Combining Ability Analysis of Maize Inbred Lines and Genotype x Environment Interaction of Hybrids for Grain Yield and Maize Streak Virus Resistance

By

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ABSTRACT

Maize streak virus is the most important leaf disease affecting maize production in Mozambique. The use of resistant varieties is an effective approach to reduce the yield losses caused by the maize streak virus disease. Therefore, it is necessary to identify hybrids that combine resistance to MSV and high yield. The objectives of this study were i) to estimate the combining ability of inbred lines and 30 experimental hybrids developed using a 15 x 2 line x tester mating scheme, ii) to determine genotype x environment (G x E) interaction effects for grain yield and maize streak virus and iii) the relationship between secondary traits and grain yield. This was achieved using a 6 x 6 alpha lattice design with six checks, two replications, in trials conducted in Mozambique and Zimbabwe, in six environments. Artificial inoculation of MSV with leafhoppers (*Cicadulina mbila*) was done in one environment and natural infestation in the other five environments. The trials were planted in Mozambique in three different locations: Umbéluzi (two environments), Chókwè and Sussudenga, and in Zimbabwe in one location (Muzarabani) under two different environments; artificial inoculation of MSV and in non-disease stress conditions. Data were collected using a CIMMYT protocol and statistical analyses were done using ANOVA and REML in GENSTAT 14th edition and PATHSAS macros in SAS 9.3 computer software procedures. Mean yield for the hybrids varied from 2.5 t ha^{-1} to 10 t ha^{-1} with an average of 5.29 t ha^{-1}. No G x E interaction was observed for grain yield implying hybrids ranked similarly at the different locations. There was significant G x E interaction for MSV indicating the different disease pressure at the different sites. The best performing hybrid across the sites was MSV-122T2. None of the checks was in the top 10 performing hybrids. The line x tester interaction effects were highly significant ($P>0.001$) for maize streak virus, while not significant ($P>0.05$) for grain yield of the maize hybrids. This indicated that SCA effects were important for MSV resistance but were less important for conferring grain yield in the hybrids tested. The ear position had the highest heritability of 95.07% and plant height had the lowest of 0.29 %. The highest genotypic coefficient of variation (GCV) for the hybrids was observed for ear position with 93.03%, while phenotypic coefficient of variation (PCV) was highest (266.64%) for ear position. For the hybrids, anthesis days, anthesis silking interval, and ear aspect were all significant and negatively correlated with grain yield. Plant height was significant and positively correlated with grain yield, while maize streak virus showed no significant correlation with grain yield. Plant height had the highest direct effect on grain yield followed by the ear position with the second highest direct effect on grain yield. The hybrids MSV-129T2, LP21/LP19, MSV-62T2 and MSV-135T2 were the most stable for grain yield, qualifying them as candidates for advancement. On the cultivar superiority index, the hybrid MSV122T2 ranked first.

DECLARATION

I **Sheila Juma** declare that**:**

I. The research presented in this thesis, except where otherwise indicated, is my original research.

II. This thesis has not been submitted for any degree or examination any other university.

III. This thesis does not contain other scientists' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from other scientists.

IV. This thesis does not contain other scientists writing, unless specifically acknowledged as being sourced from other scientists. Where other written sources have been quoted, then:

  a) Their words have been re-written but the general information attributed to them has been referenced;

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DEDICATION

I dedicate this dissertation to my late father (Mr Luis Manuel Juma) and my brother (Mr Luis Manuel Juma Junior (Lulu). To my family: my mom (Mrs Matilde), my son (Yanick) and my husband (Celso).

Special dedication is to my daughter (Siyabonga) my little princess.

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LIST OF ABBREVIATIONS

AD	Anthesis date
ANOVA	Analysis of variance
ASI	Anthesis to silking interval
CIMMYT	International Maize and Wheat Improvement Centre
CML	CIMMYT Maize Line
CV	Coefficient of variation
D.F	Degrees of Freedom
DM	Downy mildew
EA	Ear aspect
EH	Ear height
EPO	Ear position
EPP	Ears per plant (no.)
ER	Ear rot
F1	Fist filial generation
FAOSTAT	Food and Agriculture Organization Statistics
GCA	General combining ability
GCV	Genotypic coefficient of variance
GCV	Genotypic coefficient of variation
GGE	Genotype main effect plus genotype x environment interaction
G X E	Genotype x environment interaction
GYG	Grain yield
H^2	Heritability in a broad sense
HC	Husk cover
IIAM	Instituto de Investigação Agrária de Moçambique (Agricultural Research Institute of Mozambique)
ISPG	Instituto superior politécnico de Gaza (Gaza Polytechnic Higher Institute)
IPCA	Interaction principal component axis
LSD	Least significant difference
LXT	Line by tester
MOI	Grain moisture
MSV	Maize streak virus
MUZARABANI MSV	Muzarabani station under artificial inoculation of Maize streak virus
PCV	Phenotypic coefficient of variation
PH	Plant height
RL	Root lodging
SCA	Specific combining ability
SE	Standard error
SL	Stem lodging
SSA	Sub-Saharan Africa
T/ha	Tonnes per hectare
TEX	Grain texture
UMBÉLUZI MSV	Umbéluzi station under natural infestation of maize streak virus

CHAPTER 1 : INTRODUCTION TO DISSERTATION

1.1 General background

Maize (*Zea mays* L.) is the principal crop in Mozambique and the sub-Saharan Africa (SSA) region. It is considered as the staple food crop in most of eastern and southern African countries (Barrow, 1993; DeVries and Toenniessen, 2001). It has multi-purpose uses, ranging from food for humans, feed for livestock, to raw materials for agro-allied industries (Badu-Apraku et al., 2012). In terms of production in the world, it is the third most important crop after wheat and rice with a total of more than 1018 million tonnes produced in 2013 from an area of about 185 million hectares (FAOSTAT, 2017). Maize is adapted to a wide range of environmental conditions and is cultivated in all agro-ecologies of SSA (Denić et al., 2008; Badu-Apraku et al., 2012; Beyene et al., 2015). As indicated in Table 1-1, the major maize producing countries in Africa as of 2013 were South Africa, followed by Nigeria, with Mozambique occupying 16th position in the ranking (FAOSTAT, 2017). However, in terms of yield, Egypt ranked first with an average of 7.8 t ha^{-1}, followed by South Africa with 5.3 t ha^{-1}. Yield in Mozambique is currently very low averaging about 0.7 t ha^{-1} (Table 1-1). The yield is highest in Egypt because they irrigate all the maize, while it is mainly rain-fed in other countries.

Table 1-1. Top 20 maize producing countries in Africa

Country	**Production (Tonnes)**	**Area Harvest (ha)**	**Yield ha^{-1}**
South Africa	14,250,000	2,688,200	5.3
Nigeria	10,790,600	5,849,800	1.8
Egypt	8,059,906	1,039,241	7.8
Ethiopia	7,234,955	2,114,876	3.4
United Republic of Tanzania	6,737,197	4,146,000	1.6
Kenya	3,513,171	2,116,141	1.6
Zambia	3,350,671	1,205,202	2.7
Malawi	2,776,277	1,676,213	1.6
Uganda	2,763,000	1,105,000	2.5
Ghana	1,762,000	1,019,000	1.7
Mali	1,744,026	803,136	2.1
Angola	1,686,869	1,624,186	1.0
Cameroon	1,600,000	799,254	2.0
Zimbabwe	1,456,000	2,283,803	0.6
Burkina Faso	1,433,085	749,935	1.9
Mozambique	1,357,220	1,703,500	0.7
Benin	1,354,344	968,030	1.3
Democratic Republic of the Congo	1,174,427	1,506,884	0.7
Togo	833,044	696,588	1.1
Ivory Coast	680,000	336,836	2.0

(FAOSTAT, 2017)

Furthermore, most of the low yields realised in African countries, including Mozambique are attributed to various production constraints that include drought, low soil fertility, diseases and insect pests. Diseases in particular, pose the biggest threat to the attainment of high yields in Mozambique. Since maize is an important food crop in Mozambique, improving its production is considered to be one of the most important strategies for food security for the majority of the people (Cavane, 2011). Therefore, the main focus of the Mozambique maize breeding programme is on selection for tolerance/resistance to maize streak virus (MSV), downy mildew (DM), stem borers, drought and soil infertility (Denić et al., 2007) and high yield performance under tropical lowland conditions.

Maize streak virus (transmitted by leafhoppers of the genus *Cicadulina*) and downy mildew (caused by the *Perenosclerospora sorghi*) are considered as the most important diseases in lowland areas of Mozambique (Denic et al., 2012). These diseases contribute to low yield, affecting about 68% of the population living in rural areas (FAOSTAT, 2017). As a result of low yield, Mozambique relies on maize imports to meet the local demand. Damage to maize from MSV can be insignificant in some years but epidemics of the disease in other years can be devastating.

Development of cultivars, which are resistant to the MSV, is the most economically viable approach to improve maize production and reduce yield losses due to this disease. In Mozambique, potential inbred lines with some levels of resistance to MSV have been developed. However, their combining ability is unknown, yet this forms the basis of selecting suitable parents for use in the production of resistant hybrid varieties. Information on the combining ability of the inbred lines is an essential and critical factor in this regard. Studies on combining ability will provide information that is useful in the breeding for resistance to MSV, since the maize breeding programme in Mozambique is targeting development of hybrid varieties. Therefore, the information from combining ability studies can be used to estimate gene action controlling the traits and thus assist the breeders to select the best strategy for improving grain yield and MSV resistance in maize hybrids.

Using genotype x environment (GXE) interaction to determine the stability in yield performance of new genotypes bred for growing in wider or specific target growing environment its helpful for cultivar development and release (Dehghani et al., 2009; Hooyer, 2012; Adu et al., 2013; Kamut et al., 2013). According to Abuali et al. (2014), additive main effects and multiplicative interaction (AMMI) biplot models were able to identify genotypes with large and small GXE interaction on grain yield of inbred lines and F1- hybrids in maize. The genotype, and genotype x environment interaction (GGE) biplot analysis provides visual interpretation of GXE interaction effects on each of the genotypes evaluated. The GGE biplot has the ability to identify areas of adaptations of genotypes through its utility view of which won where pattern of multi-environmental yield trials. It is also a useful tool for visual identification of mega environments within a large target region and identification of discriminating and representative environments (Tonk et al., 2011; Mohammadi and Amri, 2012).

Selection based on secondary traits is also useful for the breeding programme. It is important to understand the relationship between secondary traits and yield because this can help in devising an effective method to achieve high breeding gain in yield. The secondary traits which have been targeted in maize are mainly plant height, number of ears per plant, tassel branches, ear prolificacy, and reduced anthesis-silking interval (Bekavac et al., 2007). Mohammadi et al. (2003) in studies with hybrids and inbred lines concluded that yield is a sum of contributions by several traits having different contributory effects. The efficiency of selection in plant breeding can be improved by the knowledge of association between yield and its component traits and among the component parameters themselves (Bello et al., 2010; Raghu et al., 2011).

Knowledge of heritability and predictability of genetic gains, and the association between grain yield and secondary traits in the base germplasm population is crucial (Maphumulo et al., 2015). The estimation of heritability is useful in developing relevant selection strategies, because it determines the expression of the trait in the next generation.

1.2 Research Goal and Specific objective

1.2.1 Overall Goal

The overall goal of the study was to identify maize hybrid combinations with high yielding potential and high levels of resistance to maize streak virus for potential deployment in the Mozambican lowlands.

1.2.2 Specific Objective

The specific objectives were:

- To estimate the combining ability effects for grain yield and resistance to MSV of 15 selected maize inbred lines and 30 maize hybrids.

- To determine performance of FI hybrids and their particular lines for grain yield performance and MSV resistance
- To study the genotype x environment (G x E) interaction for grain yield and maize streak virus resistance of the hybrids grown in different environments.
- To determine the relationship between secondary traits and grain yield.

1.3 Research Hypotheses

The study tested the following hypotheses:

- The 15 selected maize inbred lines have high combining ability (GCA) for both grain yield and maize streak virus resistance making them suitable parents for use in hybrids;
- Grain yield and levels of resistance to maize streak virus disease of the hybrids are highly affected by the different environmental conditions with implications for hybrid deployment strategy.
- There is a significant genetic gain through selection and relationship between secondary traits and grain yield.

1.4 Dissertation Structure

The specific objectives mentioned were achieved and are addressed in the various chapters that constitute this dissertation. The chapters are divided as follows:

Chapter 1: Introduction to the dissertation

Chapter 2: Literature review

Chapter 3: Materials and methods

Chapter 4: Results

Chapter 5: Discussion

Chapter 6: Conclusions and recommendations

CHAPTER 2 : LITERATURE REVIEW

2.1 Introduction

This literature review covers topics relevant to the research focus to provide the theoretical base for the study. The section covers information on the importance of maize in Mozambique, the biotic constraints that affect maize production with special emphasis on maize streak virus disease and its importance. Combining ability effects for grain yield and MSV resistance in maize including mating designs such as line x tester used to estimate them and the mode of gene action governing inheritance of these traits and implications in plant breeding are covered. The implication of genotype x environment interaction in breeding is discussed to create an important frame of reference for the research study.

2.2 Importance of maize

Maize (*Zea mays* L) is the second major food crop in Mozambique after cassava (FAOSTAT, 2017). Smallholder farmers produce it mostly in central and northern parts of Mozambique. It is grown for home consumption and the surplus is sold to generate income. The southern part of the country obtains its maize supply from the north where production is higher due to availability of rain all year round (Alemu and Van Schalkwyk, 2008). Maize production by the smallholder farming sector in Mozambique accounts for 39% of total arable land over an area of 1.74 million hectares (Denić et al., 2007). However, the average grain yield is less than 1.0 t ha^{-1}, and is characterized by huge fluctuations across the years as shown in Figure 2-1. The trend in maize production in Mozambique shows relative increase of maize harvested area, but declining production per unit area. Therefore, improving maize production is considered to be one of the most important strategies for increasing food security in Mozambique (Cavane, 2011).

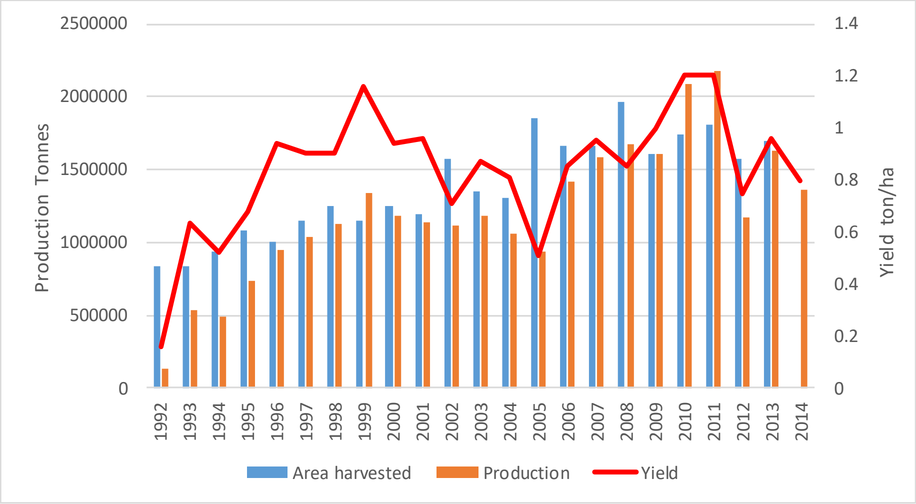

Figure 2-1 Maize production in Mozambique between 1992 and 2014 (FAOSTAT, 2017)

2.3 Biotic constraints affecting maize production in Mozambique

A number of biotic constraints affect maize production in Mozambique. These include diseases (maize streak virus, downy mildew, leaf blights, rusts, grey leaf spot, stem/cob rots) and insect pests (borers and storage pests) (Bosque-Pérez, 2000; Denić et al., 2008). Downy mildew (DM) is a major disease in the tropics, sub-tropics and mid-altitude regions and can cause economic losses as high as 30% (Jeffers et al., 2000). However, the challenge in breeding for host-plant resistance to DM has been the spill-over of resistance across DM pathogens and even variants within species, and also its prolonged and widespread use in an environment favourable for DM disease development (Rashid et al., 2013). Resistance to maize streak virus (MSV) is an essential trait of improved maize varieties in sub-Saharan Africa. Maize streak virus strain A (MSV-A), the causal agent of maize streak disease, is currently one of the most serious biotic threats to food security in sub- Saharan Africa (Monjane et al., 2011).

2.4 Importance of maize streak virus

Although there are numerous viral diseases that affect maize in Africa, maize streak virus remains the most important and widespread disease (Thottappilly et al., 1993). Losses in yield due to MSV are more serious when infection occurs at seedling stage (Efron et al., 1989). Yield reduction in susceptible varieties has been noted to exceed 70% (Bosque-Perez et al., 1998). Maize streak virus disease contributes to poverty throughout the tropical regions in SSA, due to its devastating effects on maize production (Martin et al., 2009). Maize streak virus reduces plant height by 50% and yield losses can reach 100%, especially if plants are infected before seven weeks after planting (Wambugu and Wafula, 1999).

2.5 Symptoms of maize streak virus

Symptoms of MSV can be seen on the leaves. They appear as narrow streaks mainly along the veins of the leaf laminae and are distributed uniformly over the leaf surface. In highly susceptible genotypes, chlorotic streaks may coalesce to form large chlorotic and later necrotic leaf areas, whereas partially or highly resistant genotypes produce few or no streaks. Severe chlorosis occurs in very susceptible maize cultivars, leading to stunted growth and premature death, poor ear formation, reduced seed setting, and heavy yield losses (Mawere et al., 2006). The virus is transmitted by the leafhopper *Cicadulina mbila* (Welz et al., 1998; Magenya et al., 2008).The disease is naturally erratic like most virus diseases (Efron et al., 1989). Maize streak virus is transmitted into the phloem sieve tubes of cereal host plants via the leafhopper vector *Cicadulina mbila* (Lucy et al., 1996). The spread of MSV is encouraged by some agricultural production systems such as mono-cropping in rain fed and irrigated conditions. The irrigated winter crop facilitates over-wintering of both the virus and the vectors (Mawere et al., 2006).

2.5.1 Epidemiology of maize streak virus

Maize streak virus disease is endemic to Africa, and has been reported in southern, eastern and western Africa (Wambugu and Wafula, 1999). It occurs in the lowland humid and savanna areas, as well as in the mid-altitude ecological zones. The disease is caused by a geminivirus called maize streak virus (MSV) which occurs across most of Africa (Martin and Shepherd, 2009). Most geminivirus are transmitted by insect vector species under natural conditions (Martin and Rybicki, 2000). According to Martin and Shepherd (2009), epidemics of MSV disease are often erratic and may not be predicted. The presence of susceptible hosts during the early growth stages is an important factor enhancing MSV disease epidemics. The influence of agro-ecological factors are the reason for the distribution of leafhopper vector populations and the viral diseases (Magenya et al., 2008).

2.5.3 Cultural control

Maize streak virus is difficult to control as chemical control cannot eradicate the virus, but only the vector. However, cultural control measures including early planting have been effective. Early planting can result in avoidance of vector build-up later in the season. Other cultural practices include crop rotations with a non-host crop where and when possible to reduce disease incidence, avoiding relay planting of maize, rouging out diseased plants which are important sources of the virus, and intercropping which makes it more difficult for male and female leafhoppers to mate (Wambugu and Wafula, 1999; Mawere et al., 2006).

2.5.4 Breeding for resistance to maize streak virus disease

Resistance to MSV is an essential trait of improved maize varieties in sub-Saharan Africa (Welz et al., 1998). Several techniques have been applied in breeding maize for MSV resistance (Gichuru, 2013). Conventional breeding involves making crosses between selected parent plants that have desirable characteristics such as high yield or maize streak virus resistance. Therefore, identifying inbred lines to be used to develop hybrids with MSV resistance is very important (Gichuru, 2013; Ige et al., 2017). These inbred lines need to be evaluated to determine the genetic variability for MSV resistance that is available. For example, line Oh1V1 shows resistance to a number of viruses (at least 10) and when it was crossed with a susceptible line Oh28, the F_1 and F_2 progeny was either resistant or susceptible to about six viruses with ≥ 95% infection, suggesting resistance to these viruses is largely dominant and additive (Zambrano et al., 2014).

Studies for MSV resistance have been conducted and these studies showed significant differences in the resistance of inbreds and experimental hybrids (Gichuru et al., 2011b; Gandiwa, 2012; Nyaligwa, 2014; Mathew, 2015; Ige et al., 2017). Ige et al. (2017) identified lines including TZEI-7 and TZEI-22 as resistant to MSVD and with good combining ability for grain yield.

2.6 Line x test mating design

Line by tester (L x T) is one of the mating designs that can be used to estimate combining ability and gene action that govern inheritance of traits. It is basically an extension of topcross design in the sense that instead of one tester used in topcross, more than one tester is used under L x T mating design providing progenies that include full-sibs and half-sibs simultaneously (Nduwumuremyi et al., 2013). Line x tester crosses can be used to identify new lines with good specific combining ability in a relatively smaller number of field crosses (Xia et al., 2005). Studies done in Kenya using line x tester helped to identify two new lines that had high general combining ability effects for grain yield and other secondary traits (Ertiro et al., 2017). Using line by tester mating design, good lines and testers that can be used across management conditions can be identified.

2.6.1 Combining ability

Combining ability of inbred lines is the ultimate factor determining future usefulness of the lines for hybrid production. Combining ability initially was a general concept considered collectively for classifying an inbred line relative to performance of its cross (Hallauer et al., 2010). General and specific combing ability reveal the worth of genotypes in hybrid combinations (Mutengwa et al., 2012). General combining ability (GCA) is defined as the average performance of a line in hybrid combinations (Sprague and Tatum, 1942), and specific combining ability (SCA) as those instances in which certain hybrid combinations are either better or poorer than would be expected on the average performance of the parent inbred lines included. In statistics GCA is the main effect of the lines while SCA is their interaction (Olfati et al., 2012). The variance of GCA measures the additive gene action whereas that of SCA measures the non-additive gene actions (Gichuru et al., 2011a; Olfati et al., 2012).

According to Vivek et al. (2010) and Gichuru et al. (2011b), additive effects were predominant for MSV resistance in maize hybrids. A study done by Ige et al. (2017) found that general combining ability (GCA) and specific combining ability (SCA) mean squares were significant for MSVD severity mean score and only SCA for grain yield. The additive gene effect was preponderant for MSVD severity mean score, whereas grain yield was influenced by non-additive gene effect. Seyoum et al. (2016) also found in his study that GCA mean squares due to lines were highly significant for most of the traits, while SCA mean squares were significant for some traits. The higher relative contribution of GCA sum of squares over SCA sum of squares in all studied traits indicated the predominance of additive gene effect in controlling the inheritance of those traits. Ertiro et al. (2017) identified two new lines (L4 and L6), that had high general combining ability effects for grain yield and other secondary traits across three management conditions. These lines can be nominated as candidate inbred testers for evaluating new inbred lines under optimum, managed drought stress and low-nitrogen conditions. Ali et al. (2014a) found in their study that in general there was no relationship between GCA effects of the parents and the SCA effects of the maize single crosses. The study done by Sibiya et al. (2011) found lines A1220-4, N3-2-3-3 and CML488 had negative

GCA effects for *Phaeosphaeria leaf* spot (PLS) disease indicating good combining ability for PLS resistance.

2.7 Heritability

Heritability was originally defined by Lush (1940) as the proportion of phenotypic variance among individuals in a population that is due to heritable genetic effects (Holland et al., 2003).

The heritability reflects the amount of variation which is due to genetic effects (Maphumulo et al., 2015). Higher values of heritability and genetic advance indicate that selection of high yielding maize genotypes can be helpful to improve maize yield (Ali et al., 2014b). It is also the key parameter which determines the efficiency of a breeding programme (Nzuve et al., 2014). Ertiro et al. (2017) found highest heritability no stress in the sites compared with the stress sites. Low environmental influence contributes to high heritability, and thus is useful in predicting gain under selection (Begum et al., 2016).

2.8 Genotype x environment interaction

Genotype by environment (G x E) interaction is the differential genotype expression across environments. G x E interaction is the major element in determining many key aspects of a breeding programme including whether to aim for wide or specific adaption, choice of locations for selection, and whether selection in early generations is conducted in stressed or stress-free environments (Kempton and Fox, 1997). G x E interaction is considered quantitative if the ranking of genotypes does not change from one environment to another, that is, if the differential response of one genotype compared with another is a matter of scale, and qualitative in which genotypes change rank and is considered less important to the breeders (Romagosa and Fox, 1993). Studies done in Kenya on G x E found significant differences for genotype, environment and G x E interaction mean squares for grain yield in seven drought-tolerant inbred lines crossed with seven single-cross testers from complimentary heterotic group (Ertiro et al., 2017). This indicated that the performances of the hybrids was influenced by the environment (Mary, 2016).

2.8.1 Stability and adaptability analysis

One of the main reasons for growing genotypes in a wide range of environments is to estimate their stability (Freeman, 1973). Becker (1981) defined stability in two ways; (i) biological stability where genotypes perform constantly in different environments and is assessed by genotypic variance across environments and (ii) agronomic stability which is determined by a genotype's ability to respond to improved conditions. Breeders and farmers desire a stable genotype in different environmental conditions and that has the lowest probability of producing yield less than some minimally acceptable value (Kempton and Fox, 1997). Studies done by Gichuru et al. (2016) identified hybrids, with high yield with desirable performance in two different mega-environments, which is desirable by the breeders (Golparvar, 2013). Studies to assess the stability of the hybrids across major production environments showed highly significant differences for grain yield and identified hybrids that were high yielding and stable (Kamut et al., 2013; Boshev et al., 2014).

2.8.2 Determination of G x E interaction

The most important G x E interaction is the crossover type which implies changes in the ranking of the genotypes across environments, while with non-crossover interaction, genotypes with superior means can be recommended for all environments (Becker and Leon, 1988; Kempton and Fox, 1997). Four statistical procedures that can be used to assess the agronomic stability include analysis of variance (ANOVA) only if the error terms from different environments are homogeneous, simple linear regression using Finlay and Wilkinson (1963) approach, non-parametric methods and multivariate exploration of relationship among sites and among genotypes using additive main effects and multiplicative interaction (AMMI) (Romagosa and Fox, 1993). Genotype and genotype x environment interaction (GGE) biplot analysis is another method used to evaluate hybrid performance and GxE interaction in multi-environment trials (Boshev et al., 2014). Both AMMI and GGE biplot were used to identify the best hybrids and the lines with superior performance. The AMMI model is a powerful tool for estimating genotype environments and GXE interactions components as it compresses the interactions into principal components depending on the amount of interactions that are significant (Babić et al., 2011; Bose et al., 2014). GGE biplot combines tools from several methods such as regression and AMMI in a scatter plot that enables the simultaneous visualization of row and column factors and their underlying interactions (Yan and Tinker, 2006; Ding et al., 2007).

2.8 Correlation, regression and path coefficient analyses

Kwon and Torrie (1964) indicated that genetic correlations for yield and yield contributing traits provide information on the extent and direction of association of plant traits. Path analysis furnishes information of the influence of each contributing trait to yield under drought stress directly as well as indirectly and also enables the breeders to rank the genetic attributes according to their contribution (Dewey and Lu, 1959). Path-coefficient analysis measures the direct influence of one variable on another (Pavlov et al., 2015). Studies by Haider et al.,(2012) reported the magnitude of direct or indirect effects on rice yield responses. Correlations are found where variables have a cause and effect relationship in which one variable is dependent on the other such that a change in the independent variable causes a change in the dependent variable (Bello et al., 2010).

2.9 Summary and conclusion

This literature review has highlighted that maize streak is one of the most important diseases that affect maize production in Mozambique. It results in high yield losses despite its occurrence fluctuating every season. Identifying hybrids with resistance to this disease is one of the biggest challenges to the maize breeding programme in Mozambique. Study of combining ability for grain yield and the influence of GXE interaction are important in identifying suitable environments for each hybrid. Methods such as cultivar superiority index and mean ranks can be used to determine stability of the genotypes.

The literature review identified the following gaps that need to be addressed:

- Combining ability of the MSV resistant inbred lines from Mozambique maize breeding programme has not been evaluated
- It is necessary to identify the performance of the genotypes in different environments and to assess which secondary traits with high heritability can be used for indirect selection of grain yield because the high heritability provides an opportunity for yield improvement.

CHAPTER 3 : MATERIALS AND METHODS

3.1 Introduction

This chapter presents the general materials and procedures that were used to develop the experimental hybrids used in the study. It also presents the evaluation of hybrids that was carried out and outlines the methodologies used for the genetic analyses.

3.2 Germplasm

One elite inbred line LP23 from the Agrarian Research Institute of Mozambique (IIAM), which is susceptible to MSV was crossed to two MSV resistant inbred lines (CML505 and CML509) from the International Centre for Maize and Wheat Improvement (CIMMYT). The F1 progeny from the two populations were selfed to F2. The 118 F3 families were derived by self-pollination from the two F2 populations at Makhathini Research Station in South Africa. These were advanced to F4 in Chókwè under natural infestation by MSV, and only the lines showing resistance to MSV and down mildew were selected. The following season, the F4 progenies were advanced to F5 under high incidence of MSV in Mozambique. The three parental lines (LP23, CML505 and CML509) were included as genetic checks. This allowed simultaneous evaluation for resistance to both MSV and downy mildew under field conditions as both are the most important diseases that affect maize production in Mozambique. A total of 15 F5 lines were selected based on the level of resistance to MSV and were used to create the 30 F1 hybrids following the line x tester mating design using the principal tester lines LP19 and LP21 (Hallauer et al., 2010). Inbred lines LP19 and LP21 are susceptible to MSV (Mafu et al., 2014) and belong to the elite line from maize breeding programme, having high resistance to downy mildew. The parental lines were also evaluated and are listed in Table 3-1. The 30 testcross hybrids used in the study and six check hybrids are presented in Table 3-2. There was not sufficient seed of the parental donors CML505 and CML509 during the preparation of the trial, hence they were not included in the trials. The MSV resistant line CML539 and the susceptible line CML312 were used as inbred line checks.

Table 3-1 Pedigree of maize parental lines used in study

Entry	Name	Pedigree	Origin	Role in crosses
1	MSV-36	MSV CH-15-2-1-4	IIAM	Line
2	MSV-40	MSV CH-15-2-2-4	IIAM	Line
3	MSV-62	MSV CH-22-3-4-1	IIAM	Line
4	MSV-65	MSV CH-22-3-5-1	IIAM	Line
5	MSV-72	MSV CH-24-1-1-3	IIAM	Line
6	MSV-101	MSV CH-34-1-1-3	IIAM	Line
7	MSV-119	MSV CH-39-2-1-3	IIAM	Line
8	MSV-121	MSV CH-39-2-2-2	IIAM	Line
9	MSV-122	MSV CH-39-2-2-3	IIAM	Line
10	MSV-123	MSV CH-39-2-2-4	IIAM	Line
11	MSV-128	MSV CH-39-2-3-3	IIAM	Line
12	MSV-129	MSV CH-39-2-3-4	IIAM	Line
13	MSV-135	MSV CH-43-1-1-3	IIAM	Line
14	MSV-142	MSV CH-51-1-1-3	IIAM	Line
15	MSV-156	MSV CH-54-1-1-1	IIAM	Line
16	CHECK-1	LP19	IIAM	TESTER
17	CHECK-2	LP21	IIAM	TESTER
18	CHECK-3	LP23	IIAM	Line: Founder parent line
19	CHECK-4	CML539	CIMMYT	Line check
20	CHECK-5	CML312	CIMMYT	Line check

Table 3-2 Pedigrees of maize hybrids used in the study

Entry	Name	Pedigree	Origin	Type of hybrid
1	MSV-36T1	MSV CH-15-2-1-4/ LP19	IIAM	SC hybrid
2	MSV-40T1	MSV CH-15-2-2-4/ LP19	IIAM	SC hybrid
3	MSV-62T1	MSV CH-22-3-4-1/ LP19	IIAM	SC hybrid
4	MSV-65T1	MSV CH-22-3-5-1/ LP19	IIAM	SC hybrid
5	MSV-72T1	MSV CH-24-1-1-3/LP19	IIAM	SC hybrid
6	MSV-101T1	MSV CH-34-1-1-3/ LP19	IIAM	SC hybrid
7	MSV-119T1	MSV CH-39-2-1-3/ LP19	IIAM	SC hybrid
8	MSV-121T1	MSV CH-39-2-2-2/LP19	IIAM	SC hybrid
9	MSV-122T1	MSV CH-39-2-2-3/LP19	IIAM	SC hybrid
10	MSV-123T1	MSV CH-39-2-2-4/ LP19	IIAM	SC hybrid
11	MSV-128T1	MSV CH-39-2-3-3/LP19	IIAM	SC hybrid
12	MSV-129T1	MSV CH-39-2-3-4/LP19	IIAM	SC hybrid
13	MSV-135T1	MSV CH-43-1-1-3/ LP19	IIAM	SC hybrid
14	MSV-142T1	MSV CH-51-1-1-3/ LP19	IIAM	SC hybrid
15	MSV-156T1	MSV CH-54-1-1-1/ LP19	IIAM	SC hybrid
16	MSV-36T2	MSV CH-15-2-1-4/LP21	IIAM	SC hybrid
17	MSV-40T2	MSV CH-15-2-2-4/ LP21	IIAM	SC hybrid
18	MSV-62T2	MSV CH-22-3-4-1/ LP21	IIAM	SC hybrid
19	MSV-65T2	MSV CH-22-3-5-1/ LP21	IIAM	SC hybrid
20	MSV-72T2	MSV CH-24-1-1-3/ LP21	IIAM	SC hybrid
21	MSV-101T2	MSV CH-34-1-1-3/ LP21	IIAM	SC hybrid
22	MSV-119T2	MSV CH-39-2-1-3/ LP21	IIAM	SC hybrid
23	MSV-121T2	MSV CH-39-2-2-2/ LP21	IIAM	SC hybrid
24	MSV-122T2	MSV CH-39-2-2-3/ LP21	IIAM	SC hybrid
25	MSV-123T2	MSV CH-39-2-2-4/ LP21	IIAM	SC hybrid
26	MSV-128T2	MSV CH-39-2-3-3/ LP21	IIAM	SC hybrid
27	MSV-129T2	MSV CH-39-2-3-4/ LP21	IIAM	SC hybrid
28	MSV-135T2	MSV CH-43-1-1-3/ LP21	IIAM	SC hybrid
29	MSV-142T2	MSV CH-51-1-1-3/ LP21	IIAM	SC hybrid
30	MSV-156T2	MSV CH-54-1-1-1/ LP21	IIAM	SC hybrid
31	Check-1	Hluvukane	IIAM	TWC hybrid
32	Check-2	SP-01	CIMMYT	TWC hybrid
33	Check-3	PAN53	PANNAR	TWC hybrid
34	Check-4	Molocue	CIMMYT	TWC hybrid
35	Check-5	Pristine-1	CIMMYT	TWC hybrid
36	Check-6	LP21/LP19	IIAM	SC hybrid

[*] SC- single cross, TWC -three way cross

3.3 Description of sites

The testcrosses between lines and testers were made at Umbéluzi, and the F1s planted in four sites, with six environments. All sites in Mozambique, excluding Sussudenga and Zimbabwe had high incidence of MSV and presented different climatic conditions. At Umbéluzi there were two environments established on 29 December 2015 and 10 May 2016 one under low MSV infestation and another with no MSV, at Chókwè there was one environment established on 10 January 2016, and Sussudenga one environment established on 30 December 2015. All these sites are located at the Agriculture Research Stations in Mozambique that are owned and operated by the IIAM. In Zimbabwe, trials were planted on the 20th of April 2016 at the Muzarabani station, which is operated by CIMMYT (Table 3-3).The parental trial was planted in Chókwè for grain yield and at Muzarabani for MSV evaluation and was not evaluated for yield at Muzarabani. The sites description is given in Table 3-3; Umbéluzi (12 masl) and Chókwè (33 masl) represent the tropical lowland environment and Sussudenga (64 masl) is a mid-altitude environment for Mozambique (Fato, 2010). Muzarabani is classified as tropical low land environment (348 masl) based on CIMMYT standards (Vivek et al., 2005). The parental lines were evaluated at two sites; Chókwè under MSV natural infestation and at Muzarabani under maize streak virus artificial inoculation. The average weather parameters of the sites during the growing period of the trials is shown in Figure 3-1.

Table 3-3: Description of the sites

Location	Latitude (S)	Longitude (E)	Altitude (m.a.s.l)	Max (ºC)	Min (ºC)	Rainfall (mm)
Umbéluzi	26º03’S	32º23’E	12	29	23	700
Chókwè	24° 31′ S	33° 0′ E	33	30	17	600
Sussudenga	19° 19.324’ S	33°13.491’E	641	29	14	800
Muzarabani	17°43'26"S	31°1'23"E	348	29	14	800

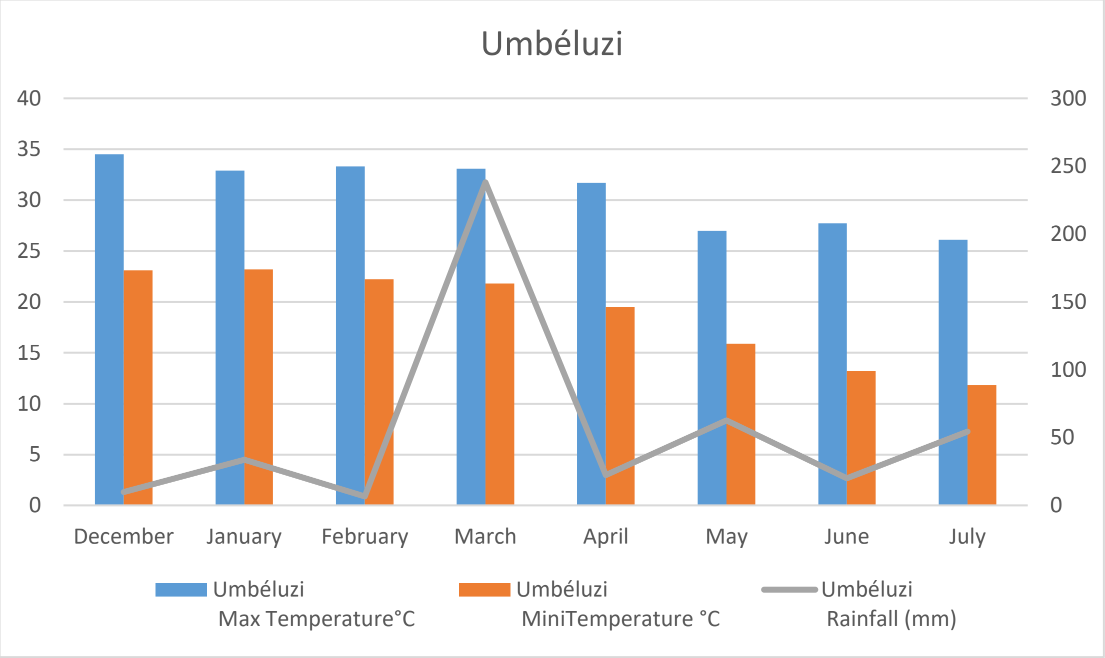

Figure 3-1 Average weather for Umbeluzi, Temperature on the right axis and rainfall on the left axis of the graph

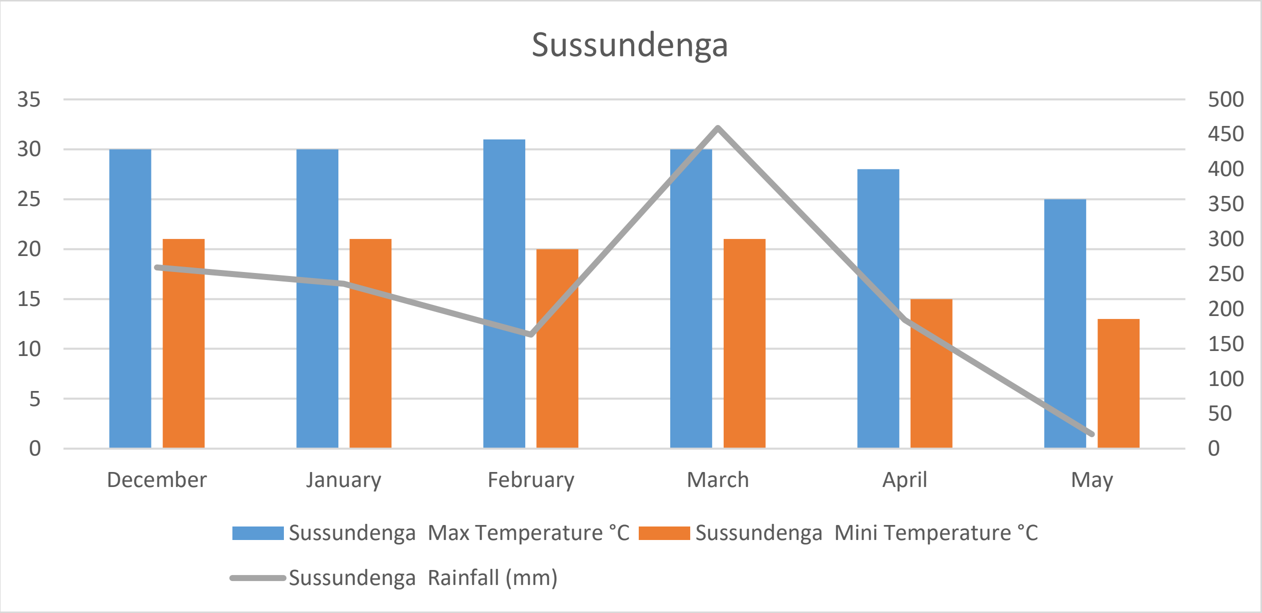

Figure 3-2 Average weather for Sussundenga, Temperature on the right axis and rainfall on the left axis of the graph

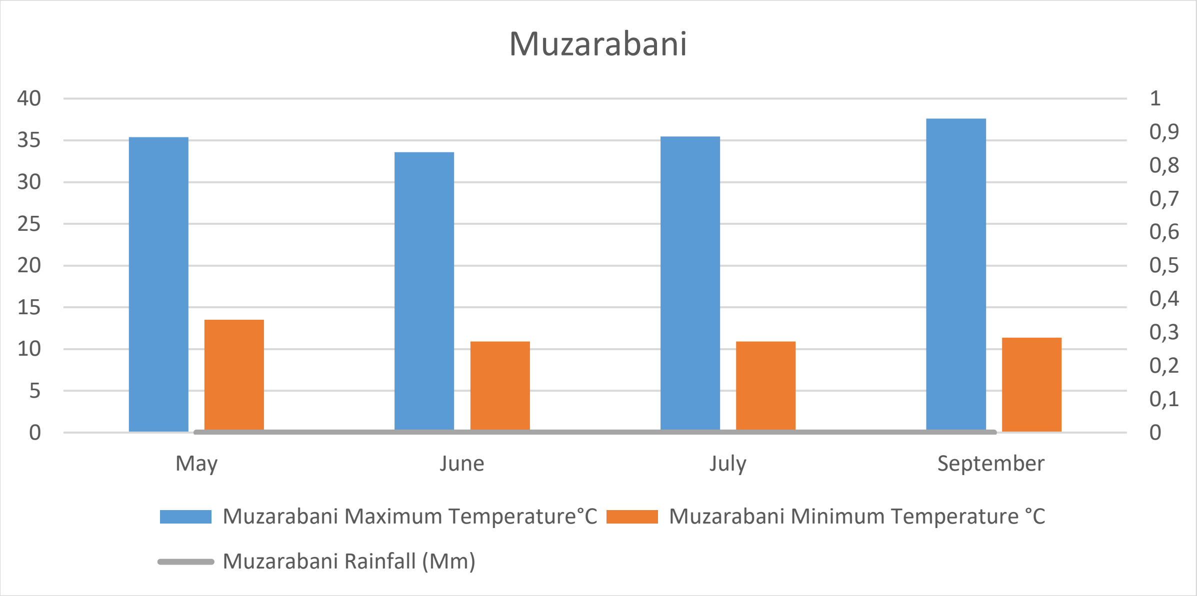

Figure 3-3 Average weather for Muzarabani, Temperature on the right axis and rainfall on the left axis of the graph

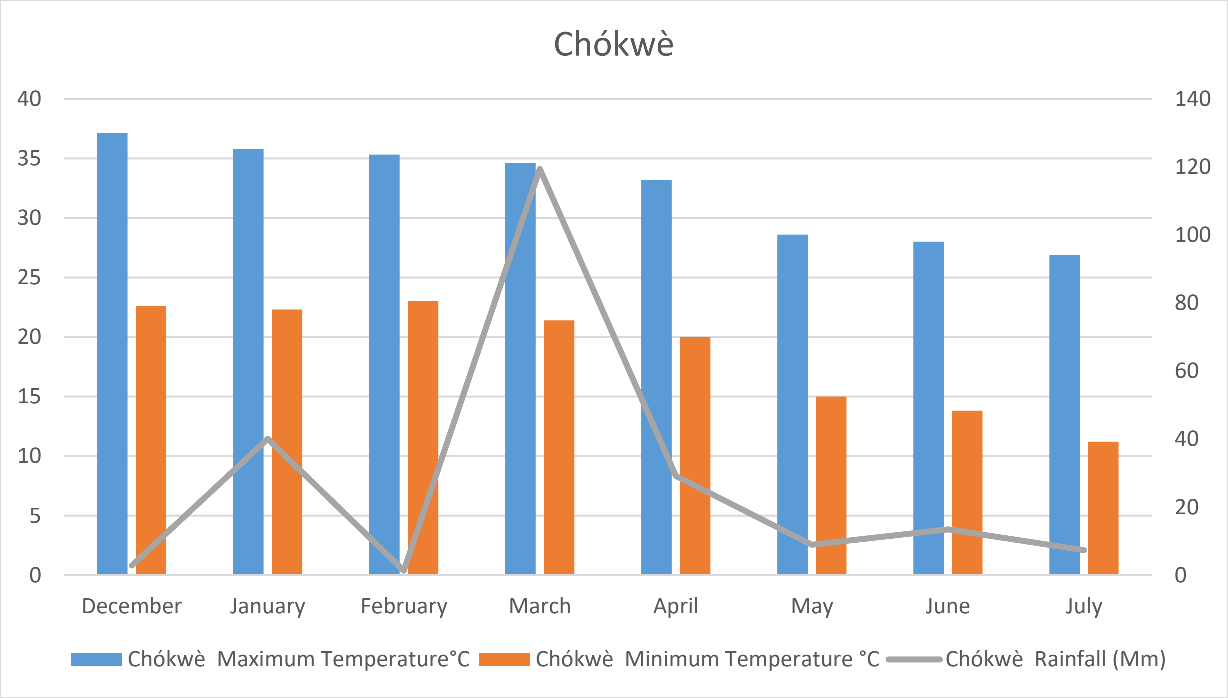

Figure 3-4 Average weather for Chókwè, Temperature on the right axis and rainfall on the left axis of the graph

3.4 Experimental design and field management

The experiment was laid as a 6 x 6 alpha lattice design for hybrid trials and for the parental trial 4 x 5 alpha lattice design with two replications at all sites.

The hybrid and parental trial consisted of two rows per plot at all sites. They were planted with two seeds per station that were later thinned to one plant per station. The plot size was 5 m long with an inter-row and intra-row spacing of 0.80 m and 0.25 m, respectively. This translated to an average plant population of 50 000 plants per hectare in all the six environments. Weeds were controlled manually by hand weeding at all sites in Mozambique and using herbicides, which was complemented by manual hand weeding at Muzarabani. A different commercial variety was used as border at all sites in Mozambique including the hybrid trial in Zimbabwe. The susceptible line CML312 was used as the border for the parental trial. In Mozambique sites, the basal fertiliser NPK (12%-24%-12%) was applied at planting. Topdressing fertiliser urea (46%N) was applied two times, three weeks and eight weeks after planting, respectively. This was consistent with cultural practices in Mozambique.

3.5 Inoculation

Inoculation was done three weeks after planting (Figure 3-5), using leafhoppers *Cicadulina mbila* which are routinely used for field infestations in CIMMYT's breeding nurseries in Zimbabwe using the same methodology as reported by Mafu (2013).

Figure 3-5: Artificial inoculation *Cicadulina mbila*

1: collecting insects using modified vacuum cleaners; **2:** insects anaesthetised with carbon dioxide to ease infestations; **3:** leafhoppers *Cicadulina mbila* before infestion after anaesthetisation; **4:** dispensing leafhoppers in the plant whorl (Photos by Sheila Juma taken at CIMMYT, Harare and Muzarabani, Zimbabwe Date: 5/05/2016).

3.7 Data collection

Data collected included MSV severity scores, days to anthesis and silking, plant and ear heights, total number of plants at harvest, ear aspect, stem lodging, weight of grain, and grain moisture at harvest. All these variables were taken based on the procedures used by CIMMYT (Vivek et al., 2004) and adopted by the National Maize Programme at the Mozambique Agricultural Research Institute (IIAM).

Disease assessment for maize streak virus was done four weeks after planting (1st score). The subsequent scores were taken at five-day intervals using a 1–5 scale with half points as follows: 1 = no symptoms on leaves, 1.5 = very few streaks on leaves, 2 = light streaking on old leaves, gradually decreasing on young leaves, 2.5 = light streaking on old and young leaves, 3 = moderate streaks on old and young leaves, 3.5 = moderate streaks on old and young leaves and slight stunting, 4 = severe streaking on 60% of leaf area, plants stunted, 4.5 = severe streaking on 75% of leaf area, plants severely stunted, 5 = severe streaking on 75% or more of the leaf area (Welz et al., 1998).

Days to anthesis (AD) - recorded as the number of days from planting to the date when 50% of the plants in a plot had tassels shedding pollen.

Days to silking (ASI) -recorded as the number of days from planting to the date when 50% of the plants in a plot had emerged silks.

Plant and ear height (PH and EH) –were measured as height between the base of a plant to the insertion of the first tassel branch and of the top ear of the same plant.

Husk cover (HC) –recorded when ears were fully developed and husk leaves drying out (1–3 weeks before harvest.

Stalk lodging (SL or RL)- recorded as the number of plant stalks broken below the ear.

Grain yield (GYG) – was assessed using shelled grain weight per plot adjusted to 12.5% grain moisture and converted to tons per hectare. The conversion of grain yield to grain moisture-standardized yield was done using the formula:

Yield (at 12.5% grain moisture) kg = Grain yield kg × (100 – actual grain moisture %) / 87.5.

Ear aspect (EA) –that is the general appearance of all ears in the plot, was recorded using a score of 1–5. Factors considered were ear size, grain filling, disease and insect damage. The scale was relative for a given trial, so that: 1 = best, 3 = average, 5 = poorest ear aspect.

Grain hardness (TEX) – that is the grain texture was recorded using a score of 1–5, where 1 = very flint, 5 = very dent.

Moisture percentage (MOI) – that is grain moisture content measured using a moisture tester at harvest. Grains were sampled from a minimum of five representative ears, by either breaking the ears in half or sampling rows at the centre of each ear.

3.8 Data analysis

Analyses of variance for single environment and across environment, and regression analysis were carried out in GenStat 14th edition. The path coefficient analyses and correlation was carried out in SAS 9.3 (SAS Institute,2002) computer software.

3.8.1 Frequency distribution and mean ranking

The means of hybrids were generated using GenStat 14th edition. Entries were ranked in descending order according to the mean grain yield. Frequency histograms were generated for a selected set of traits.

3.8.2 Line x tester analysis

3.8.2.1 Analysis of variance

The entries and sites were considered fixed effects, while the replications and blocks were taken as random. The variance components were estimated from their respective mean squares (Table 3-4 and Table 3-5) as shown in the linear model for the line x tester mating design was be expressed as:

$Y_{ijkl} = \mu + a_l + r_{kl} + b_{mkl} + g_i + g_j + s_{ij} + (ag)_{il} + (ag)_{jl} + (as)_{ijl} + \varepsilon_{ijklm}$, [Equation 3-1]

Where Y_{ijkl} =observed value from each site

- Y_{ijkl} is the observed value from each experimental unit;
- μ is the mean of the population
- a_l is the site effect
- r_{kl} is the effect of replication within a site
- b_{mkl} is block effect within each replication within each site
- g_i is general combining ability (GCA) for the i^{th} parental line
- g_j is the GCA effect of j^{th} tester;
- s_{ij} is the specific combining ability (SCA) for the ij^{th} F1 hybrid
- $(ag)_{il}$ is the interaction effect of i^{th} line and l^{th} site
- $(ag)_{jl}$ is the interaction effect of j^{th} tester and l^{th} site
- $(as)_{ijl}$ is the interaction effect of the i^{th} hybrid and l^{th} the site
- ε_{ijklm} the residual effect

Table 3-4: The skeleton ANOVA and expected mean squares for line x tester mating design

Source	**DF**	**Mean Square**	**Expected MS**
Env	s-1		$\sigma^2e + \sigma^2\, b(r*s) + stl\, \sigma^2r(s) + tlr\, \sigma^2s$
Env/Rep	s(r-1)		$\sigma 2e + \sigma^2\, b(r*s) + stl\, \sigma^2r(s)$
Env.Rep.Blk	b-1		$\sigma^2e + \sigma^2b(r*s)$
Line	l-1	MSl	$\sigma^2e + rt\, \sigma^2sl + str\, \sigma^2l$
Tester	t-1	MSt	$\sigma^2e + rl\, \sigma^2st + sr\, \sigma^2lt$
Line ×Tester	(l-1) (t-1)	MSlt	$\sigma^2e + r\, \sigma^2stl + rs\, \sigma^2lt$
Site ×Testcross	(s-1) (h-1)	MSsh	$\sigma^2e + r\, \sigma^2sh$
Site ×Line	(s-1) (l-1)	MSsl	$\sigma^2e + rt\, \sigma^2sl$
Site ×Tester	(s-1) (t-1)	MSst	$\sigma^2e + rl\, \sigma^2st$
Site × Line × Tester	(s-1) (lt-1)	MSslt	$\sigma^2e + r\, \sigma^2stl$
Residual	srtl-1	MSe	σ^2e

Where s=number of sites, r = number of replications, t= number of testers, l =number of lines

Table 3-5: General ANOVA for testcross by sites interaction

Source	**DF**	**Mean Square**	**Expected MS**
Site	a-1		$\sigma^2e + b\, \sigma^2\, (r*a) + h\, \sigma^2\, (r*a) + rh\, \sigma^2a$
Rep/Site	a(r-1)		$\sigma^2e + \sigma^2b(r*a) + h\, \sigma^2r(a)$
Block/ Rep/Site	ar(b – 1)		$\sigma^2e + \sigma^2b(r*a)$
Testcross (TC)	(h-1)	MSh	$\sigma^2e + r\, \sigma^2ha + a\, \sigma^2rH$
Site × TC	(a-1)(h-1)	MSsh	$\sigma^2e + r\, \sigma^2ha$
Residual	a(h-1) (r-1)	MSe	σ^2e

Where a=number of sites, r = number of replications

3.8.2.2 Estimation of combining ability effects

The general combining ability (GCA) effects of the parents and specific combining ability (SCA) effects of hybrids, their corresponding standard error and their mean square were estimated using the line x tester analysis as indicated below:

$GCA_l = \frac{y_l}{rl} - \mu \qquad GCA_t = \frac{y_t}{rt} - \mu$, [Equation 3-2]

Where;

GCA_l and GCA_t = the general combining ability of the l^{th} line and t^{th} tester, Respectively

$y_{l.}$ and y_t = the grand total of the l^{th} line mated with all testers and the t^{th} tester mated.

With all lines, respectively

μ = the grand mean of all crosses in all sites

r = the number of replication

l^{th} = the number of lines

t^{th} = the number of testers

Standard error for general combining ability

SE=$\sqrt{\frac{MSE}{E*T}}$,[Equation 3-3]

Where:

SE= standard error

MSE= error mean square for line

T= number of tester

E= number of environments

Specific combining ability effects were calculated using

$SCA_{ij} = yo - yp$,[Equation 3-4]

Where SCA_{ij} = the specific combining ability effect of ij^{th} cross

yo = observed yield

yp = predicted yield

Standard error for the specific combining ability

SE=$\sqrt{\frac{MSE}{E*r}}$, [Equation 3-5]

Where:

SE= standard error

MSE= error mean square for line x tester

E= number of environments

r= number of replications per environment

3.8.3 Genetic gain

3.8.3.1 Phenotypic and genotypic variances

Genotypic variance $(\delta_g^2) = \frac{[\mathrm{MSg-MSe}]}{\mathrm{r}}$, [Equation 3-6]

Phenotypic variance $\left(\delta_p^2\right) = \delta_g^2 + \delta_e^2$, [Equation 3-7]

Where:
MS_g - genotypic mean squares
MS_e - residual mean squares
r- Number of replications

3.8.3.2 Heritability

The broad-sense heritability was estimated as the ratio of genotypic variance to the phenotypic variance expressed in percentage (Darbeshwar, 2000).

Within environments, $\mathrm{H}^2 = \frac{\delta_g^2}{\delta_p^2}\, x\ 100$, [Equation 3-8]

Across environments $\mathrm{H}^2 = \left[\frac{\sigma^2 \mathrm{g}}{\frac{\sigma^2}{\mathrm{re}} + \frac{\sigma^2 \mathrm{ge}}{\mathrm{e}} + \sigma^2\ \mathrm{g}}\right] \mathrm{x}\ 100$, [Equation 3-9]

H^2 - broad sense heritability
δ^2p -phenotypic variance
δ^2g -genotypic variance
δ^2ge - genotype x environment variance
δ^2 - error variance
r -number of replications
e -number of environments

3.8.3.3 Coefficient of variation

$\mathrm{GCV} = \frac{\sqrt{\sigma^2 \mathrm{g}}}{\mathrm{x}}\ \mathrm{x}\ 100$, [Equation 3-10]

$\mathrm{PCV} = \frac{\sqrt{\sigma^2 \mathrm{p}}}{\mathrm{x}}\ \mathrm{x}\ 100$, [Equation 3-11]

Where:

GCV- Genotypic coefficient of variation

PCV-Phenotypic coefficient of variation

δ^2p -phenotypic variance

δ^2g -genotypic variance

X – General mean of the character

3.8.3.4 Predicted genetic gain

$R = i\sigma_p h^2$, [Equation 3-12]

Where:

i- Efficacy of selection, which is 2.06% at 5% selection intensity

σ_p – Phenotypic standard deviation

H^2 – heritability in a broad sense

3.8.4 Relation between grain yield and secondary traits

To determine the relationship between grain yield and secondary traits three different approaches were used which are correlation, regression and path analyses.

3.8.4.1 Correlation analysis

Correlations were performed in GenStat 14th edition following the method of (Payne et al., 2009) based on Pearson's phenotypic correlation analysis.

3.8.4.2 Regression analysis

On the regression analysis, yield and agronomic traits were treated as response and independent variables, respectively using the model:

$\mathrm{Y} = \propto + \beta\mathrm{X} + \varepsilon$, [Equation 3-13]

Where:

Y – yield response of the genotype (dependent variable)

$\propto$ - yield response when the independent variable X=0

β- rate of change for Y for each unit of X

X – value of the independent variable

ε- the error associated with prediction of Y from X

Regressions with a coefficient of determination less than 10% were considered negligible.

3.8.4.3 Path analysis

The Cramer and Wehner (2000) PATHSAS approach was used to do path analysis in SAS version 9.3 to deduce direct and indirect effects of secondary traits on grain yield of hybrids.

3.8.5 Genotype x environment interaction (GxE)

The additive main effects and multiplicative interaction analysis (AMMI), genotype and genotype x environment interaction analysis, cultivar superiority index and cultivar stability and mean rank analysis models were used for GxE analysis.

3.8.5.1 Additive main effects and multiplicative interaction analysis (AMMI)

The AMMI model was combined with ANOVA into a single model with additive and multi traits, to determine hybrids stability and the equation below was used (Crossa, 1990).

$yij = \mu + G_i + E_j + \sum_{k=1}^{n}(\lambda_k \propto_{tk}\gamma_{fk}) + e_{tj}$, [Equation 3-14]

Where:

yij= is the yield of the ith genotype in the jth environment

μ - is the grand mean

G_i - genotype deviations from the grand mean

E_j - environment deviations from the grand mean

λ_k –Is the Eigen value of the PCA analyses axis k

$\propto_{tk}$–Ggenotype principal component scores for axis k

γ_{fk} – Environment principal component scores for axis k

n- Number of principal components retained in the model

e_{tj} – Random experimental error

3.8.5.2 Cultivar Superiority Index

The genotype performance was analysed based on the model Lin and Binns (1988).

$Pi = \sum_{j}^{n} \ 1 \left(\frac{xij-Mj}{n}\right)^{2}$, [Equation 3-15]

Where:

Pi - mean square between the cultivar yield and the overall yield for each location

X_{ij} - yield of i^{th} genotype grown in j th location

M_j - maximum yield response among all cultivar’s in j^{th} location.

n- number of location

3.8.5.4 Cultivar Stability and Mean Rank Analysis

The model from (Huehn, 1990) was used to determine the cultivar stability and the mean ranking.

$\boldsymbol{S^{3}} = \sum_{\boldsymbol{j}} \left(\frac{\boldsymbol{rij-rt}}{\boldsymbol{ri}}\right)^{\boldsymbol{2}}$, **[**Equation 3-16]

Where:

S^3- nonparametric statistic

r_{ij} – ran of i^{th} genotype j^{h} environment

r_i – mean of ranks overall all environment for i^{th} genotype

CHAPTER 4 : RESULTS

4.1 Introduction

This chapter presents the results obtained from the statistical analysis of data collected in this study.

4.2 General analysis of variance

Table 4-1 shows that the mean squares for grain yield was not significant ($P > 0.05$) amongst the entries, but highly significant ($P \leq 0.001$) for ear position, ear height, husk cover, plant height and grain texture. The mean squares were significant ($P \leq 0.05$) for ear aspect and grain moisture, significant ($P \leq 0.01$) for number of ears per plant. The environment main effects were highly significant ($P \leq 0.001$) for all the traits. The mean squares of interaction of environment effects and entry main effects were not significant ($P > 0.05$) for grain yield, ear aspect, ears per plant, grain moisture and plant height, but significant ($P \leq 0.05$) for ear height, ear position, highly significant ($P \leq 0.001$) for husk cover and significant ($P \leq 0.01$) for grain texture.

The mean squares of maize streak virus and anthesis date were highly significant ($P \leq 0.001$), and variation among entries for anthesis silking interval was not significant ($P > 0.05$) as shown in Table 4-2. The mean squares of interaction of environment with entry was significant ($P \leq 0.01$) for maize streak virus and not significant ($P > 0.05$) for anthesis silk interval and anthesis date. The mean of grain yield and maize streak virus severity score were 5.29 t ha $^{-1}$ and 1.47, respectively. The mean squares for the parental trial in Table 4-2 showed non-significant ($P > 0.05$) differences for grain yield and maize streak virus amongst the lines.

The individual analysis for each site are shown in the appendices (Appendix 4-1 to Appendix 4-6). The mean squares of grain yield at Umbéluzi (Appendix 4-2) were significant ($P \leq 0.05$), while these were not significant ($P > 0.05$) for the rest of the sites. In Muzarabani under MSV artificial infestation, the hybrids were highly significant ($P \leq 0.001$) for maize streak virus trait (Appendix 4-5).

Table 4-1 Mean squares for grain yield and secondary traits for the hybrids across environments

Source	D.F	GYG	EA	EH	EPO	EPP	ER	HC	MOI	PH	TEX	D.F.	MSV	D.F	AD	ASI
Environment	5	595.7***	115.1***	18334.9***	0.1***	0.4***	80.8***	25985.2***	435.3***	52465.6***	3.83***	1	29.4***	3	700.7***	59.4***
Environment/replication	6	15.50	10.9	1075.5	0.00	0.06	14.2	1107.5	3.30	2110.0	0.6	2	0.07	4	30.9	2.3
Environment/replication/block	10	2.64	3.4	346.8	0.00	0.05	14.5	479.7	3.04	408.1	0.4	10	0.07	10	21.3	2.2
Entry	35	1.60	2.3*	611.9***	0.01***	0.06**	12.1	2104.2***	1.5*	610.9***	1.18***	35	0.1***	35	19.6***	1.4
Entry x Environment.	175	1.41	2.1	233.3	0.00	0.03	11.0	463.3***	0.97	330.6	0.27*	35	0.08**	105	8.7	1.7
Residual	197	1.58	1.6	184.7	0.00	0.03	13.7	203.3	0.91	266.2	0.2	60	0.03	129	7.1	1.4
Mean		5.29	2.7	97.5	0.54	1.07	4.5	30.3	15.87	179.8	2.1		1.47		60.1	1.9
%cv		23.78	23.5	13.9	9.27	16.34	129.0	47.0	6.01	9.1	21.1		12.22		4.4	61.4
Se		1.26	1.2	13.6	0.05	0.18	3.7	14.3	0.95	16.3	0.4		0.18		2.7	1.2
LSD		0.87	2.5	11.0	0.04	0.35	4.0	28.2	0.77	13.2	0.4		0.25		4.0	1.2

*, **, ***, level of significance at P ≥0.05, P≥ 0.01 and P≥0.001, respectively, D.F - degrees of freedom, GYG – grain yield, EA- ear aspect ,EH- ear height, EPO- ear position, EPP- ear per plant, ER- ear rot, HC- husk cover, MOI- grain moisture content, PH- plant height, TEX -grain texture, MSV- maize streak virus AD- anthesis days, ASI- anthesis silking interval.

Table 4-2. Mean square of grain yield and secondary traits for the parental trial

Source	D.F	GYG	D.F.	AD	ASI	EA	EH	EPO	EPP	MSV	D.F.	HC	PH	TEX	D.F.	MOI
REP	1	6.4	1	14.4	0.3498	0.4427	129.4	0.001019	0.1222	0.7562	1	202.8	249.92	0.0607	1	11.31
REP.BLK	10	1.7523	6	18.1	1.3263	1.3	182.3	0.01	0.2692	0.1229	6	560.6	425.8	0.3386	6	11.258
ENTRY	35	1.2075	19	9.3	1.6245	0.96	78.38	0.004	0.6161	0.1896	19	1479.2*	285.88**	0.1996	18	2.792
Residual	25	0.9568	13	0.825	0.7612	0.3868	19.01	0.00054	0.7294	0.1614	12	435.4	54.31	0.1507	8	8.959
Mean		0.98183		61.2	1.281	3.6325	46.0355	0.41707	1.1071	1.8375		21.983	110.67	1.46365		15.5875
%CV		13.12		1.48	66.72	17.02	9.51	5.61	75.41	21.86		92.46	6.65	26.56		18.17
Se		0.9782		0.9083	0.8725	0.622	4.36	0.02324	0.854	0.4017		20.87	7.37	0.3882		2.993
LSD		2.015		1.962	1.945	1.387	9.72	0.05182	1.904	0.8679		46.52	16.43	0.8655		7.333

*, **, ***, level of significance at P ≥0.05, P≥ 0.01 and P≥0.001, respectively, D.F - degrees of freedom, GYG – grain yield, AD- anthesis days, ASI- anthesis silking interval, EA- ear aspect, EH- ear height, EPO- ear position, EPP- ear per plant, MSV- maize streak virus, HC- husk cover, PH- plant height, TEX -grain texture, MOI- grain moisture content.

4.3 Frequency distribution

Maize streak virus was not normally distributed, but discontinuous at Umbéluzi, while the distribution was continuous and normal at Muzarabani (Figure 4-1a and b). For grain yield the distribution was discontinuous at Umbéluzi under MSV while it was continuous and negatively skewed at Umbéluzi under no MSV (Fig 4-2a and b). Yield was normally distributed at Chókwè (Figure 4-2c). The grain yield was also normally distributed at Muzarabani (both under MSV and no MSV) and Sussudenga (Figure 4-3a,b,c). For the parental trial, MSV was skewed to the right showing that most of the maize inbred lines were resistant to MSV, while grain yield showed that some lines were outliers (Figure 4-4a,b).

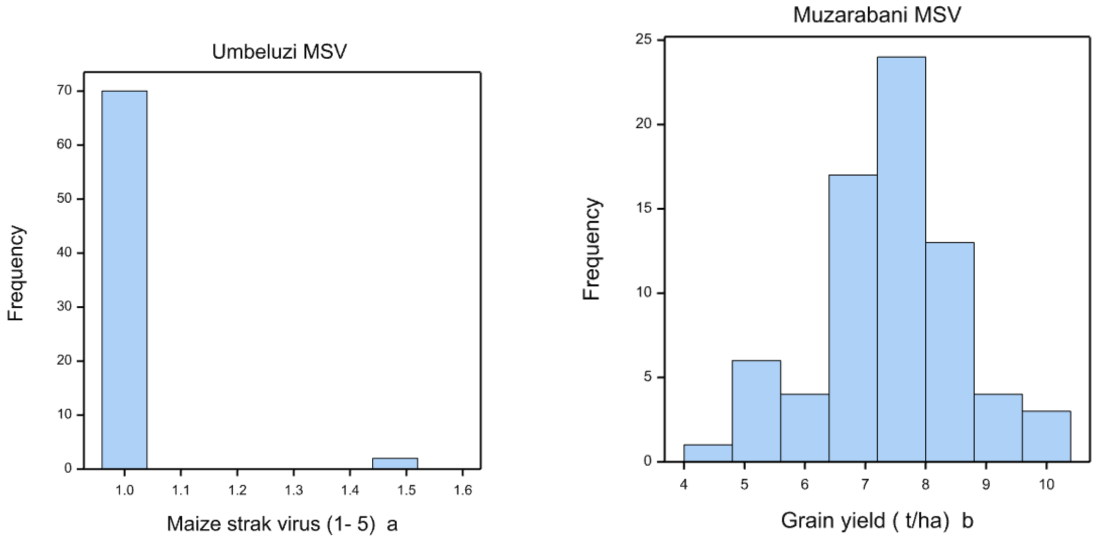

Figure 4-1. Histogram of maize streak virus for Umbeluzi and Muzarabani MSV for hybrids

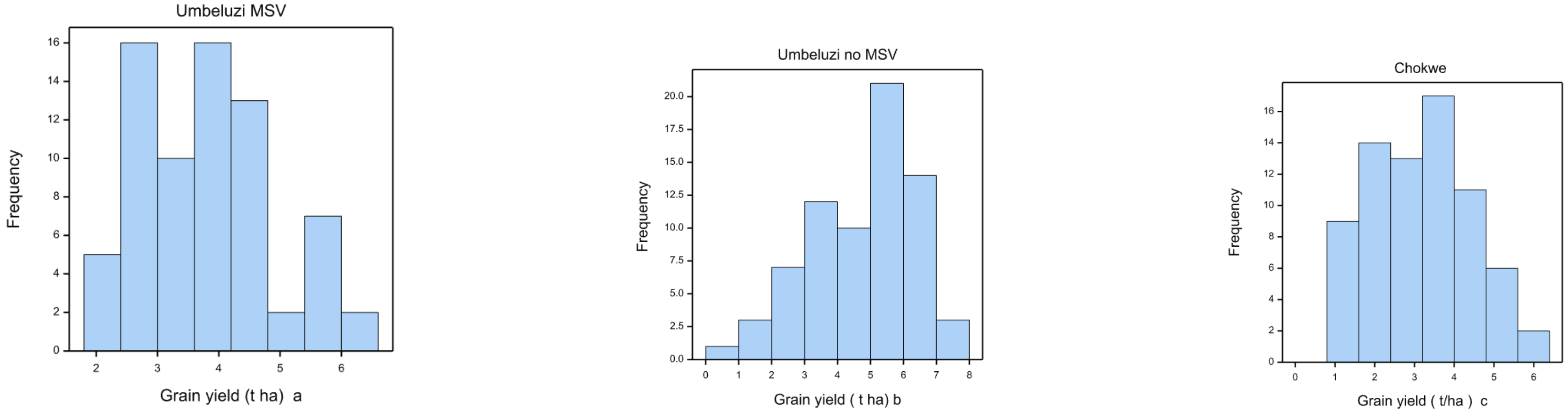

Figure 4-2. Histogram of grain yield for Umbéluzi MSV, Umbéluzi and Chókwè

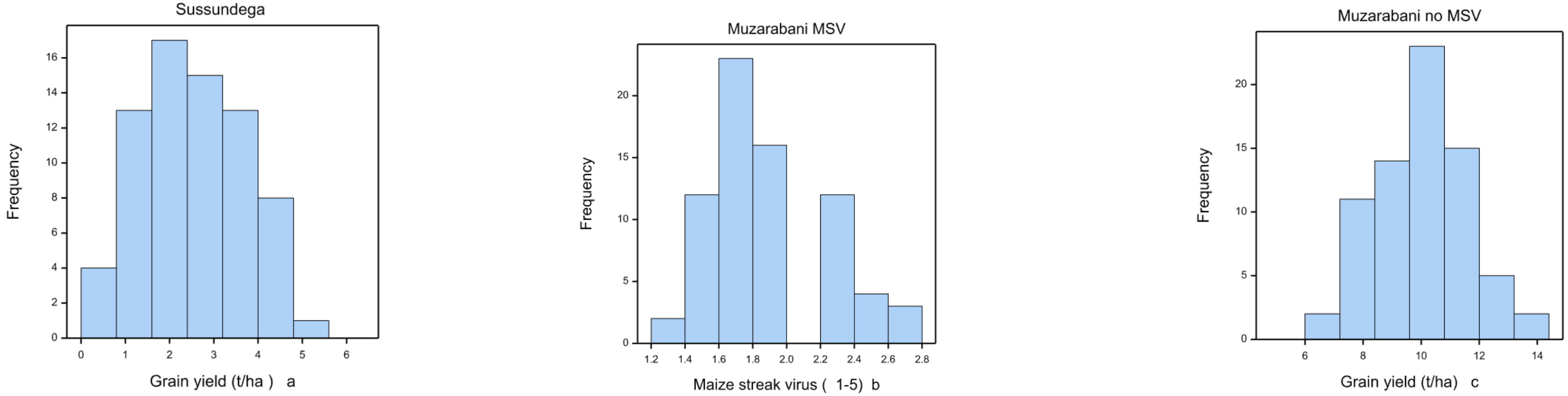

Figure 4-3. Histogram of grain yield for Sussundega, Muzarabani MSV and Muzarabani

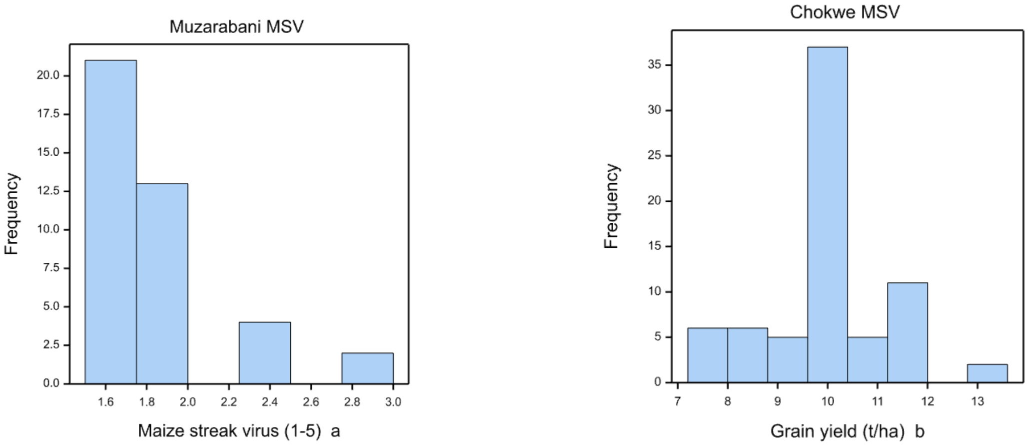

Figure 4-4. Histogram of grain yield and maize streak virus for the parental linesl

4.4 Line x tester analysis

The mean squares for grain yield were only significant ($P \leq 0.001$) for the environment main effects and reps (Table 4-3). For MSV, the mean squares were highly significant ($P \leq 0.001$) for line main effects, interaction of line with tester effects, interactions of environment x tester and environment x line ($P \leq 0.05$) effects (Table 4-4).

Table 4-3. Mean squares of grain yield and secondary traits for the hybrids across six sites

SOURCE	D.F.	GYG	EH	EPO	MOI	D.F.	EPP	HC	D.F.	EA	TEX
ENV	5	505.7***	14269.3***	0.1***	360.2***	5	0.3***	25544.7***	5	24.0***	3.2***
ENV.REP	6	12.1***	945.6***	0.0	2.2*	6	0.01	1074***	6	2.7***	0.3
ENV.REP.BLK	60	3.4***	381.1***	0.0**	1.5*	60	0.1**	609***	60	0.8***	0.3**
LINE	14	1.2	233.1*	0.0*	1.6*	14	0.1**	1635.5***	14	0.6***	1.1***
TESTER	1	0.1	12224.3***	0.2***	0.1	1	0.2*	20111***	1	0.8*	4.4***
LINE.TESTER	14	0.6	188.9	0.0	0.4	14	0.0	498.8**	14	0.2	0.5**
ENV.LINE	70	1.0	200.2*	0.0*	0.9	70	0.0	419***	70	0.5***	0.3*
ENV.TESTER	5	0.6	958.8***	0.0***	0.9	5	0.0	2750.4***	5	1.3***	0.9***
ENV.LINE.TESTER	70	0.8	124.7	0.002	0.71	70	0.0	222.2	70	0.3*	0.2
Residual	112	1.6	133.8	0.002	0.91	113	0.0	182.2	114	0.2	0.2
Mean		5.3	97.0	0.5	15.5		1.0	24.6		2.4	3
%CV		23.5	11.9	8.9	6.0		16.3	41.3		17	20.6
SE		1.2	11.6	0.04	0.9		0.1	13.5		0.4	0.4
LSD		2.5	16.3	0.06	1.9		0.3	18.9		0.6	0.8

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, D.F - degrees of freedom, GYG – grain yield, EH- ear height, EPO- ear position, MOI- grain moisture content, EPP- ear per plant, HC- husk cover, EA- ear aspect, TEX -grain texture.

Table 4-4. Mean squares of maize streak virus (MSV) and secondary traits for the hybrids across four and three sites

Source	D.F.[¥]	AD	ASI	D.F.	ER	RL	D.F.	MSV
ENV	3	671.6***	59.0***	2	77.0***	1239.7***	2	12.1***
ENV.REP	4	23.5	2.3	3	10.3	263.1	2	0.1
ENV.REP.BLK	40	21.9	1.9	30	17.6	133.9	20	0.1***
LINE	14	17.6***	0.7	14	11.9	94.8	14	0.1***
TESTER	1	24.1*	1.2	1	0.15	56.8	1	0.0^{ns}
LINE.TESTER	14	8.5***	1.7	14	14.9	44.7	14	0.1***
ENV.LINE	42	5.0	1.5	28	10.4	0.6	1	0.0
ENV.TESTER	3	6.8	1.1	2	29.2	54.5	14	0.1*
ENV.LINE.TESTER	42	4.5	0.9	28	15.6	37.5	14	0.1***
Residual	76	3.6	1.4	57	10.5	56.9	38	0.0
Mean		60.1	2.1		2.9	5.5		1.9
%CV		3.2	63.6		108.8	124.2		9.9
SE		1.9	1.2		3.2	7.5		0.1
LSD		0.5	0.3		3.9	6.4		0.3

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, NS = non- significant (P>0.05); ¥, D.F - degrees of freedom, AD- anthesis days, ASI- anthesis silking interval, ER- ear rot, RL- root lodging, MSV- maize streak virus.

4.5 Combining ability

Only six lines had GCA effects that were positive and significant (P<0.05-0.001) for grain yield (Table 4-7). These were MSV-65, MSV-72, MSV-122, MSV-129, MSV-135 and MSV-142. None of the lines had a significant GCA effect for MSV, although eight of the lines (MSV-62, MSV-101, MSV-119, MSV-121, MSV-123, MSV-129, MSV-135 and MSV-142) had negative GCAs.

For SCA effects, only two crosses: LP19 x MSV-122 and LP19 x MSV-135 had significant (P< 0.05) effects, but these were negative (Table 4-6). All the crosses between LP19 and the 15 lines had highly significant (P<0.001) SCA effects for maize streak virus, either positive or negative. The negative SCA effects are desirable for MSV resistance and these were displayed by -LP19 crossed to MSV-40, MSV-72, MSV-119, MSV-128, MSV-129 and MSV-156.

Positive SCA effects were significant (P< 0.05) for grain yield for crosses between LP21 and MSV-122 and MSV-135 (Table3-9). Both lines had negative SCA effects for maize streak virus but only MSV-135 was significant (P< 0.001). All the crosses except LP21 x MSV-122 had highly significant SCA effects for MSV. Eight crosses had desirable negative SCA effects for MSV and these were crosses between LP21 with MSV-36, MSV-62, MSV-65, MSV-101, MSV-121, MSV-123, MSV-135 and MSV-142

Table 4-5. General combining ability (GCA) effects of 15 maize lines for grain yield and secondary traits[¥]

Line	GYG [¥] (t ha^{-1})	AD (days)	ASI (days)	EA (score)	EH (m)	EPO (ratio)	EPP (no.)	ER (score)	HC	MOI	MSV	PH (m)	TEX	RL	SL	SB
MSV-36	0.078	-0.49*	0.19*	0.26***	3.53	0.03***	0.04***	1.734**	8.6	-0.16**	0.17	-3.16	0.03*	1.8389	0.067***	-2.9693
MSV-40	-0.120 *	0.34*	0.0933	-0.11***	-4.78	-0.003***	-0.04***	-0.0923	-16.08*	-0.09*	0.0869	-8.1667	-0.30***	5.84*	-0.219***	10.79*
MSV-62	-0.470 ***	-1.26***	-0.1117	-0.17***	-2.5700	0.007***	-0.07***	-1.31*	-9.4813	-0.23***	-0.0041	-6.0667	-0.09***	-3.8051	0.446***	-5.9493
MSV-65	0.150*	-0.88***	-0.15*	0.09***	5.6600	0.008***	0.04***	-0.5863	8.2587	-0.23***	0.0439	7.4333	-0.11***	3.0789	0.794***	-7.2693
MSV-72	0.180*	-1.76***	0.42***	-0.08***	0.4200	0.0094***	-0.02***	-1.09*	-8.6713	0.60***	0.0229	-2.8667	0.32***	0.2759	-0.599***	15.12**
MSV-101	-0.117	0.1213	-0.16*	-0.03	-4.6200	-0.009***	-0.05***	-0.4483	-10.2713	0.27***	-0.1461	-5.2667	-0.20***	0.7169	-0.113***	-4.6493
MSV-119	-0.160*	0.45*	0.43***	0.05***	-2.4400	-0.01***	-0.07***	-0.1053	10.8587	0.08*	-0.1781	-0.7667	0.54***	-4.98*	-0.122***	-0.6893
MSV-121	-0.650***	-0.85***	-0.26**	0.21***	2.3600	0.007***	0.06***	1.35*	13.8087	-0.16**	-0.1681	2.2333	0.039**	-1.1551	-0.154***	-5.0393
MSV-122	0.580***	-0.70**	0.13*	0.04***	5.7500	0.019***	0.01***	0.4067	-10.5213	-0.40***	0.1499	4.5333	-0.46***	-3.3671	-0.101***	-4.3193
MSV-123	-0.350***	2.38***	-0.35***	0.12***	-3.7600	-0.007***	0.09***	-0.6653	-7.4413	0.07	-0.0981	-3.3667	0.038**	0.2309	-0.373***	7.0407
MSV-128	0.109	0.2213	-0.0827	0.12***	-2.0900	-0.014***	-0.04***	-0.1093	1.8187	-0.09*	0.1149	1.4333	0.0011	1.5849	0.206***	5.4207
MSV-129	0.230**	1.88***	-0.1157	-0.14***	1.5600	-0.018***	-0.04***	1.30*	10.0987	0.01	-0.0311	7.4333	0.30***	-3.2241	0.114***	8.57**
MSV-135	0.260**	0.36*	-0.53***	-0.29***	2.7500	-0.015***	-0.01***	-0.0903	1.8087	0.40***	-0.0741	9.7333	-0.021*	2.5699	0.127***	-13.20**
MSV-142	0.410***	0.0313	0.22**	-0.24***	-1.7700	0.001***	-0.02***	-0.5033	3.7087	0.25***	-0.1391	-1.8667	-0.108***	-0.9731	-0.348***	1.7707
MSV-156	-0.097	0.1713	0.23**	0.15***	0.0000	0.002***	0.13***	0.1997	3.50	-0.30***	0.2489	-1.2667	0.031**	1.3759	0.282***	-4.6193
SE	0.3617	0.5515	0.3465	0.1299	3.3392	0.0129	0.0500	0.9359	3.8966	0.2754	0.0426	3.6968	0.1237	2.1793	0.1436	2.7574

*, **, ***, level of significance at $P \leq 0.05$, $P \leq 0.01$ and $P \leq 0.001$, respectively, GYG – grain yield, AD- anthesis days, ASI- anthesis-silking interval, EA- ear aspect ,EH-ear height, EPO- ear position, EPP- ear per plant, ER- ear rot, HC- husk cover, MOI- grain moisture content, MSV- maize streak virus, PH- plant height, TEX -grain texture, RL-root lodging, SL- stem lodging, SB- stem borer.

Table 4-6. SCA effects for grain yield and secondary traits for maize hybrids derived from crosses between line and tester 1 (LP19)

Line	GYG ¥ (t ha^{-1})	AD (days)	ASI (days)	EA (score)	EH (m)	EPO (ratio)	EPP (no.)	ER (score)	HC	MOI	MSV	PH (m)	TEX	RL	SL	SB
MSV-36	0.258	-0.302	0.44**	0.004	5.293	0.025***	0.031***	-2.47*	-3.946	0.083	0.027***	1.333	-0.109***	-4.811	-2.95***	-27.98**
MSV-40	0.134	-2.57***	0.057	-0.037*	1.273	0.0008***	0.0452***	1.120	5.334	-0.077	-0.104***	2.833	-0.109***	-2.210	-2.99***	-12.65*
MSV-62	0.209	0.248	-0.077	-0.005	-1.217	-0.0018***	0.0682***	0.065	0.494	-0.037	0.081***	-1.667	0.169***	-1.341	-2.54***	-16.06*
MSV-65	-0.013	-1.222	-0.054	-0.002	-3.097	-0.023***	-0.0137***	-0.202	4.534	-0.037	0.081***	1.033	-0.342***	3.702	-2.52***	-17.95*
MSV-72	-0.060	0.69*	-0.196	-0.116***	3.363	-0.0083***	-0.0158***	-0.548	-0.796	-0.127	-0.057***	8.833	0.115***	-0.391	-2.62***	-8.950
MSV-101	-0.092	0.258	0.30*	-0.002	-1.747	-0.0028***	0.0362***	-0.094	6.964	0.023	0.060***	-1.967	0.257***	-0.687	-2.60***	-13.13*
MSV-119	-0.150	0.358	-0.598	-0.102***	4.963	0.0223***	-0.023***	-0.229	-7.746	0.20*	-0.035***	1.933	-0.003	-0.165	-2.11***	-22.61**
MSV-121	-0.188	-0.452	-0.070	0.027	-1.337	-0.0033***	0.0352***	0.452	-6.706	0.093	0.055***	-0.067	0.090***	-1.475	-2.03***	-4.800
MSV-122	-0.36*	0.198	-0.158	0.04*	-4.817	-0.0035***	-0.049***	-0.796	2.644	-0.057	0.0004***	-6.967	0.090***	-0.056	-2.62***	-24.71**
MSV-123	0.127	-0.262	-0.007	-0.075**	0.163	-0.01***	-0.039***	1.261	-1.286	0.123	0.059***	4.033	-0.123***	-1.658	-2.86***	-29.55***
MSV-128	0.199	-0.182	0.138	-0.043*	-0.447	-0.0091***	0.0202***	0.877	-3.986	0.093	-0.168***	2.233	0.081***	6.380	-2.85***	-30.03***
MSV-129	0.033	0.81*	0.42**	0.002	2.253	0.005***	0.0243***	0.763	1.134	-0.087	-0.019***	0.833	-0.038*	0.669	-2.86***	-14.96*
MSV-135	-0.40*	1.28*	-0.113	-0.020	-3.047	-0.0051***	-0.048***	0.340	-3.886	0.063	0.017***	-6.467	0.016	1.691	-2.87***	-18.66*
MSV-142	0.111	0.95*	0.048	0.201***	-1.537	0.013***	0.0162***	0.134	-3.246	0.073	0.018***	-5.767	0.040*	1.358	-2.88***	-11.970
MSV-156	0.192	0.088	-0.176	0.116***	-0.737	-0.0021***	-0.092***	-0.750	10.894	-0.30**	-0.0506***	-0.667	-0.107***	-1.058	-2.16***	-25.65**
SE	**0.512**	**0.780**	**0.490**	**0.184**	**4.722**	**0.018**	**0.071**	**1.324**	**5.511**	**0.389**	**0.060**	**5.228**	**0.175**	**3.082**	**0.203**	**3.900**

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, GYG – grain yield, AD- anthesis days, ASI- anthesis-silking interval, EA- ear aspect ,EH- ear height, EPO- ear position, EPP- ear per plant, ER- ear rot, HC- husk cover, MOI- grain moisture content, MSV- maize streak virus, PH- plant height, TEX -grain texture, RL- root lodging, SL- stem lodging, SB- stem borer.

Table 4-7. Specific combining ability (SCA) effects for grain yield (GYG) and secondary traits of maize hybrids derived from crosses of lines with Tester 2 (LP21)

Line	**GYG ¥ (t ha^{-1})**	**AD (days)**	**ASI (days)**	**EA (score)**	**EH (m)**	**EPO (ratio)**	**EPP (no.)**	**ER (score)**	**HC**	**MOI**	**MSV**	**PH (m)**	**TEX**	**RL**	**SL**	**SB**
MSV-36	-0.237	0.298	-0.47*	-0.002	-5.537	-0.026***	-0.03***	2.50*	4.224	-0.067	-0.03***	-1.367	0.109***	5.007	-2.983***	-12.94*
MSV-40	-0.143	2.67***	-0.057	0.05*	-1.777	-0.0025***	-0.05***	-1.196	-5.086	0.083	0.10***	-3.167	0.107***	2.170	-3.028***	2.393
MSV-62	-0.198	-0.212	0.070	0.003	1.393	0.002***	-0.06***	-0.065	-0.776	0.033	-0.07***	1.733	-0.156***	1.224	-2.576***	-1.017
MSV-65	0.011	1.18**	0.051	0.002	3.183	0.023***	0.01***	0.195	-4.546	0.033	-0.07***	-0.967	0.335***	-3.392	-2.559***	-2.907
MSV-72	0.054	-0.70*	0.195	0.12***	-3.207	0.008***	0.01***	0.543	0.674	0.123	0.05***	-8.667	-0.112***	0.361	-2.653***	6.093
MSV-101	0.088	-0.242	-0.31*	0.001	1.883	0.004***	-0.03***	0.094	-6.946	-0.027	-0.05***	2.033	-0.246***	0.652	-2.634***	1.913
MSV-119	0.144	-0.332	0.57**	0.1002***	-4.687	-0.021***	0.02***	0.230	7.344	-0.19*	0.03***	-1.867	0.005	0.147	-2.145***	-7.567
MSV-121	0.189	0.438	0.072	-0.026	1.203	0.003***	-0.03***	-0.462	7.144	-0.107	-0.05***	-0.067	-0.096***	1.536	-2.064***	10.243
MSV-122	0.37*	-0.242	0.170	-0.04*	4.753	0.002***	0.05***	0.834	-2.316	0.053	-0.003	7.233	-0.103***	0.029	-2.655***	-9.667
MSV-123	-0.125	0.268	0.006	0.07**	-0.037	0.010***	0.03***	-1.261	1.174	-0.117	-0.05***	-3.867	0.121***	1.640	-2.891***	-14.51*
MSV-128	-0.191	0.188	-0.133	0.05*	0.583	0.009***	-0.01***	-0.875	3.744	-0.097	0.15***	-2.267	-0.079***	-6.615	-2.889***	-14.99*
MSV-129	-0.031	-0.78*	-0.41*	-0.003	-1.937	-0.005***	-0.02***	-0.729	-1.366	0.073	0.01***	-0.767	0.039*	-0.625	-2.896***	0.083
MSV-135	0.39*	-1.36**	0.119	0.020	3.023	0.005***	0.04***	-0.332	3.754	-0.067	-0.01***	6.333	-0.016	-1.629	-2.903***	-3.617
MSV-142	-0.112	-0.94*	-0.048	-0.202	1.423	-0.014***	-0.01***	-0.140	3.544	-0.077	-0.01***	5.733	-0.045*	-1.480	-2.916***	3.073
MSV-156	-0.204	-0.152	0.201	-0.119***	0.423	0.0009***	0.08***	0.742	-10.956	0.31**	0.04***	0.433	0.105***	1.020	-2.198***	-10.607
SE	0.511534	0.779957	0.490068	0.183757	4.722288	0.018257	0.070711	1.323505	5.510596	0.389444	0.06018	5.228129	0.174881	3.081937	0.20306	3.899573

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, NS = non- significant (P >0.05) ¥, GYG – grain yield, AD- anthesis days, ASI- anthesis silking interval, EA- ear aspect ,EH- ear height, EPO- ear position, EPP- ear per plant, ER- ear rot, HC- husk cover, MOI- grain moisture content, MSV- maize streak virus, PH- plant height, TEX -grain texture, RL- root lodging, SL- stem lodging, SB- stem borer.

4.6 Heritability estimates and genetic gain

The ear position had the highest heritability of 95.07% and plant height the lowest of 0.29% (Table 4-8). The genotypic coefficient of variation (GCV) mean ranged from 0.60% to 93.03%, the highest being for ear position. The phenotypic coefficient of variation (PCV) ranged from 8.50% to 266.64 % and the highest was also for ear position. The Table 4-9 shows that the parental trial had the highest heritability (0.93%) for anthesis days, and highest GCV (461.35%) and PCV (461.36%) for ear position. On individual sites, Umbéluzi MSV had the highest heritability (0.99%), GCV (293.27%) and PCV (293.28%), respectively, for ear position.

Table 4-8. Estimates of variance components,heritability and genetic gains across enviroments for the hybrids

Trait	**δ^2g**	**δ^2e**	**δ^2ge**	**δ^2e**	**δ^2p**	**H^2 %**	**GCV%**	**PCV%**	**R^2**
Grain yield	0.51	188.3	0.45	0.79	190.0	17.15	13.46	260.63	0.15
Ear Aspect	0.74	37.1	0.67	0.78	39.3	23.34	32.46	236.52	0.23
Ear Height	1.66	49.6	0.63	92.35	144.3	0.59	1.32	12.32	0.00
Ear Position	1.98	19.8	0.59	0.00	22.4	95.07	259.83	873.48	1.91
Ear Per Plant	1.00	6.7	0.50	0.02	8.2	88.63	93.03	266.64	1.72
Ear rot	0.44	3.0	0.40	6.84	10.6	2.10	14.85	73.15	0.01
Husk Cover	5.18	63.9	1.14	101.65	171.9	1.67	7.50	43.21	0.00
Grain Moisture Content	0.83	239.7	0.53	0.45	241.5	36.28	5.74	97.94	0.45
Plant Height	1.15	98.5	0.62	133.10	233.4	0.29	0.60	8.50	0.00
Anthesis Days	1.38	49.5	0.61	3.54	55.0	16.06	85.22	506.01	0.13
Anthesis-Silking Interval	0.49	21.4	0.60	0.69	23.2	24.29	1.95	12.34	0.25
Maize streak virus	1.56	458.7	1.25	0.02	461.5	70.9	36.53	251.23	1.23

δ^2g =genotypic variance, δ^2p =phenotypic variance, H^2 =broad sense heritability, PCV =phenotypic coefficient of variance, GCV =genotypic coefficient of variance, h^2=narrow sense.

Table 4-9.Estimates of variance components,heritability and genetic gains of parental lines

Trait	**δ^2g**	**δ^2e**	**δ^2p**	**H^2 %**	**GCV%**	**PCV%**	**R^2**
Grain yield	0.6	0.5	1.1	56.88	80.91	107.28	1.2
Anthesis Days	5.6	0.4	6.0	93.18	3.88	4.02	4.7
Anthesis Silking Interval	1.1	0.4	1.4	73.71	80.64	93.93	1.8
Ear Aspect	1.2	0.2	1.4	86.52	30.67	32.97	2.1
Ear Height	2.1	9.5	11.6	17.82	3.12	7.39	1.2
Ear Position	3.7	0.0	3.7	99.99	461.35	461.36	4.0
Ear Per Plant	0.4	0.4	0.8	53.66	58.70	80.13	1.0
Husk Cover	1.7	217.7	219.4	0.77	41.71	44.48	0.2
Grain Moisture Content	0.2	4.5	4.6	3.36	5.93	67.38	0.1
Maize streak virus	0.6	0.1	0.7	87.92	1.47	4.93	1.5
Plant Height	2.6	27.2	29.8	8.84	55.60	58.68	1.0
Grain Texture	0.7	0.1	0.7	89.78	2.53	13.81	1.6

δ^2g =genotypic variance, δ^2p =phenotypic variance, H^2 =broad sense heritability, PCV =phenotypic coefficient of variance, GCV =genotypic coefficient of variance

5.1 Relationship between grain yield and secondary traits

5.1.1 Correlation

Maize streak virus scores did not show any significant correlations with grain yield across the six environments (Table 4-10). Grain yield was significant (P<0.001-0.05) and positively correlated with plant and ear height, while negatively correlated with anthesis-silk interval, anthesis days and ear aspect. The parental trial had no significant correlations between grain yield and maize streak virus but positive and highly significant correlations for plant and ear height. Positive and highly significant (P<0.001) correlations were observed between grain yield and ear per plant in Umbéluzi and Chókwè (Appendix 4-14 Appendix 4-15). All other correlations between grain yield and ear per plant at Sussudenga (Appendix **4-16**), MSV and grain yield at Muzarabani MSV (Appendix **4-17**) and ear per plant and grain yield at Muzarabani under no MSV were not significant (Appendix **4-18**).

Table 4-10. Correlation of grain yield and secondary traits across six sitesfor the hybrids

Trait	Grain yield	Anthesis Days	Anthesis Silking Interval	Ear Aspect	Ear Height	Ear Position	Ear Per Plant	Husk Cover	Grain Moisture Content	Maize streak virus	Plant Height	Grain Texture
Grain yield	-											
Anthesis Days	-0.27*	-										
Anthesis Silking Interval	-0.24*	-0.01	-									
Ear Aspect	-0.31**	-0.36***	0.12	-								
Ear Height	0.50***	-0.22	-0.38***	-0.24*	-							
Ear Position	0.14	-0.11	-0.13	-0.24*	0.63***	-						
Ear Per Plant	-0.12	0.46***	0.05	-0.15	-0.16	-0.18	-					
Husk Cover	-0.14	-0.12	-0.12	0.49***	-0.30**	-0.55***	0.01	-				
Grain Moisture Content	0.03	0.31**	0.06	-0.19	0.12	0.19	-0.04	-0.30**	-			
Maize streak virus	0.03	-0.06	-0.01	0.13	-0.07	-0.02	0.13	0.17	-0.06	-		
Plant Height	0.56***	-0.21	-0.40***	-0.14	0.84***	0.11	-0.10	0.00	0.03	-0.08	-	
Grain Texture	0.07	0.28*	0.12	-0.31**	0.03	0.14	-0.03	-0.19	0.32**	-0.05	-0.07	-

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively,

Table 4-11 Correlation of grain yield and secondary traits for the parental trial

Traits	Grain yield	Anthesis days	Anthesis Silking interval	Ear Aspect	Ear Height	Ear Position	Ear Per Plant	Husk Cover	Grain Moisture Content	Maize streak Virus	Plant Height	Grain Texture
Grain yield	-											
Anthesis days	0.67***	-										
Anthesis Silking interval	0.12	-0.08	-									
Ear Aspect	0.59***	0.44**	0.18	-								
Ear Height	0.71***	0.46**	0.07	0.60***	-							
Ear Position	0.38*	-0.47	0.03	-0.43**	0.62***	-						
Ear Per Plant	0.26	-0.33*	-0.01	-0.26	0.13	0.00	-					
Husk Cover	0.34*	-0.35*	0.14	-0.04	-0.07	-0.18	0.57***	-				
Grain Moisture Content	-0.13	0.30	0.15	-0.05	-0.10	-0.29	0.02	-0.04	-			
Maize streak Virus	0.20	-0.13	0.04	-0.12	0.18	0.17	0.05	-0.02	-0.10	-		
Plant Height	0.56***	-0.14	0.06	-0.38	0.73***	-0.06	0.17	0.07	0.12	0.06	-	
Grain Texture	0.09	-0.02	-0.01	-0.03	0.10	-0.12	0.04	0.19	-0.09	0.07	0.27	-

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively,

5.1.2 Regression Analysis

Table 4-12 presents the regression analysis across six environments. All traits except ear rot, stem lodging and grain tester were significant (P≤0.001 or P ≤0.05). Anthesis days and ear aspect were the only traits with moderate regressions on yield with the coefficients of determination (R^2) values of 14.9 % and 15.5%, while ear height, ear rot, maize streak virus, plant height and stem borer had R^2 >25%.

Table 4-12. Regression of secondary traits on yield across six environments

	Model		**……………….ß……………………**		
Tait	**F pr**	**R^2 (%)**	**estimate**	**SE**	**t pr**
Root Lodging	0.217	0.7	0.0	0.0	<.001
Grain Moisture Content	0.028	0.9	-0.1	0.1	<.001
Ear Position	0.005	1.6	5.8	2.1	<.001
Husk Cover	<.001	2.9	0.0	0.0	<.001
Anthesis Silking Interval	<.001	3.6	-0.2	0.1	<.001
Ear Per Plant	<.001	7.9	4.4	0.7	<.001
Anthesis Days	<.001	14.9	-0.1	0.0	<.001
Ear Aspect	<.001	15.5	-0.6	0.1	<.001
Stem borer	<.001	28.1	0.0	0.0	<.001
Ear Rot	<.001	34.9	-0.5	0.1	<.001
Ear Height	<.001	42.9	0.1	0.0	<.001
Maize streak virus	<.001	54.7	3.1	0.2	<.001
Plant Height	<.001	54.9	0.1	0.0	<.001
Stem lodging	0.343		-0.3	0.4	<.001
Grain Texture	0.85		0.0	0.2	<.001

R2 (%) =coefficient of determination, β =regression coefficient, SE=standard error, t pr=t test probability, *, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively,

4.7.3 Path coefficient analysis

Plant height had the highest direct effect on grain yield followed by the ear position with the second highest direct effect (Table 4-13). Anthesis days had the highest direct negative effect followed by the ear aspect which had the second highest direct negative effect. The traits with low direct effect on grain were maize streak virus, ear per plant and ear rot. Table 4-14 shows the direct effects for the parental trial; the trait with highest direct effect was ear height. Maize streak virus contributed to positive direct effects on grain yield.

Table 4-13. Direct (diagonal, underlined and bold data) and indirect effects of secondary traits on grain yield across environments for the hybrids

Trait	Anthesis Days	Anthesis Silking Interval	Ear Aspect	Ear Height	Ear Position	Ear Per Plant	Ear Rot	Husk Cover	Grain Moisture Content	Plant Height	Grain Texture	Maize streak virus	**Total**
Anthesis Days	**-0.36**	0.15	0.09	1.13	-0.28	0.00	0.00	0.00	0.02	-0.89	0.05	-0.01	**-0.10**
Anthesis Silking Interval	-0.10	**0.56**	0.02	0.14	0.53	-0.02	-0.01	-0.07	-0.16	-0.77	-0.01	-0.01	**0.11**
Ear Aspect	0.09	-0.03	**-0.37**	0.50	-0.08	0.03	0.02	-0.01	-0.06	-0.52	-0.04	-0.01	**-0.48**
Ear Height	0.10	-0.02	0.04	**-4.27**	2.16	0.00	-0.05	0.00	-0.07	2.22	-0.02	0.04	**0.13**
Ear Position	0.03	0.10	0.01	-3.05	**3.02**	0.01	-0.03	-0.07	-0.09	0.03	-0.03	0.05	**-0.01**
Ear Per Plant	-0.01	-0.08	-0.06	0.05	0.22	**0.15**	0.00	0.07	-0.09	-0.31	-0.07	0.06	**-0.07**
Ear Rot	0.01	-0.02	-0.06	1.34	-0.67	0.00	**0.15**	0.01	0.09	-0.82	0.00	0.01	**0.04**
Husk Cover	0.00	-0.16	0.01	0.05	-0.86	0.04	0.01	**0.26**	-0.05	0.79	0.04	-0.03	**0.10**
Grain Moisture Content	-0.02	-0.22	0.05	0.71	-0.66	-0.03	0.03	-0.03	**0.41**	-0.04	-0.02	-0.04	**0.15**
Plant Height	0.10	-0.14	0.06	-3.01	0.03	-0.02	-0.04	0.06	-0.01	**3.15**	0.00	0.00	**0.21**
Grain Texture	-0.09	-0.03	0.07	0.40	-0.44	-0.05	0.00	0.05	-0.05	0.01	**0.20**	0.01	**0.08**
Maize streak virus	0.03	-0.05	0.04	-1.12	0.90	0.06	0.01	-0.05	-0.09	0.06	0.01	**0.16**	**-0.05**

Table 4-14.Direct (diagonal, underlined and bold data) and indirect effects of secondary traits on grain yield of parental trial

	Anthesis Days	Anthesis Silking Interval	Ear Aspect	Ear Height	Ear Position	Ear Per Plant	Husk Cover	Grain Moisture Content	Maize streak virus	Plant Height	Grain Texture	Total
Anthesis Days	**-0.31**	0.00	-0.10	-0.27	0.10	0.06	-0.12	-0.01	-0.01	0.00	0.00	**-0.67**
Anthesis Silking Interval	0.03	**0.05**	-0.04	0.04	-0.01	0.00	0.05	-0.01	0.00	0.00	0.00	**0.12**
Ear Aspect	-0.14	0.01	**-0.22**	-0.35	0.09	0.04	-0.01	0.00	-0.01	-0.01	0.00	**-0.59**
Ear Height	0.14	0.00	0.13	**0.58**	-0.13	-0.02	-0.02	0.00	0.01	0.02	-0.01	**0.71**
Ear Position	0.15	0.00	0.10	0.36	**-0.20**	0.00	-0.06	0.01	0.01	0.00	0.01	**0.38**
Ear Per Plant	0.10	0.00	0.06	0.07	0.00	**-0.17**	0.19	0.00	0.00	0.00	0.00	**0.26**
Husk Cover	0.11	0.01	0.01	-0.04	0.04	-0.10	**0.33**	0.00	0.00	0.00	-0.01	**0.34**
Grain Moisture Content	-0.09	0.01	0.01	-0.06	0.06	0.00	-0.01	**-0.04**	-0.01	0.00	0.01	**-0.13**
Maize streak virus	0.04	0.00	0.03	0.10	-0.03	-0.01	-0.01	0.00	**0.08**	0.00	-0.01	**0.20**
Plant Height	0.04	0.00	0.08	0.42	0.01	-0.03	0.02	0.00	0.00	**0.02**	-0.02	**0.56**
Grain Texture	0.01	0.00	0.01	0.06	0.03	-0.01	0.06	0.00	0.01	0.01	**-0.08**	**0.09**

*direct=underlined, total=bold

4.8 Genotype x environment interaction

4.8.1 Additive main effects and multiplicative interactions (AMMI)

Genotype by environment interactions were explored further only for maize streak virus which had significant GxE interaction (Table 4-15). AMMI analysis showed highly significant (P>0.001) mean squares for the maize streak virus treatments, environments, interaction main effect, genotypes and IPCA1 across two environments (Table 4-15).

Table 4-15. AMMI ANOVA for maize streak virus across two environments

Source	**Degree freedom**	**Mean square**	**F**	**F pr**
Total	431	0.092		
Treatments	215	0.172	4.91	<0.001
Genotypes	35	0.115	3.29	<0.001
Environments	1	29.385	436.12	<0.001
Block	2	0.067	1.92	0.154
Interactions	35	0.102	2.92	<0.001
IPCA 1	39	0.09	2.56	<0.001
IPCA 2	37	0.002	0.06	1.00
Residuals	41	0.00	0.00	
Error	70	0.035		

4.8.2 Stability and cultivar superiority analysis

The hybrids were ranked according to the mean yield across six environments. The hybrid MSV-129T2 was the most stable with cultivar superiority in eleventh positions while hybrid MSV-119T1 was less stable and in last position (Table 4-16). The check PAN53 was the only check in the top ten most stable hybrids followed by Molocue in 14th position.

Table 4-16.Static stability of the hybrid and cultivar superiority based on the mean yield

Entry	**Cultivar superiority index**	**Rank**	**Static Stability index**	**Rank**
MSV-122T2	0.435	1	10.388	28
MSV-135T2	0.771	2	6.432	4
MSV-36T1	0.884	3	8.202	13
MSV-142T1	0.943	4	10.395	29
MSV-142T2	0.961	5	8.889	20
MSV-129T1	1.014	6	8.898	21
MSV-156T1	1.265	7	7.978	11
MSV-65T1	1.265	8	8.954	22
MSV-122T1	1.268	9	8.736	18
MSV-128T1	1.283	10	13.349	34
MSV-129T2	1.347	11	5.699	1
MSV-65T2	1.424	12	8.031	12
MSV-40T1	1.546	13	8.417	16
MSV-135T1	1.613	14	10.1	26
MSV-119T2	1.629	15	10.162	27
MSV-72T2	1.72	16	11.084	33
MSV-128T2	1.786	17	10.567	31
MSV-101T2	1.847	18	8.804	19
MSV-72T1	1.875	19	7.731	9
SP-01	1.885	20	10.767	32
Pristine-1	1.961	21	9.846	24
MSV-36T2	1.973	22	8.366	15
Hluvukane	1.974	23	9.515	23
MSV-62T1	1.994	24	10.002	25
MSV-123T1	1.998	25	7.257	7
MSV-121T2	2.376	26	13.376	35
MSV-156T2	2.427	27	7.15	6
MSV-101T1	2.468	28	6.511	5
PAN53	2.485	29	7.493	8
MSV-123T2	2.804	30	7.741	10
MSV-40T2	2.823	31	8.688	17
MSV-119T1	3.019	32	15.02	36
LP21/LP19	3.131	33	5.919	2
MSV-62T2	3.244	34	5.978	3
MSV-121T1	3.389	35	10.524	30
Molocue	3.653	36	8.275	14

CHAPTER 5 : DISCUSSION

5.1 Introduction

This chapter presents the discussion of the results obtained in the study.

5.2. Analysis of Variance

The hybrids were not significantly different for grain yield across environments, indicating that, in general, selection based on grain yield would not be possible. This could be because the hybrids were developed from related lines thus there would not be genetic variation. The results are in contrast with findings by other researchers (Badu-Apraku et al., 2011; Gethi et al., 2013; Ali et al., 2014a; Moradi, 2014), who have reported significant hybrid differences for grain yield. However, the individual site analysis revealed that hybrids were significantly different for grain yield in specific sites. The mean squares from the Umbéluzi Research Station showed that hybrid effects were significantly different.

In sharp contrast with yield data, maize streak virus disease data indicated that the hybrids were significantly different across the environments. The disease severity scores recorded for each environment were different indicating differences in disease pressure for both locations. Most of the hybrids showed a resistant reaction to MSV at the Umbéluzi and Muzarabani MSV sites. The resistant x susceptible crosses were resistant meaning that the resistance is controlled by genes with dominant effects. This result agrees with Gichuru et al. (2011a) who reported in their study that the physical expression of the MSV disease showed great differentiation. However, the response of the hybrids to MSV differed across environments, suggesting an uneven transmission of MSV by the vectors to all the hybrids, resulting from possible escapes of some hybrids under natural infestation. This led to higher disease pressure under artificial infestation as compared to natural infestation as shown by the differences in maize streak virus disease severity mean scores between the environments.

The hybrids were significantly different for some other secondary traits such as ear height, ear position, husk cover, plant height, grain texture and anthesis dates. The result agree with Ejigu et al. (2017) who found significant differences for plant height and ear height. This means that hybrids could be selected based on these secondary traits when yield data was not significant. The environment main effects were highly significant for all traits, indicating that multi-location testing is important before hybrids could be selected for advancement and deployment, the result agree with the study done by Gichuru et al. (2016) who report significant differences for grain yield across environment and concluded that the hybrids responded differently to locations. The data from the parental trials showed that the lines were not significantly different for grain yield and maize streak virus resistance. The results disagree with Gichuru et al. (2016) who found in their parental line evaluation that grain yield was significant. These inbred lines could be exploited in hybrid breeding to develop high yielding and MSV resistant varieties.

5.2.2 Combining ability effects

Positive combining ability effects for grain yield potential are desired. Lines with positive GCA effects for yield would confer genes for high yield potential in their hybrid progenies. The line MSV-142 showed positive and highly significant GCA effects. Favourable GCA effects for grain yield were also observed for other lines including MSV-129, MSV-135, MSV-65 and MSV-72. This result agrees with Ertiro et al. (2017) who found lines L4 and L6 with positive GCA for grain yield under all management conditions. These lines could be considered as good general combiners for grain yield potential, which is desired and qualify as high utility lines for the maize breeding programme in Mozambique. The positive GCA effects for the lines MSV-36, MSV-128 were not significant, indicating that these lines would be less useful for the programme, but can be subjected to further observation in future evaluation trials. There were also lines with negative significant GCA effects for grain yield, such as MSV-40 and MSV-119, which were considered to be poor general combiners and would not be considered for use in future crosses.

The negative GCA effects for MSV resistance were desirable for the maize lines under study as they conferred resistance in their hybrids. Negative and highly significant GCA effects were observed for lines MSV-62, MSV-121, MSV-122 and MSV-123.This result agrees with Sibiya et al. (2011) who reported negative and significant ($P \leq 0.01$) GCA effects for disease resistance for parents A1220-4, N3-2-3-3 and CML488 in different environments, whereas parents; CML445, CZL00009, CML205 and CML443 had positive GCA effects in the same environments. All the other lines had non-significant GCA effects for maize streak virus, indicating that they would not be useful parental lines on a breeding programme targeting MSV resistance maize. However, eight lines had negative GCA effects and these were; MSV-62, MSV-101, MSV-119, MSV-121, MSV-123, MSV-129, MSV-135 and MSV-142, which makes them useful to the MSV breeding, programme. They will be used in hybrid development targeting MSV prone environments.

Eight lines crossed with tester 1(LP19) showed positive SCA effects for grain yield and seven lines crossed with tester 2 (LP21) also showed positive SCA effects which is desirable for development of high yielding hybrids. However, these were not significant. Tester LP19 had two lines with significant SCA effects for grain yield, but were negative. Tester LP21 had two crosses with lines MSV-122 and MSV-135 with significant and positive SCA effects. These results agree with those found by other researchers (Sibiya et al., 2012) who reported significant specific combining ability effects associated with reduced disease levels in some hybrids when one parent was resistant, and these may be exploited in developing single cross maize hybrids. The cross between tester LP21 and line MSV-135 had the highest SCA effects for grain yield and highly significant (P<0.001) negative SCA effects for maize streak virus which is desirable. This indicated that both additive and non-additive gene effects were important for the resistance to MSV disease and grain yield in the maize lines used.

Both testers had highly significant (P<0.001) negative or positive SCA effects for maize streak virus. These hybrids would be advanced in the breeding programme and used as female of three way crosses.

5.2.3 Heritability estimates, coefficients of variation and correlation

According to Robinson et al. (1949) the heritability estimates can be categorized as: low, 0 - 30%; moderate, 30 - 60%; and high >60%. The heritability across environments for grain yield was very low (17.15%). This result agrees with findings by other researchers who reported 16.67% to 38% (Asghar and Mehdi, 2010; Abady et al., 2013; Mathew, 2015) heritability estimates for grain yield. These results are in contrast with other reports where very high heritability estimates between 85.4 5 to 99.3% were observed for grain yield (Mahmood et al., 2004; Nadagoud, 2008; Khoza, 2012). This indicate that genetic variation was lower than the environmental variation in the study. Phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the environments, indicating a high influence of the environment on the traits. Similar results were reported by Khoza (2012). The parental trial had moderate heritability estimates of 56% for grain yield. High heritability estimates of 70.9% were observed for maize streak virus in the hybrids and 87% in the parental trial. This indicated that the environments in which the hybrids and the parents were evaluated had less influence on the expression of the trait. This is in agreement with the results reported by Gichuru (2013) who report heritability for MSV and grain yield of 88% and 90% respectively.

Positive correlation between grain yield and plant height and ear height were highly significant across environments indicating strong association between grain yield and both traits. These traits can positively influence grain yield which is in agreement with previous authors (Nazir et al., 2010; Bello et al., 2012). The maize streak virus was negatively correlated with plant and ear height, although not significant. Previous authors reported similar results that maize streak virus reduced significantly the height of the plants (Bosque-Perez et al., 1998; Bua and Chelimo, 2010). Another important trait, which was negatively correlated with the grain yield, was ear per plant, thus contributed to low yield.

The traits with high coefficient of determination ($R^2 \geq 30\%$) were plant height, maize streak virus, ear height, ear rot, the high determination means the model for the experiment was strong and the experimental error was minimum, thus the results are therefore reliable. According to the results from the regression analysis all of traits with high coefficient of determination (≥30%) are important in improving yield. The low R^2 value means the hybrids were not very different for those traits because parents of these hybrids were developed from an F2 Population with narrow genetic base, most of the differences could be attributed to the environment effects as reflected by large CVs or error mean squares.

5.3 Path coefficient analysis

The high direct effects shown by plant height were considered important as the regression of plant height on grain yield was highly significant. This result agrees with (Begum et al., 2016). Path coefficient analysis showed that ear position was second to plant height in contribution to grain yield. Regression analysis also revealed that ear position correlation with grain yield was significant and positive. The ear height had negative direct effect on yield and this agreed with findings by other researchers (Pavlov et al., 2015; Begum et al., 2016).

5.4 Genotype x environment interactions, stability and cultivar superiority analysis

The genotype and genotype x environment interaction effects were not significant ($P>0.05$), for grain yield but only for MSV, indicating high differential hybrid response to MSV across the environments. Variation of the disease pressure, might have contributed immensely to these differences. For example, Muzarabani was under artificial inoculation while at Umbéluzi-MSV the hybrids were under natural infestation.

Superior genotypes have smaller indices (Lin and Binns (1988). The stability analysis showed that the most stable hybrid was MSV-122T2 with 0.43, more stable than MSV-135T2 with 0.77. The hybrid Molocue was the least stable among the 36 performing hybrids with 3.65. Stable performance of maize hybrids is important for recommending hybrids across environments (wide adaptation) (Boshev et al., 2014). The hybrid MSV-122T2, therefore, can be considered for wide adaptation across the six environments it was tested in.

CHAPTER 6 : CONCLUSION AND RECOMMENDATIONS

6.1 Introduction

This chapter summarises main findings from the study and draws conclusion and recommendations for the future study and implications for breeding.

6.2 Conclusion

- The study found significant combining ability effects for resistance to MSV and grain yield of 15 selected maize inbred lines. Lines MSV- 129, MSV-135 and MSV-142 had high GCA for yield and MSV.
- The hybrids MSV-122T2 and MSV-119T1 were most adapted to Muzarabani and Chókwè. Umbéluzi MSV and Muzarabani MSV had hybrids PAN 53 and MSV-135T2 as the most adapted. Sussudenga had Molocue and MSV-40T2 as the most adapted.
- The hybrids MSV-122T2, MSV-135T2, MSV-36T1, MSV-142T1 and MSV-142T2 showed high cultivar superiority. This means that they combined high yield potential and high levels of dynamic stability.
- Plant height had the highest direct effects on grain yield and ear height showed the highest indirect effects to yield determination.

6.3 Recommendation

- The lines that showed high levels of GCA imply that phenotypic selection for MSV in these lines can be effective as this is the component of variation that is transferable to next generations. These lines will be used as parents of new hybrids in Mozambique. These include MSV-129, MSV-135 and MSV-142.
- In general, the hybrids would be deployed to all environments that were represented in this study because the GxE was not significant for yield. Therefore, the study should be repeated at many locations to confirm whether specific adaptation or general adaptation would be important factors in selecting hybrids for deployment in Mozambique.

- The breeders would be encouraged to pay attention to plant height for improvement of these hybrids as it was the trait that was highly and positive correlated with grain yield.

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APPENDICES

Appendix 4-1. Means square for grain yield and secondary trait of Umbéluzi under natural infestation of MSV

Source	D.F.¥	GYG	MSV	AD	ASI	EA	EH	EPO	EPP	HC	MOI	PH	SB	SL	TEX
REP	1	33.60	0.01	6.1	6.7	2.3	3598.4	0.00	0.00	635.20	338	8202.7	0.70	9208.9	1.00
REP.BLK	10	2.10	0.01	51.6	3.5	0.6	497.9	0.00	0.05	755.20	161.6	836.8	0.30	677.6	0.82
ENTRY	35	0.50*	0.01^{ns}	6.0***	2.4**	0.5***	163.8*	0.00***	0.03	1552.20***	44.12	222.8	0.09	116.3	0.78***
Residual	24	0.24	0.01	1.8	0.9	0.1	73.1	0.00	0.02	227.00	27.15	147.9	0.09	81.6	0.23
Mean		3.79	1.01	59.5	2.1	3.5	95.6	0.59	1.15	62.04	17.69	161.7	1.31	18.8	2.23
CV		12.79	7.35	2.3	45.1	10.2	8.9	3.66	11.31	24.28	29.45	7.5	22.40	48.2	21.29
Se		0.48	0.07	1.3	0.9	0.4	8.5	0.02	0.13	15.06	5.21	12.2	0.29	9.0	0.47
LSD		1.01	0.15	2.8	1.9	0.74	17.6	0.04	0.27	31.03	10.73	25.1	0.60	18.6	0.98

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, NS = non- significant (P >0.05);¥,D.F - degrees of freedom, GYG – grain yield, MSV- maize streak virus, AD - anthesis days, ASI- anthesis silking interval, EA- ear aspect, EH- ear height, EPO- ear position, EPP- ear per plant, HC- husk cover, MOI- grain moisture content, PH- plant height ,SB- stem borer, RL- root lodging, SL- stem lodging, TEX -grain texture.

Appendix 4-2. Means square grain yield and secondary traits of Umbéluzi

Source	**D.F.**[¥]	**GYG**	**ASI**	**AD**	**EA**	**EH**	**EPO**	**EPP**	**HC**	**MOI**	**PH**	**RL**	**TEX**
REP	1	10.4	0.125	14.222	4.3	1.02	0.003	0.03139	1352.7	6.6	230.6	1238.5	0.1701
REP.BLK	10	9.3	0.936	23.4	0.26	619.3	0.003	0.2	1499.3	2.7	943.9	345.4	0.43
ENTRY	35	1.076^{ns}	1.454	14.6*	0.16*	243.8***	0.004***	0.03057	897.2***	1.8***	193.3***	110.29	0.33***
Residual	24	1.749	2.105	7.662	0.07847	25.76	0.000457	0.07383	239.7	0.4911	55.84	91.71	0.1001
Mean		4.75	59.89	0.76	1.92	103.37	0.53	1.03	43.49	17.83	193.98	11.97	1.91
%cv		27.82	189.93	4.62	14.56	4.91	4.01	26.36	35.6	3.93	3.85	79.98	16.57
Se		1.323	1.451	2.768	0.2801	5.075	0.02137	0.2717	15.48	0.7008	7.472	9.576	0.3164
LSD			1.451	5.701	0.5769	10.61	0.04466	0.5596	31.89	1.465	15.39	19.72	0.6517

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, NS = non- significant (P >0.05); [¥], D.F - degrees of freedom, GYG – grain yield, ASI- anthesis silking interval, AD- anthesis days, EA- ear aspect, EH- ear height, EPO- ear position, EPP- ear per plant, HC- husk cover, MOI- grain moisture content, PH- plant height ,RL- root lodging, TEX -grain texture.

Appendix 4-3. Means square of grain yield and secondary of Chókwè

Source	D.F.¥	GYG	ASI	AD	EA	EH	EPO	EPP	HC	MOI	PH	TEX
REP	1	19.7	0.056	82.3	0.125	1863.8	0.008939	0.25	2109.6	2.8	2714.6	0.59
REP.BLK	10	4.6	3.056	27.1	0.7	531.5	0.00392	0.01982	893.3	0.846	1541.8	0.18
ENTRY	35	0.9421^{ns}	1.951	13.4*	0.28*	269.9**	0.01*	0.0433	898.2***	0.6411	308.1**	0.46**
Residual	25	0.7285	1.962	6.534	0.1483	87.71	0.002415	0.02658	160.1	0.4753	105.8	0.1451
Mean		3.16	56.76	2.97	2.38	80.64	0.55	0.99	28.35	11.63	144.89	2.47
%cv		27.03	47.13	4.5	16.22	11.61	8.86	16.46	44.63	5.93	7.1	15.45
Se		0.8535	1.401	2.556	0.3851	9.365	0.04915	0.163	12.65	0.6894	10.29	0.381
LSD		1.758	2.885	5.264	0.7932	19.58	0.1027	0.3358	26.45	1.42	21.18	0.7846

*, **, ***, level of significance at $P \leq 0.05$, $P \leq 0.01$ and $P \leq 0.001$, respectively, NS = non- significant ($P > 0.05$); ¥,D.F - degrees of freedom, GYG – grain yield, ASI- anthesis silking interval, AD- anthesis days, EA- ear aspect, EH- ear height, EPO- ear position, EPP- ear per plant, HC- husk cover, MOI- grain moisture content, PH- plant height, TEX -grain texture.

Appendix 4-4. Means square of grain yield and secondary traits of Sussudenga

Source	D.F.¥	GYG	AD	ASI	EA	EH	EPO	EPP	ER	HC	MOI	PH	TEX
REP	1	22.2	0.125	10.889	24.5	712.2	0.004547	0.007517	27.13	2474.6	0.367	1435.4	8
REP.BLK	10	3.6	6.492	1.594	12.128	206.4	0.00395	0.007398	51.3	115.5	1.633	294.9	2.483
ENTRY	35	0.4576^{ns}	3.115	2.127	2.99	135.8	0.003742	0.00406	29.03	67.1	0.837	315	1.467
Residual	24	0.7439	2.712	2.089	2.667	129.1	0.003939	0.004794	20.1	132.3	1.192	171.5	1.733
Mean		2.52	4.88	5.25	6.39	77.15	0.47	1.03	4.02	15.89	18.50	162.79	3.58
%cv		34.17	33.78	27.53	25.56	14.73	13.23	6.72	111.42	72.38	5.9	8.04	36.74
Se		0.8625	1.647	1.445	1.633	11.36	0.06276	0.06924	4.483	11.5	1.092	13.09	1.317
LSD			3.391	2.977	3.363	23.75	0.1312	0.1447	9.371	24.04	2.282	27.37	2.712

*, **, ***, level of significance at $P \leq 0.05$, $P \leq 0.01$ and $P \leq 0.001$, respectively, NS = non- significant ($P > 0.05$); ¥,D.F - degrees of freedom, GYG – grain yield, ASI- anthesis silking interval, AD- anthesis days, EA- ear aspect, EH- ear height, EPO- ear position, EPP- ear per plant, HC- husk cover, MOI- grain moisture content, PH- plant height, TEX -grain texture.

Appendix 4-5. Means square of grain yield and secondary traits Muzarabani site under artificial inoculation of MSV

Source	**D.F.¥**	**GYG**	**MSV**	**EA**	**EH**	**EPO**	**EPP**	**ER**	**HC**	**MOI**	**PH**	**RL**	**TEX**
REP	1	6.3	0.12087	0.5	138.9	0.00248	0.01237	15.199	72.91	1.5022	8.7	71.84	0.0139
REP.BLK	10	1.7523	0.1	0.3611	346.9	0.002515	0.00884	3.291	288.5	0.9522	677.8	25.47	0.2222
ENTRY	35	1.2075^{ns}	0.2***	0.5**	241	0.003031	0.02994	6.915	300.1**	1.4**	237.1	21.74	0.3**
Residual	25	0.9568	0.0452	0.1883	198.2	0.002665	0.02107	4.252	98.98	0.5655	207.5	24.78	0.1239
Mean		7.46	1.92	2.47	111.67	0.55	1.07	2.67	17.93	15.36	201.18	3.50	2.10
%cv		13.12	11.09	17.55	12.61	9.31	13.53	77.27	55.49	4.9	7.16	142.43	16.78
Se		0.9782	0.2126	0.434	14.08	0.05162	0.1452	2.062	9.949	0.752	14.41	4.978	0.352
LSD		2.015	0.4379	0.8938	29	0.1063	0.2989	4.247	20.49	1.549	29.67	10.25	0.7249

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, NS = non- significant (P >0.05);¥,D.F - degrees of freedom, GYG – grain yield, MSV- maize streak virus, EA- ear aspect, EH- ear height, EPO- ear position, EPP- ear per plant, ER- ear rot, HC- husk cover, MOI- grain moisture content, PH- plant height, RL- root lodging, TEX -grain texture.

Appendix 4-6. Means square of grain yield and secondary traits of Muzarabani

Source	**D.F.**$^{¥}$	**GYG**	**EA**	**EH**	**EPO**	**EPP**	**ER**	**MOI**	**PH**	**RL**	**TEX**
REP	1	0.854	0.0313	138.9	0.002095	0.0805	0.229	0.017	68.1	2.11	0.0556
REP.BLK	10	1.401	0.1507	700.6	0.010523	0.0616	2.776	1.175	526.9	34.02	0.1028
ENTRY	35	1.987^{ns}	0.2741	437.5	0.004895	0.01929	2.128	0.707	495.7	45.1	0.2651
Residual	25	3.58	0.2346	330.2	0.004415	0.03337	5.034	1.838	360.1	57.19	0.1856
Mean		9.99	2.26	116.11	0.54	1.17	1.93	15.15	213.75	4.17	2.08
%cv		18.94	21.46	15.65	12.25	15.56	116.5	8.95	8.88	181.25	20.68
SE		1.892	0.4843	18.17	0.06644	0.1827	2.244	1.356	18.98	7.563	0.4308
LSD		3.897	0.9975	37.43	0.1368	0.3762	4.621	2.792	39.08	15.58	0.8872

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, NS = non- significant (P >0.05));¥,D.F - degrees of freedom, GYG – grain yield, EA- ear aspect, EH- ear height, EPO- ear position, EPP- ear per plant, ER- ear rot, HC- husk cover, MOI- grain moisture content, PH- plant height, RL- root lodging, TEX -grain texture.

Appendix 4-7. Estimates of variance components, heritability and genetic gains at Umbéluzi MSV

Trait	**δ^2g**	**δ^2e**	**δ^2p**	**H^2**	**GCV%**	**PCV%**	**R**
Grain yield	1.06	0.12	1.18	0.90	27.22	28.69	2.02
Maize streak virus	0.42	0.00	0.42	0.99	63.66	63.89	1.32
Anthesis Days	1.65	0.90	2.55	0.65	2.16	2.68	2.13
Anthesis Silking Interval	1.36	0.44	1.80	0.76	56.05	64.46	2.09
Ear Aspect	1.90	0.06	1.97	0.97	39.08	39.74	2.79
Ear Height	1.12	36.53	37.65	0.03	1.11	6.42	0.38
Ear Position	3.00	0.00	3.00	1.00	293.27	293.28	3.57
Ear Per Plant	0.77	0.01	0.78	0.99	76.17	76.59	1.80
Husk Cover	3.42	113.50	116.92	0.03	2.98	17.43	0.65
Grain Moisture Content	0.81	13.58	14.39	0.06	5.09	21.44	0.44
Plant Height	0.75	73.95	74.70	0.01	0.54	5.35	0.18
Stem borer	0.51	0.04	0.55	0.92	54.46	56.72	1.41
Stem lodging	0.71	40.80	41.51	0.02	4.50	34.35	0.23
Grain Texture	1.73	0.11	1.85	0.94	59.05	60.94	2.63

δ^2g =genotypic variance, δ^2p =phenotypic variance, H^2 =broad sense heritability, PCV =phenotypic coefficient of variance, GCV =genotypic coefficient of variance

Appendix 4-8.Estimates of variance components, heritability and genetic gains at Umbéluzi

Trait	**δ^2g**	**δ^2e**	**δ^2p**	**H^2**	**GCV%**	**PCV%**	**R**
Grain yield	0.3	0.9	1.2	0.3	11.67	22.87	0.6
Anthesis Days	1.0	3.8	4.8	0.2	1.63	3.65	0.9
Anthesis Silking Interval	0.3	1.1	1.4	0.2	76.93	154.78	0.6
Ear Aspect	1.0	0.0	1.1	1.0	52.49	53.49	2.0
Ear Height	4.7	12.9	17.6	0.3	2.10	4.06	2.3
Ear Position	4.4	0.0	4.4	1.0	393.20	393.21	4.3
Ear Per Plant	0.2	0.0	0.2	0.8	44.14	47.91	0.9
Husk Cover	1.9	119.9	121.7	0.0	3.15	25.37	0.3
Grain Moisture Content	1.8	0.2	2.1	0.9	7.59	8.08	2.6
Plant Height	1.7	27.9	29.7	0.1	0.68	2.81	0.7
Root Lodging	0.6	45.9	46.5	0.0	6.48	56.92	0.2
Grain Texture	1.6	0.1	1.7	1.0	67.23	68.24	2.6

δ^2g =genotypic variance, δ^2p =phenotypic variance, H^2 =broad sense heritability, PCV =phenotypic coefficient of variance, GCV =genotypic coefficient of variance

Appendix 4-9. Estimates of variance components, heritability and genetic gains at Chókwè

Trait	δ^2g	δ^2e	δ^2p	H^2	GCV%	PCV%	R
Grain yield	0.6	0.4	1.0	0.6	25.46	31.84	1.3
Anthesis Days	1.0	3.3	4.3	0.2	1.78	3.65	1.0
Anthesis Silking Interval	0.5	1.0	1.5	0.3	23.72	40.91	0.8
Ear Aspect	0.9	0.1	1.0	0.9	40.91	42.49	1.9
Ear Height	1.5	43.9	45.4	0.0	1.54	8.36	0.5
Ear Position	2.1	0.0	2.1	1.0	259.51	259.59	3.0
Ear Per Plant	0.8	0.0	0.8	1.0	91.10	91.84	1.8
Husk Cover	2.8	80.1	82.9	0.0	5.91	32.10	0.6
Grain Moisture Content	0.7	0.2	0.9	0.7	7.06	8.21	1.5
Plant Height	1.5	52.9	54.4	0.0	0.83	5.09	0.4
Grain Texture	1.6	0.1	1.7	1.0	51.07	52.23	2.5

δ^2g =genotypic variance, δ^2p =phenotypic variance, H^2 =broad sense heritability, PCV =phenotypic coefficient of variance, GCV =genotypic coefficient of variance

Appendix 4-10. Estimates of variance components, heritability and genetic gains at Sussudenga

Trait	**δ^2g**	**δ^2e**	**δ^2p**	**H^2**	**GCV%**	**PCV%**	**R**
Grain yield	0.3	0.4	0.7	0.5	21.97	32.66	0.8
Anthesis Days	0.6	1.4	1.9	0.3	15.55	28.50	0.9
Anthesis Silking Interval	0.5	1.0	1.6	0.3	13.59	23.74	0.8
Ear Aspect	0.6	1.3	1.9	0.3	11.72	21.54	0.8
Ear Height	0.5	64.6	65.1	0.0	0.94	10.46	0.1
Ear Position	0.5	0.0	0.5	1.0	145.32	145.62	1.4
Ear Per Plant	0.4	0.0	0.4	1.0	63.15	63.33	1.3
Ear Rot	0.7	10.1	10.8	0.1	21.12	81.57	0.5
Husk Cover	0.3	66.2	66.4	0.0	3.17	51.29	0.1
Grain Moisture Content	0.4	0.6	0.9	0.4	3.20	5.26	0.7
Plant Height	0.9	85.8	86.7	0.0	0.59	5.72	0.2
Grain Texture	0.4	0.9	1.3	0.3	18.16	31.69	0.8

δ^2g =genotypic variance, δ^2p =phenotypic variance, H^2 =broad sense heritability, PCV =phenotypic coefficient of variance, GCV =genotypic coefficient of variance

Appendix 4-11.Estimates of variance components,heritability and genetic gains at Muzarabani MSV

Trait	δ^2g	δ^2e	δ^2p	H^2	GCV%	PCV%	R
Grain yield	0.63	0.48	1.11	0.57	10.65	14.12	1.23
Maize streak virus	2.21	0.02	2.23	0.99	77.58	77.97	3.05
Ear Aspect	1.33	0.09	1.42	0.93	46.61	48.23	2.29
Ear Height	0.61	99.10	99.71	0.01	0.70	8.94	0.13
Ear Position	0.57	0.00	0.57	1.00	136.04	136.19	1.55
Ear Per Plant	0.71	0.01	0.72	0.99	78.54	79.12	1.72
Ear Rot	0.81	2.13	2.94	0.28	33.79	64.24	0.98
Husk Cover	1.52	49.49	51.01	0.03	6.87	39.84	0.44
Grain Moisture Content	1.24	0.28	1.52	0.81	7.25	8.03	2.07
Plant Height	0.57	103.75	104.32	0.01	0.38	5.08	0.12
Root Lodging	0.44	12.39	12.83	0.03	18.95	102.47	0.25
Grain Texture	1.21	0.06	1.27	0.95	52.46	53.79	2.21

δ^2g =genotypic variance, δ^2p =phenotypic variance, H^2 =broad sense heritability, PCV =phenotypic coefficient of variance, GCV =genotypic coefficient of variance

Appendix 4-12. Estimates of variance components,heritability and genetic gains at Muzarabani

Trait	δ^2g	δ^2e	δ^2p	H^2	GCV%	PCV%	R
Grain yield	0.28	1.79	2.07	0.13	5.27	14.39	0.40
Ear Aspect	0.58	0.12	0.70	0.83	33.87	37.11	1.44
Ear Height	0.66	165.10	165.76	0.00	0.70	11.09	0.11
Ear Position	0.55	0.00	0.56	1.00	137.25	137.52	1.53
Ear Per Plant	0.29	0.02	0.31	0.95	45.81	47.11	1.08
Ear Rot	0.21	2.52	2.73	0.08	23.87	85.77	0.26
Grain Moisture Content	0.19	0.92	1.11	0.17	2.90	6.96	0.38
Plant Height	0.69	180.05	180.74	0.00	0.39	6.29	0.11
Root Lodging	0.39	28.60	28.99	0.01	15.05	129.04	0.15
Grain Texture	0.71	0.09	0.81	0.89	40.56	43.12	1.64

δ^2g =genotypic variance, δ^2p =phenotypic variance, H^2 =broad sense heritability, PCV =phenotypic coefficient of variance, GCV =genotypic coefficient of variance

Appendix 4-13. Correlation of grain yield and secondary triats at Umbeluzi MSV

Trait	Grain yield	Anthesis Silking Interval	Anthesis Days	Ear Height	Ear Position	Ear Per Plant	Husk Cover	Grain Moisture Content	Maize streak virus	Plant Height	
Grain yield	-										
Anthesis Silking Interval	-0.24*	-									
Anthesis Days	-0.27*	-0.0058	-								
Ear Aspect	-0.31**	0.1**	-0.3614	-							
Ear Height	0.5096	-0.3883	-0.2214	-0.2355	-						
Ear Position	0.1372	-0.1258	-0.1071	-0.2401	0.6255	-					
Ear Per Plant	-0.1235	0.045	0.4566	-0.1525	-0.1638	-0.176	-				
Husk Cover	-0.135	-0.1158	-0.1204	0.4909	-0.2961	-0.5551	0.0087	-			
Grain Moisture Content	0.0372	0.0644	0.2882	-0.1646	0.1196	0.1799	-0.0345	-0.2898	-		
Maize streak virus	0.0275^{ns}	-0.0137	-0.0579	0.1268	-0.0673	-0.0238	0.1293	0.1699	-0.0696^{ns}	-	
Plant Height	0.5566	-0.4042	-0.2087	-0.1375	0.8431	0.1127	-0.0991	-0.0001	0.0427	-0.0796	-

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, NS = non- significant (P >0.05)

Appendix 4-14. Correlation of grain yield and secondary traits at Umbeluzi

Trait	Grain yield	Plant Height	Ear Height	Ear Position	Ear Per Plant	Husk Cover	Grain Texture	Grain Moisture Content	Ear Aspect	Root Lodging
Grain yield	-									
Plant Height	0.46***	-								
Ear Height	0.39***	0.81***	-							
Ear Position	0.2244	0.41***	0.87***	-						
Ear Per Plant	0.45***	-0.0756	-0.1076	-0.1144	-					
Husk Cover	0.34*	0.1116	-0.197	-0.42***	0.45***	-				
Grain Texture	0.0395	0.1713	0.1168	0.0313	0.1051	0.0572	-			
Grain Moisture Content	0.0602	0.2043	0.0935	-0.0207	-0.1401	-0.0258	0.39**	-		
Ear Aspect	-0.38***	-0.2087	-0.1394	-0.0426	-0.28*	-0.1157	-0.1364	-0.39**	-	
Root Lodging	-0.2088	-0.25*	-0.1664	-0.0302	0.1853	-0.1411	-0.1217	-0.34*	0.1722	-

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, NS = non- significant (P >0.05)

Appendix 4-15. Correlation of grain yield and secondary traits at Chókwè

Trait	Grain yield	Anthesis Days	Anthesis Silking Interval	Ear Aspect	Ear Height	Ear Position	Ear Per Plant	Husk Cover	Grain Moisture Content	Plant Height	Grain Texture
Grain yield	-										
Anthesis Days	-0.74***	-									
Anthesis Silking Interval	0.1378	-0.37**	-								
Ear Aspect	-0.39***	0.24*	0.2241	-							
Ear Height	0.55***	-0.54***	0.0652	-0.0486	-						
Ear Position	0.0592	-0.2098	0.1192	0.29*	0.71***	-					
Ear Per Plant	0.52***	-0.55***	0.1264	-0.27*	0.2759	-0.0447	-				
Husk Cover	0.42***	-0.51***	0.1156	-0.1022	0.1611	-0.1482	0.40***	-			
Grain Moisture Content	0.3027	-0.34**	0.2135	-0.1718	-0.0077	-0.0945	0.051	0.1135	-		
Plant Height	0.73***	-0.59***	0.0024	-0.3147	0.81***	0.166	0.44***	0.36**	0.0846	-	
Grain Texture	0.0819	-0.0314	0.1929	0.3003	0.2245	0.2609	-0.078	0.0227	0.0761	0.1121	-

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, NS = non- significant (P >0.05)

Appendix 4-16. Correlation of grain yield and secondary traits at Sussundenga

Trait	Grain yield	Ear Aspect	Ear Height	Ear Position	Ear Per Plant	Ear Rot	Husk Cover	Grain Moisture Content	Plant Height	Root Lodging	Grain Texture	Maize streak Virus
Grain yield	-											
Ear Aspect	-0.39***	-										
Ear Height	0.1297	-0.2952	-									
Ear Position	-0.0462	-0.2291	0.79***	-								
Ear Per Plant	-0.1948	0.33**	-0.0416	0.0289	-							
Ear Rot	-0.25***	0.39***	-0.29*	-0.38***	0.1359	-						
Husk Cover	-0.0441	0.42***	-0.33**	-0.37**	0.1243	0.58***	-					
Grain Moisture Content	0.112	-0.1144	0.0623	0.002	-0.0787	-0.1292	-0.0419	-				
Plant Height	0.25*	-0.208	0.72***	0.1626	-0.1072	-0.0312	-0.0988	0.1029	-			
Root Lodging	-0.1695	-0.0489	0.0484	0.025	0.0673	0.1998	-0.079	-0.0628	0.0625	-		
Grain Texture	0.1467	-0.209	0.0983	0.0653	-0.29*	-0.0234	0.0119	-0.0455	0.0915	-0.0129	-	
Maize streak Virus	-0.069	-0.1304	-0.0061	0.0696	0.36**	-0.0349	-0.0713	-0.1598	-0.0891	0.031	-0.1606	-

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, NS = non- significant (P >0.05)

Appendix 4-17. Correlation of grain yield and secondary traits of Muzarabani MSV

Trait	Grain yield	Ear Aspect	Ear Height	Ear Position	Ear Per Plant	Ear Rot	Husk Cover	Grain Moisture Content	Plant Height	Root Lodging	Grain Texture	Maize streak Virus
Grain yield	-											
Ear Aspect	-0.39***	-										
Ear Height	0.1297	-0.2952	-									
Ear Position	-0.0462	-0.2291	0.79***	-								
Ear Per Plant	-0.1948	0.33**	-0.0416	0.0289	-							
Ear Rot	-0.25***	0.39***	-0.29*	-0.38***	0.1359	-						
Husk Cover	-0.0441	0.42***	-0.33**	-0.37**	0.1243	0.58***	-					
Grain Moisture Content	0.112	-0.1144	0.0623	0.002	-0.0787	-0.1292	-0.0419	-				
Plant Height	0.25*	-0.208	0.72***	0.1626	-0.1072	-0.0312	-0.0988	0.1029	-			
Root Lodging	-0.1695	-0.0489	0.0484	0.025	0.0673	0.1998	-0.079	-0.0628	0.0625	-		
Grain Texture	0.1467	-0.209	0.0983	0.0653	-0.29*	-0.0234	0.0119	-0.0455	0.0915	-0.0129	-	
Maize streak Virus	-0.069^{ns}	-0.1304	-0.0061	0.0696	0.36**	-0.0349	-0.0713	-0.1598	-0.0891	0.031	-0.1606	-

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, NS = non- significant (P >0.05)

Appendix 4-18. Correlation of yield and secondary traits in Muzarabani

Traits	Grain yield	Plant Height	Ear Height	Ear Position	Ear Per Plant	Husk Cover	Grain Texture	Grain Moisture Content	Ear Aspect	Root Lodging
Grain yield	-									
Plant Height	0.1381	-								
Ear Height	0.2247	0.71***	-							
Ear Position	0.177	0.1014	0.76***	-						
Ear Per Plant	0.0494	-0.0724	0.1074	0.24*	-					
Husk Cover	0.0196	-0.0685	-0.146	-0.1511	0.0877	-				
Grain Texture	0.0095	0.1777	0.1743	0.0893	-0.0663	-0.2134	-			
Grain Moisture Content	-0.0629	0.053	0.0244	-0.0026	-0.0125	-0.0628	0.1102	-		
Ear Aspect	-0.1337	-0.1627	-0.1772	-0.102	0.1561	0.49***	-0.26*	-0.38**	-	
Root Lodging	0.0824	0.1025	0.1101	0.0623	-0.0571	-0.1531	0.061	-0.35**	0.26*	-

*, **, ***, level of significance at P ≤0.05, P≤ 0.01 and P≤0.001, respectively, NS= non- significant (P >0.05)

Appendix 4-19.Direct (diagonal, underlined and bold data) and indirect effects of secondary traits on grain yield of Umbeluzi MSV

Trait	Anthesis Days	Anthesis Silking Interval	Ear Aspect	Ear Height	Ear Position	Ear Per Plant	Husk Cover	Grain Moisture Content	Maize streak virus	Plant Height	**Total**
Anthesis Days	**-0.04**	0.00	-0.05	-0.04	0.02	0.00	0.00	0.00	0.00	-0.14	**-0.24**
Anthesis Silking Interval	0.00	**-0.34**	0.14	-0.02	0.01	0.00	0.00	0.02	-0.01	-0.07	**-0.27**
Ear Aspect	0.00	0.12	**-0.37**	-0.03	0.03	0.00	-0.02	-0.01	0.01	-0.05	**-0.31**
Ear Height	0.01	0.08	0.09	**0.11**	-0.08	0.00	0.01	0.01	-0.01	0.29	**0.51**
Ear Position	0.00	0.04	0.09	0.07	**-0.13**	0.00	0.02	0.01	0.00	0.04	**0.14**
Ear Per Plant	0.00	-0.15	0.06	-0.02	0.02	**0.00**	0.00	0.00	0.01	-0.03	**-0.12**
Husk Cover	0.00	0.04	-0.18	-0.03	0.07	0.00	**-0.03**	-0.02	0.02	0.00	**-0.13**
Grain Moisture Content	0.00	-0.10	0.06	0.01	-0.02	0.00	0.01	**0.07**	-0.01	0.01	**0.04**
Maize streak virus	0.00	0.02	-0.05	-0.01	0.00	0.00	-0.01	0.00	**0.10**	-0.03	**0.03**
Plant Height	0.01	0.07	0.05	0.09	-0.01	0.00	0.00	0.00	-0.01	**0.35**	**0.56**

Appendix 4-20.Direct (diagonal, underlined and bold data) and indirect effects of secondary traits on grain yield of Umbeluzi

Trait	Anthesis Days	Anthesis Silking Interval	Ear Aspect	Ear Height	Ear Position	Ear Per Plant	Husk Cover	Grain Moisture Content	Plant Height	Root Lodging	Grain Texture	**Total**
Anthesis Days	**-0.12**	-0.01	-0.02	0.16	-0.18	-0.05	-0.01	0.00	-0.01	-0.02	0.00	**-0.27**
Anthesis Silking Interval	0.06	**0.01**	-0.01	0.04	0.05	0.05	0.00	0.00	-0.12	0.01	0.01	**0.10**
Ear Aspect	-0.01	0.00	**-0.14**	0.20	-0.05	-0.12	-0.02	0.00	-0.25	-0.02	0.02	**-0.38**
Ear Height	0.01	0.00	0.02	**-1.45**	0.92	-0.05	-0.03	0.00	0.96	0.02	-0.01	**0.40**
Ear Position	0.02	0.00	0.01	-1.25	**1.07**	-0.05	-0.05	0.00	0.48	0.00	0.00	**0.22**
Ear Per Plant	0.02	0.00	0.04	0.16	-0.12	**0.42**	0.06	0.00	-0.09	-0.03	-0.01	**0.44**
Husk Cover	0.01	0.00	0.02	0.29	-0.44	0.19	**0.13**	0.00	0.13	0.02	-0.01	**0.34**
Grain Moisture Content	-0.02	0.00	0.05	-0.14	-0.02	-0.06	0.00	**0.01**	0.24	0.05	-0.04	**0.06**
Plant Height	0.00	0.00	0.03	-1.19	0.44	-0.03	0.01	0.00	**1.18**	0.04	-0.02	**0.46**
Root Lodging	-0.02	0.00	-0.02	0.24	-0.03	0.08	-0.02	0.00	-0.30	**-0.14**	0.01	**-0.21**
Grain Texture	0.00	0.00	0.02	-0.17	0.03	0.04	0.01	0.00	0.20	0.02	**-0.11**	**0.04**

Appendix 4-21.Direct (diagonal, underlined and bold data) and indirect effects of secondary traits on grain yield of Chókwè

Trait	Anthesis Days	Anthesis Silking Interval	Ear Aspect	Ear Height	Ear Position	Ear Per Plant	Husk Cover	Grain Moisture Content	Plant Height	Grain Texture	Total
Anthesis Days	**-0.40**	0.01	-0.03	0.52	-0.11	-0.03	0.00	-0.03	-0.66	0.00	**-0.73**
Anthesis Silking Interval	0.15	**-0.02**	-0.03	-0.06	0.06	0.01	0.00	0.02	0.00	0.01	**0.14**
Ear Aspect	-0.10	-0.01	**-0.14**	0.05	0.15	-0.02	0.00	-0.01	-0.35	0.02	**-0.40**
Ear Height	0.22	0.00	0.01	**-0.96**	0.36	0.02	0.00	0.00	0.89	0.02	**0.54**
Ear Position	0.08	0.00	-0.04	-0.68	**0.50**	0.00	0.00	-0.01	0.18	0.02	**0.06**
Ear Per Plant	0.22	0.00	0.04	-0.26	-0.02	**0.06**	0.00	0.00	0.49	-0.01	**0.52**
Husk Cover	0.20	0.00	0.01	-0.15	-0.07	0.02	**0.00**	0.01	0.40	0.00	**0.42**
Grain Moisture Content	0.14	0.00	0.02	0.01	-0.05	0.00	0.00	**0.09**	0.09	0.01	**0.30**
Plant Height	0.24	0.00	0.04	-0.77	0.08	0.03	0.00	0.01	**1.10**	0.01	**0.73**
Grain Texture	0.01	0.00	-0.04	-0.21	0.13	0.00	0.00	0.01	0.12	**0.07**	**0.08**

Appendix 4-22.Direct (diagonal, underlined and bold data) and indirect effects of secondary traits on grain yield of Sussundenga

Trait	Anthesis Days	Anthesis Silking Interval	Ear Aspect	Ear Height	Ear Position	Ear Per Plant	Husk Cover	Grain Moisture Content	Plant Height	Grain Texture	**Total**
Anthesis Days	**-0.41**	0.02	-0.10	0.00	-0.04	-0.01	-0.06	0.15	-0.02	-0.01	**-0.48**
Anthesis Silking Interval	0.16	**-0.06**	0.02	0.00	0.02	0.01	0.00	-0.09	-0.09	0.02	**-0.01**
Ear Aspect	-0.12	0.00	**-0.35**	0.00	0.00	0.01	0.02	0.08	-0.04	-0.01	**-0.41**
Ear Height	0.14	0.00	0.03	**0.01**	0.06	0.02	0.04	0.02	0.21	0.00	**0.54**
Ear Position	0.17	-0.01	-0.01	0.01	**0.09**	0.01	0.02	-0.08	-0.02	0.02	**0.19**
Ear Per Plant	0.03	0.00	-0.02	0.00	0.01	**0.15**	0.06	0.04	0.03	0.00	**0.29**
Husk Cover	0.13	0.00	-0.04	0.00	0.01	0.05	**0.18**	-0.01	0.05	0.01	**0.38**
Grain Moisture Content	-0.24	0.02	-0.11	0.00	-0.03	0.02	0.00	**0.26**	0.12	-0.02	**0.02**
Plant Height	0.03	0.02	0.05	0.01	-0.01	0.02	0.03	0.11	**0.30**	-0.01	**0.53**
Grain Texture	0.07	-0.01	0.06	0.00	0.02	-0.01	0.01	-0.08	-0.05	**0.07**	**0.10**

Appendix 4-23 Direct (diagonal, underlined and bold data) and indirect effects of secondary traits on grain yield of Muzarabani MSV

Trait	Ear Aspect	Ear Height	Ear Position	Ear Per Plant	Ear Rot	Husk Cover	Grain Moisture Content	Plant Height	Root lodging	Grain Texture	Maize streak virus	Total
Ear Aspect	**-0.39**	0.01	0.04	0.01	-0.10	0.09	0.00	-0.05	0.01	-0.01	0.01	**-0.39**
Ear Height	0.12	**-0.04**	-0.12	0.00	0.08	-0.07	0.00	0.18	-0.01	0.00	0.00	**0.13**
Ear Position	0.09	-0.04	**-0.16**	0.00	0.10	-0.08	0.00	0.04	0.00	0.00	-0.01	**-0.05**
Ear Per Plant	-0.13	0.00	0.00	**0.02**	-0.04	0.03	0.00	-0.03	-0.01	-0.01	-0.03	**-0.19**
Ear Rot	-0.15	0.01	0.06	0.00	**-0.26**	0.12	0.00	-0.01	-0.03	0.00	0.00	**-0.25**
Husk Cover	-0.17	0.01	0.06	0.00	-0.15	**0.21**	0.00	-0.02	0.01	0.00	0.01	**-0.04**
Grain Moisture Content	0.04	0.00	0.00	0.00	0.03	-0.01	**0.00**	0.03	0.01	0.00	0.01	**0.11**
Plant Height	0.08	-0.03	-0.03	0.00	0.01	-0.02	0.00	**0.25**	-0.01	0.00	0.01	**0.26**
Root lodging	0.02	0.00	0.00	0.00	-0.05	-0.02	0.00	0.02	**-0.13**	0.00	0.00	**-0.17**
Grain Texture	0.08	0.00	-0.01	-0.01	0.01	0.00	0.00	0.02	0.00	**0.04**	0.01	**0.15**
Maize streak virus	0.05	0.00	-0.01	0.01	0.01	-0.01	0.00	-0.02	0.00	-0.01	**-0.08**	**-0.07**

Appendix 4-24.Direct (diagonal, underlined and bold data) and indirect effects of secondary traits on grain yield of Muzarabani

Trait	Ear Aspect	Ear Height	Ear Position	Ear Per Plant	Ear Rot	Grain Moisture Content	Plant Height	Root lodging	Grain Texture	Total
Ear Aspect	**-0.23**	-0.11	0.03	0.01	0.04	0.03	0.05	0.02	0.02	**-0.13**
Ear Height	0.04	**0.64**	-0.24	0.01	0.00	0.00	-0.22	0.01	-0.01	**0.22**
Ear Position	0.02	0.49	**-0.31**	0.01	-0.01	0.00	-0.03	0.01	-0.01	**0.18**
Ear Per Plant	-0.04	0.07	-0.07	**0.06**	0.01	0.00	0.02	-0.01	0.00	**0.05**
Ear Rot	-0.12	-0.02	0.02	0.01	**0.07**	0.02	0.00	0.01	0.00	**-0.01**
Grain Moisture Content	0.08	0.02	0.00	0.00	-0.01	**-0.09**	-0.02	-0.03	-0.01	**-0.06**
Plant Height	0.04	0.46	-0.03	0.00	0.00	0.00	**-0.31**	0.01	-0.01	**0.14**
Root lodging	-0.06	0.07	-0.02	0.00	0.01	0.03	-0.03	**0.09**	0.00	**0.08**
Grain Texture	0.06	0.11	-0.03	0.00	0.00	-0.01	-0.06	0.01	**-0.07**	**0.01**