hilum is strongly protruberant.

Trichometasphaeria turcica is hardly found naturally. The causative pathogen of NLB

normally exists at *E.turcicum*.

The fungus is in the division Eumycota, sub-division Deuteromycotina, order Moniliales and family Dematiaceae. The teleomorph *Setosphaeria turcica* belongs to division Eumycota, sub-division Ascomycotina, order Pleosporales and family Pleosporaceae. The fungus exists as olive grey, spindle shaped conidia with lengths 5 x 20 µm with upto around 9 septations.

Robert (1960) identified two races of *Helminthosporium turcicum* and ten strains of corn and noticed the cultural changes in the two races as they grew on artificial media. He concluded that *H.turcicum*, *H.carbonum* and *H.sativum* consisting of two or more parasitic races. Physiologic specialization in maize and sorghum isolates tested in their respective host was reported by Robert (1960). Morphological and cultural variations were also observed. The effect humid conditions and high temperature levels in creation of a maize isolate of *H.turcicum* were studied and found that the growth of the fungus in culture and for infection and disease development were 20-30⁰ C, 25-30⁰ C and 30⁰ C respectively.

Abebe and Narong Singburaudom (2006) reported variation in the cultural characters of 28 isolates and they showed variation in colony growth, colony colour and pigmentation in a study they conducted.

Isolates differing in agro-ecological regions displayed differences in biology, colouration growing rates and spore formation in varying medium (Muiru *et al.*, 2008). The different lightings had significant effects on the growth rates of the different isolates.

E.turcicum is a common pathogen of sorghum, teosinte, paspalum and zea in nature. Triticum, Hordeum, Oryza are susceptible to the pathogen when inoculated artificially. There is a tendency for isolates from one species to infect the same species. Robert (1960) analysed on the effect of *E.turcicum* on 8 lines to 27 isolates of conidia through scoring at a range of 1-11. The 14 isolates reacted hence displaying some variance in performance. He made an observation on important inbred isolate relation that was

linked to gene differentials within the isolates. Robert and Sprague (1960) recorded minor differences in the isolates in relation to the performance.

2.5 Description

The disease begins with minor spots on the leaf surface, greyish in colour and water like. The spots change colour to green as the crop matures and merge getting larger. Spores of the fungus develop on all sides of the spots in large numbers. Crops that are affected highly have a scorch like look Abebe and Narong Singburadom (2006).

The disease is recognized by long elliptical tan lesions. These lesions are first noted on lower leaves and as the crop matures their number increases and all the leaves are covered hence the plant appears dead.

2.6 Genetics of Resistance to *E. turcicum*

Hooker (1961) first reported some outstanding lesion on chlorophyll matter with some resistance level in maize lines that developed late and with some minor necrosis at the center of some scarce green margin. Fewer spores were produced by these lesions in comparison to the fast growing susceptible lesions with necrosis. A single Ht gene for resistance was in control of this trait. Dominating plants with homozygosity hairy had these lesions. Conclusions on the line P.1 217407 in which occurrence of the minor lesions had some chlorotic circles surrounding them had minimal spore formation in the germplasm with resistance (Ullstrup, 1963).

The chlorotic resistance was controlled with one gene having dominance from the GE440 inbred line. Symptoms for resistant or susceptible lines were similar from 2 to 7 days and they were visible when inoculation with *E.turcicum* was carried out in the lines and variety seedlings and were visualized as minute white to faded green specks (Hilu and Hooker, 1963). The susceptible inbred had the lesions present as flecks which later had grown to lesions which were wilting followed by necrosis development. The disease cycle took around 15 days.

The polygenes controlling resistance are in expression through a minimal lesion population and small lesions also reduced spore formation (Ullstrup, 1970). The mean resistance amounts to NLB, average area covered by lesions, the speed in development of lesions and the appearance could be highly affected by the variety genetics as per the parental combinations (Singulas *et al.*, 1988).

2.7.0 Combining Ability analysis

Maize plays a very key role with the diets in East Africa. It records more than 35% of the calorie intake (Specu, 2013). Maize is Kenya's staple crop and is almost entirely dependent on rain. About 17% of the country can be utilized for rain fed maize farming.

Different maize varieties are grown in Kenya and this is determined by the weather characteristics of the different agro-ecological zones. Altitude and moisture are the limitations influencing varieties in every ecological region. In Kenya, the maize breeders have taken into account all these hence inbred lines are developed for the arid and semi-arid areas that are characterized by earlier maturity and drought tolerance. Varieties with a longer growing season of around 8 months have been developed for the medium altitude regions and the highlands (Gebrekidan *et al.*, 1982).

Use of hybrids amongst the smallholder farmers has eventually not resulted to an increase in their production despite adoption of the seed by over half of the farmers. With a large number of small holder farmers growing maize, having farmers to grow varieties that are bred for their environments would be a key thing.

Breeding for resistance in diseases has been done for maize but with inadequate data that results in release of maize varieties without field and green house acclimatization to the disease. Kenya has therefore produced varieties of high disease risk. Poor yields in third-world countries are due to disease pressure and ineffective disease control strategies. The other reason for the poor yields is use of selfed or farm saved diseased seed in their various stages of segregation.

After development of inbred lines, they are crossed to other lines and the production in either single or double crosses evaluated. Combining ability is hence the ability of an inbred to pass on desirable traits to its progeny (Kumar *et al.*, 2007). Combining ability evaluations are of importance since hybrid performance can never be determined visually. Combining ability of lines determines the potential of inbred lines in hybrid development and conclusive evaluation of inbred lines is best determined through hybrid performance (Sharma *et al.*, 2005).

2.7.1 General combining Ability

The mean performance of an inbred line within a number of hybrid combinations is hence termed as its general combining ability (GCA) (Kumar *et al.*, 2007). It is referred to as the deviation from the overall of the crosses developed from other parent lines in a diallel design. A deviation that is positive could be suitable or unsuitable depending on the trait of interest. Negative deviations are not suitable for yield but are considered suitable in traits like days to 50% anthesis (AD) where the trait of earliness is important (Venkateson *et al.*, 2007).

General combining ability (GCA) is associated with alleles that have additive gene effects. They are predictable effects hence termed useful to plant breeders (Baloch *et al.*, 2010). The GCA tests are useful in a breeding program to evaluate many lines. They are also used to verify the gene action governing traits of interest.

High GCA estimates are an indication of additive gene action. Genotypes of low GCA are disposed. Crosses may deviate in value from the expectation to a greater or lesser extent which is termed the SCA of the trait (Vacaro *et al.*, 2002).

2.7.2 Specific Combining Ability

The SCA is described as performance of the crosses as better as or poorer than the expectations based on the average performance of the potential lines used in the cross. SCA is an indication that the value of superior genotypic crosses in intra group crosses is represented in selection of inbred lines as it assists in identifying specific inbred lines

for use in hybrid development and also determine heterotic grouping for different genotypes. Lines obtained from different heterotic groups that give high and positive SCA estimates are said to compliment each other (Fan *et al.*, 2008).

2.8 Testers

Testers are genotypes with well determined heterotic groups and of good GCA. They are used to identify and select superior genotypes for use in breeding programs (Melania and Carena, 2005). They are of importance in determining heterotic groups of new inbred lines and populations and in evaluation of breeding values of genotype in population improvement.

Testers could be inbred lines, single crosses or heterogenous material. Good testers should be able to determine good from bad genotype hence provide information that describes the advantages of lines and optimize genetic gains. Testers should have broad adaptation to the target environment (Rawlings and Thompson, 1962).

Identification of superior genotypes by use of testers involves evaluation of the GCA effects of the testcrosses. The choice of testers to use (narrow or broad based) depends on the availability, type of material to be tested and the type of hybrids to be developed using the lines (Parentoni *et al.*, 2001).

Productivity of an inbred line is highly determined by its ability to transmit genes that are desirable to the hybrid progenies (Pixley and Banziger, 2002). The genetic base of the germplasm, environmental interaction and correlation studies for various quantitative traits, heterosis and combining ability are of importance to plant breeders in selection and breeding maize varieties of good yield potential.

2.9 Heterotic Classification

Maize is grown all over the world with the United States as the maize leading producer accounting for 40% of the entire world's harvest (Martinez, 2011). While maize comprises a consumption of over 60% in developing countries, it is of less importance in the developed countries.

Maize was introduced to Africa in the 16th-18th century. It has since become Africa's staple food. In Kenya, the counties that produce maize include: uasing Gishu, Trans Nzoia, Nakuru, Nyeri, Embu, Kakamega, Taita taveta, Kirinyaga and Kwale. The estimate area under maize is at 1.5million hectares. Maize production in Kenya has been on decline since 2006 having dropped from 34 million bags in 2006 to 25 million bags in 2008 from an estimated area of 1.6 million hectares (Kamau, 2013).

The decline in production has been attributed to factors like drought, high cost of inputs, low soil fertility, pest and diseases (Mearns, 2015). In Kenya, 80% of the land mass receive less than 250mm of rainfall in a season hence the need to breed maize varieties that can utilize the low water levels and varieties that can tolerate diseases and pests.

In a maize breeding program, inbred lines classification into heterotic groups is the first step. This would provide the exploitation of maximum heterosis of lines. In the availability of large numbers of inbred lines and determined testers, performance of the lines through testcrosses would be used as a criterion to group the lines (Melchinger, 1999). Murenga *et al.*, 2015 used the approach to evaluate the performance of 66 lines and classified them into their respective heterotic groups.

In the recent past, molecular markers have been used in classification of lines and populations hence obtaining a clear picture on the heterotic patterns that are promising (Reif *et al.*, 2003). Testcrosses are used to determine the potential of inbred lines in a breeding program. Choice of testers is hence crucial for selection of genotypes for their use in hybrid development.

Maize breeders have in the past used several techniques to study genetics of quantitative traits amongst them grain yield. Line by tester is an efficient method and allows the inclusion of a large number of lines hence provide combining ability estimates that are reliable.

The SCA is described as performance of the crosses as better as or poorer than what was expected as per the average performance of the potential lines used in the cross

(Menkir *et al.*, 2004). SCA is an indication that the value of superior genotypic crosses in intra group crosses is represented in selection of inbred lines as it assists in identifying specific inbred lines for use in hybrid development and also determine heterotic grouping for different genotypes. According to Murenga *et al.*, (2015), lines that complement each other are obtained from heterotic groups that differ and that exhibit high and positive SCA estimates.

The SCA estimates for grain yield according to Menkir *et al.*, (2004) have been used in classification of maize into different heterotic groups (Melani and Carena, 2005, Fan *et al.*, 2008). A line, depending on its performance could also be in more than one heterotic group in a particular combination since heterotic groups may be conceptual (Hallauer and Carena, 2009).

Melchinger and Gumber (1998) recorded that heterotic groups classify entries of related or unrelated genotypes from a similar or different population that shows combining abilities or the heterotic response that are similar once crossed with distinct genotypes.

Maize lines are classified into various heterotic groups through various ways. These are applied across the globe (Fan *et al.*, 2009). Use of SCA estimates is the traditional way used in the availability of line-pedigree data and cross yield data to allocate inbred to various heterotic groups. The second way is through use of molecular markers in order to attain the genetic similarity (GS) or distance (GD) estimates in order to classify the inbred lines to given heterotic groups. The methods accuracy is not guaranteed. Fan *et al.*, (2009) applied a different method through use of heterotic groups specific and general combining ability to assign inbred to heterotic groups. This method was said to have efficiency in comparison to SSR markers. Menkir *et al.*, (2004) used both yield based SCA and molecular markers to categorize the lines into various heterotic groups.

Melchinger (1999) concluded that in the existence of a large number of germplasm and with availability of proven testers, the line by tester should be a better criterion to classify lines into heterotic groups.

Barata and Carena (2006) recorded massive inconsistency in molecular marker classification and field trial based in diverse inbred entries. They were for the opinion that the groups with germplasm and heterotic properties that were similar could not be accurately identified using molecular markers. Extensive field tests were recommended across different environments to categorize the lines to different heterotic groups.

Hallauer *et al.*, (2010) concluded that in testing large numbers of progeny, mating designs could be of importance as they are used broadly across locations in a number of years to categorize inbred lines into heterotic groups. However, stability of heterotic groups differs depending on the situation.

Identification of heterotic groups that could be crosses of known genotypes is important and they express higher levels of heterosis (Carena and Hallauer, 2001, Troyer, 2006, Mandes *et al.*, 2015). They are key in development of maize hybrids (Barata and carena, 2006, Carena and Wicks III, 2006).

Maize breeding depends almost entirely on identifying heterotic patterns and heterotic groups for utilization (Melani and Carena, 2005). A groups of germplasm source that can be inter-crossed consistently to develop crosses that are better compared to when crosses are made from lines in a similar group represents heterotic groups 1 (Hallauer and Carena, 2009)

Maize breeding in Kenya depends on four heterotic groups developed from collections from growers and introduction. The variations of the collections could be high due to interchange of germplasm across the borders.

Existence of the groups indicates that there is heterosis within the groups from farmers and heritability of this and the heterotic patterns is not established. In any breeding programme, population improvement through selection is influenced mostly by heterotic groups. Understanding of heterotic patterns is hence crucial in exploitation of heterosis .Knowledge on heterotic groups of various collection or introductions is hence crucial in breeding to allow exploitation of heterosis in any breeding programme. This

results in good heterotic pattern combinations to obtain disease resistant, early or late maturing and high yielder hybrids.

Information on heterotic groups is of importance in developing high performing hybrid crosses and improving populations obtained from collections and introductions. Heterosis is attained when the progeny of crosses from inbred perform above the average of the parents. Heterotic manifestation is dependent on genetic divergence of two parental varieties. Genotypes can be classified into heterotic groups which are dependent on the similarity in CA and the heterosis once crossed with genotypes from different genetic groups (Murenga *et al.*, 2015).

Different patterns have been in use in different countries for hybrid development which depends on their adaptability. For USA and Europe, Reid x Lancaster pattern is common and is exploited (Orda's 1991). Major pattern used in China is domestic x LSC in the North maize area while summer region exploit domestic x PN (Li *et al.*, 2004). Japan uses the US dent x Northern/European flint (Enoki *et al.*, 2002). In East Africa, the pattern used is KSII x EC573 for highlands in Kenya. Pool A and Pool B have been developed for the medium altitude areas of Kenya.

Breeders are therefore able to group genotypes into heterotic patterns in order to develop high performing hybrids by use of the knowledge on heterosis (Reif *et al.*, 2005).

CHAPTER THREE

MATERIALS AND METHODS

3.1 Experimental site

The experiment was carried out in 2017 main growing season in three mid-altitude agro-ecological zones of Kenya. The experiment was conducted in Kakamega, Embu and Muranga which are medium altitude maize growing regions in Kenya.

Muranga County is located in Central Kenya. The altitude of the place is approximately 1530 metres above sea level. The average annual rainfall received is 1600 mm annually. The mean temperature of the region ranges from 21-35⁰ C.

Embu County is located in Eastern Kenya. The temperature ranges between 12⁰C – 27⁰C and an average annual rainfall of 1495mm annually.

Kakamega County is located in the former western province of Kenya. The temperature ranges between 14⁰C-27⁰C. It is a maize growing region with high incidences and occurrence of Northern leaf blight in maize. The various factors that contribute to this are the high humidity due to regular rainfall and the high temperatures hence creating a favorable environment for development of the fungal disease (NLB).

3.2 Experimental Designs and management

The trials were planted in an alpha lattice design. Each plot comprised of 1 row of 5 meters long with a spacing of 0.75meters between the rows and 0.25 meters between plants replicated thrice. Two seeds were planted per hill and later thinned to one plant per hill after establishment. A population of 21 plants per plot was attained.

DAP was applied at planting at the rate of 100kg/ha while CAN was applied at the seven leaf stage at the rate of 100kg/ha. Other cultural practices including weeding, pest management was done throughout the entire growing season.

3.3 Experimental Materials

A total of 98 test crosses developed by crossing 49 lines with two testers (CML 312/CML 412) and (CML 395/CML 444) and two checks which were the testers were used for the study.

The two testers were used as the female parents (CIMMYT tester A and tester B) and a segregating population in the F4 (Population Y) were used as male parents.

The experimental lines were selected from a population segregated from some Indian introductions. The two testers were obtained from CIMMYT Kenya.

Table 3.1: Stock ID and Pedigree of the Lines Used in the Study

Entry	Stock ID	Pedigree	Entry	Stock ID	Pedigree
Line 1	EABN3-1	Y1-1-1B	Line 46	EABN3-20	Y5-5-2-1
Line 2	EABN3-2	Y1-2-1B	Line 47	EABN3-20	Y5-5-2-2
Line 4	EABN3-4	Y1-4-2B	Line 48	EABN3-20	Y5-5-3B
Line 5	EABN3-4	Y1-4-3B	Line 50	EABN3-20	Y5-5-5-1
Line 9	EABN3-8	Y3-1-1-2	Line 51	EABN3-20	Y5-5-5-2
Line 12	EABN3-12	Y4-4-1-1	Line 52	EABN3-20	Y5-5-6B
Line 17	EABN3-12	Y4-4-4-1	Line 53	EABN3-21	Y5-6-1B
Line 18	EABN3-12	Y4-4-4-2	Line 54	EABN3-21	Y5-6-2B
Line 19	EABN3-13	Y4-5-1-1	Line 58	EABN3-23	Y5-8-1B
Line 24	EABN3-14	Y4-6-3-2	Line 61	EABN3-24	Y5-9-3B
Line 26	EABN3-14	Y4-6-4-2	Line 62	EABN3-25	Y5-10-1B
Line 27	EABN3-15	Y4-7-1B	Line 63	EABN3-26	Y5-11-1B
Line 29	EABN3-15	Y4-7-3B	Line 66	EABN3-27	Y5-12-1-2
Line 31	EABN3-16	Y5-1-1-1	Line 67	EABN3-27	Y5-12-2B
Line 32	EABN3-16	Y5-1-1-2	Line 69	EABN3-28	Y5-13-1B
Line 33	EABN3-16	Y5-1-2B	Line 71	EABN3-28	Y5-13-3-1
Line 34	EABN3-16	Y5-1-3B	Line 72	EABN3-28	Y5-13-3-2
Line 35	EABN3-16	Y5-1-4B	Line 73	EABN3-28	Y5-13-4B
Line 38	EABN3-17	Y5-2-2-2	Line 74	EABN3-29	Y6-1-1-1
Line 40	EABN3-18	Y5-3-1B	Line 75	EABN3-29	Y6-1-1-2
Line 41	EABN3-18	Y5-3-3B	Line 76	EABN3-29	Y6-1-1B
Line 43	EABN3-19	Y5-4-1B	Line 78	EABN3-30	Y6-2-1B
Line 44	EABN3-19	Y5-4-2B	Line 79	EABN3-30	Y6-2-2B
Line 45	EABN3-20	Y5-5-1B	Line 81	EABN3-31	Y6-3-1-2
Tester A	CIMMYT	CML312/CML442	Line 87	EABN3-32	Y6-4-2-2
Tester B	CIMMYT	CML395/CML444			

3.4.1 Methods

To evaluate on resistance of maize crosses to NLB

This was achieved by carrying out disease scores of the maize plants before flowering and post flowering.

To evaluate on the disease severity in relation to yield

This was achieved by recording visual disease scores of the crosses before flowering (booting stage) and at 50% grain filling. The field weight for all the entries was recorded during harvest hence allowing the direct relation of the disease occurrence and severity in the maize to the effect on the yields.

To evaluate on the resistance levels of the crosses to that of testers

This was obtained by analyzing on the disease scores for both the testcrosses and the testers. The consistency on resistance was observed across all the replicates in all the sites hence giving a valid conclusion on the resistance and tolerance of the testcrosses.

3.4.2 Data Collection

Data collected included AD- days to 50% anthesis, SD- days to 50% silking, EA- ear aspect, PH- Plant height after physiological maturity, EH- ear height after physiological maturity, NLB- northern leaf blight visual scores, NP- number of plants during harvest, NE- number of ear during harvest, FW- field weight of the harvested cobs per plot and GW-Grain weight of the threshed maize per plot.

Data on disease (NLB) severity based on percent leaf area infected was recorded at 50% grain filling stage (post-flowering) stage using visual scales of 0-5 (Muiru *et al.*, 2007; Durrishahwar *et al.*, 2008) with little modification. Disease severity rating was as follows; 0 = leaves free from infection, 1 = a few restricted lesions on the lower leaves ($\leq 5\%$), 2 = several small and large lesions on many leaves (5.1-10 %), 3 = numerous small and large lesions on many leaves (10.1-25 %), 4 = many enlarged and coalesced

lesions on many leaves above the upper cob (25.1-50 %) and 5 = several coalesced lesions, leaf showing wilting, tearing and blotching typical blight symptoms (> 50%).

3.5 Data Analysis

The data collected during the research was analyzed using the CIMMYT META R. The GCA and SCA means for NLB and other yield related traits were used to determine crosses that exhibited tolerance or susceptibility to NLB. The yield was evaluated by analyzing the grain weight of the crosses using CIMMYT IMIS field book. The analyzed data was used to classify the testcrosses according to their GCA and SCA estimates hence determine good combiners for NLB and other yield related traits. This information could be used in future to advance the lines in breeding for NLB tolerance and high yielding maize varieties in the country.

3.5.1 Analysis of Variance

The data collected for NLB and other yield related traits was analyzed using the CIMMYT META R and AGD R (2015). In the analysis, lines, plots and site were used as fixed factors. Replications, incomplete blocks were used as random factors.

Combining abilities were analyzed and the GCA and SCA were estimated.

The linear model used for combining ability analysis was:

$$Y_{ijk} = \mu + r_k + g_i + g_j + S_{ij} + e_{ijk}$$

Where, Y_{ijk} = the value of a character measured on cross of line i by tester j in k^{th} replication

μ = Population mean

r_k = Effect of k^{th} replication

g_i = general combining ability (GCA) effects of i^{th} line

g_j = general combining ability (GCA) effects of the j^{th} tester

S_{ij} = specific combining ability (SCA) of i^{th} line and j^{th} testers such that S_{ij} equal to S_{ji}

e_{ijk} = Experimental error for ijk^{th} observation

CHAPTER FOUR

RESULTS

4.1 Kakamega

4.1.1 General Combining Ability Analysis

The GCA estimates of the lines for NLB differed significantly ($P \leq 0.01$) in Kakamega.

Table 4.1: General Combining Ability Estimates for Northern Leaf Bight in Kakamega

Line	NLB	Line	NLB
1	0.515**	47	-0.205
2	-0.419**	48	0.351
4	0.576	50	-0.151
5	-0.109	51	0.038
9	-0.053	52	-0.129
12	-0.206	53	-0.222
17	0.072	54	0.149
18	0.514**	58	-0.512**
19	0.241	61	-0.230
24	-0.532**	62	0.178
26	-0.038	63	-0.459**
27	-0.102	66	-0.249
29	0.343	67	0.176
31	-0.625**	69	0.173
32	0.585**	71	-0.177
33	-0.364	72	-0.477**
34	0.716	73	-0.201
35	0.440	74	-0.500**
38	0.206	75	-0.242
40	0.707**	76	-0.628**
41	0.442	78	-0.028
43	-0.110	79	0.197
44	0.178*	81	-0.164
45	0.486**	87	-0.167
46	0.011	Tester A	0.173
		Tester B	0.173

Lines 1, 18, 32 and 40 exhibited positive and significant GCA effects for NLB. Lines 2, 24, 31, 58, 63, 72, 74 and 76 exhibited negative and significant GCA estimates for NLB. Positive and significant GCA effects for NLB indicate susceptibility to NLB disease. Negative and significant GCA effects for NLB could be used in breeding for resistance to the disease in maize. In this case, lines 2, 24, 31, 58, 63, 72, 74 and 76 could be used in breeding to develop NLB resistant maize hybrids. Lines 4, 17, 19, 29, 32, 34, 35, 38, 41, 48, 51, 54, 62, 67, 69 and 79 exhibited positive and non-significant GCA effects for NLB. Lines 5, 9, 12, 26, 27, 33, 43, 47, 50, 52, 53, 61, 66, 71, 73, 75 and 78 exhibited negative and non-significant GCA estimates for NLB.

Table 4.2: General Combining Ability Estimates of the Lines for Days to Anthesis and Days to Silking in Kakamega

Line	AD	SD	Line	AD	SD
1	-0.233	-0.484	47	-1.165	-0.612
2	1.182	1.140	48	0.411	1.071
4	0.977	0.815	50	-0.466	-0.174
5	-0.866	-0.835	51	-1.518	-1.247
9	-0.614	-0.103	52	0.216	0.469
12	-0.884	-1.004	53	-0.178	-0.388
17	1.622	1.218	54	-0.709	0.332
18	0.459	0.485	58	-0.936	-0.163
19	-1.577	-1.205	61	-0.920	-0.058
24	0.491	0.714	62	-0.282	-0.188
26	-0.377	-0.453	63	0.340	0.723
27	0.062	-0.289	66	1.190	0.862
29	-1.278	-1.235	67	0.285	0.012
31	1.101	0.885	69	0.223	0.159
32	-1.977	-2.786**	71	1.173	1.118
33	-0.379	-0.642	72	0.356	0.093
34	-0.251	-0.830	73	0.339	-0.208
35	0.336	0.550	74	1.146	0.825
38	-0.329	0.065	75	1.323	0.514
40	-0.811	-0.247	76	1.432	1.034
41	0.595	0.984	78	1.024	0.912
43	-0.019	-0.152	79	1.053	0.563
44	-0.849	-0.438	81	-0.253	-0.739
45	0.672	0.725	87	0.722	0.261
46	-1.857	-2.050**	Tester A	-1.15	-1.03
			Tester B	1.15	1.03

For days to anthesis, the lines did not exhibit significance for the trait. For days to silking, lines 32 and 46 exhibited negative and significant estimates for SD with estimates of -2.786 and -2.050 respectively.

4.1.2 Specific Combining Ability Analysis

Table 4.3: Specific combining ability Estimates of the crosses with Tester A for Grain Weight

Testcross	GW	Testcross	GW
L1 x T A	0.893	L47 x T A	-2.540
L2 x T A	0.977**	L48 x T A	-0.244
L4x T A	-1.040	L50 x T A	-0.032
L5 x T A	0.388	L51 x T A	-2.618
L9 x T A	1.831	L52 x T A	-0.146
L12 x T A	-0.790	L53 x T A	0.038
L17 x T A	-1.821**	L54 x T A	-0.663
L18 x T A	-1.874**	L58 x T A	-0.630
L19 x T A	-1.143	L61 x T A	1.154
L24 x T A	0.598	L62 x T A	-0.714
L26 x T A	-2.214**	L63 x T A	-3.445
L27 x T A	0.284	L66 x T A	0.767
L29 x T A	1.516**	L67 x T A	-4.143
L31 x T A	1.416**	L69 x T A	0.692
L32 x T A	-0.512	L71 x T A	0.717
L33 x T A	1.415**	L72 x T A	0.743
L34 x T A	1.160**	L73 x T A	2.086
L35 x T A	1.373**	L74 x T A	0.443
L38 x T A	-0.475	L75 x T A	0.124
L40 x T A	-0.134	L76 x T A	-0.428
L41 x T A	1.162**	L78 x T A	1.551
L43 x T A	0.723	L79 x T A	2.048
L44 x T A	-0.908	L81 x T A	-1.250
L45 x T A	2.142**	L87 x T A	0.530
L46 x T A	0.036		

Testcross L2xTA, L29xTA, L31xTA, L33xTA, L35xTA, L41xTA and L45xTA exhibited positive and significant SCA effects for yield. Testcross L17xTA, L18xTA and L26xTA exhibited negative and significant SCA effects for yield.

Crosses L4xTA, L19xTA, L32xTA, L38xTA, L40xTA, L44xTA, L47xTA, L48xTA, L50xTA, L51xTA, L52xTA, L54xTA, L58xTA, L62xTA, L63xTA, L76xTA and L81xTA exhibited negative and non-significant SCA estimates for grain yield in the

Kakamega environment. The rest of the crosses had positive and non-significant SCA estimates for the yield trait.

Table 4.4: Specific Combining Ability Estimates of the Crosses with Tester B for Grain Weight

Testcross	GW	Testcross	GW
L1 x T B	1.340**	L47 x T B	0.445
L2 x T B	-0.680	L48 x T B	0.753
L4 x T B	-0.288	L50 x T B	-0.044
L5 x T B	-0.466	L51 x T B	0.634
L9 x T B	-0.204	L52 x T B	-0.815
L12 x T B	-0.218	L53 x T B	-0.177
L17 x T B	0.482	L54 x T B	-0.177
L18 x T B	-0.843	L58 x T B	-0.711
L19 x T B	1.302	L61 x T B	0.772
L24 x T B	0.332	L62 x T B	-0.924
L26 x T B	0.492	L63 x T B	0.223
L27 x T B	-0.458	L66 x T B	-0.689
L29 x T B	0.112	L67 x T B	-0.865
L31 x T B	-0.138	L69 x T B	0.443
L32 x T B	-0.133	L71 x T B	-0.072
L33 x T B	-0.148	L72 x T B	-0.107
L34 x T B	0.022	L73 x T B	0.699
L35 x T B	-0.237	L74 x T B	-0.016
L38 x T B	0.260	L75 x T B	1.189**
L40 x T B	-0.215	L76 x T B	0.753
L41 x T B	0.153	L78 x T B	-0.072
L43 x T B	-0.247	L79 x T B	-0.391
L44 x T B	0.055	L81 x T B	0.207
L45 x T B	-0.357	L87 x T B	-0.242
L46 x T B	0.225		

Testcrosses L1xTB and L75xTB exhibited positive and highly significant SCA estimates for grain yield.

Crosses L17xTB, L19xTB, L24xTB, L26xTB, L29xTB, L34xTB, L38xTB, L41xTB, L44xTB, L46xTB, L47xTB, L48xTB, L51xTB, L61xTB, L63xTB, L69xTB, L73xTB,

L76xTB, and L81xTB had positive and non-significant SCA estimates for yield. The rest of the crosses exhibited negative and non-significant SCA estimates for yield.

Crosses with significant SCA estimates can be used for maize improvement (Motamedi *et al.*, 2014). Significant and highly significant SCA estimates on maize grain yield were recorded by Shushay *et al.*, (2013).

Table 4.5: Specific Combining Ability Effects of the Crosses to Northern Leaf Blight in Kakamega

Line	Tester A	Tester B	Line	Tester A	Tester B
1	5.415	3.552	47	-4.489	2.860
2	-1.002	-2.329	48	4.229	-1.436
4	2.953	1.626	50	2.232	-3.433
5	4.566	-5.436	51	-1.355	1.656
9	-3.883	3.466	52	1.522	-1.175
12	2.014	-3.651**	53	1.950	-3.714
17	-3.390	3.958	54	1.255	-7.189
18	5.373	3.548	58	-1.370	-2.697
19	5.960	-4.042	61	-2.419	5.922
24	-3.618**	-6.071	62	3.538	-2.126
26	5.143	-8.127	63	-1.161	-2.488
27	2.564	-1.071	66	-6.832**	4.855
29	2.028	7.006	67	5.702	-4.300
31	-3.987	-9.767	69	1.352	2.450
32	5.159	-5.062	71	-2.209	8.018
33	-7.826	-2.110	72	-3.403	-3.921
34	1.342	4.353	73	-1.369	-1.464
35	2.445	3.255	74	-3.492	-4.816
38	-2.854	4.494	75	-2.468	5.426
40	3.475	2.148	76	-4.000	-9.889
41	2.522	3.263	78	-3.786	3.563
43	2.276	-1.099	79	3.614	-2.051
44	-7.998	2.211	81	1.240	-1.315
45	4.766	-8.992	87	8.930	-1.326
46	2.877	-2.788			

4.1.3 Heterotic Classification

Table 4.6: Heterotic Classification of the Lines using the SCA for Grain Weight in Kakamega

Line	Heterotic Group	Tester A	Tester B	Line	Heterotic Group	Tester A	Tester B
1		0.217	-0.149	47		-0.187	0.483
2		0.084	-0.298	48		-0.115	-0.107
4		-0.170	-0.112	50		0.181	0.107
5		0.236	-0.082	51		-0.250	-0.064
9		0.041**	0.093	52		-0.101	0.005
12	B	0.249*	-0.063	53		0.036	-0.016
17	B	0.152	-0.149	54		-0.040	-0.050
18		0.095	-0.268	58		-0.036	0.216
19		0.114	0.032	61		-0.193	0.353
24		0.059	-0.075	62		0.128	0.170
26		-0.262	-0.100	63		-0.213	0.275
27		-0.013	-0.105	66		0.199	-0.165
29	B	0.010	-0.072**	67		-0.241	-0.143
31		-0.099	0.059	69		0.129	-0.001
32		0.257	0.237	71		-0.098	-0.034
33		0.145	-0.067	72		-0.028	-0.154
34		-0.129	0.191	73		-0.036	-0.295
35		-0.021	0.153	74		-0.238	-0.062
38		-0.007	0.333	75		0.156	-0.324
40		-0.239	0.035	76		0.150	-0.191
41		0.025	0.079	78		0.271	-0.383
43		-0.083	0.331	79		0.030	-0.056
44		0.244	0.055	81		0.015	0.271
45		-0.047	0.109	87		-0.442	-0.136
46		0.200	-0.002				

Classification of the lines into heterotic group A and group B using Tester A (CML312/CML442) and Tester B (CML 395/CML444) were dependent on the SCA effects for grain yield. Lines exhibiting positive and significant SCA effects with Tester A (TA) were classified into the opposite heterotic group B while lines exhibiting

positive and significant SCA effects with Tester B (TB) were classified into the opposite heterotic group A.

Lines exhibiting positive and significant SCA with the two testers were oriented to group AB. Lines exhibiting negative and significant SCA with tester A were oriented into heterotic group A while lines exhibiting negative and significant SCA with tester B were oriented to heterotic group B.

For the Kakamega site (Table 4.6), line 29 exhibited negative and significant SCA with Tester B (TB) with an estimate of -0.072 and was classified into heterotic group B. Lines 9 and 12 exhibited positive and significant SCA with Tester A (TA) and were classified to heterotic group B.

A total of three lines were classified to heterotic group B in this location. The rest of the lines could not be classified with the two testers.

4.1.4 Yield of the Crosses

The yield of the testcrosses (Table 4.7) in Kakamega differed significantly for all the entries. The highest yield recorded was at 6.17t/ha from Tester A/L46. The lowest yield recorded was at 1.86t/ha from tester A. The highest yielding crosses were Tester A/L46 with 6.17t/ha, Tester A/L62=6.1t/ha, Tester A/L9=5.71t/ha, Tester A/L79=5.53t/ha, Tester B/L81=5.51t/ha and Tester A/L50=5.47t/ha.

A total of 18 crosses with tester A yielded 5t/ha and above while with Tester B only one of the crosses yielded 5.51t/ha. Crosses with line 81 performed well in this site yielding 5.51t/ha with tester B and 5.33t/ha with tester A.

The 18 crosses that had a yield of above 5t/ha with tester A were: Tester A/L46=6.17t/ha, Tester A/L62=6.1t/ha, Tester A/L9=5.71t/ha, Tester A/L79=5.53t/ha, Tester A/L50=5.47t/ha, Tester A/L5=5.43t/ha, Tester A/L24=5.42t/ha, Tester A/L2=5.38t/ha, Tester A/L44=5.38t/ha, Tester A/L32=5.37t/ha, Tester A/L18=5.34t/ha, Tester A/L81=5.33t/ha, Tester A/L78=5.33t/ha, Tester A/L58=5.32t/ha, Tester

A/L19=5.23t/ha, Tester A/L17=5.19t/ha, Tester A/L12=5.13t/ha and Tester A/L34=5.05t/ha.

Crosses Tester A/L2 and Tester A/L44 had a similar yield of 5.38t/ha, Tester A/L81 and Tester a/L78 also had a similar yield of 5.33t/ha.

The crosses with the lowest yield were Tester B/L87=1.86t/ha, Tester A=2.07t/ha and Tester B/L2=2.08t/ha.

Table 4.7: Yield of the Crosses in Kakamega

Testcross	Yield mt/ha Tester A	Yield mt/ha Tester B	Testcross	Yield mt/ha Tester A	Yield mt/ha Tester B
Tester/Line 1	4.94	3.29	Tester/Line 47	4.04	4.97
Tester/ line 2	5.38	2.08	Tester/Line 48	4.52	2.99
Tester/Line 4	3.89	2.26	Tester/Line 50	5.47	3.63
Tester/Line 5	5.43	3.87	Tester/Line 51	3.52	3.05
Tester/Line 9	5.71	3.84	Tester/Line 52	4.61	3.44
Tester/Line 12	5.13	3.55	Tester/Line 53	4.32	3.99
Tester/Line 17	5.19	3.18	Tester/Line 54	4.48	3.01
Tester/Line 18	5.34	2.17	Tester/Line 58	5.32	4.78
Tester/Line 19	5.23	3.48	Tester/Line 61	3.65	4.64
Tester/Line 24	5.42	2.94	Tester/Line 62	6.10	4.39
Tester/Line 26	3.27	2.83	Tester/Line 63	3.65	4.65
Tester/Line 27	4.79	2.58	Tester/Line 66	4.29	3.03
Tester/Line 29	4.98	3.00	Tester/Line 67	3.65	2.67
Tester/Line 31	4.46	3.88	Tester/Line 69	4.85	2.73
Tester/Line 32	5.37	3.99	Tester/Line 71	4.28	3.70
Tester/Line 33	4.47	3.64	Tester/Line 72	3.43	2.36
Tester/Line 34	5.05	4.63	Tester/Line 73	4.37	2.31
Tester/Line 35	4.65	4.38	Tester/Line 74	3.09	2.49
Tester/Line 38	4.99	4.07	Tester/Line 75	4.99	2.23
Tester/Line 40	3.37	4.26	Tester/Line 76	4.41	3.32
Tester/Line 41	4.39	3.46	Tester/Line 78	5.33	3.21
Tester/Line 43	4.72	4.63	Tester/Line 79	5.53	3.25
Tester/Line 44	5.38	4.12	Tester/Line 81	5.33	5.51
Tester/Line 45	4.90	4.02	Tester/Line 87	3.38	1.86
Tester/Line 46	6.17	3.74	Tester	2.07	2.68

4.2 Embu

4.2.1 General Combining Ability Analysis

Table 4.8: General Combining Ability Estimates of the Lines to Northern Leaf Blight in Embu

Line	NLB	Line	NLB
1	0.001	47	-0.007
2	0.001	48	0.127
4	-0.016	50	0.007
5	-0.026	51	-0.008
9	-0.026	52	-0.001
12	-0.004	53	-0.006
17	-0.042	54	-0.003
18	0.012	58	-0.003
19	-0.011	61	0.009
24	-0.011	62	0.006
26	0.007	63	0.020
27	0.009	66	0.013
29	-0.023	67	-0.026
31	-0.014	69	-0.003
32	-0.006	71	0.016
33	0.008	72	0.010
34	0.008	73	0.012
35	-0.003	74	-0.008
38	-0.001	75	-0.014
40	-0.014	76	0.004
41	-0.007	78	0.004
43	-0.007	79	0.005
44	0.014	81	0.003
45	0.003	87	-0.011
46	0.002	Tester A	0
		Tester B	0

The GCA estimates for NLB (Table 4.8) were not significant ($P < 0.01$) for any of the lines in Embu. Lines 4, 5, 9, 12, 17, 19, 24, 29, 31, 32, 35, 38, 40, 41, 43, 47, 51, 52, 53, 54, 58, 67, 69, 74, 75, and 87 exhibited negative and non-significant GCA effects for NLB with estimates of -0.016, -0.026, -0.026, -0.004, -0.042, -0.011, -0.011, -0.023, -

0.014, -0.006, -0.003, -0.001, -0.014, -0.007, -0.007, -0.007, -0.008, -0.001, -0.006, -0.003, -0.003, -0.026, -0.003, -0.008, -0.014 and -0.011 respectively.

Lines 1, 2, 18, 26, 27, 33, 34, 44, 45, 46, 48, 50, 61, 62, 63, 66, 71, 72, 73, 76, 78, 79 and 81 exhibited positive and non-significant GCA effects for NLB with estimates of 0.001, 0.001, 0.012, 0.007, 0.009, 0.008, 0.008, 0.014, 0.003, 0.002, 0.127, 0.007, 0.009, 0.006, 0.020, 0.013, 0.016, 0.010, 0.012, 0.004, 0.004, 0.005 and 0.003 respectively.

Table 4.9: General Combining Ability Estimates of the lines for Days to Anthesis (AD) and Days to Silking (SD) in Embu

Line	AD	SD	Line	AD	SD
1	0.094	-0.150	47	-0.314	-0.251
2	-0.193	0.072	48	0.012	-0.068
4	0.162	0.398	50	0.299	0.128
5	0.319	0.210	51	-0.205	-0.316
9	-0.023	-0.057	52	0.156	0.124
12	-0.138	0.186	53	0.027	0.059
17	-0.284	0.282	54	-0.457	-0.201
18	-0.103	-0.015	58	-0.248	-0.328
19	0.123	0.455	61	0.341	0.532
24	-0.245	-0.114	62	-0.166	-0.021
26	0.225	0.450	63	-0.046	-0.018
27	0.044	-0.123	66	0.186	-0.054
29	0.113	-0.096	67	0.346	0.083
31	-0.002	-0.204	69	0.403	0.277
32	-0.515*	-0.639	71	0.045	0.391
33	-0.233	-0.287	72	0.548*	1.238**
34	-0.209	-0.294	73	0.215	0.150
35	0.606*	0.056	74	0.315	0.188
38	0.089	-0.337	75	0.241	-0.119
40	-0.446*	0.144	76	-0.139	-0.290
41	0.013	-0.085	78	0.305	0.061
43	0.207	0.210	79	-0.276	-0.121
44	-0.320	0.009	81	-0.432*	-0.583*
45	-0.219	-0.519	87	-0.126	-0.294
46	-0.094	-0.116			

Lines 32, 40, 81 (Table 4.9) had negative and significant GCA for days to Anthesis (AD) with estimates of -0.515, -0.446 and -0.432 respectively. The GCA for days to anthesis was positive and significant for lines 35 and 72 with estimates of 0.606 and 0.548 respectively. Positive and highly significant estimates were recorded for line 72 with an estimate of 1.238.

Lines 32, 40 and 81 could be utilized in breeding for earliness in maize hybrids. The same was observed in other studies Roy *et al.* (1998), Hussein *et al.* 2013 and Uddin *et al.* (2006).

Line 72 exhibited positive and significant effects for both days to anthesis at 0.548 and for days to silking at 1.238.

4.2.2 Specific Combining Ability Analysis

Table 4.10: Specific Combining Ability Estimates of Tester A Crosses for Grain Weight in Embu

Testcross	GW	Testcross	GW
L1 x T A	-0.044**	L47 x T A	-0.157**
L2 x T A	0.165	L48 x T A	0.092
L4x T A	-0.190	L50 x T A	0.306
L5 x T A	0.017	L51 x T A	-0.016
L9 x T A	0.059	L52 x T A	-0.229
L12 x T A	0.175	L53 x T A	-0.103
L17 x T A	0.019	L54 x T A	0.060
L18 x T A	0.214	L58 x T A	-0.337
L19 x T A	-0.184	L61 x T A	-0.308
L24 x T A	-0.074	L62 x T A	0.092
L26 x T A	-0.225**	L63 x T A	-0.249**
L27 x T A	0.177	L66 x T A	-0.064
L29 x T A	0.108	L67 x T A	-0.049
L31 x T A	0.015	L69 x T A	-0.081
L32 x T A	-0.100	L71 x T A	0.073
L33 x T A	0.020	L72 x T A	-0.138
L34 x T A	-0.052	L73 x T A	0.038
L35 x T A	-0.139	L74 x T A	0.245
L38 x T A	0.310	L75 x T A	0.202
L40 x T A	-0.106	L76 x T A	0.036
L41 x T A	0.066	L78 x T A	0.079
L43 x T A	0.0445	L79 x T A	0.056
L44 x T A	-0.236	L81 x T A	0.256
L45 x T A	0.241	L87 x T A	0.089
L46 x T A	-0.042		

Testcrosses`L1xTA, L26xTA, L47xTA and L63xTA (Table 4.10) had negative and significant SCA effects for grain weight with estimates of -0.044, -0.225, -0.157 and -0.249 respectively.

Crosses L4xTA, L19xTA, L24xTA, L32xTA, L34xTA, L35xTA, L40xTA, L44xTA, L46xTA, L51xTA, L52xTA, L53xTA, L58xTA, L61xTA, L66xTA, L67xTA, L69xTA

and L72xTA had negative and non-significant SCA effects for grain weight with estimates of -0.19, -0.184, -0.074, -0.100, -0.052, -0.139, -0.106, -0.236, -0.042, -0.016, -0.229, -0.103, -0.337, -0.308, -0.064, -0.049, -0.081 and -0.138 respectively.

Negative SCA effects for yield are not suitable in a breeding program. Crosses with positive and significant SCA for grain weight could be used in a breeding programme to evaluate further and develop crosses for high yields.

Table 4.11: Specific combining ability Estimates of Tester B Crosses for Grain Weight in Embu.

Testcross	GW	Testcross	GW
L1 x T B	-0.005	L47 x T B	0.307
L2 x T B	0.089	L48 x T B	-0.062
L4 x T B	-0.183	L50 x T B	-0.099
L5 x T B	0.026	L51 x T B	0.029
L9 x T B	-0.196**	L52 x T B	-0.287
L12 x T B	0.027	L53 x T B	-0.114
L17 x T B	0.010**	L54 x T B	-0.146
L18 x T B	-0.118	L58 x T B	0.105
L19 x T B	0.057	L61 x T B	-0.097
L24 x T B	0.020	L62 x T B	0.017
L26 x T B	0.140	L63 x T B	0.059**
L27 x T B	0.160	L66 x T B	0.089
L29 x T B	0.342	L67 x T B	-0.304
L31 x T B	0.174	L69 x T B	0.178
L32 x T B	-0.001	L71 x T B	-0.140
L33 x T B	0.218	L72 x T B	-0.195
L34 x T B	0.179	L73 x T B	-0.304
L35 x T B	0.081	L74 x T B	-0.030
L38 x T B	0.086	L75 x T B	-0.376
L40 x T B	-0.022	L76 x T B	0.038
L41 x T B	0.032	L78 x T B	-0.124
L43 x T B	0.211	L79 x T B	0.143
L44 x T B	0.121	L81 x T B	0.100
L45 x T B	-0.123	L87 x T B	-0.068
L46 x T B	-0.184		

Testcross L9xTB (Table 4.11) had negative and significant SCA effects for NLB with an estimate of -0.196.

L1xTB, L4xTB, L18xTB, L32xTB, L40xTB, L45xTB, L46xTB, L48xTB, L50xTB, L52xTB, L53xTB, L54xTB, L61xTB, L67xTB, L71xTB, L72xTB, L73xTB, L74xTB, L75xTB, L78xTB and L87xTB had negative and non-significant SCA for grain weight with estimates of -0.005, -0.183, -0.118, -0.001, -0.022, -0.123, -0.184, -0.062, -0.099, -0.287, -0.114, -0.146, -0.097, -0.304, -0.140, -0.195, -0.304, -0.030, -0.376, -0.124 and -0.068 respectively.

L17xTB and L63xTB had positive and significant SCA effects for grain weight with estimates of 0.010 and 0.059. Crosses L2xTB, L5xTB, L12xTB, L19xTB, L24xTB, L26xTB, L27xTB, L29xTB, L31xTB, L33xTB, L34xTB, L35xTB, L38xTB, L41xTB, L43xTB, L44xTB, L47xTB, L51xTB, L58xTB, L62xTB, L66xTB, L69xTB, L76xTB, L79xTB and L81xTB had positive and non-significant SCA for grain weight.

Positive and significant SCA for grain weight could be used in breeding to evaluate and further develop high yielding crosses.

4.2.3 Heterotic Classification

Significance was recorded for some of the lines (Table 4.12). Lines 17 and 63 recorded positive and significant SCA for grain yield with tester B with estimates of 0.01 and 0.059 respectively hence were grouped into heterotic group A. Line 12 recorded positive and significant SCA for grain yield with Tester A with an estimate of 0.175 hence classified under heterotic group B.

Line 9 recorded negative and significant SCA with tester B with an estimate of -0.196 and grouped into heterotic group B. Line 1, 26 and 47 had negative and significant SCA for yield with estimates of -0.044, -0.225 and -0.517 respectively and were classified under heterotic group A.

Line 63 recorded significance with both testers. Positive and significant SCA was recorded with tester B while negative and significant SCA was recorded with tester A hence the line was classified into heterotic group A.

The rest of the lines could not be classified with the two testers

Table 4.12: Heterotic classification of the Lines using the Specific Combining Ability for Grain Weight in Embu

Line	Heterotic Group	Tester A	Tester B	Line	Heterotic Group	Tester A	Tester B
1	A	-0.044**	-0.005	47	A	-0.157**	0.307
2		0.165	0.089	48		0.092	-0.062
4		-0.190	-0.183	50		0.306	-0.099
5		0.017	0.0265	51		-0.016	0.029
9	B	0.059	-0.196**	52		-0.229	-0.287
12	B	0.175**	0.027	53		-0.103	-0.114
17	A	0.019	0.010**	54		0.060	-0.146
18		0.214	-0.118	58		-0.337	0.105
19		-0.184	0.057	61		-0.308	-0.097
24		-0.074	0.020	62	A	0.092	0.017
26	A	-0.225**	0.140	63		-0.249**	0.059**
27		0.177	0.160	66		-0.064	0.089
29		0.108	0.342	67		-0.049	-0.304
31		0.015	0.174	69		-0.081	0.178
32		-0.100	-0.001	71		0.073	-0.140
33		0.020	0.218	72		-0.138	-0.195
34		-0.052	0.179	73		0.038	-0.304
35		-0.139	0.081	74		0.245	-0.030
38		0.310	0.086	75		0.202	-0.376
40		-0.106	-0.022	76		0.036	0.038
41		0.066	0.032	78		0.079	-0.124
43		0.044	0.211	79		0.056	0.143
44		-0.236	0.121	81		0.256	0.100
45		0.241	-0.123	87		0.089	-0.062
46		-0.042	-0.184				

4.2.4 Yield of the Crosses

The highest yielding cross (Table 4.13) in Embu recorded a yield of 7.34t/ha (TesterAxL74) while the lowest recorded a yield of 1.6mt/ha (TBxL75).

The ten best performing crosses were: TesterAxL74=7.34t/ha, TesterAxL38=7.2t/ha, TesterAxL12=6.93t/ha, TesterAxL27=6.89t/ha, TesterAxL75=6.6t/ha, TesterAxL50=6.37 t/ha, TesterAxL81=6.29t/ha, TesterAxL18=6.14t/ha and TesterAxL62=6.11t/ha.

All the top performing crosses are those crossed with Tester A for this location. Tester A had a yield of 2.62t/ha while Tester B had a yield of 5.31t/ha.

Table 4.13: Yield of the Crosses in Embu

Testcross	Yield mt/ha Tester A	Yield mt/ha Tester B	Testcross	Yield mt/ha Tester A	Yield mt/ha Tester B
Tester/Line 1	4.47	3.94	Tester/Line 47	4.81	5.82
Tester/ line 2	6.08	3.64	Tester/Line 48	5.44	3.10
Tester/Line 4	5.16	2.75	Tester/Line 50	6.37	3.13
Tester/Line 5	5.49	3.66	Tester/Line 51	5.12	4.38
Tester/Line 9	5.55	2.73	Tester/Line 52	3.18	1.93
Tester/Line 12	6.93	4.36	Tester/Line 53	4.27	3.53
Tester/Line 17	5.69	4.19	Tester/Line 54	4.86	2.85
Tester/Line 18	6.14	2.69	Tester/Line 58	3.03	4.45
Tester/Line 19	4.33	4.28	Tester/Line 61	3.94	3.74
Tester/Line 24	5.08	4.42	Tester/Line 62	6.11	4.60
Tester/Line 26	3.78	5.06	Tester/Line 63	3.88	3.95
Tester/Line 27	6.89	5.32	Tester/Line 66	4.75	4.21
Tester/Line 29	5.52	5.51	Tester/Line 67	4.95	2.21
Tester/Line 31	5.59	4.51	Tester/Line 69	4.57	5.39
Tester/Line 32	4.65	3.58	Tester/Line 71	5.94	2.42
Tester/Line 33	5.18	4.51	Tester/Line 72	4.21	2.42
Tester/Line 34	4.66	5.45	Tester/Line 73	5.29	2.44
Tester/Line 35	4.66	4.00	Tester/Line 74	7.34	3.37
Tester/Line 38	7.20	4.43	Tester/Line 75	6.60	1.61
Tester/Line 40	5.29	3.46	Tester/Line 76	5.39	3.88
Tester/Line 41	5.39	3.57	Tester/Line 78	5.29	2.77
Tester/Line 43	5.63	5.17	Tester/Line 79	5.88	5.04
Tester/Line 44	3.38	5.18	Tester/Line 81	6.29	4.06
Tester/Line 45	6.66	3.41	Tester/Line 87	5.82	3.52
Tester/Line 46	4.06	2.09	Tester	2.62	5.31

4.3 Muranga

4.3.1 General Combining ability Analysis

Table 4.14: General Combining Ability Estimates for Northern Leaf Blight in Muranga

Line	NLB	Line	NLB
1	-0.043	47	0.233
2	-0.223	48	-0.100
4	-0.042	50	0.053
5	-0.028	51	-0.159
9	-0.119	52	0.151
12	-0.114	53	0.058
17	0.045	54	-0.105
18	-0.020	58	-0.013
19	0.063	61	-0.050
24	-0.133	62	-0.025
26	0.225	63	0.135
27	-0.117	66	-0.126
29	-0.022	67	0.072
31	-0.039	69	-0.045
32	-0.042	71	-0.039
33	-0.036	72	-0.036
34	-0.140	73	-0.106
35	0.057	74	0.000
38	-0.046	75	0.108
40	0.056	76	0.045
41	0.136	78	0.059
43	-0.056	79	0.058
44	0.046	81	0.239
45	-0.016	87	0.238
46	-0.035		

None of the lines exhibited significance for NLB in Muranga (Table 4.14). Line 1, 2, 4, 5, 9, 12, 18, 24, 27, 29, 31, 32, 33, 34, 38, 43, 45, 46, 48, 51, 54, 58, 61, 62, 66, 69, 71, 72 and 73 exhibited negative and non-significant GCA for NLB with estimates of -0.043, -0.223, -0.042, -0.028, -0.119, -0.114, -0.020, -0.133, -0.117, -0.022, -0.039, -

0.042, -0.036, -0.140, -0.046, -0.056, -0.016, -0.035, -0.100, -0.159, -0.105, -0.013, -0.050, -0.025, -0.126, -0.045, -0.039, -0.036 and -0.106 respectively.

Lines 17, 19, 26, 35, 40, 41, 44, 47, 50, 52, 53, 63, 67, 74, 75, 76, 78, 79, 81 and 87 exhibited positive and non-significant GCA effects for NLB.

Table 4.15: General Combining Ability of the lines for Days to Anthesis and Days to Silking in Muranga

Line	AD	SD	Line	AD	SD
1	0.267	0.467	47	-0.438	-0.603
2	-0.564	-0.228	48	-0.355	-0.095
4	1.755**	1.083	50	-0.234	0.243
5	-1.170**	-1.062	51	-1.075**	-0.217
9	-0.228	-1.180	52	-0.151	-0.337
12	-1.427**	-0.448	53	0.942	-0.319
17	-1.171**	-0.656	54	-0.529	-0.328
18	1.328	2.512**	58	0.782	0.161
19	-0.200	-0.715	61	0.780	1.281
24	-1.930	-1.086	62	0.103	-0.821
26	1.851	2.387**	63	0.093	-0.334
27	0.777	0.139	66	-1.058**	-1.345
29	0.250	0.276	67	-0.394	0.011
31	-0.627*	0.096	69	-0.779*	-0.674
32	-0.181	-0.688	71	0.334	0.355
33	-0.375	-0.468	72	1.175	0.280
34	0.388	0.593	73	0.330	0.015
35	1.296	0.946	74	1.004	0.644
38	-0.421	0.862	75	1.723	1.223
40	-0.748	-1.636	76	0.047	0.344
41	-0.156	1.161	78	1.115	1.238
43	0.549	1.026	79	-0.466	0.356
44	-0.044	0.120	81	-0.373	-0.517
45	-0.701*	-2.101**	87	-0.841**	-1.309
46	-0.253	-0.650			

Line 4 exhibited positive and significant ($P < 0.01$) GCA for days to anthesis with an estimate of 1.755 (Table 4.15).

Lines 5, 12, 17, 31, 45, 51, 66, 69 and 87 exhibited negative and significant GCA for days to anthesis with estimates of -1.170, -1.427, -0.627, -0.701, -1.075, -1.058, 0.779 and -0.841 respectively.

Line 2, 19, 24, 32, 33, 38, 40, 41, 44, 45, 46, 47, 48, 50, 54, 67, 69, 79 and 81 exhibited negative and non-significant GCA for days to anthesis. Line 1, 18, 26, 27, 29, 34, 35, 43, 53, 58, 61, 62, 63, 71, 72, 73, 74, 75, 76 and 78 exhibited positive and non-significant GCA for days to anthesis.

Line 18 and 26 exhibited positive and significant GCA for days to silking with estimates of 2.512 and 2.387. Line 45 exhibited negative and significant GCA for days to silking with an estimate of -2.101.

Line 2, 5, 9, 17, 19, 24, 32, 33, 40, 46, 47, 48, 51, 52, 53, 54, 62, 63, 66, 69, 81 and 87 had negative and non-significant GCA effects for days to silking.

Lines with negative and significant GCA for AD and SD could be used to breed for earliness.

4.3.2 Specific Combining Ability Analysis

Testcross L9xTA and L12xTA had positive and significant ($P < 0.01$) SCA effects for grain weight (Table 4.16) with estimates of 0.041 and 0.249.

Crosses L1xTA, L2xTA, L5xTA, L5xTA, L17xTA, L18xTA, L19xTA, L24xTA, L29xTA, L32xTA, L33xTA, L41xTA, L44xTA, L46xTA, L50xTA, L53xTA, L62xTA, L66xTA, L69xTA, L75xTA, L76xTA, L78xTA, L79xTA and L81xTA exhibited positive and non-significant SCA for grain weight.

Positive and significant SCA for yield could be utilized to breed for high yielding varieties.

Table 4.16: Specific Combining Ability Estimates of the Crosses with Tester A for Grain Weight in Muranga

Testcross	GW	Testcross	GW
L1 x T A	0.217	L47 x T A	-0.187
L2 x T A	0.084	48 x T A	-0.115
L4 x T A	-0.170	L50 x T A	0.181
L5 x T A	0.236	L51 x T A	-0.250
L9 x T A	0.041**	L52 x T A	-0.101
L12 x T A	0.249**	L53 x T A	0.036
L17 x T A	0.152	L54 x T A	-0.040
L18 x T A	0.095	L58 x T A	-0.036
L19 x T A	0.114	L61 x T A	-0.193
L24 x T A	0.059	L62 x T A	0.128
L26 x T A	-0.262	L63 x T A	-0.213
L27 x T A	-0.013	L66 x T A	0.199
L29 x T A	0.010	L67 x T A	-0.241
L31 x T A	-0.099	L69 x T A	0.129
L32 x T A	0.257	L71 x T A	-0.098
L33 x T A	0.145	L72 x T A	-0.028
L34 x T A	-0.129	L73 x T A	-0.036
L35 x T A	-0.021	L74 x T A	-0.238
L38 x T A	-0.007	L75 x T A	0.156
L40 X T A	-0.239	L76 x T A	0.150
L41 x T A	0.025	L78 x T A	0.271
L43 x T A	-0.083	L79 x T A	0.030
L44 x T A	0.244	L81 x T A	0.015
L45 x T A	-0.047	L87 x T A	-0.442
L46 x T A	0.200		

Table 4.17: Specific Combining Ability Estimates of the Crosses with Tester B for Grain Weight in Muranga

Testcrosses	GW	Testcrosses	GW
L1 x T B	-0.149	L47 x T B	0.483
L2 x T B	-0.298	L48 x T B	-0.107
L4 x T B	-0.112	L50 x T B	0.107
L5 x T B	-0.082	L51 x T B	-0.064
L9 x T B	0.093	L52 x T B	0.005
L12 x T B	-0.063	L53 x T B	-0.016
L17 x T B	-0.149	L54 x T B	-0.050
L18 x T B	-0.268	L58 x T B	0.216
L19 x T B	0.032	L61 x T B	0.353
L24 x T B	-0.075	L62 x T B	0.170
L26 x T B	-0.100	L63 x T B	0.275
L27 x T B	-0.105	L66 x T B	-0.165
L29 x T B	-0.072 **	L67 x T B	-0.143
L31 x T B	0.059	L69 x T B	-0.001
L32 x T B	0.237	L71 x T B	-0.034
L33 x T B	-0.067	L72 x T B	-0.154
L34 x T B	0.191	L73 x T B	-0.295
L35 x T B	0.153	L74 x T B	-0.062
L38 x T B	0.333	L75 x T B	-0.324
L40 x T B	0.035	L76 x T B	-0.191
L41 x T B	0.079	L78 x T B	-0.383
L43 x T B	0.331	L79 x T B	-0.056
L44 x T B	0.055	L81 x T B	0.271
L45 x T B	0.109	L87 x T B	-0.136
L46 x T B	-0.002		

Testcross L29xTB exhibited negative and significant ($P < 0.01$) SCA for grain weight with an estimate of -0.072 (Table 4.17).

L9xTB, L19xTB, L31xTB, L32xTB, L34xTB, L35xTB, L38xTB, L40xTB, L41xTB, L43xTB, L44xTB, L45xTB, L47xTB, L50xTB, L52xTB, L58xTB, L61xTB, L62xTB, L63xTB and L81xTB exhibited positive and non-significant SCA effects for grain weight.

L1xTB, L2xTB, L4xTB, L5xTB, L12xTB, L17xTB, L18xTB, L24xTB, L26xTB, L27xTB, L33xTB, L46xTB, L48xTB, L51xTB, L53xTB, L54xTB, L66xTB, L67xTB, L71xTB, L72xTB, L73xTB, L74xTB, L75xtB, L76xtB, L78xtB, L79xTB and L87xTB had negative and non-significant SCA for grain weight.

Table 4.18: Specific combining ability Effects of the Crosses to Northern Leaf Blight in Muranga

Line	Tester A	Tester B	Line	Tester A	Tester B
1	0.019	-0.087	47	0.120	0.248**
2	-0.124	-0.229**	48	0.091	-0.249**
4	0.019	-0.086	50	-0.022	0.107
5	0.031	-0.074	51	-0.249	-0.003
9	-0.159	-0.030	52	0.172	0.067
12	0.080	-0.260**	53	-0.019	0.110
17	-0.029	0.100	54	-0.148	-0.019
18	-0.197	0.165	58	0.042	-0.063
19	-0.015	0.114	61	0.013	-0.092
24	0.064	-0.275**	62	-0.201	0.162
26	0.348**	0.008	63	0.159	0.054
27	-0.157	-0.028	66	0.070	-0.269**
29	0.035	-0.070	67	0.227**	-0.113
31	-0.212	0.150	69	0.017	-0.088
32	0.020	-0.086	71	0.021	-0.084
33	0.024	-0.081	72	0.025	-0.081
34	-0.409**	0.188	73	0.086**	-0.253
35	-0.019	0.109	74	0.111	-0.111
38	-0.218	0.145	75	0.079	0.091
40	-0.020	0.109	76	-0.029	0.100
41	0.160	0.055	78	-0.018	0.111
43	0.009	-0.097	79	-0.019	0.110
44	-0.028	0.100	81	0.125**	0.254**
45	0.040	-0.065	87	0.124	0.252
46	0.025	-0.081			

Testcross L2xTB, L12xTB, L24xTB, L48xTB and L66xTB exhibited negative and significant SCA for NLB with estimates of -0.229, -0.260, -0.275, -0.249 and -0.269 respectively (Table 4.18).

L26xTA, L47xTA, L67xTA, L67xTA, L73xTA, L81xTA and L81xTB exhibited positive and significant SCA for NLB with estimates of 0.348, 0.248, 0.227, 0.086, 0.125 and 0.254 respectively.

Both Line 81 crosses had positive and significant SCA effects for NLB.

L4xTB, L5xTB, L9xTA, L9xTB, L17xTA, L18xTA, L19xTA, L27xTA, L27xTB, L29xTB, L31xTA, L32xTA, L33xTB, L35xTA, L38xTA, L40xTA, L43xTB, L44xTA, L44xTB, L46xtB, L50xTA, L51xTA, L51xTB, L53xTA, L54xTA, L54xTB, L58xTB, L61xTB, L62xtA, L67xTb, L69xTB, L71xTB, L72xTB, L73xTB, L74xTB, L76xTA, L78xTA and L79xTA had negative and non-significant SCA for NLB.

4.3.3 Heterotic Classification

Table 4.19: Heterotic Classification of the Lines in Muranga

Line	Heterotic Group	Tester A	Tester B	Line	Heterotic Group	Tester A	Tester B
1	A	1.340	1.340**	47	A	-2.540**	0.445
2	B	0.977**	-0.680	48		-0.244	0.753
4	A	-1.040**	-0.288	50	A	-0.032	-0.044
5	B	0.388	-0.466	51		-2.618**	0.634
9		1.831**	-0.204	52		-0.146	-0.815
12		-0.790	-0.218	53		0.038	-0.177
17	A	-1.821**	0.482	54		-0.663	-0.177
18	A	-1.874**	-0.843	58	B	-0.630	-0.711
19	A	-1.143**	1.302**	61		1.154**	0.772
24	A	0.598	0.332	62		-0.714	-0.924
26		-2.214**	0.492	63		-3.445**	0.223
27	B	0.284	-0.458	66	A	0.767	-0.689
29	B	1.516**	0.112	67		-4.143**	-0.865
31		1.416**	-0.138	69		0.692	0.443
32	B	-0.512	-0.133	71		0.717	-0.072
33	B	1.415**	-0.148	72	B	0.743	-0.107
34	B	1.160**	0.022	73		2.086**	0.699
35		1.373**	-0.237	74	A	0.443	-0.016
38	B	-0.475	0.260	75	B	0.124	1.189**
40		-0.134	-0.215	76		-0.428	0.753
41		1.162**	0.153	78	B	1.551**	-0.072
43		0.723**	-0.247	79	A	2.048**	-0.391
44	B	-0.908	0.055	81		-1.250**	0.207
45		2.142**	-0.357	87		0.530	-0.242
46		0.036	0.225				

Line 1, 19 and 75 expressed positive and significant ($P < 0.01$) SCA for grain weight (GW) with tester B with estimates of 1.340, 1.302 and 1.189 respectively (Table 4.19). These lines were classified under the opposite heterotic group B.

Line 2, 9, 29, 31, 33, 34, 35, 41, 43, 45, 61, 73, 78 and 79 exhibited positive and significant SCA for grain weight with Tester A with estimates of 0.977, 1.831, 1.516,

1.416, 1.415, 1.160, 1.373, 1.162, 0.723, 2.142, 1.154, 2.086, 1.551 and 2.048 hence were classified under heterotic group B.

Line 4, 17, 18, 19, 26, 47, 51, 63, 67 and 81 exhibited negative and significant SCA for grain weight with Tester A with estimates of -1.040, -1.821,-1.874, -1.143, -2.214, -2.540, -2.618, -3.445, -4.143 and -1.250 hence were classified under heterotic group A.

The rest of the lines could not be classified by the two testers.

4.4.4 Yield of the Crosses (Muranga)

The highest yielding cross (Table 4.20) recorded a yield of 10.32t/ha (TesterBxL19).

The highest yielding crosses were TesterBxL19=10.32t/ha, TesterBxL1=10.25t/ha, TesterBxL73=10.13t/ha, TesterAxL73=9.73t/ha, TesterBxL75=9.31t/ha, TesterBxL74=9.47t/ha, TesterAxL79=9.33t/ha, TesterAxL45=9.31t/ha, TesterAxL9=9.21t/ha, TesterBxL76=9.07t/ha and TesterBxL61=9.02t/ha. These crosses recorded yields of 9t/ha and above.

The lowest yielding cross was TesterAxL67 with a yield of 2.17t/ha.

Table 4.20: Yield of the Crosses in Muranga

Testcross	Yield mt/ha		Testcross	Yield mt/ha	
	Tester A	Tester B		Tester A	Tester B
Tester/Line 1	8.16	10.25	Tester/Line 47	4.09	8.95
Tester/ line 2	8.18	7.42	Tester/Line 48	6.56	9.03
Tester/Line 4	5.98	8.37	Tester/Line 50	7.26	8.46
Tester/Line 5	7.68	7.95	Tester/Line 51	3.99	8.99
Tester/Line 9	9.21	8.50	Tester/Line 52	7.03	7.21
Tester/Line 12	6.27	8.40	Tester/Line 53	7.25	8.57
Tester/Line 17	4.72	8.82	Tester/Line 54	6.34	8.20
Tester/Line 18	5.02	8.23	Tester/Line 58	6.50	8.59
Tester/Line 19	6.02	10.32	Tester/Line 61	8.52	9.02
Tester/Line 24	8.02	8.89	Tester/Line 62	6.22	7.17
Tester/Line 26	4.30	8.53	Tester/Line 63	3.12	9.00
Tester/Line 27	7.45	7.98	Tester/Line 66	8.02	7.96
Tester/Line 29	8.69	8.67	Tester/Line 67	2.17	7.58
Tester/Line 31	8.50	8.47	Tester/Line 69	7.55	8.90
Tester/Line 32	6.19	8.24	Tester/Line 71	7.56	8.19
Tester/Line 33	8.42	8.43	Tester/Line 72	7.62	8.00
Tester/Line 34	8.42	8.54	Tester/Line 73	9.73	10.13
Tester/Line 35	8.59	8.18	Tester/Line 74	7.68	9.47
Tester/Line 38	6.56	8.96	Tester/Line 75	7.37	9.50
Tester/Line 40	6.87	8.30	Tester/Line 76	6.37	9.07
Tester/Line 41	8.18	8.64	Tester/Line 78	8.97	7.93
Tester/Line 43	7.67	7.84	Tester/Line 79	9.33	7.99
Tester/Line 44	5.88	8.53	Tester/Line 81	5.68	8.88
Tester/Line 45	9.31	7.68	Tester/Line 87	7.71	8.00
Tester/Line 46	6.83	8.58	Tester	6.29	6.18

4.4: Across Sites Analysis

4.4.1: Yield of the Crosses across the Locations

The highest yielding testcross across the locations (Table 4.21) was Tester A/Line 62 with an average yield of 8.14t/ha. The crosses developed from Tester A had a higher mean performance with yield of above 5mt/ha. Crosses developed from Tester B had yields ranging from 2.77t/ha (Tester B/Line 75) which was the lowest and 6.91t/ha (Tester B/Line 47).

The top high yielding crosses were Tester A/Line62=8.14t/ha, Tester A/Line50=7.59t/ha, Tester A/Line9=7.56t/ha, Tester A/line46=7.52t/ha, Tester A/Line79=7.49t/ha, Tester A/Line 12=7.44t/ha, Tester A/Line81=7.43t/ha, Tester A/Line2= 7.41t/ha, Tester A/Line18 and Tester A/Line38=7.39t/ha.

Tester B had a yield of 4.45t/ha while Tester A had an average yield of 2.94t/ha. The lowest yielding testcross had a yield of 2.77t/ha (Tester B/line75) followed by Tester A which was a check.

Table 4.21: Across sites Yield in mt/ha

Testcross	Tester A	Tester B	Testcross	Tester A	Tester B
Tester/Line 1	6.43	4.60	Tester/Line 47	5.64	6.91
Tester/ line 2	7.41	3.29	Tester/Line 48	6.33	4.02
Tester/Line 4	5.61	3.18	Tester/Line 50	7.59	4.67
Tester/Line 5	7.26	5.09	Tester/Line 51	5.23	4.51
Tester/Line 9	7.56	4.75	Tester/Line 52	5.67	4.08
Tester/Line 12	7.44	5.00	Tester/Line 53	5.74	5.17
Tester/Line 17	7.09	4.58	Tester/Line 54	6.10	3.96
Tester/Line 18	7.39	3.07	Tester/Line 58	6.33	6.26
Tester/Line 19	6.67	4.91	Tester/Line 61	4.96	5.89
Tester/Line 24	7.11	4.41	Tester/Line 62	8.14	5.92
Tester/Line 26	4.53	4.52	Tester/Line 63	4.94	5.97
Tester/Line 27	7.09	4.35	Tester/Line 66	5.87	4.43
Tester/Line 29	6.82	4.84	Tester/Line 67	5.30	3.41
Tester/Line 31	6.32	5.38	Tester/Line 69	6.37	4.53
Tester/Line 32	6.92	5.18	Tester/Line 71	6.26	4.51
Tester/Line 33	6.20	5.14	Tester/Line 72	4.83	3.17
Tester/Line 34	6.60	6.45	Tester/Line 73	6.13	3.12
Tester/Line 35	6.20	5.71	Tester/Line 74	5.54	3.61
Tester/Line 38	7.39	5.55	Tester/Line 75	7.19	2.77
Tester/Line 40	5.13	5.41	Tester/Line 76	6.21	4.61
Tester/Line 41	6.19	4.65	Tester/Line 78	7.09	4.13
Tester/Line 43	6.60	6.35	Tester/Line 79	7.49	4.93
Tester/Line 44	6.51	5.85	Tester/Line 81	7.43	6.86
Tester/Line 45	7.12	5.16	Tester/Line 87	5.32	3.03
Tester/Line 46	7.52	4.44	Tester	2.94	4.45

CHAPTER FIVE

DISCUSSION

Lines and crosses that exhibited negative and significant GCA and SCA for AD and SD differed across the three locations. Negative and significant GCA effects for AD and SD could be used to breed for earliness in maize hybrids. The same was observed in other studies Hussein *et al.*, (2003) and Uddin *et al.*, (2006).

Positive and significant GCA effects for NLB are an indication of susceptibility to the disease hence the lines exhibiting positive and significant GCA effects for the trait cannot be used to breed for NLB resistance. Negative and significant GCA effects for NLB exhibit resistance hence lines exhibiting negative and significant GCA estimates for NLB could be used to breed for resistance to the disease.

Classification of the lines into heterotic group A (CML312/CML442) and B (CML395/CML444) were dependent on the SCA effects for grain weight such that lines exhibiting positive and significant SCA with (CML312/CML442) tester A were oriented into the opposite heterotic group which is B and lines exhibiting positive and significant SCA with (CML395/CML444) tester B were oriented into the opposite heterotic group which is A.

Lines exhibiting positive and significant SCA to the two testers were oriented to group AB. Lines exhibiting negative and significant SCA with tester A were oriented into heterotic group A while lines exhibiting negative and significant SCA with tester B were oriented into heterotic group B. Lines classified into heterotic group A could be crossed with germplasm in heterotic group B in order to exploit higher levels of heterosis. Lines classified into heterotic group B could also be crossed with germplasm from heterotic A in order to exploit maximum levels of heterosis. Hallauer and carena (2009) reported that heterotic groups represent a group of genotypes that when crossed consistently give better crosses than when crosses are made within the same group.

According to Menkir *et al.*, (2004), SCA estimates for grain yield have been used widely to classify maize lines into heterotic groups.

Crosses with significant SCA estimates can be used for maize improvement (Motamedi *et al.*, 2014). Significant and highly significant SCA estimates on maize grain yield were recorded by Shushay *et al.*, 2013 (Motamedi *et al.*, 2014, Shushay *et al.*, 2013).

CHAPTER SIX

CONCLUSION AND RECOMMENDATION

6.1 CONCLUSION

Combining Ability Analysis

- Positive and significant GCA effects for NLB are an indication of susceptibility to the disease hence the lines exhibiting positive and significant GCA effects for the trait cannot be used to breed for NLB resistance. Negative and significant GCA effects for NLB exhibit resistance hence lines exhibiting negative and significant GCA estimates for NLB could be used to breed for resistance to the disease. More lines in Kakamega exhibited significance for NLB. A total of 8 lines exhibited negative and significant estimates for the trait hence could be recommended for further testing to breed for resistance to the disease.
- More lines in Muranga exhibited negative and significant GCA effects for AD than in the other locations. These lines could further be tested and utilized to breed for earliness.
- Crosses with significant SCA estimates can be used for maize improvement.

Heterotic Classification

- The classification of the lines differed across the three locations having most of the lines in Muranga falling under the heterotic groups A and B. For Embu and Kakamega, fewer lines were classified into either heterotic group a and B having none of the lines in heterotic group A in Kakamega. Lines classified into heterotic group A could be crossed with germplasm in heterotic group B in order to exploit higher levels of heterosis. Lines classified into heterotic group B could also be crossed with germplasm from heterotic A in order to exploit maximum level of heterosis. SCA estimates for grain yield have been used widely to classify maize lines into heterotic groups. Some of the lines were classified under different heterotic groups across the environments. Line 17 was classified

into heterotic group A in Muranga and into heterotic group B in Embu. Line 9 was classified into heterotic group B in both Embu and Kakamega and into heterotic group A in Muranga. Lines could be in more than one heterotic groups and this would depend on the performance in the particular combination as heterotic groups could be conceptual.

- Knowledge of heterotic groups of the lines is of importance in the introductions in order to exploit their use in the breeding programme. The lines may hence require some further testing with alternative testers in order to fully classify them into their various heterotic groups. Significant interactions between the lines and the testers is evidence that the rank of the lines differs depending on testers used, a suitable tester may then be selected to classify new germplasm.

Yield of the Testcrosses

- The maize crosses exhibited different yield performance across the three locations even under similar agronomic management practices. Testcrosses developed with Tester A recorded higher yields in Kakamega and Embu while in Muranga the crosses developed from Tester B recorded higher average yields. Yield can be considered as a result of interaction between genotype, agronomic management and the environment.
- The top performing crosses could hence be subjected to further trials hence recommended for high yielding varieties in best suited regions in the country. The lines could further be developed to breed for high performing hybrids that would be best suited for different agro-ecological zones across the country in different combinations.

6.2 RECOMMENDATIONS

- Lines exhibiting negative and significant GCA for NLB could be evaluated further to develop hybrids for NLB prone areas.
- Crosses with negative and significant SCA for AD and SD could be evaluated for earliness and recommended for use in the short seasons.
- High yielding crosses could be recommended for further trialing in order to avail high performing varieties for farmers in different Agro-ecological areas of the country.
- Further testing to identify the heterotic groups of the lines using markers and different testers could be recommended for the lines that were not classified with Tester A and Tester B in order to place the lines in their respective heterotic groups for use in the breeding programme.

REFERENCES

- Abebe, T., Arron, A.C., Martin. and B., Cushman, J.C. (2003).Tolerance of mannitol accumulating transgenic wheat to water stress and salinity. *Plant Physiology* 131: 1748-1755.
- Adipala, E., P.E., Lipps. and L.V. Madden. (1993). Reaction of maize cultivars from Uganda to *Exserohilum turcicum*. *Phytopathology* 83:217-223.
- Alake, C.O., Ojo, D.K., Oduwaye, O.A., Adekoya, M.A. (2008) Genetic variability and correlation studies in yield and yield related characters of tropical maize (*Zea mays* L.). *Asset Series A*, 8(1), 14-27.
- Albrecht, T., Wimmer V., Auinger H.-J., Erbe M., Knaak C. (2011) Genome based prediction of testcross values in maize. *Theor. Appl. Genet.* 123: 339–350
- Al-Tabbal, J.A., Al-Fraihat, A.H. (2012) Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. *Journal of Agricultural Science*, 4(3), 193.
- Asoro, F.G., Newell M.A., Beavis W.D., Scott M.P., Jannink J.-L. (2011) Accuracy and training population design for genomic selection on quantitative traits in elite North American oats. *Plant Gen* 4: 132–144.
- Baloch, A.W., Baloch, M.J., Jatoi, W.A. and Veesar, N.F (2010). Production of superior F1 hybrids; genetic analysis for estimating combining ability in upland cotton yield and its component traits in *Gossypium hirsutum* L. *Cotton Research Development*, 19 (2): 161- 164.
- Barata, C and Carena M.J. (2006). Classification of North Dakota maize inbred lines into heterotic groups based on molecular and testcross data. *Euphytica* 151: 339-349.

- Bernardo, R., Yu J., (2007) Prospects for genome wide selection for quantitative traits in maize. *Crop Sci.* 47: 1082–1090.
- Bocanski, J., Sreckov, Z., Nastasic, A. (2009). Genetic and phenotypic relationship between grain yield and components of grain yield of maize (*Zea mays* L.). *Genetika*, 41(2), 145-154.
- Browning, B.L., Browning, S.R., (2009). A unified approach to genotype imputation and haplotype-phase inference for large data sets of trios and unrelated individuals. *J. Hum. Genet.* 84: 210–223.
- Carena, M.J. and Hallauer, A.R. (2001). Response to inbred progeny recurrent selection in Leaming and Midland Yellow Dent populations. *Maydica* 46: 1-10.
- Carena, M.J. and Wicks III Z.W. (2006). Maize early maturing hybrids: An exploitation of U.S. temperate public genetic diversity in reserve. *Maydica* 51: 201-208.
- Carson, M.L., (1995). Inheritance of latent period length in maize infected with *Exserohilum turcicum*. *Plant Dis.* 79: 581–585.
- Chenulu, V.V. and Hora, T.S. (1962). Studies on losses due to Helminthosporium blight of maize. *Indian Phytopathology*, 15: 235-237.
- Chung, C.L., Jamann T, Longfellow J, Nelson R (2010). Characterization and fine-mapping of a resistance locus for northern leaf blight in maize bin 8.06. *Theor Appl Genet* 121(2):205–227.
- CIMMYT, (1985) Managing trials and reporting data for CIMMYT's International Maize Testing Programme. CIMMYT, El Batan, Mexico.
- Collard, B. C. Y., Mackill D. J. (2008). Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. *Philos T Roy Soc B* 363: 557–572.

- Cukandor, O.B., J.F. Miller and J.J. Hammond, (1997). Combining ability of the stay green trait and seed moisture content in sun flower. *Crop Sci.* 37: 378-382.
- Daetwyler, H.D., Hickey J. M., Henshall J. M., Dominik S., Gredler B. (2010a). Accuracy of estimated genomic breeding values for wool and meat traits in a multi-breed sheep population. *Anim. Prod. Sci.* 50: 1004–1010.
- Daetwyler, H.D., Pong-Wong R., Villanueva B., Woolliams J. A. (2010b). The impact of genetic architecture on genome-wide evaluation methods. *Genetics* 185: 1021–1031
- De Roos, A.P.W., Hayes B. J., Goddard M. E. (2009). Reliability of genomic predictions across multiple populations. *Genetics* 183: 1545–1553.
- Dingerdissen, A., Geiger H., Lee M., Scheckert A., Welz H. (1996). Interval mapping of genes for quantitative resistance of maize to *Setosphaeria turcica*, cause of northern leaf blight, in a tropical environment. *Mol. Breed.* 2: 143–156.
- Dodds, P.N., Rathjen J.P. (2010). Plant immunity: Towards an integrated view of plant-pathogen interactions. *Nat Rev Genet* 11(8):539–548.
- Drechsler, C. (1923). Some graminicolous species of *Helminthosporium*. I. *J. Agri. Res.* 24:641-739.
- Dunn, G.M, and T. Namm. (1970). Gene dosage effects on monogenic resistance to northern corn leaf blight. *Crop Sci.* 10:352-354.
- Durrishahwar, H., Rehman, S.M.A., Shah,I.A.K and Ali, F. (2008). Recurrent selection for yield and yield associated traits under leaf blight (*Helminthosporium maydis*) stress in maize. *Sarhad Journal of Agriculture*, 24(4): 599-605.

- Elshire, R.J., Glaubitz J.C., Sun Q., Poland J. a., Kawamoto K. (2011). A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. *PLoS ONE* 6: e19379].
- Enoki, H., H. Sato, and K. Koinuma. (2002). SSR analysis of genetic diversity among maize inbred lines adapted to cold regions of Japan. *Theoretical Applied Genetics* 104:1270-1277.
- Fageria, N.K., Baligar VC, Wright RJ. (1988). Aluminum toxicity in crop plants. *Journal of Plant Nutrition* 11: 303-319.
- Falconer, D.S and Mackay, T.F.C. (1996). Introduction to quantitative genetics. 4th ed., pp 200-215.
- Falconer, D.S. (1989). Introduction to Quantitative Genetics. 3rd ed. *Longman, London, England*, pp 125-132.
- Falconer, D.S., Mackay T.F.C. (1996). Correlated response to selection, Longmans Green, Harlow, Essex, UK. *Introduction to Quantitative Genetics* Ed. 4: 320-322.
- Fan, X.M., Chen H.M., Tan J, Xu C.X., Zhang Y.M., Huang Y.X., and Kang M.S. (2008). A new maize heterotic pattern between temperate and tropical germplasms. *Agronomy Journal* 100: 917-923.
- Ganal, M.W., Durstewitz G., Polley A., Bérard A., Buckler E.S. (2011). A large maize (*Zea mays* L.) SNP genotyping array: development and germplasm genotyping, and genetic mapping to compare with the B73 reference genome. *PLoS ONE* 6: e28334.
- Gaunt, R.E. (1995). New technologies in disease measurement and yield loss appraisal. *Can. J. Plant Pathol.* 17:185-189.

- Gebrekidan, B, Wafula, B., and Njoroge, K. (1992) Agroecological zoning in relation to maize research priorities in Kenya. In: *KARI: Review of the National Maize Research Program*. Proceedings of a Workshop Held between November 19 and 23, 1991, Kakamega, Kenya. Kenya Agricultural Research Institute (KARI) and the International Service for National Agricultural Research (ISNAR), Nairobi, Kenya.
- Gevers, H.O. (1975). A new major gene for resistance to *Helminthosporium turcicum* leaf blight of maize. *Plant Dis Rep* 59:296–299.
- Gravois, K.A. and R.W. McNew. (1993). Combining ability and heterosis in U.S. southern long rice grain. *Crop Sci.* 33: 90-95.
- Guzman, P., Lamkey K. (2000). Effective population size and genetic variability in the BS11 maize population. *Crop Sci.* 40: 338–346.
- Hadfield, J.D., (2010). MCMC Methods for multi-response generalized linear mixed models: *The MCMCglmm R Package*. *J. Stat. Softw.* 33: 1–22.
- Hallauer, A.R. and J.B. Miranda. (1988) Quantitative genetics in maize breeding. 2nd ed. Iowa State Univ. Press. Ames. pp. 64-71.
- Hallauer, A.R. and Miranda Fo, J.B. (1981). Quantitative genetics in maize breeding. 2nd ed. Iowa State University press, Ames, Iowa. pp 26-40.
- Hallauer, A.R., Carena M.J., and Miranda F.J.B. (2010). Quantitative genetics in maize breeding. 3rd edn, *Springer, New York*, 663p.
- Hallauer, AR and Carena MJ. (2009) Maize Breeding. In Carena MJ (ed) Handbook of plant breeding: *Cereals*. *Springer, New York*, p. 3-98.

- Hayes, B.J., Bowman P.J., Chamberlain A.C., Verbyla K., Goddard M. E. (2009a). Accuracy of genomic breeding values in multi-breed dairy cattle populations. *Genet. Sel. Evol.* 41: 51.
- Hayes, B.J., Bowman P.J., Chamberlain A.J., Goddard M.E. (2009b). Invited review: genomic selection in dairy cattle: progress and challenges. *J. Dairy Sci.* 92: 433–443
- Heffner, E.L., Lorenz A.J., Jannink J.-L., Sorrells M.E. (2010). Plant breeding with genomic selection: gain per unit time and cost. *Crop Sci.* 50: 1681–1690.
- Hilu, H.M. and A.L.Hooker, (1963). Host-pathogen relationship of *Helminthosporium turcicum* in resistant and susceptible corn seedlings. *Phytopathology.* 54:570-575.
- Hooker, A.L. (1961). A new type of resistance in corn infected with *Helminthosporium turcicum*. *Plant Dis. Repr.* 45:780-781.
- Joshi, V.N., R.B. Dubey and S. Marker, (2002). Combining ability for polygenic traits in early maturity hybrids of maize (*Zea mays* L.). *Indian J. Plant Breed. Genet.* 62: 312-315.
- Kachapur, M.R. and Hegde, R.K. (1988). Studies on turcicum blight of maize (*Zea mays* L.) caused by *Exserohilum turcicum* (Pass) Leonard & Suggs with special reference to crop loss assessment. *Plant pathology newsletter*, 6: 33-35.
- Kang'ethe, W.G. (2004). Agricultural development and food security in Kenya: A case for more support. A paper prepared for agriculture and food organisation (September).
- Kang'ethe, E. (2011). Situation analysis: Improving food safety in the maize value chain in Kenya. 1-89 College of Agriculture and Veterinary Science: FAO.

- Karkkainen, H.P., Sillanpaa M.J., (2012). Back to basics for bayesian model building in genomic selection. *Genetics* 191: 969–987.
- Kempthorne, O. (1957). *An Introduction to Genetic Statistics*. New York: John Wiley & Sons, Inc. London: *Chapman & Hall Ltd*. pp. 458-471.
- Khalil, I.A., Rahman, H.U., Rehman, N.U., Arif, M.; Khalil, I.H.; Iqbal, M.; Hidayatullah; Afridi, K.; Sajjad, M., Ishaq, M. (2011). Evaluation of maize hybrids for grain yield stability in north-west of Pakistan. *Sarhad J. Agric.*, 27, 213–218.
- Kumar, S., Singh, H. B., Sharma, J.K., (2007). Combining ability analysis for grain yield and other associated traits in rice. *Oryza*, 44(2): 108-114.
- Legarra, A., Robert-Granié C., Manfredi E., Elsen J.-M. (2008). Performance of genomic selection in mice. *Genetics* 180: 611–618.
- Levy, Y. and Cohen, Y. (1983) Biotic and environmental factors affecting infection of sweet corn with *Exserohilum turcicum*. *Phytopathology* 73:722-725.
- Li, Y., Shi, Y. Song, J. Du, R. Tuberosa, and T. Wang. (2004) Analysis of genetic diversity in maize inbred lines based on AFLP markers. *Maydica* 49:89-95.
- Longman, Essex, England Erbe, M., Hayes B.J., Matukumalli L.K., Goswami S., Bowman P.J. (2012). Improving accuracy of genomic predictions within and between dairy cattle breeds with imputed high-density single nucleotide polymorphism panels. *J. Dairy Sci.* 95: 4114–4129.
- Lorenz, A.J., Smith K., Jannink J.L., (2012). Potential and optimization of genomic selection for Fusarium head blight resistance in six-row barley. *Crop Sci.* 52: 1609–1621.

- Madden, L.V., Hughes G, van den Bosch F. (2007). The study of plant disease epidemics (*APS Crop Sci Press, St. Paul, MN*), p 432.
- Makumbi, D. (2005). Phenotypic and genotypic characterization of white maize inbreds, hybrids and synthetics under stress and non-stress environments. In Office of Graduate Studies, Vol. PhD: Texas A and M University.
- Manwiller, A., W.K.K. Mmatta & T. Ambeta. (1985). Breeding Hybrid maize at Muguga. Record of Research. KARI Annual Report 61-62.
- Martin, M., Miedaner T., Dhillon B.S., Ufermann U., Kessel B. (2011). Colocalization of QTL for gibberella ear rot resistance and low mycotoxin contamination in early european maize.. 51: 1935–1945.
- Martinez, A. (2011). Fertilizer Use Statistics and crop yields. Muscle shoals, Alabama:IFDC.
- Mbithi, L.M. (2000). Agricultural policy and maize production in Kenya: *Universiteit Gent, Unpublished Ph.D Thesis*.
- Melania, M.D. and Carena, M.J. (2005). Alternative maize heterotic patterns for Northern Corn Belt. *Crop Science*, 45: 2186-2194.
- Melchinger, A. E. (1999). Genetic diversity and heterosis. In: Coors, J. G. and Pandey, S. (Eds). The genetics and exploitation of heterosis in crops. American society of Agronomy/crop Science Society of America Inc., *Madison, Winconsin*, pp 99-118.
- Melchinger, A.E., R.K. Gumber. (1998). Overview of heterosis and heterotic groups in agronomic crops. pp. 29-44. In K.R. Lamkey, J.E. Staub (ed.), Concepts and breeding of heterosis in crop plants. *CSSA, Madison, WI*.

- Mendes, U.C., Miranda-Filho J.B., Oliveira A.S. and Reis E.F. (2015). Heterosis and combining ability in crosses between two groups of open-pollinated maize populations. *Crop Breeding and applied Biotechnology* 15: 235-243.
- Menkir, A., Berhan, M., Ingelbrecht, C. L and Adepoju, A. (2004). Grouping of tropical midium altitude maize inbred lines on the basis of yield data and molecular analysis. *Theoretical Applied Genetics*, 108: 1582-1590.
- Messmer, M.M., Melchinger A.E., Boppenmaier J., Brunklaus-Jung E., Herrmann R. G. (1993). Relationship among early European maize inbreds: I. Genetic diversity among Flint and Dent lines revealed by RFLPs. *Crop Sci.* 32: 1301–1309.
- Meuwissen, T.H., Hayes B.J., Goddard M.E. (2001). Prediction of total genetic value using genome-wide dense marker maps. *Genetics* 157: 1819–1829 Nadeau C., Bengio Y., 2003. Inference for the generalization error. *Mach. Learn.* 52: 239–281.
- Motamedi, M., Choukan, R., Hervan, E.M., Bihamta, M.R. & Kajouri, F.D. (2014). Investigation of genetic control for yield and related traits in maize (*Zea mays* L.) lines derived from temperate and sub-tropica germplasm. *Internatinal Journal of Bioscience* 5(12): 123-129.
- Muiru, W.M., Mutitu, E.W. and Kimenju, J.W. (2007). Reactions of some Kenyan maize genotype to turcicum leaf blight under greenhouse and field conditions. *Asian Journal Plant Science*, 6: 1190-1196.
- Murenga, M. Derera, J., Tongoona, P., Mugo, S., and Gichuru, L. (2015). Combining ability for stem borer resistance and heterotic orientation of maize inbred lines using CIMMYT single cross testers under *Busseola fusca* infestation. *Euphytica*. 7. 10.1007/s10681-015-1602-1.

- Nicholason, R.L. and H.L. Warren, (1975). Criteria for evaluation of resistance to Maize anthracnose. *Phytopathology* 66:86-66.
- Nyoro, J., Kirimi, L and Jayne, T.S. (2004), “Competitiveness of Kenyan and Ugandan maize production: Challenges for the future”, Working Paper 10, Egerton University, Tegemeo Institute, Nairobi.
- Nyoro, J.K. (2002). Competitiveness in domestic maize production: Implications for food security. Paper presented in a seminar at the African Study Center, University of Leiden. November 7, 2002, Leiden, Netherlands: Tegemeo Institute, Egerton University, Kenya, 2002.
- Packer, D.J. (2007). Comparing the Performance of F1 Testers Versus Their Inbred Line Parents in Evaluating Experimental Sorghum R and B Lines in Testcrosses. Vol. Master of science plant breeding: Brigham Young University.
- Parentoni, S.N., Magalhaes, J.V., Pacheco, C.A.P., Santos, M. X., Abadie, T., Gamap, E.E.G., Guimavaes, E. O., Meirelles, M.F., Lopes, M.A., Vasconcelos, M.J.V. and Paiva, E. (2001). Heterotic groupings based on yield- specific combining ability data and phylogenetic relationship determined by RAPD markers for 28 tropical maize open pollinated varieties. *Euphytica*, 121: 197-208.
- Pataky, J.K. (1994). Effects of races 0 and 1 of *Exserohilum turcicum* on sweet corn hybrids differing for Ht-and partial resistance to northern leaf blight. *Plant Dis.*78:1189-1193.
- Payak, M.M., and Sharma, R.C. (1985). Maize diseases and their approach to their management. *Tropical Pest Management*, 31: 302-310.
- Pedersen, W.L. and M.G. Oldham. (1992). Effect of three tillage practices on development of northern corn leaf blight *Exserohilum turcicum* under continuous corn. *Phytopathology* 76:1161-1164.

- Perkins, J.M., Pedersen W.L. (1987). Disease development and yield losses associated with northern corn leaf blight on corn. *Plant Dis.* 71: 940–943.
- Pixley, K. and Banziger, M. (2001). Open-pollinated maize varieties. A backward step or valuable option for farmers? Integrated Approaches to higher maize productivity in the new millennium. Proceedins of the seventh Eastern and Southern Africa Maize Regional Conference. 5-11 February, 2001. Nairobi, Kenya: CIMMYT and KARI, 2001: 22-28.
- Poland, J.A., Bradbury P.J., Buckler E.S., Nelson R.J. (2011). Genome-wide nested association mapping of quantitative resistance to northern leaf blight in maize. *Proc. Natl. Acad. Sci. USA* 108: 6893–6898.
- Pratt, R.C., E. Adipala, and P.E., Lipps, (1993). Characterization of race-specific resistance to *Exserohilum turcicum* races 0 and 1 in maize OhS0 S1 progenies. *Plant Dis.* 77:1227-1232.
- Pratt, R.C., Gordon S.G. (2005). Breeding for resistance to maize foliar pathogens. Plant Breeding Reviews, ed Janick J (*John Wiley & Sons, Oxford*), pp 119–173.
- Pswarayi, A. and Vivek, B. (2004). Combining ability of CIMMYTs early maturing maize (*Zea mays* L.) germplasm under stress and non stress conditions and identification of testers
- Rawlings, J.O. and D.L. Thompson, (1962). Performance level as criterion for the choice of maize testers. *Crop Sci.* 2: 217-220.
- Raymundo, A.D. (1978). Epidemiology of northern corn leaf blight as affected by host resistance and yield losses following simulated epidemics. Ph.D.Thesis, *University of Illinois, Urbana -Champaign.* 111pg.
- Raymundo, A.D., Hooker A.L. (1981). Measuring the relationship between northern corn leaf blight and yield losses. *Plant Dis.* 65: 325–327

- Rebourg, C., Chastanet M., Gouesnard B., Welcker C., Dubreuil P. (2003) Maize introduction into Europe: the history reviewed in the light of molecular data. *Theor. Appl. Genet.* 106: 895–903.
- Reif, J.C., A.R. Hallauer, A.E. Melchinger. (2005) Heterosis and heterotic patterns in maize. *Maydica* 50:215-223.
- Riedelsheimer. C., Czedik-Eysenberg A., Grieder C., Lisec J., Technow F. (2012). Genomic and metabolic prediction of complex heterotic traits in hybrid maize. *Nat. Genet.* 44: 217–220.
- Rutkoski, J., Benson J., Jia Y., Brown-Guedira G., Jannink J.-L. (2012). Evaluation of genomic prediction methods for fusarium head blight resistance in wheat. *Plant Gen* 5: 51–61.
- Shakoor, M.S., Akbar,M., & Hussain, A. (2007). Correlation and path coefficients studies of some morphophysiological traits in maize double crosses. *Pak. J. Agri. Sci.*, 44(2), 213-216.
- Shanthi, P., Shanmugasundaram, P. and Nagarajan, P. (2003). Combining ability analysis in rice. *Oryza*, 40(1/2): 11-13.
- Sharma, D., and Aujla S.S. (1968). *J. Res. Punjab Agric.Univ. Ludhiana* 5: 501-504.
- Sharma, P., Khoyumthem, P., N.B. and Singh, N.K. (2005) Combining ability and gene action for quality studies in Basmati rice (*Oryza sativa* L.). *Indian Journal of Genetics*, 65(4): 290-292.
- Sharma, S.M., S. Narwal, R. Kumar and S. Dass, (2004). Lin x tester analysis in maize (*Zea mays* L.). *Forage Res.* 30: 28-30.

- Shushay, W., Abrha, H.Z., Zeleke & Gissa, D. (2013). Line \times tester analysis of maize inbred lines for grain yield and yield related traits. *Asian Journal of Plant Science Research* 3(5).
- Sibiya, J., Tongoona, P., Derera, J., Rij, N. (2012). Genetic analysis and genotype by environment (G \times E) for grey leaf spot disease resistance in elite African maize (*Zea mays* L.) germplasm. *Euphytica*, 185: 349–362.
- Singh, R.K., and B.D. Chaudhary. (1979). Biometrical methods in quantitative genetic analysis. *Kalyani publs.* Pp: 127-223.
- Singh, Rajesh; Mani, V.P., Koranga, K.S., Bisht, G.S., Khandelwal, R.S., Bhandari, P. and Pant, S.K. (2004). Identification of additional sources of resistance to *Exserohilum turcicum* in maize (*Zea mays* L.). *SABRAO Journal of Breeding and Genetics*. 36 (1) 45-47.
- Slopeck, S.W. (1989). An improved method of estimating percent leaf area diseased using a 1 to 5 disease scale. *Can. J. Plant Pathol.* 11:381-387.
- Solomonovich, S. Levy Y., and J.K. Pataky (1992). Yield losses in sweet corn hybrids in response to defoliation and infection by *Exserohilum turcicum*. *Phytoparasitica* 20(2):113-121.
- Specia, A. (2013). Kenya food security brief. In United States Agency for International Development Famine Early Warning Systems Network (FEWS NET): USAID.
- Sprague, G.F., and Tatum, L.A. (1942). General Vs Specific Combining ability in single crosses of corn. *Journal of American Maize Society of Agronomy*, 34: 923-932.
- Technow F., Riedelsheimer C., Schrag T.A., Melchinger A.E. (2012). Genomic prediction of hybrid performance in maize with models incorporating dominance and population specific marker effects. *Theor. Appl. Genet.* 125: 1181–1194.

- Troyer A.F. (2006). Adaptedness and heterosis in corn and mule hybrid. *Crop Science* 46: 528-543.
- Uddin, M.S., F. Khatun, S. Ahmed, M.R., Ali and S.A. Bagum, (2006). Heterosis and Combining Ability in Field Corn (*Zea mays* L.). *Bangladesh J. Bot.* **35** (2): 109-116.
- Ullstrup, A.J. (1970). A comparison of monogenic and polygenic resistance to *H. turcicum* in corn. *Phytopathology* 60:1597-1599.
- Vacaro, E., Barbosa-Neto, J.F., Pegoraro, D.G., Nuss, C.N. and Conceicano, L.D.H. (2002). Combining ability of twelve maize populations. *Pesquisa-Brasileira*, 37: 67-72.
- Van, Inghelandt D., Melchinger A.E., Martinant J.-P., Stich B. (2012). Genome-wide association mapping of flowering time and northern corn leaf blight (*Setosphaeria turcica*) resistance in a vast commercial maize germplasm set. *BMC Plant Biol.* 12: 56.
- Van, Raden P. M. 2008. Efficient methods to compute genomic predictions. *J. Dairy Sci.* 91: 4414–4423.
- Venkatesan, M., Anbuselvam, Y., Elangaimannan, R. and Karthikeyan, P. (2007). Combining ability for yield and physical characters in rice. *Oryza*, 44(4): 296-299.
- Vivek, B.S., Kasango, J.S., Chisoro, S. and Magorokosho, C. (2007) Fieldbook: Software for managing maize breeding program: A Cookbook for handling field experiments, data, stocks and pedigree information. CIMMYT, pp 12-30.
- Weber, K.L., Thallman R.M., Keele J.W., Snelling W.M., Bennett G.L. (2012). Accuracy of genomic breeding values in multi-breed beef cattle populations

derived from deregressed breeding values and phenotypes. *J. Anim. Sci.* 10.2527/jas.2011-4586.

Welz, H.G., Geiger H.H. (2000). Genes for resistance to northern corn leaf blight in diverse maize populations. *Plant Breed* 119(1):1-14.


Wisser, R.J., Balint-Kurti P.J., Nelson R.J., (2006). The genetic architecture of disease resistance in maize: a synthesis of published studies. *Phytopathology* 96: 120-129.


Zeeshan, M., Ahsan, M., Arshad, W., Ali, S., Hussain, M., and Khan, M.I. (2013). Estimate of correlated responses for some polygenic parameters in yellow maize (*Zea mays* L.) hybrids. *International Journal of Advanced Research*, 1(5), 24-29.

Zhao, Y., Gowda M., Liu W., Wurschum T., Maurer H.P. (2011). Accuracy of genomic selection in European maize elite breeding populations. *Theor. Appl. Genet.* 124: 769-776.

APPENDICES


Appendix I: NACOSTI Research License


REPUBLIC OF KENYA


NATIONAL COMMISSION FOR
SCIENCE, TECHNOLOGY & INNOVATION

Ref No: **291773** Date of Issue: **22/December/2020**


RESEARCH LICENSE




This is to Certify that Ms. Ferista Wanjiku Ndungu of Kenyatta University, has been licensed to conduct research in Embu, Kakamega, Muranga on the topic: ASSESSED LINE BY TESTER ANALYSIS OF MAIZE INBREDS FOR NORTHERN LEAF BLIGHT AND OTHER YIELD RELATED TRAITS for the period ending : 22/December/2021.

License No: **NACOSTI/P/20/8266**

291773
Applicant Identification Number


Director General
NATIONAL COMMISSION FOR
SCIENCE, TECHNOLOGY &
INNOVATION

Verification QR Code



NOTE: This is a computer generated License. To verify the authenticity of this document, Scan the QR Code using QR scanner application.