DEVELOPING TOP CROSS MAIZE (*Zea mays L.)* HYBRIDS TOLERANT AGAINST MAIZE STREAK VIRUS (MSV) DISEASE FOR THE EASTERN ZONE ECOLOGIES

SALUM JALALA MBEGU

DISSERTATION TO BE SUBMITTED IN PARTIAL FULFILMENT OF THE REQUIREMENT FOR THE DEGREE AWARD OF MASTER OF SCIENCE IN CROP SCIENCE OF SOKOINE UNIVERSITY OF AGRICULTURE, MOROGORO, TANZANIA.

2014

ABSTRACT

Maize production in smallholder farming community has remained low due to a number of constraints which include biotic and abiotic. Among biotic constraints, Maize streak virus (MSV) disease is one of the major causes of low yield if not controlled. Genetic resistance appears to be the best economical option to control MSV and it is readily adopted as method for smallholder farmers, because of less cost and environmentally friendly. The main objective of this study was to produce high yielding top cross maize hybrids which are tolerant to MSV disease for growing in the Eastern ecologies of Tanzania. Staha (female) and fourteen inbred lines (male) were used to produce top cross hybrid genotypes. Evaluation for MSV resistance was done under natural infection. RCBD replicated three times was used in three selected MSV hot spots of Eastern areas of Tanzania. Fourteen top cross hybrid genotypes and two checks were used. Highly significant variation ($P \leq 0.001$) was found among the genotypes for MSV and grain yield. Dak0127, Dak0122, Dak0125 and Dak0124 genotypes were identified as the best materials for yield and tolerant to MSV disease while Dak0123, Dak01211 and Dak01210 genotypes were not good for locations having high MSV disease pressure. Significant and positive correlations between yield and plant height, ear length, hundred seed weight and ears/plant were observed. Path coefficient analysis indicated importance of the same variables through their direct contribution on grain yield. High heritability was observed for grain yield, ear length, number of rows/ear, grains/ear and grains/row, MSV disease incidence and severity, ear height, ears/plant, ear circumference, plant height. Based on correlation analysis earlier silking should be used for increased yield at these locations. High yielding MSV disease tolerant top cross genotypes which were identified are recommended for more seasons' evaluation for identifying genotypes to replace existing inferior cultivars.

DECLARATION

I, **Salum Jalala Mbegu,** do hereby declare to the Senate of Sokoine University of Agriculture that the work presented here is my own original work and has not been submitted or concurrently being submitted for a higher degree award in any other Institution.

15.10.2014

Salum Jalala Mbegu — Date

(MSc. Crop Science Candidate)

The above declaration confirmed by:

17/10/2014

Prof. S.O.W.M Reuben — Date

(MSc. Supervisor)

COPYRIGHT

ACKNOWLEDGEMENTS

I would like to give thanks and glory to God and his prophet Mohammad (S.A.W) for having been my source of wisdom, strength and determination while writing this dissertation. I thank my supervisor, Prof. Reuben, S.O.W.M, for his patience, understanding, guidance, encouragement and suggestions during this study and writing of the dissertation. I am also greatly indebted to ARI Chollima, particularly Mr. George Iranga for providing the germplasm used in this study. I am grateful to the Government of Tanzania for providing financial assistance for my study through COSTECH. Special thanks to the Demonstration Centre of China Agricultural Technology, ARI Ilonga and Mgambo JKT for allowing me to utilize their facilities.

Sincerely thanks go to all course instructors for their course coverage whose contributions lead to strong foundation and confidence to this study. I would like to thank all staff members of Crop Science, in particular Head of department Prof. Rweyemamu C. L, for their valuable critics, encouragement and assistance in academics. Special thanks also go to my employer, Ministry of Agriculture, Food security and Cooperatives for granting me the study leave to continue with training.

Last but not least, I wish to thank my family who, in a very special way, enabled me to realize my dream of completing my studies. To Azimina Salum, my Wife, thank you for your encouragement and taking care of our teenage children while I was away. To Salmin, Omary, Shadya and my last born Sharisa, thank you for your support, unwavering love, encouragement and patience throughout the two year study period.

DEDICATION

I would like to dedicate this work to all members of my family for their moral support during my study.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

LIST OF ABBREVIATIONS AND SYMBOLS

ANOVA	Analysis of Variance
a.s.l	Above sea level
ARI	Agricultural Research Institute
N	Nitrogen
CV	Coefficient of Variation
DF	Degree of freedom
DMRT	Duncan Multiple Range Test
EGA	Expected genetic adance
FAO	Food and Agriculture organization
FSD	Food security Department
GEI	Genotype × Environmental Interaction
LSD	Least significance difference
MSV	Maize streak virus
MSVD	Maize streak virus disease
MSTAT-C	Michigan State University Computer Software
r	Correlation Coefficient
RCBD	Randomized Complete Block Design
SE	Standard error
SUA	Sokoine University of Agriculture
SV	Source of variation
TSP	Triple supper phosphate

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background Information

Maize is known to be an important staple food crop in many tropical, subtropical and warm temperate countries. Essentially it is a crop of the warm environment although adapted to a wide range of environments. Current maize production in the world surpasses that of traditionally grown cereals such as sorghum and millet (Onwueme and Sinha, 1991).

In Africa maize is grown in a wide range of agro-ecological zones (Magenya *et al.*, 2008). Over 30% of the dietary calories in East Africa are contributed through maize production (Salasya *et al.*, 1998). Many African countries experience maize shortages which affect approximately 100 million people (Alexander and Bindiganavile, 2008). Resource poor small-scale farmers produce over 70% of maize in Africa (Salasya *et al.*, 1998). According to FAO (2006), the average maize yield in Africa stood at 1.3 t/ha compared to 3.0 t/ha elsewhere.

In Tanzania maize is known to be the major cereal consumed. It is estimated that annual per capita consumption of maize in Tanzania is 112.5 kg while national maize consumption is estimated to be three million tons per year (FSD, 1992). Maize accounts for 60% of dietary calories as well as up to 50% of utilizable protein for the majority of the Tanzanian rural population (Lyimo, 2006). It is the most widely cultivated crop in the country, covering about 45% of the area under annual crop production. Small holder farmer's produce is on 1-3 ha holdings, which accounts for about 85% of the total crop production (Moshi *et al.,* 1987). According to Mduruma and Ngowi, (1997) despite being important food crop, maize contributes substantial amount of cash income among small holder farmers. Maize is grown in all twenty regions on average of two million hectares of the cultivated area in Tanzania.

1.2 Setbacks to Attainment of Potential Yields of Maize

Despite the importance of crop maize in Tanzania, yields under farmers fields are only 1.2 tons per hectare compared to the estimated potential yields of 4-5 tons per ha (Kaswende *et al.,* 1998).

The low grain yields can be attributed to a number of constraints which include abiotic stresses (unreliable and poor distributed rainfall, low soil fertility and lack of capital to purchase inputs, lack of suitable varieties), biotic stresses (diseases, insect pests and weeds) (Salasya *et al.,* 1998). Major maize diseases include leaf blight caused by (*Exserohilum turcicum*), common rust (*Puccinia sorghi*), maize streak virus, grey leaf spot (*Cercospora zea maydis*), ear rots (*Fusarium spp.* and *Diploidia spp.*) and head smut (*Sphacelotheca reiliana*) (Vivek *et al.,* 2004). Of these, foliar diseases mainly maize streak virus, leaf blight and common rust are the most important as they can cause a total crop failure if not controlled. Maize streak virus (MSV) disease, caused by geminivirus that is transmitted by leafhoppers of the genus *Cicadulina* has been cited to be the most important constraint (Woyengo *et al.*, 2010). The effects of MSV on maize growth and yield are most severe when the plants are infected early, and yield loss can approach 100% in plants infected less than 1 week after emergence (Smith *et al.*, 2000). Incorporating genetic resistance to host plant has been reported to be the best option to control MSV (Hilty *et al.*, 1997). According to Kaliba *et al.* (1998) released varieties, including TMV1, Kilima, Kito, Katumani and Staha have been converted to carry resistance. However, in recent years these varieties appear to lose their ability to resist the MSV especially in areas with severe MSV disease pressure, and also when there is late planting (Lyimo, 2005).

Possibility on this decline is due to introduction of inferior genes into these cultivars as effected by out crossing nature of the crop, genetic drift, inbreeding depression and occurrence of new races of the disease. Woyengo *et al.* (2010) reported that development of top cross hybrids resistant to foliar diseases (MSV and others) is among the most viable solutions for yield increase. Top cross hybrid seed is produced at low cost and the effect of seed recycling by farmers is less severe on productivity than of classical hybrids (Pixley *et al.*, 2004). Despite the release and growing of improved maize varieties such as TMV1, Kilima, Kito, Katumani and Staha in the eastern zone of Tanzania, MSV disease continues to be a major constraint to maize production. According to Kariba *et al.* (1998), 41% of the farmers in lowlands reported the incidence of the disease. Therefore breeding for disease resistant varieties and availing high yielding seeds of top cross hybrids to resource-poor small scale farmers is of paramount importance and the only feasible option to boost maize productivity in a sustainable way.

1.3 Objective of the Study

1.3.1 Overall objective

To produce high yielding top cross maize hybrids, which are tolerant to maize streak virus disease for growing in the lowland areas of the Eastern ecologies of Tanzania.

1.3.2 Specific Objectives

i. To incorporate resistance genes and identify top cross hybrid genotypes which are tolerant to MSV disease
ii. To identify yield potentials of top cross hybrid genotypes
iii. To determine inheritance and the extent of association between yield, yield components and other selected traits and their influence to grain yield

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Maize Production Constraints

Maize (*Zea mays* L.) production in tropical Africa is constrained by a number of stress factors, including a complex of insect and disease organisms that significantly reduce the quantity and quality of production (Fajemisin *et al.,* 1984). Different disease complexes affect maize production in the lowlands and mid-high altitudes, often reduce production and cause up to100% yield loss under severe epidemics depending on environmental conditions (Abebe, 2008).

2.2 Maize Streak Virus Disease

Maize Streak Virus is the major viral pathogenic constraint on maize production in African countries. Initially named as mealie variegation but later renamed as maize streak virus disease. It is caused by the geminivirus maize streak virus (Shepherd *et al.*, 2007). The disease is found from sea level up to 1 800m elevation (Fajemisin *et al.,* 1984).

2.2.1 Symptoms of maize streak virus disease in maize crop

The maize plant is susceptible to MSV disease from emergence to flowering (Magenya *et al.,* 2008). The virus has been reported to infect all cell types of the host plant, where streak symptoms are visible only on leaves produced after infection of the plant (Thottappilly *et al.,* 1993). Symptoms of MSV tend to appear quicker in younger maize plants: 3 to 5 days in a one-week-old plant, and 7 to 9 days in a 9-

week-old plant (Mesfin *et al.*, 1995). The symptoms begin as small and spherical, chlorotic spots: 0.5 to 2.0 mm in diameter on younger leaves of the maize plant (Rose, 1978). Later coalesce into broken to almost continuous longitudinal chlorotic lines, mainly along the veins of the leaf laminae (Okoth *et al.*, 1987). In severely affected plants, chlorotic stripes may merge into pale green, or yellow or even white appearance on the leaf surface of the plant (Plates 1a and 1b). The highly sensitive maize varieties develop chlorosis of the entire leaf lamina, followed by plant death, particularly if infection occurs at an early stage of plant growth (Bosque-*Pérez et al.*, 1998). The streak pattern is a result of the failure of chloroplasts to develop in tissues surrounding the vascular bundles (Bosque-Perez, 2000), and impairing the photosynthetic ability of the plant (Mesfin *et al.*, 1995).

Plate 1a: Symptoms of MSV on Maize leaves

Plate 1b: Early infestation of MSV leads to stunted growth

2.2.2 MSV disease status and yield losses

Geddes (1990) ranked maize streak disease (MSVD) as the second most important vectored disease of staple crops in Africa. According to Lyimo *et al.* (2005) in Tanzania the disease has been considered as a yield barrier of economic importance in the low land maize production areas. In general, the affected maize plants may be shorter, have less vigour and produce smaller grains and ears (Okoth *et al.*, 1987). Maize yield reduction due to MSV and other diseases ranging between 0 - 70% (Bua and Chelimo, 2010). On-station trial in Kenya showed that yield losses ranged from 24% to 62% (Guthrie, 1978). The effect of MSVD on maize growth and yield are most severe when the plants are infected early (Smith, 2000), losses of up to 100% have been reported in experiments at UTA in Nigeria (Bjarnason, 1985). However, yield losses to MSD are hard to assess over large areas.

2.2.3 Transmission of MSV

Maize streak virus is transmitted by *Cicadulina spp.* (Mesfin *et al.*, 1995). The leafhoppers transmit the virus as they feed on maize plants. The incidence of the virus is influenced by the vector population which is also influenced by climatic conditions of rainfall as well as temperature and availability of alternative hosts (Rose, 1978).

A number of studies have verified that *C. mbila* is more successful in acquiring MSV from maize than from other hosts, suggesting the occurrence of plant host adaptation (Bosque-Pérez, 2000). Proportion of MSV transmitters in populations of *C. mbila* vary between 60 and 100% (Markham *et al.*, 1984). The percentage of active transmitters among females was 2-3 times larger than that among males. *C. mbila* has been documented to spend significantly shorter time while feeding on virus infected plants than on uninfected ones (Mesfin and Bosque-Pérez, 1998). After twelve to eighty five hours of leafhopper acquisition of MSV, the virus persists in the vector throughout its life span (Smith *et al.*, 2000).

2.2.4 Control options

Use of chemicals for protection is rendered inappropriate by the recurring of invasion of Migrant hopper populations which re-infect the crop after each application (Magenya *et al.*, 2008).

Researchers generally believe that MSVD is one of the major constraints to maize production in Africa, and that breeding for disease resistance is an effective solution to control maize streak disease (Fajemisin *et al.*, 1986).

2.2.5 Breeding for resistance

Making resistance to MSV is a key target for crop improvement (Shepherd *et al.*, 2007). Newly developed maize varieties are routinely evaluated in various agro-ecological zones for adaptation, yield potential and disease reactions, to identify genotypes that can replace existing cultivars and as a part of the requirements for releasing suitable varieties for cultivation in farmers' fields (Olakojo and Iken, 2001).

Furthermore, since every agro-ecology has unique growing conditions, it is important to assess newly developed varieties for yield potential as well as reaction to other stress factors that may be unique to the environment before being recommended for cultivation (Olaoye, 2009).

The challenge of improving maize varieties for small scale farmers in Africa appears to be centered on making the maize crop more resistant to foliar diseases through the use of genetically resistant varieties (Lyimo *et al.*, 2005). Before breeding for disease resistance can commence it is essential to find a source of heritable resistance (Western, 1971).

2.3 Top Cross Maize Hybrids

Top cross hybrids are produced by crossing an open pollinated variety (OPV) used as a female with a male inbred line or Hybrid with OPV (Abebe, 2008). Vianney and Efren (2008) found that Top cross hybrids involving, one or more non inbred parents are cheaper and easier to reproduce.

2.3.1 Advantages of top cross maize hybrids

Top cross maize hybrids are very important especially in the resource poor rural communities. Bidinge *et al.* (2005) documented that cost of Producing top cross hybrid seed is low and the effect of seed recycling by farmers is less severe than of classical hybrids. Pixley and Banziger (2004) assessed the yield reduction of cultivar types incurred by planting recycled seeds relative to fresh seeds of cultivar types across five locations. Their studies proved that the effect of planting recycled seeds was negligible for OPVs (5%), severe for hybrids (>30%) and intermediate for top-cross hybrids (16%). Since many farmers in the country recycle their seeds, therefore, use of non conventional hybrids such as top cross , double cross, variety cross hybrids that are less sensitive to in breeding depression could be one way of enhancing yield stability (Vianney and Maguna, 2008).

2.4 Genotype × Environment Interaction (GEI)

The concept of genotype × environment interaction is very important in breeding work. When genotypes are compared in a series of environments, relative ranking is expected to show superiority of any genotype (Hidayat *et al.,* 2011). G× E interaction has a challenge to breeders due to the fact that they cause difficulties in selecting genotypes evaluated in diverse environments.

The influence of environments leads to considerable changes in relative performance of maize genotypes over locations (Ngowi, 2002). Consideration must be made on its cause and nature when GEI is found significant (Kang and Gorman, 1989). GEI complicates identification of genotype superiority at a single location due to the fact that magnitude of genotype by location interaction is often greater than genotype by year interaction (Badu *et al.,* 2003).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental Sites

Crosses were made in Dakawa at Demonstration Centre of China Agricultural Technology, and evaluated in Ilonga, Kwamsanga and Dakawa. Demonstration Centre of China Agricultural Technology is in Mvomero District at Latitude $6^0$5'S,$37^0$40'E with an altitude of 360 m a.s.l. Ilonga Research station is in Kilosa District (Latitude 6^0 45'S, Longitude 37^0 and 506 m.a.s.l), Dakawa Research station is located in Mvomero District (Latitude $6^0$5'S,$37^0$40'E) with an altitude of 360 m a.s.l, both are in Morogoro Region. Kwamsanga is located in Handeni District of Tanga Region. (Latitude ($4^0$6'S, Longitude $38^0$00"E), with altitude of 400 m a.s.l.

3.2 Generation of Hybrids

The nursery for crossing was set up at Demonstration Centre of China Agricultural Technology (360 m asl) during the off season of 2012. Fourteen (14) inbred lines (male) from ARI Dakawa (Table1), one OPV-staha (female) from TAN SEED were used. These inbred lines were selected according to the available data for their resistance to MSV found in Station description book. During crossing, pollen was taken from inbred lines and hand pollinated to staha to make top cross hybrid genotypes. After harvesting fourteen (14) crosses and two checks were taken for field evaluation (Table 2).

3.3 Description of the Experimental Materials

Table 1: Inbred lines used in making top cross maize hybrids

Inbred lines/variety	Origin	Collected from	Generation
1. 309	72.1	ARI-Dakawa	21
2. 305-2	(13-13-4/A20)	ARI-Dakawa	9
3. 23-1	ICW/K202	ARI-Dakawa	21
4. 341-47	93-13-4/A20)	ARI-Dakawa	20
5. 3-4-5	inbred line	ARI-Dakawa	10
6. 7	copex	ARI-Dakawa	26
7. Staha	Commercial variety	TAN SEED	-
8. 345-1	(3-4-5/408-2)	ARI-Dakawa	22
9. 246-2	(44-22-5/3-13-4)	ARI-Dakawa	9
10. Tmv1	inbred line	ARI-Dakawa	20
11. Makunja	local	ARI-Dakawa	7
12. 336-40	(1-7-1/A20)	ARI-Dakawa	10
13. 345	inbred line	ARI-Dakawa	12
14. CML	87036/87923/800-3-1	ARI-Dakawa	13
15. pool	Korea	ARI-Dakawa	19

3.4 Experimental Design

Evaluation consisting of 14 crosses and 2 checks was done for MSV disease expression, grain yield, and other agronomic traits. The trials were sown in a randomized complete block design with three blocks (Replications). Each plot consisted of 2 rows of 5.1 m length, spaced 0.75 m between rows and 0.3 m between planting hills. Blocks were separated by a distance of 1.0 m.

3.5 General Agronomy

Seeds were planted per hill and these thinned to one plant per station two weeks after emergence. Planting at all locations were done three weeks after the normal date of planting so as to give the chance for the evaluation to coincide with high MSV disease pressure. TSP was applied during planting at a rate of 30 kg P_2O_5 ha^{-1}, while a top dressing Urea of (46% N) was also applied at a rate of 80 kg N ha^{-1} three weeks after emergence. Weeds were controlled by hoeing.

Table 2: Top crosses produced and other materials used during evaluation

Genotype	Code	Pedigree
DAK 0121	1	345/staha
DAK 0 122	2	7/staha
DAK 0123	3	TMV/Staha
DAK 0 124	4	336-40/Staha
DAK 0125	6	305-2/Staha
DAK 0126	7	CML16/Staha
DAK 0127	8	345-1/Staha
DAK 0 128	9	341-47/Staha
DAK 0129	11	3-4-5/Staha
DAK 01210	12	309/Staha
DAK 01211	13	Makunja
DAK 01212	14	23-1/Staha
DAK 01213	15	Pool/Staha
DAK 01214	16	246-2/Staha
H 600 (Commercial Resistant check)	10	-
Local (Susceptible check)	5	-

3.6 Data Collection

3.6.1 Growth stages

Number of days to 50% tasselling and silking was recorded as the duration from planting to when half of the population in each plot tassled and silked respectively. Physiological maturity was recorded as the duration from planting to when the silk of the ear cut and drop off, that is when the cover of the ear became dry for the large number of plants in a plot.

3.6.2 Development variables

Five plants from each plot were randomly selected, and measured by wooden ruler from the ground surface to the first ear point of attachment on the stem to record ear height, and plant height taken from the same plants measured from the ground level to the point where the tassel of the plant starts branching.

3.6.3 Yield and yield components

Field fresh ear weight

This was recorded as the weight of all ears harvested from each plot by means of weighing balance, recorded in kg then converted into tonnes per hectare (t/ha).Also grain moisture content from each plot was taken by the use of moisture meter.

Number of grains per ear

Number of grains per ear was obtained by calculating average number of grains per ear, by summing values for five randomly selected ears and then dividing by the number of ears.

Number of grain rows per ear

Numbers of grains was recorded by counting number of grain rows on each of the five selected ears and then calculate the average grain rows number.

Number of grains per row

Obtained by selecting five ears and counting total grains from each rows of the ear and find their means.

Ear length and circumference

Measured by measuring tape whereby ear length was obtained from average length of five randomly selected dehusked ears, and circumference was calculated by use of average ear diameter, recorded from the central part of randomly selected five ears from each plot.

Number of ears per plant and 100 grains weight

Number of ears per plant recorded as the number of total ears harvested from each plot and divided by the total number of plants during harvest and 100 grain weight is the weight of hundred grains randomly selected from the total grains of each plot.

3.6.4 MSV symptoms rating

MSV severity and incidence were rated after every three weeks on all plants within a plot starting at two week stage of plant growth. Disease severity was recorded using a scale of (1-5), 1 meaning no disease symptoms on leaves while 5 indicates severe infection and stunting. Data were collected for mean symptom rating for each entry per replication. Disease incidence was recorded as numbers of infected plants per total plants stand count expressed as a percentage.

3.7 Data Analysis

Analysis of variance (ANOVA) was computed for each scored variable at each site and in combined analysis by use of GenStat 13 edition (2013) Soft ware package. Where ANOVA revealed significant differences, means were separated by using Duncan Multiple Range (DMRT) according to (Steel and Torrie, 1980) at 5%

probability level. Correlations between variables and path coefficient analysis were also done.

3.7.1 Model for ANOVA

Fixed and random statistical models were used for analyzing variance within locations and across locations respectively. The following statistical model was used for single site analysis: $R_{ijk} = \mu + \beta_i + r_j + \varepsilon_{ijk}$

Where:

R_{ijk} = measurement for i^{th} genotype of j^{th} replicate in k^{th} plot

μ = overall mean

β_i = i^{th} treatment effect

r_j = j^{th} block effect (replication) and

ε_{ijk} = random experimental error

The following was used as the statistical model for combined analysis:

$Y_{ijk} = \mu + \beta_i + E_j + K_i (Ej) + \beta_i Ej + \varepsilon_{ijk}$

Where:

Y_{ijk} = the response for i^{th} genotype

K = replicate in j^{th} location

μ = overall mean

β_i = the effect of the i^{th} variety

E_j = the effect of the j^{th} location

k_i (Ej) = Effect of i^{th} replicate/block in j^{th} location

β_i Ej = The interaction effect of i^{th} genotype and j^{th} location

ε_{ijk} = Random experimental error

3.7.2 Analysis of correlation coefficients

Simple correlation, phenotypic and genotypic correlation coefficients analyses were done by the use of Genstat statistical package and MSTATC software.

3.7.3 Estimates of variance components and method of determination

The form of ANOVA and expected composition of pertinent mean square are presented in Table 3. Variance component estimates were obtained by equating the mean square for a source of variation to its expectations and solving for unknown, hence separated the effect of genotype, location and their interaction.

Table 3: Form of variance analysis and mean square expectations

Source of variation	DF	Mean square	Expected mean square	F- value
Location (L)	l-1	M1	$\delta^2_e+r\delta^2_{G\times l}+\delta^2_g+rg\delta^2_l$	M1/M3
Block/Rep (r)	r-1	M2	$\delta^2_e+\delta^2_r/E$	M2/M5
Genotype (G)	G-1	M3	$\delta^2_e+\delta^2_{G\times l}+re\delta^2 g$	M3/M4
G × L	(G-1)(l-1)	M4	$\delta^2_e+r\delta^2_{G\times l}$	M4/M5
Error	(r-1)(G-1)l	M5	δ^2_e	

Where:

δ^2_g = component of variance due to genotypes

δ^2_l = component of variance due to location (environment)

δ^2_e = component of variance due to error term

$\delta^2_{G\times l}$ = component of variance due to genotype × location (environment)

l = number of locations (environments)

G = Number of genotypes

3.7.4 Estimates of heritability (broad sense) and Expected Genetic advance

Computation of broad sense heritability was done after estimation of phenotypic and genotypic variance, using Hanson et al. (1956) formula.

$$h^2 = (\delta^2_g / \delta^2_{ph}) \times 100$$

Where:

h^2 = Heritability in broad sense

δ^2_g = Genetic variance

δ^2_{ph} = Phenotypic variance

The expected genetic advance was calculated according to the formula proposed by Johnson *et al.*, (1955).

$$EGA = k(100\, \delta_g / l) \times \delta_g \times \delta_{ph}$$

Where:

δ_g = Genetic standard deviation

δ_{ph} = Phenotypic standard deviation

l = population mean

k = a constant which varies with selection intensity

3.7.5 Path coefficient analysis

Path coefficient analysis was performed using genotypic correlation, where grain yield was considered as the responsible variable while yield components and other selected traits ware used as predictor variables by the formula described by Dewey and Lu (1959).

The model used was arranged in matrix form as depicted below:

$r_{110} = P_{110}+r_{12}P_{210} + r_{13}P_{310}+r_{14}P_{410}+r_{15}P_{510}+r_{16}P_{610}+r_{17}P_{710}+r_{18}P_{810}+r_{19}P_{910}$

$r_{210} = P_{210}+r_{12}P_{110} + r_{23}P_{310}+r_{24}P_{410}+r_{25}P_{510}+r_{26}P_{610}+r_{27}P_{710}+r_{28}P_{810}+r_{29}P_{910}$

$r_{310} = P_{310}+r_{13}P_{110} + r_{23}P_{210}+r_{34}P_{410}+r_{35}P_{510}+r_{36}P_{610}+r_{37}P_{710}+r_{38}P_{810}+r_{39}P_{910}$

$r_{410} = P_{410}+r_{14}P_{110} + r_{24}P_{210}+r_{34}P_{310}+r_{45}P_{510}+r_{46}P_{610}+r_{47}P_{710}+r_{48}P_{810}+r_{49}P_{910}$

$r_{510} = P_{510}+r_{15}P_{110} + r_{25}P_{210}+r_{35}P_{310}+r_{45}P_{410}+r_{56}P_{610}+r_{57}P_{710}+r_{58}P_{810}+r_{59}P_{910}$

$r_{610} = P_{610}+r_{16}P_{110} + r_{26}P_{210}+r_{36}P_{310}+r_{46}P_{410}+r_{56}P_{510}+r_{67}P_{710}+r_{68}P_{810}+r_{69}P_{910}$

$r_{710} = P_{710}+r_{17}P_{110} + r_{27}P_{210}+r_{37}P_{310}+r_{47}P_{410}+r_{57}P_{510}+r_{67}P_{610}+r_{78}P_{810}+r_{79}P_{910}$

$r_{810} = P_{810}+r_{18}P_{110} + r_{28}P_{210}+r_{38}P_{310}+r_{48}P_{410}+r_{58}P_{510}+r_{68}P_{610}+r_{78}P_{710}+r_{89}P_{910}$

$r_{910} = P_{910}+r_{19}P_{110} + r_{29}P_{210}+r_{39}P_{310}+r_{49}P_{410}+r_{59}P_{510}+r_{69}P_{610}+r_{79}P_{710}+r_{89}P_{810}$

$I = P^2{}_{x10} +P^2{}_{110} +P^2{}_{210}+P^2{}_{310}+P^2{}_{410}+P^2{}_{510}+P^2{}_{610}+P^2{}_{710}+P^2{}_{810}+P^2{}_{910}+2P_{110}\, r_{12}P_{210}+$

$2P_{110}\, r_{13}P_{310}+2P_{110}\, r_{14}P_{410}+2P_{110}\, r_{15}P_{510} +2P_{110}\, r_{16}P_{610}+2P_{110}\, r_{17}P_{710}+2P_{110}\, r_{18}P_{810}+$

$2P_{110}\, r_{19}P_{910} +2P210r23P310+2P210r_{24}P_{410}+2P_{210}r_{25}P_{510} +2P_{210}r_{26}P_{610}+2P_{210}r_{27}P_{710}+$

$2P_{210}r_{28}P_{810}+2P_{210}r_{29}P_{910}+2p_{310}r_{34}P_{410}+2p_{310}r_{35}P_{510}+2p_{310}r_{36}P_{610}+2p_{310}r_{37}P_{710}+2p_{310}r_{38}$

$P_{810}+2p_{310}r_{39}P_{910}+2P_{410}r_{45}P_{510}+2P_{410}r_{46}P_{610}+2P_{410}r_{47}P_{710}+2P_{410}r_{48}P_{810}+2P_{410}r_{49}P_{910}+2P$

${}_{510}r_{56}P_{610}+2P_{510}r_{57}P_{710}+2P_{510}r_{58}P_{810}+2P_{510}r_{59}P_{910}+2P_{610}r_{67}P_{710}+2P_{610}r_{68}P_{810}+2P_{610}r_{69}P_{91}$

${}_{0}+2P_{710}r_{78}P_{810}+2P_{710}r_{79}P_{910} +2P_{810}r_{89}P_{910}.$

CHAPTER FOUR

4.0 RESULTS

4.1 Mean Performance of Genotypes Within Locations and in Combined Analysis

4.1.1 Grain yield and other variables evaluated at Kwamsanga

Results for performance of genotypes at Kwamsanga are summarized in Table 4. Yield averaged 3.0 t/ha and ranged from 3.97 t/ha for H600 to 0.99 t/ha for local check. Genotypes DAK0124 and DAK0122 showed highest means of 3.84 and 3.74 t/ha respectively. Days to 50% tasselling revealed a mean of 56.6 days with latest of 57.67 days and earliest of 55 days for DAK0127. Later genotype took shortest time to silk (58.67 days) and latest appeared for DAK01299 (61.67 days).

Ear height ranged from 130.9 cm to 71.5 cm for DAK0122 and local check respectively. Number of grains per ear was recorded highest for H600 resistant check (503.3) followed by 481.3 and 464.5 for DAK0127 and DAK0121 genotypes respectively, lowest recorded from local check (252.8). Weight of hundred grains ranged from 27.53 g for H600 and 21.13g for DAK0127. Outstanding in performance for ear circumference was obtained from DAK0122 (9.23 cm) followed by DAK0124 (8.9 cm) and DAK0127 (8.77cm), the lowest recorded from local check (5.87 cm). Numbers of rows per ear were highest as 14.0, 13.8, and 13.67 for H600, DAK0123 and DAK01210 respectively, but local check showed lowest record (10.73). DAK0127 was detected to have most lodged plants 44.09 and least number of lodged plants was recorded in local check (6.8).

Table 4: Mean performance of genotypes for the studied traits at Kwamsanga site for the 2012/2013 growing season

Genotypes	Grain yield t/ha	Days to 50% tasselling	Days to 50% Silking	Ear height (cm)	MSV disease incidence %	MSV disease severity scale 1-5	No of grains/ ear	Plant height (cm)	Weight of 100 grains (g)	Ear girth (cm)	No of rows/ ear	Plant lodging	Ear length	physiological maturity (Days)
DAK 0121	3.10bcd	57.00a	60.33a	111.2bc	24.3a-d	2.2a-c	464.5cde	218.6bc	23.13abc	8.47b	13.00bc	32.85abc	14.03b	115.0ab
DAK 0 122	3.74cd	56.33a	59.67a	130.9c	12.4a	1.7a	437.3b-e	218.8bc	27.20c	9.23b	13.27bc	26.36abc	14.47b	114.0ab
DAK 0123	3.07bcd	56.33a	60.33a	106.1bc	21.7a-d	2.2a-d	398.7a-e	207.5abc	25.87bc	8.37b	13.80c	8.10ab	12.70b	113.3ab
DAK 0 124	3.84cd	56.33a	59.33a	102.7b	17.6abc	2.0ab	440.9b-e	202.9abc	22.47ab	8.90b	12.93bc	15.08abc	14.30b	113.7ab
DAK 0125	3.45bcd	56.67a	59.67a	112.0bc	21.4a-d	1.9ab	452.9cde	206.9abc	24.00abc	8.23b	13.00bc	36.58bc	15.16b	114.3ab
DAK 0126	3.07bcd	56.00a	60.00a	122.6bc	22.2a-d	2.3a-e	448.6b-e	211.3abc	23.23abc	8.50b	13.47c	23.05abc	14.97b	116.3b
DAK 0127	3.17bcd	55.00a	58.67a	117.5bc	14.2ab	2.1abc	481.3de	206.0abc	21.13a	8.77b	12.93bc	44.09c	13.3b	112.3a
DAK 0 128	2.85bcd	57.00a	60.67a	118.3bc	26.3b-d	2.1abc	331.3a-d	230.3c	25.27abc	8.37b	13.20bc	25.99abc	13.25b	113.7ab
DAK 0129	3.10bcd	57.67a	61.67a	125.6bc	24.4a-d	2.7cde	291.5ab	216.2bc	21.43ab	7.57ab	13.53c	20.13abc	13.31b	114.3ab
DAK 01210	2.50b	57.00a	61.33a	115.5bc	28.3cd	2.8de	425.8b-e	217.9bc	22.07ab	7.53ab	13.67c	15.38abc	12.35b	115.0ab
DAK 01211	2.75bc	57.00a	59.67a	106.1bc	31.7d	2.9e	314.1abc	203.7abc	23.23abc	7.50b	12.20abc	41.70c	12.76b	114.0ab
DAK 01212	2.88bcd	56.33a	60.00a	124.9bc	23.8a-d	2.86de	373.3a-e	228.7c	21.57ab	8.30b	13.13bc	31.90abc	13.45b	112.3a
DAK 01213	2.46b	57.33a	61.33a	125.1bc	29.9cd	2.8de	364.3a-e	223.3bc	23.03abc	7.57ab	11.27ab	20.79abc	12.33b	114.3ab
DAK 01214	3.10bcd	56.67a	60.67a	103.8b	25.7b-d	2.9e	448.4b-e	199.9ab	20.83a	7.80b	13.60c	41.05c	13.18b	114.3ab
H 600	3.97d	56.67a	60.33a	121.1bc	20.1a-d	2.3a-e	503.3e	217.9bc	27.53c	8.10b	14.00c	15.47abc	14.83b	114.3ab
Local	0.99a	56.33a	60.00a	71.5a	45.9e	4.1f	252.8a	187.3a	24.07abc	5.87a	10.73a	6.86a	9.17a	115.0ab
Mean	3.0	56.60	60.23	113.4	24.4	2.51	402	212.3	23.50	8.07	12.98	25.3	13.35	114.17
SE±	0.34	1.01	1.17	7.71	3.77	0.2	46.7	8.22	1.35	0.57	0.62	8.67	0.96	0.9
CV(%)	19.4	3.10	3.40	1.4	26.8	13.7	20.1	6.7	9.90	12.10	0.82	59.3	12.5	1.57
Lsd 0.05	0.97	2.92	3.39	22.27	10.90	0.57	135	23.76	3.90	1.63	1.79	25.03	2.775	2.61

Values in each column followed by the same letters are not significantly different at 5% level test

The highest ear length was recorded from DAK0125 (15.16 cm) and lowest was revealed by local check (9.17 cm). Duration to maturity revealed no statistical difference although mean days for physiological maturity indicated that both DAK01212 and DAK0127 matured earliest (112.3 days), while DAK0126 took longest time to maturity (116.3 days).

4.1.2 Grain yield and other variables evaluated at Dakawa

Results of performance for different recorded traits at Dakawa site are summarized in Table 5. DAK0129 (6.27 t/ha) was highest in grain yield. It excelled the resistant check (5.98 t/ha) though not significantly. Other genotypes which performed relatively well are DAK01212 (5.98 t/ha), DAK0126 (5.82 t/ha), DAK01214 (5.69 t/ha) and DAK0121 (5.95 t/ha). Lowest grain yield was recorded from local check (0.61 t/ha). Longest duration in days to 50% tasselling was revealed by DAK01213 (56.33 days) and the local check (56.0 days),while DAK01210 and DAK01213 took longest duration to silking (60..33 days). However, DAK0121 tasseled and silked earliest (51.67 days) and (56.33days) respectively.

The highest ear height was observed in DAK01214 (152.6cm) which also revealed highest plant height (277.3), local check had shortest plant and ear heights (190.7 cm and72.1 cm) respectively. Weight of hundred grains varied between 35.63 g to 26.77 for DAK01212 and local susceptible check respectively. The statistical analysis of data revealed that ear girth significantly differed among genotypes. DAK01214 had biggest ear girth (11.47 cm) while local check had the smallest ear girth (4.77 cm).

Table 5: Mean performance of genotypes for the studied traits at Dakawa site for the 2012/2013 growing season

Genotypes	Grain yield t/ha	Days to 50% tassellin g	Days to 50% silking	Ear height (cm)	MSV severity scale 1-5	MSV incidence (%)	No of grain/ ear	Plant height (cm)	Weight of 100 grains (g)	Ear Girth (cm)	No of rows/ ear	Plant lodging	Ear length (cm)	physiolog ical maturiy (Days)
DAK 0121	5.95cd	51.67a	56.33a	113.4b-e	1.1abc	1.767a	490.7bc	239.1b-e	32.20ab	10.47bc	13.20bc	11.49abc	17.30c	113.7bc
DAK 0 122	4.86bcd	53.67abc	57.00ab	115.7b-f	1.6bc	12.200ab	488.7bc	233.9bcd	33.27ab	10.47bc	14.33c	14.53abc	16.25bc	114.7bc
DAK 0123	4.54bc	53.33abc	58.00bc	99.3bc	1.4abc	9.167ab	488.9bc	224.9abc	28.63ab	9.70bc	13.47bc	8.17ab	16.10bc	114.0bc
DAK 0 124	4.67bcd	54.33abc	58.00abd	111.5bcd	1.3abc	5.200ab	529.7c	234.5bcd	26.97a	9.83bc	13.07bc	14.37abc	16.73bc	114.0abc
DAK 0125	4.35bc	54.33abc	58.00abd	123.9c-f	1.6bc	17.000b	445.7bc	238.4bcd	30.10ab	10.37bc	12.93bc	7.23ab	17.28c	112.0a
DAK 0126	5.82cd	52.33ab	57.00ab	123.9c-f	1.1abc	2.867ab	494.8bc	248.1cde	34.33ab	11.03c	14.27c	7.33ab	17.24c	112.7ab
DAK 0127	5.37cd	52.33ab	57.33ab	117.1b-f	1.4abc	7.800ab	515.0c	225.3abc	30.03ab	10.87c	13.40bc	28.41cd	16.87bc	112.7ab
DAK 0 128	5.15cd	54.67abc	59.00bce	140.0efg	1.2abc	5.933ab	362.7b	264.1cde	31.67ab	10.43bc	12.93bc	13.75abc	15.93bc	113.3abc
DAK 0129	6.27d	55.67bc	58.67bce	141.7fg	1.0a	0.000a	520.9c	262.6cde	32.00ab	10.47bc	13.53bc	12.32abc	17.67c	114.0abc
DAK01210	4.96bcd	55.67bc	60.33e	135.7d-g	1.5abc	10.800ab	522.0c	265.3de	34.30ab	10.37bc	14.33c	11.16ab	17.35c	115.0c
DAK01211	3.46b	56.00c	59.00bce	92.5ab	1.7c	17.133b	363.0b	206.7ab	31.27ab	8.77b	11.93b	21.07bcd	13.70b	114.3bc
DAK01212	5.98cd	55.00abc	58.67bce	129.7d-g	1.1ab	1.900a	453.2bc	252.2cde	35.63b	10.60c	12.93bc	16.66abc	17.70c	114.3bc
DAK01213	4.96bcd	56.33c	60.33ce	128.7d-g	1.3abc	6.667ab	478.6bc	253.9cde	28.63ab	10.53bc	13.80bc	12.94abc	17.12c	114.0abc
DAK01214	5.69cd	55.67bc	59.33bce	152.6g	1.1abc	4.400ab	522.1c	277.3e	34.73ab	11.47c	13.67bc	36.20d	17.33c	114.7bc
H 600	5.98cd	54.00abc	58.00abd	116.1b-f	1.0a	0.000a	486.8bc	241.9b-e	33.70ab	10.87c	14.13c	5.87ab	16.57bc	114.3bc
Local	0.61a	56.00c	59.00bce	72.1a	3.1d	51.867c	113.5a	190.7a	26.77a	4.77a	8.47a	2.38a	9.30a	114.7bc
Mean	4.91	54.44	58.38	119.60	1.42	9.70	455	241.2	31.51	10.06	13.15	14	16.28	113.90
SE±	0.5	1	0.69	7.91	0.18	4.22	43.3	11.54	2.42	0.54	0.61	5.07	1.02	0.61
CV(%)	17.80	3.2	2.00	11.50	21.80	8.3	16.5	8.3	13.30	9.30	8.10	62.8	10.80	0.90
Lsd 0.05	1.46	2.88	1.99	22.86	0.52	33.32	125	33.32	7.00	1.56	1.77	14.64	2.94	1.77

Values in each column followed by the same letters are not significantly different at 5% level test

4.1.3 Grain yield and other variables evaluated at Ilonga

Study summary from Ilonga site is in Table 6. In the study, DAK0126 outperformed other genotypes (4.8 t/ha), followed by DAK0127 (4.7 t/ha) and DAK0128 (4.54 t/ha). The local check had the lowest mean yield of 0.99 t/ha. On the other hand days to 50% tasselling and silking were latest in local check (60.67 and 66.33 days) respectively, but earliest recorded by DAK0127 (50.67 days) in tasselling and 55 days in silking. Data revealed that ear height was highest (120.9 cm) for DAK0122 and DAK1213 (120.0 cm) and lowest for local check (64.1 cm).

Highest in plant height was revealed by DAK 0122 (209.7 cm), and lowest mean plant height was observed in local check (139.1 cm). Lowest mean number of grain per ear (188.7) and was recorded from the local check but the highest number of grains per ear was obtained from DAK0126 (573.3). However, H600 which is the resistant check outperform other genotypes in weight of hundred grains (36.07 g) followed by DAK0125 (35.93 g), DAK0128 (34.63 g) and DAK0122 (34.33 g) and the lowest was recorded by DAK0129 (29.27 g). Ear girth ranged from11.27 cm for DAK0126 to 7.77 cm for local check which also showed lowest mean performance on number of rows per ear and on ear length.

Table 6: Mean performance of genotypes for the studied traits at Ilonga site for the 2012/2013 growing season.

Genotypes	Grain yield t/ha	Days to 50% Tasselling	Days to 50% silking	Ear height (cm)	MSV severity scale 1-5	MSV incidence %	No of grain/ ear	Plant height (cm)	Weight of 100 grains (g)	Ear girth (cm)	No of rows/ ear	Plant lodging	Ear length	Physiological maturity (Days)
DAK 0121	3.04b	53.33abc	58.33abc	96.6bcd	2.3abc	21.abc	464.1cd	183.8b	29.80a	9.70ab	13.53cd	55.62a	15.05bc	110.7a
DAK 0 122	4.48cde	53.33abc	58.00abc	120.9d	2.1abc	18.3ab	444.4cd	209.7b	34.33ab	9.97b	13.00cd	26.66a	15.10bc	113.0ab
DAK 0123	2.97b	55.00bcd	57.33abc	92.1bc	2.5bc	31.1bcd	341.8bc	177.5b	30.73ab	9.77ab	12.53bc	36.03a	12.77ab	113.0ab
DAK 0 124	3.71bce	54.00abd	59.33abc	83.8ab	2.3abc	19.0ab	433.7cd	172.7b	32.33ab	9.60ab	12.73cd	41.16a	13.33ab	113.7b
DAK 0125	3.52bce	53.33abc	61.67cd	111.0cd	2.2abc	23.8abc	278.1ab	190.7b	35.93b	9.53ab	11.33ab	44.13a	14.63bc	113.3ab
DAK 0126	4.80e	54.00abd	57.67abc	106.5bcd	1.7a	14.6a	573.3d	190.2b	33.00ab	11.27b	16.53e	41.64a	14.41bc	112.7ab
DAK 0127	4.70de	50.67a	55.00a	116.5cd	2.2abc	21.4abc	375.8bc	207.8b	32.87ab	10.40b	13.93cd	61.4a	12.87ab	110.7a
DAK 0 128	4.54cde	53.33abc	58.00abc	116.0cd	1.8ab	18.2ab	373.5bc	203.1b	34.63ab	10.20b	12.60bc	39.42a	14.63bc	114.3b
DAK 0129	3.55bce	55.00bcd	60.00abc	117.1cd	2.abc	20.8abc	374.5bc	198.9b	29.27a	9.53ab	13.13cd	31.9a	16.70c	115.0b
DAK01210	3.23bc	55.00bcd	60.00abc	116.7cd	2.6c	33.4cd	380.5bc	194.1b	33.80ab	10.00b	12.67bc	60.12a	14.47bc	112.7ab
DAK01211	4.25bce	51.33ab	55.33ab	114.6cd	2.0abc	18.7ab	385.0bc	204.1b	29.87a	10.57b	13.93cd	62.5a	13.53ab	113.3ab
DAK01212	3.94bcd	53.67abc	60.33abc	109.7cd	2.1abc	19.ab	368.6bc	188.9b	34.30ab	9.37ab	13.00cd	40.4a	13.53ab	115.0b
DAK01213	3.71bce	56.33cd	61.00bcd	120.0d	2.3abc	23.8abc	437.3cd	205.2b	33.93ab	10.20b	13.13cd	28.5a	14.60bc	114.7b
DAK01214	3.36bcd	57.67dc	62.67cd	119.3cd	2.4abc	26.1abc	391.5bc	197.2b	29.47a	10.53b	13.07cd	57.97a	13.27ab	114.0b
H 600	4.44cde	53.33abc	60.33abc	113.5cd	2.1abc	20.5abc	447.2cd	199.5b	36.07b	10.90b	14.13d	32.71a	15.37bc	114.0b
Local	0.99a	60.67e	66.33d	64.1a	3.6d	41.1d	188.7a	139.1a	30.50ab	7.77a	10.87a	30.98a	11.00a	114.3b
Mean	3.70	54.38	59.46	107.4	2.3	23.2	391	191.4	32.55	9.96	13.13	43.2	14.08	113.4
SE±	0.4	1.13	1.71	8.01	0.2	4.2	45.4	10.82	1.69	0.66	0.43	12.86	0.78	0.89
CV(%)	18.70	3.6	5	12.9	15.80	31.5	20.1	9.8	9	11.4	5.7	51.6	9.6	1.4
Lsd 0.05	1.16	3.27	4.93	23.14	0.60	12.2	131.2	31.26	4.88	1.89	1.25	37.15	2.25	2.57

Values in each column followed by the same letters are not significantly different at 5% level test

4.1.4 Performance on grain yield and other variables in combined analysis

Results for combined analysis are summarized in Table 7. Grain yield is ranged from 4.8 t/ha for H600 to 0.86 t/ha for local check. Other genotypes which showed relatively better performance are DAKO126 (4.56t/ha), DAK0127 (4.42 t/ha) and DAK0122 (4.36 t/ha) (Figure 1).

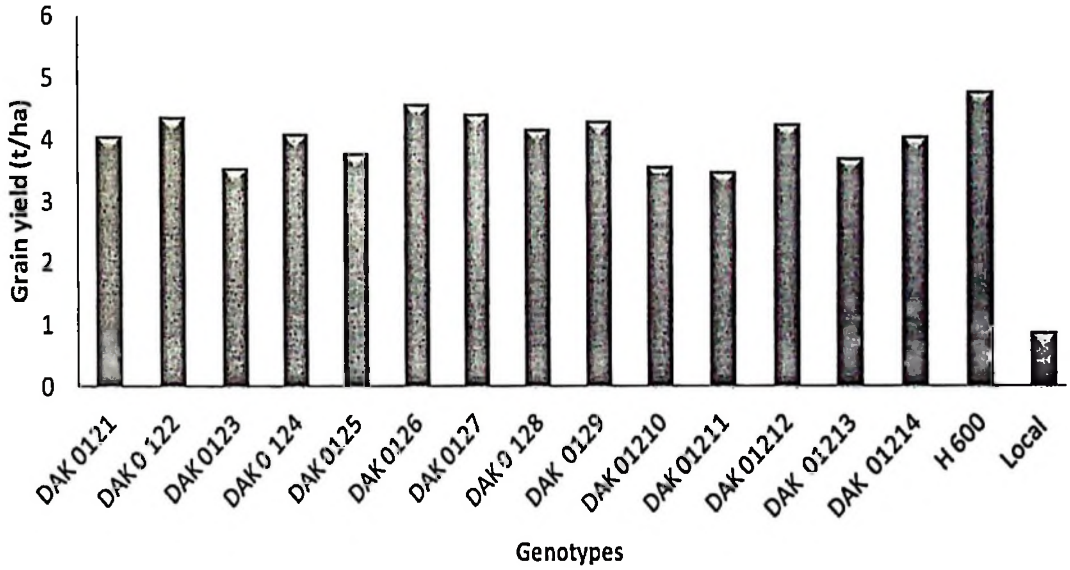

Figure 1: Average grain yield (t/ha) for genotypes across locations

Local check took longest duration to flowering, where days to 50% tasselling and silking were 57.67 and 61.78 respectively. The earliest flowering was detected from DAK0127 which had (52.67 and 57 days) for tasselling and silking respectively. However, DAK0129 had highest ear height (128.1 cm) and DAK0128 had highest plant height (232.5 cm). Number of grains per ear recorded lowest for local check (185) and highest for DAK0126 (505.6). On the other hand weight of hundred grains recorded highest (10.267 g) for DAK0126 and lowest (6.13 g) for local check.

Table 7: Mean performance of genotypes for the studied traits across sites for the 2012/2013 growing season

Genotypes	Grain yield t/ha	Days to 50% tasselling	Days to 50% Silking	Ear height (cm)	MSV severity scale 1-5	MSV incidence %	No of grain/ ear	Plant height (cm)	Weight of 100 grains (g)	Ear girth (cm)	No of rows/ Ear	Plant lodging	Ear length	Physiological maturity
DAK0121	4.031b-f	54.00ab	58.33abc	107.1bc	1.9abc	15.7ab	473.1cd	213.8b-e	9.544bc	28.38ab	13.24bcd	33.32bcd	15.46cd	113.1ab
DAK 0122	4.361c-f	54.44abc	58.22abc	122.5d	1.8ab	14.3a	456.8cd	220.8b-e	9.889bc	31.60bc	13.53bcd	22.51ab	15.27cd	113.9b
DAK 0123	3.529bc	54.89bcd	58.56a-d	99.2b	2.0abcd	20.7abc	409.8bc	203.3b	9.278bc	28.41ab	13.27bcd	17.44ab	13.86bc	113.4b
DAK 0124	4.073b-f	54.89bcd	58.89a-d	99.3b	1.9abc	13.9a	468.1cd	203.4b	9.444bc	27.26a	12.91bc	23.54ab	14.79bcd	113.8b
DAK 0125	3.775b-e	54.78bcd	59.78b-e	115.6cd	1.9abc	20.7abc	392.2bc	212.0bcd	9.378bc	30.01abc	12.42b	29.31a-d	15.69d	113.2ab
DAK 0126	4.564ef	54.11abc	58.22abc	117.7cd	1.7a	13.2a	505.6d	216.5b-e	10.267c	30.19abc	14.76c	24.01ab	15.54cd	113.9b
DAK 0127	4.415def	52.67a	57.00a	117.0cd	1.9abc	14.5a	457.4cd	213.0b-e	10.011bc	28.01ab	13.42bcd	44.63d	14.96bcd	111.9a
DAK 0128	4.179b-f	55.00bcd	59.22a-d	124.8d	1.8abc	16.8abc	355.8b	232.5e	9.667bc	30.52abc	12.91bc	26.39abc	15.29cd	113.8b
DAK 0129	4.307b-f	56.11cde	60.11bcde	128.1d	1.9abc	15.1ab	395.6bc	225.9de	9.189bc	27.57a	13.40bcd	21.45ab	14.61bcd	114.4b
DAK01210	3.562bcd	55.89b-e	60.56cde	122.6d	2.3d	24.2c	442.8cd	225.8de	9.300bc	30.06abc	13.56cd	28.89a-d	14.72bcd	114.2b
DAK01211	3.486b	54.78bcd	58.00ab	104.4bc	2.2cd	22.5bc	354.0b	204.8bc	8.944b	28.12ab	12.69bc	41.76cd	13.33b	113.9b
DAK01212	4.266b-f	55.00bcd	59.67bcde	121.4d	2.0abcd	14.9ab	398.4bc	223.8cde	9.422bc	30.50abc	13.02bcd	29.65a-d	14.89bcd	113.9b
DAK01213	3.711b-e	56.67de	60.89de	124.6d	2.1bcd	20.1abc	426.7bcd	226.9de	9.433bc	28.53ab	12.73bc	20.74ab	14.68bcd	114.3b
DAK01214	4.051b-f	56.67de	60.89de	125.2d	2.1bcd	18.7abc	454.0cd	224.8de	9.933bc	28.3ab	13.44bcd	45.07d	14.59bcd	114.4b
H 600	4.797f	54.67bcd	59.56b-e	116.9cd	1.9ab	13.6a	479.1cd	219.8b-e	9.956bc	32.43c	14.09de	18.02ab	15.59cd	114.2b
Local	0.863a	57.67e	61.78e	69.2a	3.6e	46.3d	185.0a	172.4a	6.133a	27.11a	10.02a	13.41a	9.82a	114.7b
Mean	3.87	55.14	59.35	113.5	2.06	19.07	415.9	215	9.36	29.19	13.09	27.5	14.57	113.82
SE±	0.26	0.6	0.75	4.5	0.12	2.42	26.6	5.96	1.16	0.36	0.33	5.38	0.53	0.47
CV(%)	20.00	3.3	3.8	11.9	17.6	38.00	19.2	8.3	11.6	11.9	7.6	58.7	11	1.3
Lsd 0.05	0.72	1.69	2.11	12.64	0.34	6.78	74.68	16.74	1.02	3.25	0.93	15.11	1.5	1.33

Values in each column followed by the same letters are not significantly different at 5% level test

Results show that DAK0122 recorded highest (31.6cm) for ear girth and lowest (27.11 cm) detected by local check. There is slight difference in number of rows per ear, the range being 14.76 for DAK0126 to 10.02 for local check. Mean ear length of local check was lowest (9.82 cm) but longest are for DAK0125 (15.69 cm) and H600 (15.59 cm).

Plant lodging in combined results showed that there were fewest lodged plants in local check (13.41) followed by DAK0123 (17.44). Almost all genotypes took the same duration to reach maturity although the range was 114.7 days for local check to 111.9 days for DAK0127.

4.2 MSV Disease Expression and Levels of Incidence for Different Genotypes at Studied Sites

4.2.1 Kwamsanga site

Responses of different genotypes to disease are indicated on Figures 2 and 3; disease incidence range was between 12.4% to 45.9% for DAK0122 and local check respectively. Severity of disease scored was lowest in DAK0122, DAK0125 and DAK0124 which had 1.7, 1.9 and 2.0 respectively.

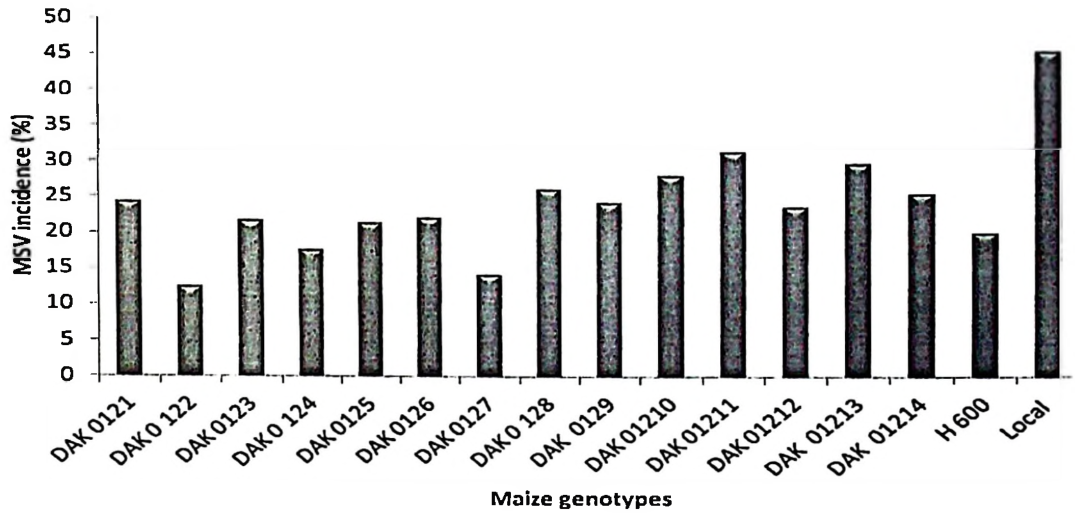

Figure 2: MSV incidence among genotypes at Kwamsanga

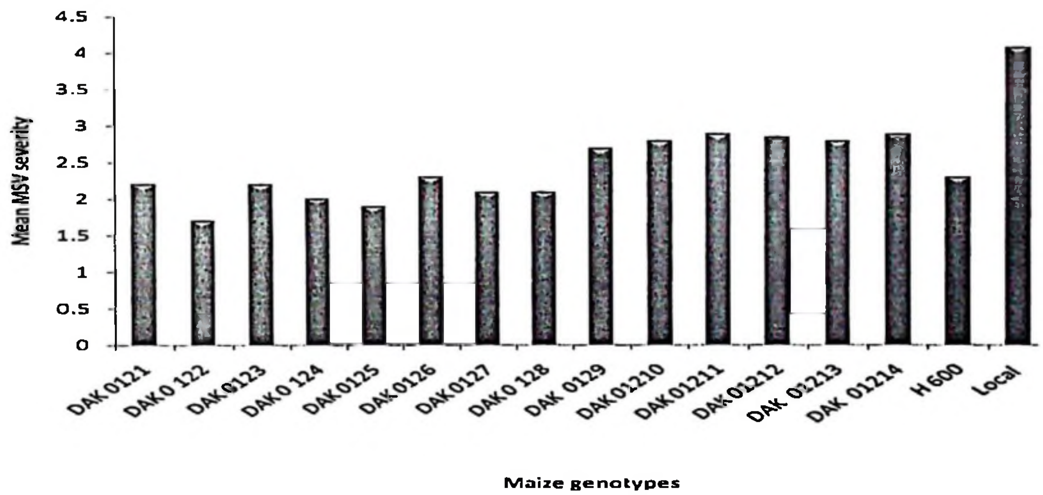

Figure 3: Mean severity of MSV disease among genotypes at Kwamsanga

4.2.2 Dakawa site

Data recorded from Dakawa revealed that MSV was not serious among genotypes (Figures 4 and 5). The mean severity of MSV was 1.42, and most of the genotypes recorded below average (Table 5). The range was 1.0 for H600 and DAK0129 to 3.1

for the susceptible check (local). MSV incidence ranged from 0 for H600 and DAK0129 to 51.9% for local check. This low rating of disease was supported by high yield, in which most of the genotypes at this site had grain yields exceeding the mean (4.91 t/ha) (Table 5). Maize cobs harvested from tolerant and susceptible genotypes are indicated in plate 2a and 2b respectively.

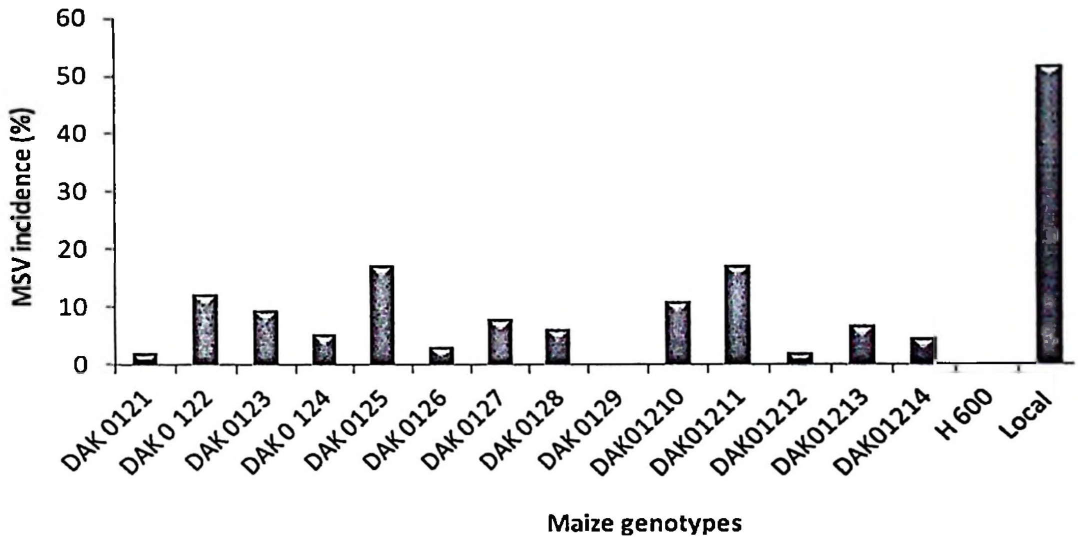

Figure 4: MSV incidence among genotypes at Dakawa

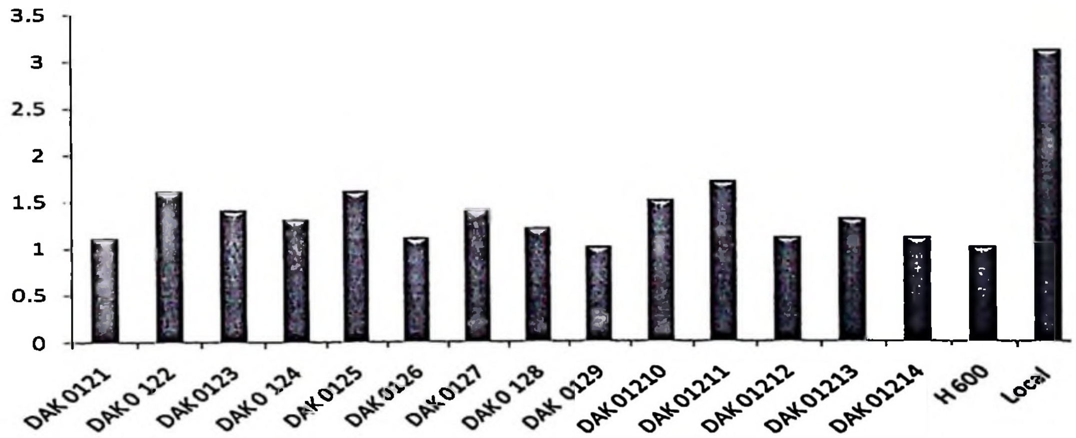

Figure 5: Mean severity of MSV disease among genotypes at Dakawa

Plate 2a: Maize harvested from resistant genotype

Plate 2b: Maize harvested from local susceptible genotype

4.2.3 Ilonga site

Expression and disease incidence for different maize genotypes are shown in Figures 6 and 7. The highest MSV incidence was shown by local check (41.1%) and lowest recorded for DAK0126 (14.6%), other genotypes with low disease incidence were DAK0122 (18.3%), DAK0128 (18.2%) and DAK01211 (18.7%).

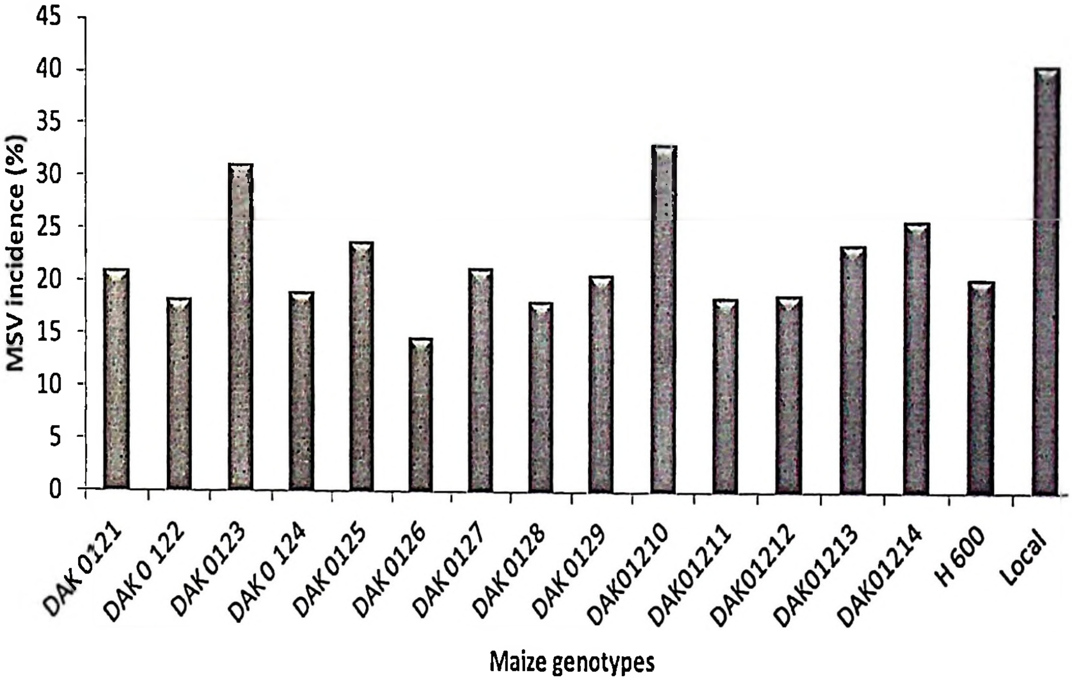

Figure 6: MSV incidence among genotypes at Ilonga

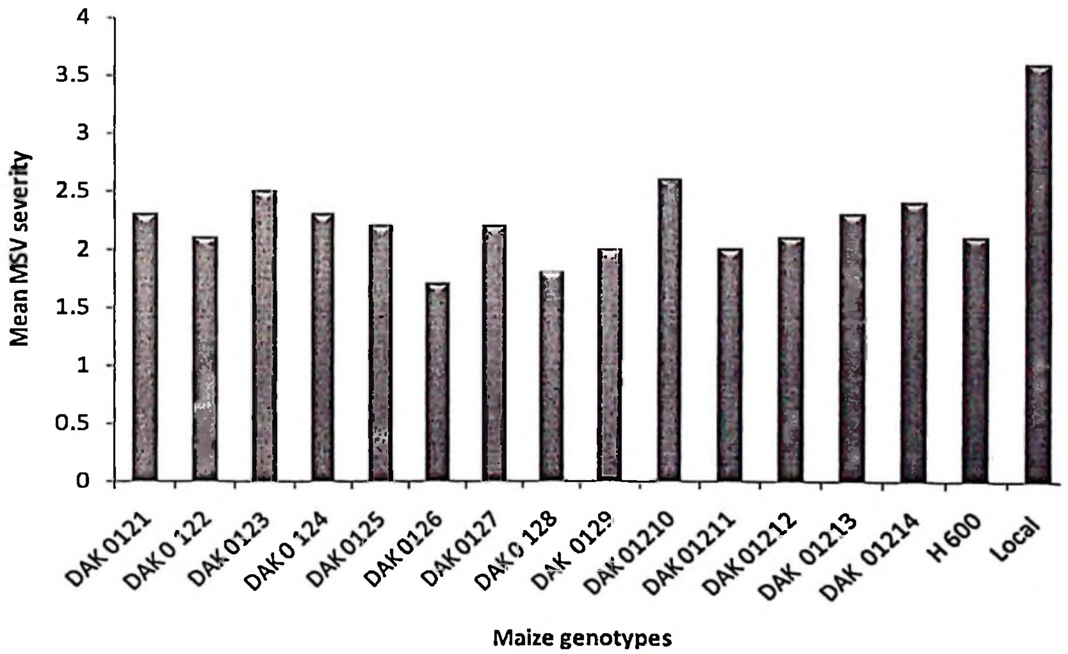

Figure 7: Mean severity of MSV disease among genotypes at Ilonga

According to MSV disease severity scale of 1-5, average severity was 2.3 and most of the genotypes had the score below average but lowest was detected by DAK0126 (1.7) followed by DAK0128 (1.8) (Plate 3a) and DAK0129 (2.0) while the local check was severely affected by MSV (3.6) (Plate 3b)

Plate 3a: **MSV tolerant genotype, DAK0128 at Ilonga site**

Plate 3b: **Local susceptible check showing symptoms of MSV at Ilonga**

4.2.4 Combined analysis

Combined results showing expression and incidence of genotypes are indicated in Figures 8 and 9, DAK0126 had the least severity (1.7) followed by resistant check H600 (1.78), DAK0122 (1.8), DAK0128 (1.84) and DAK0124 (1.87). Genotypes with the most severity scores were local check (3.6), DAK01210 (2.32), DAK01211 (2.21), DAK01213 (2.14), DAK01214 (2.12) and DAK0123 (2.02).

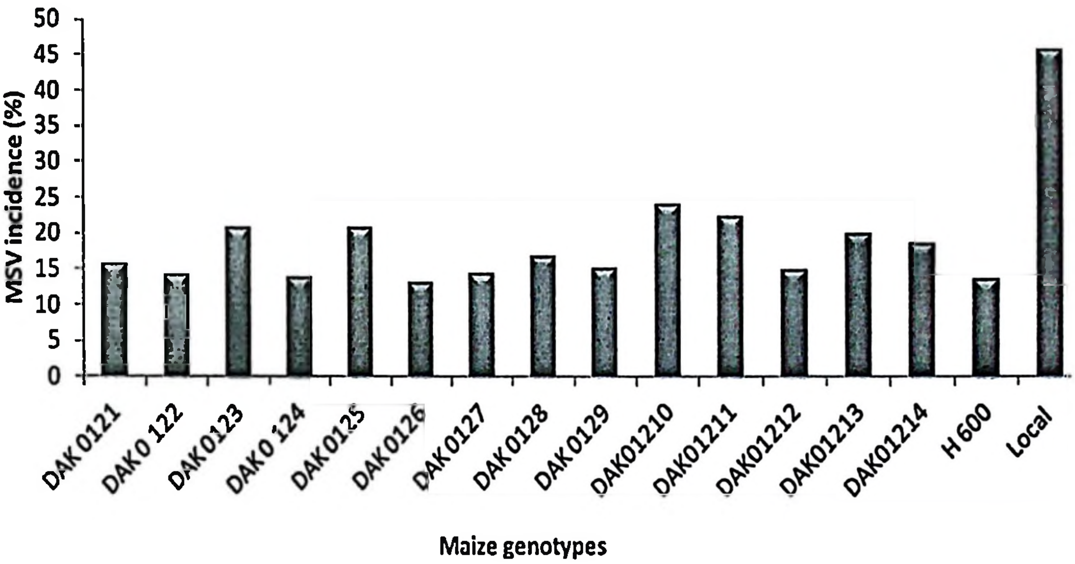

Figure 8: MSV incidence among genotypes in combined analysis

MSV incidence ranged from 46.28% to 13.22% for local susceptible check and DAK0126 respectively. The average incidence was 19.1% and most of the genotypes had mean values of below this average (Table 7). However, this resistance among genotypes is supported by high yields (Table 7).

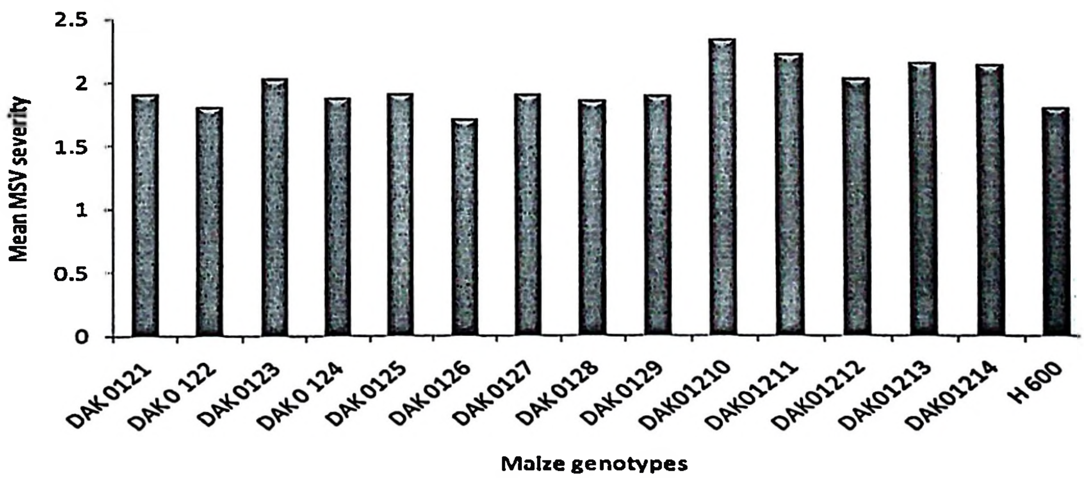

Figure 9: Mean severity of MSV disease among genotypes in combining analysis

4.3 Locations Effects for Various Variables in Studied Areas

Means showing location effects of various variables in all studied locations are indicated in Table 8. Kwamsanga revealed highest mean disease severity (2.51) and incidence (24.37%), followed by Ilonga (2.26) and (23.17%) respectively. Lowest severity (1.42) and incidence (9.67%) were recorded for Dakawa (Figures 10 and 11) respectively. Highest mean yield (4.91 t/ha) was recorded for Dakawa followed by Ilonga (3.70 t/ha) and Kwamsanga (3.0 t/ha). Longest duration for tasselling (56.6 days) was recorded for Kwamsanga followed by Dakawa (54.44 days) and Ilonga (54.38 days). Shortest duration for silking (58.38 days) was recorded for Dakawa followed by Ilonga (59.46 days) and longest was recorded for Kwamsanga (60.23 days). Highest mean plant height (241.2 cm) was revealed for Dakawa followed by Kwamsanga (212.3 cm) and Ilonga (191.4 cm).

Table 8: Location effects for various variables studied at Kwamsanga, Dakawa and Ilonga for the 2012/2013 growing season

Location	GY	DT	DSI	PH	EH	EPP	PL	DI	DS	NGPE	NGR	SW	EG	EL	PM	NRE
Kwamsanga	3.00	56.60	60.23	212.3	113.4	0.94	25.3	24.37	2.51	401.8	30.01	23.50	8.07	13.35	114.17	12.98
Dakawa	4.91	54.44	58.38	241.2	119.6	0.98	14	9.67	1.42	454.8	33.66	31.51	10.06	16.28	113.90	13.15
Ilonga	3.70	54.38	59.46	191.4	107.4	0.96	43.2	23.17	2.26	391.1	29.00	32.55	9.96	14.08	113.40	13.13
Mean	3.87	55.14	59.35	215	113.5	0.96	27.5	19.07	2.06	415.9	30.89	29.19	9.36	14.57	113.82	13.09
SE±	0.11	0.26	0.33	2.58	1.95	0.03	2.33	1.05	0.05	11.52	0.67	0.71	0.16	0.23	0.21	0.14

Grain yield (GY), tasselling days (DT), silking days (DS), plant height (PH), ear height (EH), ear per plant (EPP), plant lodging (PL), MSV incidence (DI), MSV severity (DI), number of grains/ear (NGPE), number of grains/ ear (NGR), 100 seed weight (SW), ear (EG), ear Length (EL), physiological maturity (PM), number of rows/ear

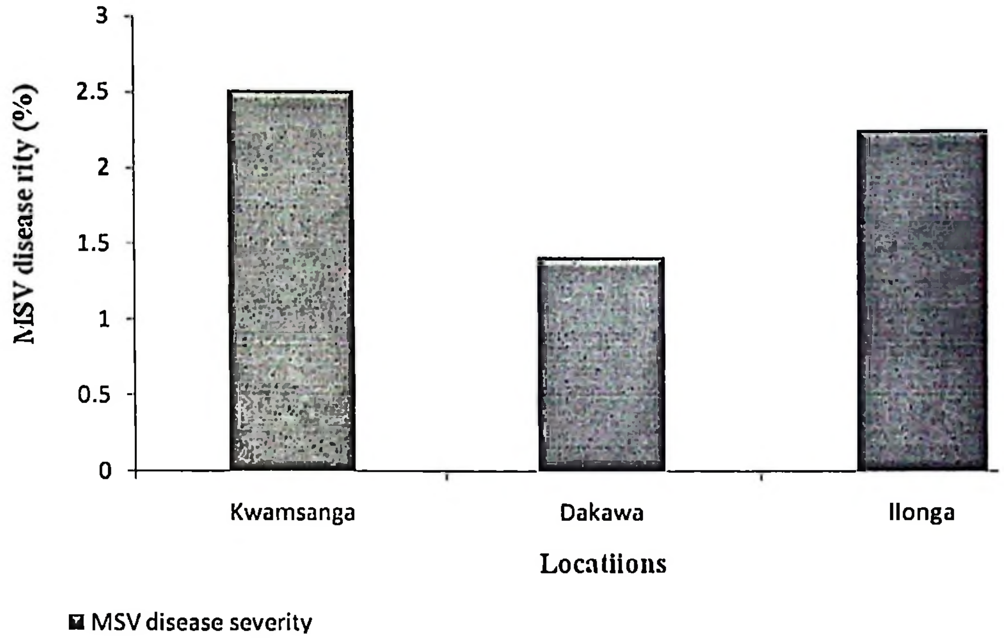

Figure 10: Location effects on MSV disease severity

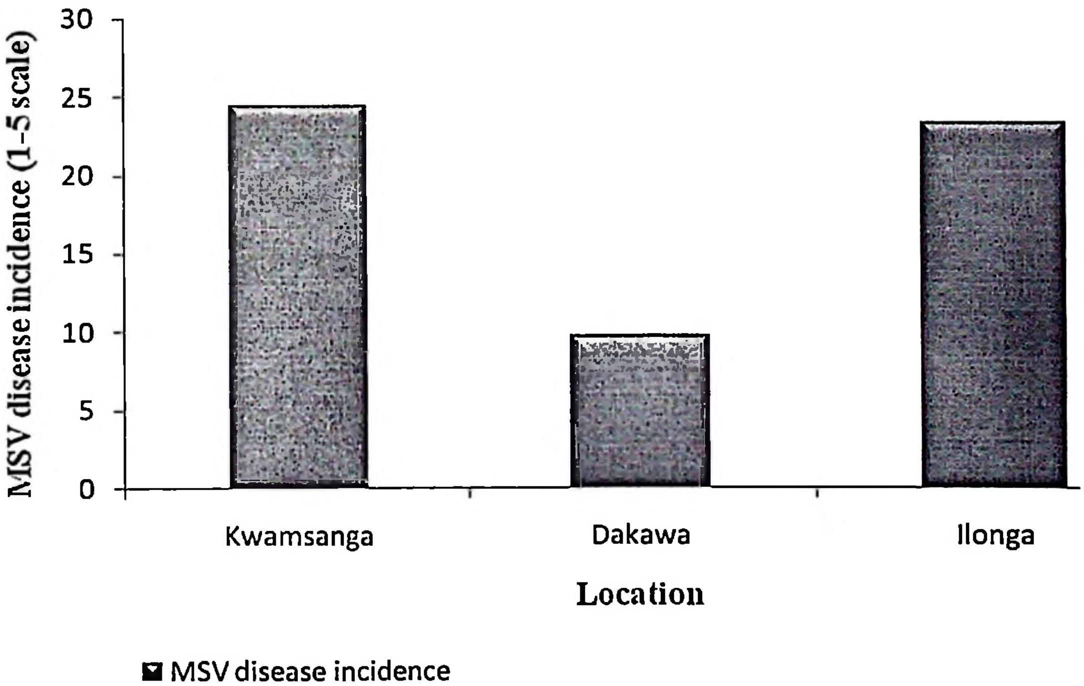

Figure 11: Locations effects on MSV disease incidence

Dakawa recorded highest ear height (119.6 cm) followed by Kwamsanga (113.4 cm) and Ilonga (107.4 cm). However, number of ears per plant (0.98) was observed for Dakawa followed by (0.96) for Ilonga and (0.94) for Kwamsanga. The study revealed highest percentage of lodging plants at Ilonga (43.2) followed by Kwamsanga (25.3) and lowest observed for Dakawa. Highest mean grains/ear and grains /row were observed for Dakawa (454.8) and (33.66) respectively, followed by Kwamsanga (401.8) and (30.1) respectively, and lowest was observed for Ilonga (391.1) and (29.0) respectively.

Hundred seed weight recorded (32.55 g) for Ilonga, followed by Dakawa (31.51 g) and Kwamsanga (23.50 g). Ear girth recorded greatest at Dakawa (10.06 cm), followed by Ilonga (9.96 cm) and Kwamsanga was recorded smallest (8.07 cm). Longest ear (16.28 cm) was observed for Dakawa, (14.08 cm) for Ilonga and shortest (13.35cm) for Kwamsanga. Number of rows/ear recorded (13.15) for Dakawa followed by (13.13) for Ilonga and (12.98) for Kwamsanga. Earliest (113.40 days) in maturity was observed for Ilonga, (113.90 days) for Dakawa and longest (114.17 days) was recorded for Kwamsanga.

4.4 Correlations Between Selected Variables for Studied Genotypes

4.4.1 Kwamsanga site

Majority of variables at this site did not show significant correlations, but ear length (0.65***), number of ears per plant (0.53***), number of grains per ear (0.39**), number of rows per ear (0.34*), MSV incidence (-0.81***) and MSV severity (-0.86***) showed significant associations with grain yield (Table 9). Plant height showed positive significant relationship with number of row per ear (0.36*) and ear length (0.32*). Days to 50% tasselling showed positive and significant relationship with days to 50% silking (0.91***), days to maturity (0.38**), MSV incidence (0.31*) and negative significant with number of grains per ear (-32*). Ear length showed significant and positive relationship with number of grains per ear (0.58***), number of row per ear (0.49***), plant height (0.32*) and number of ears per plant (0.30*). However, had negative and significant relationships with MSV disease incidence (-0.65***) and severity (-0.67***).

In this study number of grains per ear showed positive and significant association with number of rows per ear (0.46**) and ears/plant (37*), but it had negative and significant relationship with days to 50% silking (-0.32*), MSV severity (-0.42**) and MSV incidence (-0.46***). The study revealed that, days to maturity had significant positive association with days to 50% silking (0.41**) Positive and significant relationship was also shown between MSV disease severity and incidence (0.90***) and between 50% days to silking and MSV disease incidence (0.31*). Negative and significant relationship was shown between number of rows per ear and MSV disease severity (-0.30*), MSV disease incidence with number of rows per ear (-0.36*), and number of ears per plant with MSV disease severity (-0.45**).

Table 9: Correlations among selected variables, grain yield, MSV disease severity and incidence at Kwamsanga

		1	2	3	4	5	6	7	8	9	10	11	12
1	grain yield (t/ha)	1											
2	Plant height(cm)	0.22	1										
3	50%Tasselling(days)	-0.02	-0.07	1									
4	Ear length(cm)	0.65***	0.32*	-0.20	1								
5	No of grains/ear	0.39**	0.24	-0.32*	0.58***	1							
6	Days to maturity	-0.03	-0.04	0.38**	-0.15	-0.05	1						
7	50% silking(days)	-0.07	0.01	0.91***	-0.24	-0.32*	0.41**	1					
8	100 seed weight(g)	0.17	0.00	-0.05	0.13	0.08	0.14	-0.07	1				
9	No of rows/ear	0.34*	0.36*	-0.05	0.49***	0.46**	-0.01	-0.07	-0.17	1			
10	MSV incidence(%)	-0.81***	-0.28	0.31*	-0.65***	-0.46***	0.21	0.31*	-0.09	-0.36*	1		
11	MSV severity(1-5)	-0.86***	-0.23	0.16	-0.67***	-0.42**	0.12	0.21	-0.21	-0.30*	0.90***	1	
12	No of ear/plant	0.53***	0.06	-0.05	0.30*	0.37*	0.01	-0.13	0.11	0.23	-0.49***	-0.45**	1

*Significant at 5% level; **Significant at 1% level and *** Significant at 0.1% level

4.4.2 Dakawa site

The present study shows correlations among studied variables at Dakawa (Table 10). Grain yield had significant correlations with most of the traits. It showed positive and significant correlation with ear length (0.74***), number of grains per ear (0.70***), plant height (0.69***), number of rows per ear (0.66***), number of ears per plant (0.61***) and hundred seed weight (0.51***), but was significantly and negatively correlated with MSV severity (-0.90***) and MSV incidence (-0.91***). Plant height revealed significant and positive Correlation with ear length (0.68***), number of rows per ear (0.63***), number of grains per ear (0.56***), 100 seed weight (0.49***) and number of ears per plant (0.47***). 50% tasselling was significantly and positively correlated with days to 50% silking (0.89***) and days to maturity (0.53***). Number of ears per plant was significantly and negatively correlated with MSV severity (-0.64***). This study also showed that ear length had significant and positive association with number of grains per ear (0.83***), number of row per ears (0.79***), number of ear per plant (0.57***) and hundred seed weight (0.51***). On the other hand, it was significantly and negatively correlated with MSV severity (-0.75***) and MSV incidence (-0.77***). Number of grains per ear showed significant and positive association with number of rows per ear (0.84***) and number of ears per plant (0.66***). It revealed significant and negative association with MSV severity (-0.71***) and MSV incidence (-0.72***).

The study showed that days to maturity had significant and positive relationship with days to 50% silking, but also hundred seed weight showed significant and positive correlation with number of rows per ear (0.39**) and number of ears / plant (0.35*).

Table 10: Correlations among selected variables, grain yield, MSV disease severity and incidence at Dakawa

		1	2	3	4	5	6	7	8	9	10	11	12
1	Grain_yield (t/ha	1											
2	Plant height (cm)	0.69***	1										
3	50%Tasselling (days)	-0.16	-0.03	1									
4	Ear length (cm)	0.74***	0.68***	-0.10	1								
5	No of grains/ear	0.70***	0.56***	-0.17	0.83***	1							
6	Days to maturity	-0.04	-0.01	0.53***	-0.19	-0.15	1						
7	50% silking (days)	-0.06	0.10	0.89***	-0.01	-0.12	0.50***	1					
8	100 seed weight (g)	0.51***	0.49***	0.00	0.51***	0.33*	-0.01	-0.01	1				
9	No of rows/ear	0.66***	0.63***	-0.19	0.79***	0.84***	-0.18	-0.15	0.39**	1			
10	MSV incidence (%)	-0.91***	-0.67***	0.19	-0.77***	-0.72***	0.05	0.11	-0.43**	-0.74***	1		
11	MSV severity (1-5)	-0.90***	-0.70***	0.20	-0.75***	-0.71***	0.10	0.08	-0.43**	-0.70***	0.96***	1	
12	No of ear/plant	0.61***	0.47***	-0.36*	0.57***	0.66***	-0.22	-0.29*	0.35*	0.59***	-0.66***	-0.64***	1

*Significant at 5% level; **Significant at 1% level and *** Significant at 0.1% level

The same was significantly and negatively correlated with MSV incidence (-0.43**) and MSV severity (-0.43**). Significant and negative association was also shown between number of rows per ear and MSV severity (-0.70***), number of rows per ear and MSV incidence (-0.74***) and MSV incidence with number of ear per plant (-0.66***), significant and positive association was shown between number of rows per ear and number of ears per plant (0.59).

4.4.3 Ilonga site

The association of grain yield, selected variables, MSV disease severity and incidence at Ilonga was estimated by simple correlation coefficient (Table 11).

Grain yield was positively and significantly correlated with plant height (0.60***), ear length (0.54***), number of ear per plant (0.54***), number of grain per ear (0.53***), number of row per ear (0.51***) and hundred seed weight (0.50***). Grain yield was also negatively and significantly associated with MSV severity (-0.86***), MSV incidence (-0.76***), days to 50% tasselling (-0.60***) and days to 50% silking (-0.56***).

The study revealed that plant height was positively and significantly correlated with ear length (0.43**), number of grains per ear (0.33*), number of rows per ear (0.32*) and also negatively and significantly correlated with MSV incidence (-0.48***), MSV severity (-0.53***), 50% silking (-0.52***) and days to 50% tasselling (-0.62***). However, MSV incidence was positively and significantly correlated with MSV incidence (0.85***) and negatively and significantly correlated with

Table 11: Correlations among selected variables, grain yield, MSV disease severity and incidence at Ilonga

		1	2	3	4	5	6	7	8	9	10	11	12
1	Grain yield (t/ha)	1											
2	Plant height(cm)	0.60***	1										
3	50%Tasselling(days)	-0.60***	-0.62***	1									
4	Ear length(cm)	0.54***	0.43**	-0.42**	1								
5	No of grains/ear	0.53***	0.33*	-0.32*	0.43**	1							
6	Days to maturity	-0.16	-0.18	0.32*	-0.21	-0.15	1						
7	50% silking(days)	-0.56***	-0.52***	0.68***	-0.29*	-0.32*	0.53***	1					
8	100 seed weight	0.50***	0.22	-0.16	0.43**	0.11	-0.01	-0.08	1				
9	No of rows/ear	0.51***	0.32*	-0.39**	0.27	0.74***	-0.23	-0.43**	-0.09	1			
10	MSV incidence (%)	-0.76***	-0.48***	0.54***	-0.39**	-0.43**	0.03	0.55***	-0.29*	-0.47***	1		
11	MSV severity (1-5)	-0.86***	-0.53***	0.51***	-0.51***	-0.47***	0.02	0.46***	-0.46**	-0.46**	0.85***	1	
12	No of ear/plant	0.54***	0.31*	-0.54***	0.38**	0.30*	-0.11	-0.27	0.20	0.29*	-0.46**	-0.50***	1

*Significant at 5% level; **Significant at 1% level and *** Significant at 0.1% level

number of ear per plant (-0.46**). MSV severity was negatively and significantly correlated with number of ear per plant (-0.50***). Days to maturity was positively and significantly correlated with days to 50% silking (0.53***) and days to 50% tasselling.

4.4.4 Correlations studied in combined analysis

Table 12 shows simple correlations for some studied traits in combined analysis. Grain yield revealed to have positive and significant association with ear length (0.75***), plant height (0.62***), number of grains per ear (0.58***), hundred seed weight (0.54***), number of ears per plant (0.52***) and number of rows per ear (0.47***).

Plant height was showed positive and significant correlation with ear length (0.60***), number of grains per ear (0.45***), number of rows per ear (0.35***) and number of ears per plant (0.28***). But negatively and significantly associated with days to 50% tasselling (-0.21**), days to 50% silking (-0.29***), MSV severity (-0.62***) and MSV incidence (-0.64***). Days to 50% tasselling showed positive and significant correlation with days to 50% silking (0.74***), days to maturity (0.40***), MSV severity (0.39***) and MSV incidence (0.38***). On the other hand it showed negative and significant association with number of rows per ear (-0.23***), ear length (-0.33***), number of ears per plant (-0.35***) and hundred seed weight (-0.36***). Ear length was positively correlated with number of grains per ear (0.66***), number of rows per ear (0.51***), hundred seed weight (0.46***) and number of ears per plant (0.43***). Number of grains per ear was positively and

Table 12: Correlation among selected variables, grain yield, MSV disease severity and incidence in joint analysis

		1	2	3	4	5	6	7	8	9	10	11	12
1	Grain yield (t/ha)	1											
2	Plant height(cm)	0.62***	1										
3	50%Tasselling(days)	-0.42***	-0.21**	1									
4	Ear length(cm)	0.75***	0.60***	-0.33***	1								
5	No of grain/ear	0.58***	0.45***	-0.27	0.66***	1							
6	Days to maturity	-0.09	0.02	0.40***	-0.15	-0.09	1						
7	50% silking(days)	-0.39***	-0.29***	0.74***	-0.29***	-0.29***	0.46***	1					
8	100 seed weight	0.54***	0.15	-0.36***	0.46***	0.18*	-0.10	-0.20*	1				
9	No of row/ear	0.47***	0.35***	-0.23***	0.51***	0.68***	-0.15	-0.25**	0.1	1			
10	MSV incidence (%)	-0.88***	-0.64***	0.38***	-0.74***	-0.60***	0.06	0.40***	-0.4***	-0.50***	1		
11	MSV severity (1-5)	-0.89***	-0.62***	0.39***	-0.76***	-0.55***	0.06	0.39***	-0.5***	-0.41***	0.91***	1	
12	No of ear/plant	0.52***	0.28***	-0.35***	0.43***	0.47***	-0.10	-0.23**	0.2**	0.41***	-0.53***	-0.47***	1

*Significant at 5% level; **Significant at 1% level and *** Significant at 0.1% level

significantly correlated with number of rows per ear (0.68***), number of ears per plant (0.47***) and hundred seed weight (0.18*).On the other hand, it was negatively and significantly correlated with days to 50% silking (-0.29***), MSV incidence (-0.60***) and MSV severity (-0.55). Days to maturity was positively and significantly correlated with days to 50% silking (0.46***). Days to 50% silking was also positively and significantly correlated with MSV incidence (0.40***) and MSV severity (0.39***). It was also, negatively and significantly correlated with hundred seed weight (-0.20*), number of rows per ear (-0.25**) and number of ears per plant (-0.23**). Hundred seed weight had positive and significant association with number of ears per plant and negatively and significantly correlated with MSV incidence (-0.4***) and MSV severity (-0.5***).

Number of rows per ear was positive and significant correlated with number of ears/plant (0.41***) and negatively and significantly correlated with MSV incidence (-0.50***) and MSV severity (-0.41***). MSV incidence was positively and significantly correlated with MSV severity (0.91***) and negatively and significantly correlated with number of ears per plant (-0.53***). The present study indicated negative and significant association between MSV severity and number of ears per plant (-0.47***).

4.5 Phenotypic and Genotypic Correlations Among Yield, Yield Components, MSV Disease and Selected Growth Parameters

Results for genotypic and phenotypic correlations shown in Table 13 revealed that there are small differences in magnitude between phenotypic and genotypic

Table 13: Estimates of Phenotypic (lower) and genotypic (upper) correlation coefficients among selected variables, grain Yield and MSV disease in maize

		1	2	3	4	5	6	7	8	9	10	11	12
1	Grain yield (t/ha)	1	0.62***	-0.42***	0.75***	0.58***	-0.09	-0.39***	0.54***	0.47***	-0.88***	-0.89***	0.52***
			0.71***	-0.38***	0.75***	0.60***	-0.05	-0.38***	0.56***	0.47***	-0.89***	-0.89***	0.53***
2	Plant height(cm)		1	-0.21**	0.60***	0.45***	0.02	-0.29***	0.15	0.35***	-0.64***	-0.62***	0.28***
				-0.36***	0.67***	0.46***	-0.04***	-0.34***	0.47***	0.38***	-0.68***	-0.70***	0.31***
3	50%Tasselling(days)			1	-0.33***	-0.27	0.40***	0.74***	-0.36***	-0.23***	0.38***	0.39***	-0.35***
					-0.30***	-0.30***	0.36***	0.75***	-0.16	-0.23**	0.39***	0.37***	-0.36***
4	Ear length(cm)				1	0.66***	-0.15	-0.29***	0.46***	0.51***	-0.74***	-0.76***	0.43***
						0.67***	-0.13	-0.28***	0.51***	0.51***	-0.74***	-0.75***	0.43***
5	No of grain/ear					1	-0.09	-0.29***	0.18*	0.68***	-0.60***	-0.55***	0.47***
							-0.10	-0.30***	0.28***	0.69***	-0.60***	-0.56***	0.48***
6	Days to maturity						1	0.46***	-0.10	-0.15	0.06	0.06	-0.10
								0.45***	-0.04	-0.14	0.06	0.04	-0.10
7	50% silking(days)							1	-0.20*	-0.25**	0.40***	0.39***	-0.23**
									-0.16	-0.24**	0.40***	0.38***	-0.23**
8	100 seed weight								1	0.10	-0.40***	-0.50***	0.20**
										0.11	-0.46***	-0.51***	0.26***
9	No of row/ear									1	-0.50***	-0.41***	0.41***
											-0.50	-0.40***	0.41***
10	MSV incidence (%)										1	0.91***	-0.53***
												0.92***	-0.52***
11	MSV severity (1-5)											1	-0.47***
													-0.47***
12	No of ear/plant												1

***Significant at 5% level; **Significant at 1% level and *** Significant at 0.1% level**

correlations. All variables revealed significant genotypic and phenotypic correlations with grain yield except for days to maturity. Significant and positive genotypic correlations with grain yield were indicated by ear length (r= 0.75***), Plant height (r= 0.62***), Grains per ear (r= 0.58***), hundred seed weight (r=0.54***), Ears per plant (r= 0.52***) and rows per ear (r = 0.47***).

The following variables also showed phenotypic significance and positive correlation with grain yield arranged according to their magnitude: Ear length (r= 0.75***), Plant height (r= 0.71***), grains per ear (r= 0.60***), hundred seed weight (r= 0.56***), number of ears per plant (r= 0.53***) and rows per ear (r= 0.47***). Highest correlations shown between MSV disease incidence and severity (r= 0.91*** and r= 0.92***) genotypic and phenotypic respectively, followed by ear length and grain yield (r= 0.75** and r=0.75**), tasselling and silking (r= 0.74*** and r= 0.75***), grain yield and plant height (r= 0.62*** and r= 0.71***).

4.6 Influence of Yield Components and Selected Growth Variables on Grain Yield

Yield is one among the complex traits controlled by several factors, relating genotypic and environmental factors (Chinnadurai and Pothiraj, 2011). The path coefficient specifies the effective measure of direct and indirect relationship between independent variables and yield as dependent variable. In the present study, path analysis shows the direct and indirect effects (Fig. 12 and Table 14). Out of all traits used for path analysis, hundred seed weight showed maximum positive direct effect on grain yield (0.300) followed by ear length (0.274), plant height (0.264), number of ears per plant (0.185). However, residual effect was higher than all of the direct and indirect effects. Days to silking had negative direct effect and negative correlation to grain yield. Plant height had a relatively high positive indirect effect to grain yield via ear length. On the other hand, days to tasselling had relatively high negative indirect effects through days to silking (-0.103) and hundred seed weight (-0.109). Ear length recorded relatively high positive indirect effect to grain yield through plant height (0.158) and hundred seed weight (0.138). The indirect effects of grains/ear on grain yield via plant height were relatively high and positive. Positive indirect effect of hundred seed weight on grain yield was predominantly through ear length. Indirect effect of number of rows per ear on grain yield through ear length was also relatively high and positive. Thus ear length seems to interact well with plant height and hundred seed weight in influencing yield positively.

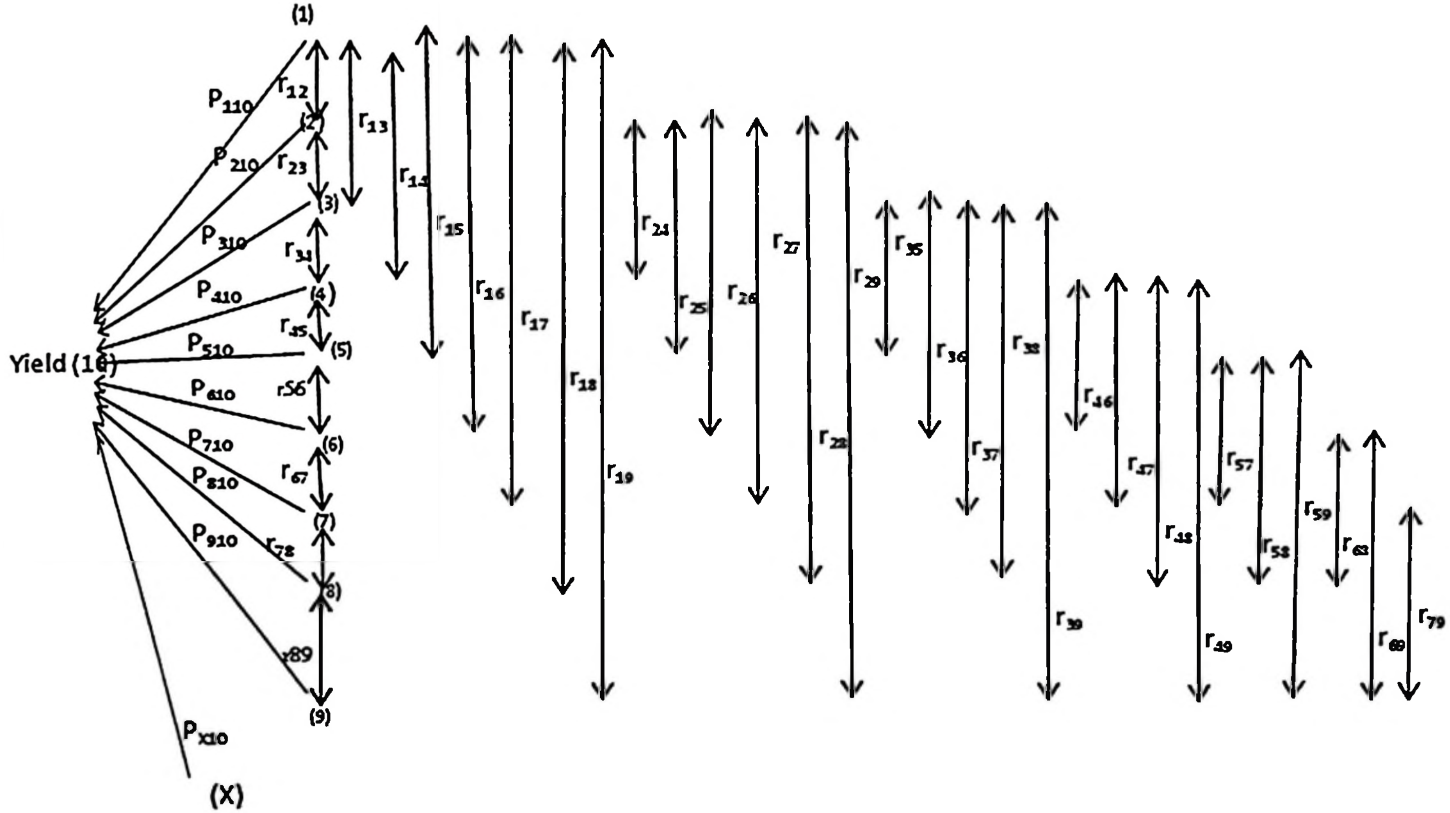

Figure 12: Path diagram showing relationships among yield components and Other selected growth variables

Legend

(1) Plant height (2) Days to tasselling (3) Ear length (4) No of grain per ear (5) Days to maturity

(6) Days to 50 % silking	r_{23}:-0.326	r_{310}:- 0.751	r_{79}: 0.221
(7) 100 seed weight	r_{24}:-0.265	r_{45}:- 0.288	r_{710}: 0.540
(8)No of row per ear	r_{25}:0.403	r_{46}:-0.288	r_{89}: 0.410
(9) No of ear per plant	r_{26}:0.739	r_{47}: 0.177	r_{810}: 0.475
(x) Residual factors	r_{27}:-0.364	r_{48}: 0.683	r_{910}: 0.524
r_{12}:- 0.215	r_{28}: -364	r_{49}: 0.474	P_{110}: 0.264
r_{13}: 0.599	r_{29}:- 0.233	r_{410}: 0.580	P_{210}: 0.008
r_{14}: 0.454	r_{210}: -0.416	r_{56}: 0.459	P_{310}: 0.274
r_{15}: 0.016	r_{34}: 0.657	r_{57}:-0.105	P_{410}: 0.058
r_{16}: -0.290	r_{35}: -0.155	r_{58}: -0.145	P_{510}: 0.077
r_{17}: 0.146	r_{36}: -0.287	r_{59}: -0.104	P_{610}: -0.139
r_{18}: 0.353	r_{37}: 0.459	r_{510}: -0.089	P_{710}: 0.300
r_{19}: 0.281	r_{38}: 0.506	r_{67}: -0.195	P_{810}: 0.074
r_{110}:0.616	r_{39}: 0.433	r_{68}: -0.247	P_{910}: 0.185
r_{69}: -0.234	r_{610}: -0.390	r_{78}: 0.108	P_x: 0.51

Table 14: Path analysis of top crosses maize (along the diagonal are the direct effects)

Characters	1	2	3	4	5	6	7	8	9	Genotypic Correlations with grain yield
1 Plant height	**0.264**	-0.002	0.164	0.026	0.001	0.04	0.044	0.026	0.052	0.616***
2 Days to tasselling	-0.057	**0.008**	-0.089	-0.015	0.031	-0.103	-0.109	-0.017	-0.064	-0.416***
3 Ear length	0.158	-0.003	**0.274**	0.038	-0.012	0.04	0.138	0.037	0.08	0.751***
4 No of grains per ear	0.12	-0.002	0.18	**0.058**	-0.007	0.04	0.053	0.051	0.088	0.580***
5 Days to maturity	0.004	0.003	-0.042	-0.005	**0.077**	-0.064	-0.032	-0.011	-0.019	-0.089
6 Days to silking	0.077	0.006	-0.079	-0.017	0.035	**-0.139**	-0.058	-0.018	-0.043	-0.390***
7 100 seed weight	0.039	-0.003	0.126	0.01	-0.008	0.027	**0.3**	0.008	0.041	0.540***
8 No of rows per ear	0.093	-0.002	0.139	0.04	-0.011	0.034	0.032	**0.074**	0.076	0.475***
9 No of ears per plant	0.074	-0.003	0.119	0.027	-0.008	0.033	0.066	0.03	**0.185**	0.524***
Residual effect (Px)										**0.51**

***** significant at 0.1% level**

4.7 Estimates of Expected Genetic Advance, Heritability and Variance Components for Top Cross Maize in the Studied Variables

Values of genotypic variance, environmental variance, phenotypic variance, G× E variance, broad sense heritability, and estimated genetic advance are given in Table 15. Moreover, relative ratios (%) of some of these variance components in phenotypic variance are also indicated. Negative values were not taken into consideration in calculating variance components ratios in phenotypic variance.

Estimates of components of variance and heritability for studied genotypes over all locations revealed high heritability for majority of recorded traits but recorded relatively low for days to maturity and hundred seed weight. Expected genetic advance (EGA) recorded high for number of grains per ear, plant height, number of grains per row, ear height, MSV disease incidence, and grain yield, but the rest of traits had below 50% EGA. Traits showed relatively higher estimates of phenotypic than genotypic variance, except for ears per plant. The genotype× location recorded lower values of variance than phenotypic variance for all traits. On the other hand, environmental variance was higher than phenotypic variance for most traits viz. ear length, days to maturity, rows per ear, silking days, hundred seed weight, ear per plant, ear circumference, plant height, grains per ear and row. The ratio of genotypic variance in phenotypic variance was 82.6%, 85%, and 82.3% for MSV disease incidence, MSV disease severity and grain yield respectively. The ratio of G × E in phenotype was found as 25.2% for MSV disease incidence, 25% for MSV disease severity and 29.1% for grain yield.

Table 15: Estimates of genetic advance, heritability (broad sense) and variance Components for recorded traits of maize genotypes across Locations

Trait	δ^2_l	δ^2_g	δ^2_{gl}	δ^2_e	δ^2_{ph}	h^2	EGA (%)
Grain yield	0.87 (110.1)*	0.65 (82.3)	0.23 (29.1)	0.6	0.79	82	68.96
Days to % tasselling	1.41 (95.3)	0.86 (58.1)	0.77 (52)	3.27	1.48	58.11	6.41
Ear length	2.3 (115)	0.25 (12.5)	0.25 (12.5)	2.57	2	81.47	46.02
Days to maturity	0.13 (28.3)	0.35 (76.1)	0.35 (76.1)	2.02	0.46	24.89	0.41
No of row/ear	-0.04	0.35 (35.4)	0.35 (35.4)	1	0.99	76.87	23.85
Days to 50% silking	0.82 (49.7)	0.69 (41.8)	0.69 (41.8)	5.08	1.65	51.85	5.94
100 seed weight	23.74 (938.3)	0.86 (34.0)	0.86 (34)	12.05	2.53	35.59	12.69
Diseaase incidence	63.72 (98.6)	53.37 (82.6)	16.3 (25.2)	52.53	64.64	82.57	1153
Disease severity	0.31 (155)	0.17 (85.0)	0.05 (25)	0.13	0.2	84.14	33.09
Ear height	33.82 (15.1)	195.08 (87.0)	20.6 (9.2)	182.3	224.2	87.01	708.1
No of ear/plant	-	0.01 (100)	-	0.02	0.01	79.15	4.25
Ear circumference	1.24 (142.5)	0.7 (80.5)	0.11 (12.6)	1.19	0.87	80.69	30.72
Plant height	620.05 (298.1)	155.44 (74.7)	50.33 (24.2)	319.9	207.97	74.84	298.3
No of grain/ear	929.64 (16.3)	939 (16.4)	939 (16.4)	6367	5718.67	82.16	4654
No of grain/row	5.35 (28.9)	2.42 (13.1)	2.42 (13.1)	21.47	18.53	82.77	204.5

Legend:

δ^2_{ph} = Phenotypic variance, EGA = Expected genotypic advance, h^2 = Heritability (broad sense), δ^2_e = components of variance due to error term
δ^2_g = components of variance due to genotypes, $_{gl}$ = components of variance due to genotype × environment, δ^2_l = Environmental (location) variance
( )* = % ge in relation to phenotypic variance, ( )* = % ge in relation to phenotypic variance

CHAPTER FIVE

5.0 DISCUSSION

Maize streak virus (MSV) disease decreases growth rate and yield of maize at significant levels. However, the growth rate and yield reduction is directly associated with time factor as well as infection stage (Bua and Chelimo, 2010). According to Bua and Chelimo (2010) the earlier the infection, the higher the yield loss but this normally depends on the level of resistance of genotype when it interacts with a particular location.

5.1 G × E Interaction

The present study revealed difference in genotypic performance at all locations (Appendices 1, 2 and 3). Selection for better genotypes on the various traits can be done at these locations. Both location and location × genotype showed significance for some of traits assessed viz. grain yield, MSV disease severity and incidence, ear girth, plant height, rows/ear, and days to silking showed suitability for Dakawa, days to tasselling revealed suitability at Ilonga (Appendix 4 and Table 8). According to Woyengo *et al.,* (2010) it shows the importance of environment and Genotype × environment interaction effects on these traits. For example although Dak0126 was ranked at tenth position at Kwamsanga on yield basis the same genotype ranked first at Ilonga. This could be due to the fact that at high disease pressure the genotype was susceptible to the disease which led to reduction of yield. The disease was low at Ilonga compared to Kwamsanga hence performance of genotypes was better. (Cock, 1985) found that genotypes performance in the field is a function of biotic and abiotic stresses such as differences in soil types, fertility and rainfall. Results of the present study also showed changes of ranking at different locations indicating the need for selection of genotypes for specific adaptability (Baker, 1978). A perusal of data revealed that variances of genotypes × location were high for variables viz. days to tasselling, days to silking, hundred seed weight, disease incidence, ear height, plant height, number of grains per ear and number of grains per row. These interactions imply that expression or relative performance of genotypes depend on environment. Significance of genotype × environment interactions observed on grain yield, days to 50% tasselling, number of row per plant, MSV incidence and severity, indicate differential genotypic response of yield, yield components and other traits across locations. Thus these traits varied from one location to another, so selection should be done basing on location.

5.2 Disease Reaction

MSV has a great impact in yield reduction. Symptoms in most susceptible lines developed rapidly resulting in severe necrosis and great reduction in photosynthetic tissues (Sibiya, 2009). MSV disease affected maize plants may be shorter, less vigorous and produce smaller grains and ears (Okoth *et al.*, 1987). Sibiya (2009) found that early appearance of disease has great potential to cause serious reduction in grain yield. Barrow (1992) reported losses as high as 94.2% for susceptible genotypes compared to 5.6% for resistant genotypes. The study revealed that there were variations in MSV disease incidence and severity for plots and locations. According to the location (Kwamsanga) which had highest MSV disease, severity ranged between 1.7- 4.1, indicating that many genotypes ranked within the intermediate position of the severity scale. Range of 12.4- 45.9 of the incidence indicates that the occurrence of the disease is below 50%. Results showed that there is lowest mean disease rating at Dakawa (1.42) and (9.67%) for severity and incidence respectively.

The study revealed that disease pressures differed within and between locations, where Kwamsanga had highest disease pressure followed by Ilonga and lastly Dakawa site. This gives opportunity to distinguish genotypes and locations according to their superiority in performance under disease pressure. Dak0122, Dak0124 and Dak0125 possess the potential to perform well under MSV high pressure conditions (Tables 4 and 6). Disease resistance is one of the major aim of plant breeders and according to Furhan *et al.* (2012) production of genotypes having resistant background is the primary objective of plant breeding. Variability for traits in the present study indicated possession of remarkable genetic diversity for disease resistance traits and other traits of economic importance.

5.3 Grain Yield and Yield Components

Difference in performance of yield and other traits among genotypes occurred due to inherent genetic differences exhibited by genotypes. Results of grain yield revealed that resistant check (H600), Dak0126, Dak0127, Dak0122, Dak0129 and Dak01212 genotypes were superior basing on yield among the all tested genotypes in combined analysis (Table 7). However, Dak01214 and Dak0129 showed that they are tolerant to MSV disease as besides having disease severity of approximate to 3 at high disease pressure site, they performed well as indicated by their average yield of 3.1

t/ha (Table 4). Therefore these genotypes can be considered when high yielding cultivars are required in areas having high MSV disease pressure. Present results showed that high overall mean yield was observed at Dakawa (4.91 t/ha) followed by Ilonga (3.70 t/ha) and the lowest recorded from Kwamsanga (3.0 t/ha).The highest yield at Dakawa could be due to low MSV disease incidence and severity and other environmental variation. According to observed results (Table 8) high yields were contributed by number of grains/ear, number of grains/row, ear girth, ear length and number of rows/ear. Overall higher yield obtained during growing time and low disease epidemics could be due to the fact that the same conditions that favored yield were not conducive for disease development (Kimoone *et al.*, 2005). The low yield at Kwamsanga could be due to high disease infestation at the early stage of the crop growth and environmental variation and on individual genotype performance.

5.4 Relationships among Variables and Inheritance Studies

There was slight difference in magnitude between phenotypic and genotypic correlations Table 13. The very close values shown by phenotypic and genotypic coefficients of correlation might be due to the fact that associations between traits are predominantly due to genetic causes which are not easily affected by environmental changes. Dewey and Lu, (1959) documented the same as a result of minimized error (environmental) variance on correlation to minor proportions. This implies that selection for higher yield basing on plant height, ear length, grains/ear, hundred seed weight, rows/ear and number of ears/plant should be done. Yadav, (2010) documented that selection basing on recorded traits having high significance association with yield would be reliable. Data from Table 13 revealed that grain yield had negative and significant association with days to maturity, 50% silking, suggesting that genotypes that silk, tassel and mature late will have low yields in these locations. Eastern zone area covers low and mid-altitude zone with low to moderate rainfall (Kaliba *et al.* (1998). Late maturing genotypes yielded less because tasselling, silking and grains filling coincided with dry spell. MSV incidence and severity had negative and significant correlation with grain yield at both genotypic and phenotypic levels indicating that disease had negative effects to grain yield as shown at Kwamsanga where overall mean yield reduced coincided with highest MSV occurrence. Understanding genetic variation as well as association of recorded variables enable the breeder in selection of traits to be improved (Bozokadfa *et al.*, 2010).

Path coefficient permits separation of correlation coefficients into components of direct and indirect effects which gives information on the contribution of certain traits to yield hence form basis of selection for yield improvement. Table 14 depicted that hundred seed weight had highest direct positive contribution to grain yield followed by ear length, plant height and number of ears per plant, also these traits were positively and significantly correlated with grain yield suggesting independently higher contribution to grain yield. The high positive correlation of hundred seed weight on grain yield was predominantly due to its direct contribution to grain yield and indirect positive effect through ear length. Manal (2011) documented that hundred seed weight, number of ears/plant, ear length and plant height should be considered as selection criteria for yield improvement in the studied materials. According to the present study genotypes which had high weight of hundred seeds resulted into increased grain yield. On the other hand, the indirect influence of number of rows/ear on grain yield through ear length was relatively high and positive which indicated that these variables interact well in influencing yield. The significant negative correlation between days to tasselling with yield was predominantly due to the negative indirect effects through days to silking and hundred seeds weight, thus these variables interact negatively with days to tasselling in influencing grain yield. On the other hand, the significant negative correlation between days to silking with yield was mostly due to the negative direct effect of this variable on yield showing that days to silking is an important factor in influencing yield at these locations. Thus early silking will result to higher yields at these locations for the genotypes under study.

The negative significant correlation of days to maturity with grain yield was mainly contributed by its negative indirect effects via ear length, days to silking and hundred seeds weight. Bekele and Nagasha (2013) documented negative and significant correlations between grain yield with 50% days to silking, maturity and 50% days to tasselling, such results are in accordance with the findings of Mruthunjaya *et al.* (2006) and Immanuel (2011). Meanwhile residual effect (0.51) indicated that error variation and other variables might have contributed to the effect so in future work other variables not included in the model need to be included to determine their contribution to grain yield.

Determination of variance components and heritability is of more importance in deciding criteria for assessment and testing procedures in breeding. Table 15 indicates that estimate of phenotypic variances (δ^2_{ph}) were higher compared to genetic variances (δ^2_g), indicating higher environmental influence. This implies that phenotypic selection for these traits will not be very effective and that the traits are more likely to be controlled by many genes. Heritability estimates revealed low for days to maturity indicating high influence by environmental factors and improvement is difficult based on standard selection procedures. MSV disease and other remaining traits have high heritability indicating less influence of environmental factors. Kim and Brewbaker (1977) and Randle *et al.* (1989) documented high values of heritability (60- 90%) for the quantitatively inherited diseases.

High heritability along with genetic advance is an important factor for predicting the resultant effect for selection of the best individuals (Bello, 2012). The estimates of genetic advance seemed to be useful as a selection tool when considered together with heritability estimates (Johnson *et al.*, 1955). This study revealed that grain yield, plant height, grains/ear and grains/row have high heritability and genetic advance, indicating presence of additive gene action for expression of these traits and that larger proportion of phenotypic variance was contributed by genetic variance hence reliable selection has to be made basing on phenotypic expression.

These results are supported by Najeebs *et al.* (2009) who also found greater magnitude of broad sense heritability and high genetic advance in grain yield and plant height, suggesting that the variables were controlled by additive genetic effects. On the other hand low heritability and genetic advance observed for ear length, rows/ear, ears/plant and ear girth may be caused by non additive gene action implying that in order to make improvement of recorded traits several seasons are needed to evaluate these genotypes. Rafique *et al.* (2008) documented that improvement of traits controlled by non additive genes should be done by hybridization and several seasons of evaluation.

CHAPTER SIX

6.0 CONCLUSION AND RECOMMENDATIONS

6.1 Conclusions

The main objective of this study was to produce high yielding top cross maize hybrids which are tolerant to MSV disease among 16 maize genotypes which were evaluated. In general the ANOVA revealed highly significant differences among the genotypes for most of the recorded traits. The differences observed among the top cross genotypes could provide a basis for choosing superior genotypes for future breeding works. Among the three selected hot spots, Kwamsanga and Ilonga were the best for genetic differentiation of genotypes tolerant against maize streak virus disease, while Dakawa was the least representative basing on disease severity and incidence. Based on the highest selected hot spot, Dak0127, Dak0122, Dak0125 and Dak 0124 and commercial resistant variety (H600) was the best materials for yield and tolerance to MSV disease.

The combination of heterozygous genes from staha and homozygous genes from inbred lines used to form these genotypes showed that they fit for MSV disease resistance. Local susceptible check, Dak01213, Dak01211 and Dak 01210 were not good materials for areas having high maize streak disease pressure. High heritability values observed for MSV disease severity and incidence indicate a relatively less environmental influence on this trait implying more chances of genetic improvement for MSV resistance via reduction of its severity and incidence on maize genotypes. Based on independent effect and correlation analysis earlier silking will result into increased yield at these locations. From the study G × E interaction of the genotypes evaluated was found to be significant for grain yield, days to 50% tasselling, MSV incidence and severity, ear girth and number of rows per ear. Presence of genetic variability for these traits indicated that good progress can be made in selecting for grain yield under the different environments.

6.2 Recommendations

i. Identified best materials and intermediate for MSV resistance should be further evaluated in more seasons in order to come with more conclusive information on their resistance to MSV, their stability and pattern of response across locations and years.

ii. In order to confer complete resistance for MSV it is recommended that more materials should be used during crossing work.

iii. At both locations selection for increased yield should be based on ear length, number of rows/ear and ears/plant.

iv. Combined analysis showed that plant height, ear length, hundred seed weight, number of ears per plant should be considered during future breeding work since they showed high correlation with grain yield.

v. Path analysis revealed the importance of number of ears per plant, hundred seed weight and plant height due to their high direct contribution and correlation on grain yield. Earlier silking genotypes should be used for increased yield at these locations.

vi. Heritability along with genetic advance is more helpful in predicting genetic gain under selection. In the present study, high heritability and genetic advance was observed for grain yield, plant height, grains/ear and grains/row, therefore selection based on these traits will be effective.

REFERENCES

Abebe, M. (2008). Breeding for resistance to disease. *In proceedings of DTMA Maize breeders workshop, 17Aug-3Sept, 2008*, Nairobi, Kenya.1-4pp.

Alexander, P. and Bindiganavile, V. (2008). Combining Ability of CIMMYT's early maturing maize (Zea maysL.) germplasm under stress and non-stress conditions and identification of testers. Euphytica 162: 353-362.

Bekele, A. and Nageshwar, R. T. (2013). Estimates of Heritability, Genetic Advance and Correlation Study for Yield and it's Attributes in Maize (*Zea ays L.*). *Journal of Plant Sciences*. 2 (1): 1- 4.

Badu, B., Abamu, F. J., Menkir, A., Fakorede, M. A. B. and Obeng-Antwi, K. (2003). Genotype by Environment interactions in the regional early maize variety trials in west and central Africa. *Maydica*. 48 (2): 93-104.

Baker, R. J. (1978). Issues in diallel analysis. *Crop Science* 18: 533-536.

Barrow, M. R. (1992). Increasing maize yields in Africa through the use of maize streak Virus resistant hybrids. *African crop science. Journal*.1 (2):139-144.

Bjarnason, M. (1985). Progress in breeding for resistance of the maize streak virus disease. In: *To Feed Ourselves. Proceedings of the First Eastern, Central, and Southern Africa Regional Maize Workshop, Lusaka, Zambia*, 10-17 March, pp 197-207.

Bosque-Perez, N. A., Olojede, S. O., Buddenhagen, I. W. (1998). Effect of maize streak virusdisease on the growth and yield of maize as influenced by varietal resistance levels and plant stage at time of challenge. *Euphytica* 101: 307-317.

Bosque-Perez, N. A. (2000). Eight decades of maize streak virus research. *Virus Research*. 71(1/2): 107-121.

Bello, (2012). Heritability and Genetic Advance for grain yield and its related attributes. In: *maize (Zea mays L.) Instascience. Journal. of micro and Biotechnology*. 2 (1) 1-14.

Bozokalfa, K, M., Esiyokhulya, I, D. and Kaygisiz, A. T. (2010). Estimates of Genetic variability and association studies in quantitative plant traits of *Eruca spp*. Landraces. *Genetika*, 42 (3) pp501.

Bidinge, F. R., Bhasker Raj, A. G., Negusse, A., Adam, M. A., Obilana, A. B. and Jones R. B. (2005). Topcross hybrids as an entry into commercial seed production of pearl millet in Eastern Africa. *Experimental Agriculture* 41: 335-356.

Bua, B. and Chelimo, B. M. (2010). The reaction of maize genotypes to the maize streak virus in central Uganda. In: second RUFORUM biennial Regional conference on "*Building capacity for food security in Africa*. Sept. 2010. Entebbe, Uganda. pp 293-297.

Chinnadurai, I. S. and Pothiraj, N. (2011). Interrelationship and Path-coefficient Studies for Qualitative Traits, Grain Yield and other Yield Attributes among Maize *(Zea mays L.)*. *International Journal of Plant Breeding and Genetics.* 5: 209-223.

Cock, J. H. (1985). Stability of performance of cassava. In: Cassava breeding: a multidisciplinary review. Proceedings of a workshop in the Philippines, *4-7 March* 1985. Pp177-207.

Dewey, J. R., Lu, K. H. (1959). A correlation and path co-efficient analysis of components of crested wheat seed production. *Agronomy* Journal 51, 515-518.

FAO statistics (2006): www.fao.org.

Fajemisin, J. M., Kim, S. K., Efron, Y. and Alam, S. M. (1984). Breeding for durable disease resistance in Tropical maize with special reference to maize streak *virus. Cereal improvement programme* IITA Ibadan, Nigeria. (55): 49-71.

Fajemisin, J. M., Dabrowski, Z. T., Efron, Y. and Kim, S. K. (1986). Weather factors associated with recurring maize streak epidemics. In: *Proceedings of the Seminar on Agrometeorology and Crop Protection in the Lowland Humid and Sub-Humid Tropics.* Cotonou, Benin, 7-11 July. (World Meteorological Organization), pp. 267-276.

Furhan, A., Mareeya, M., Jie, X., Durrishahwar, J., Hidayat ur, R., Yan, L., Wassem, H., Hidayat, U., Muhammad, N., Iltaf, U. and Jianbing Y. (2012). Accumulation of desirable alleles for southern leaf blight in maize (Zea mays L.) under the epiphytotic of Helminthosporium maydis. *Australian Journey of Crop Science* 6(8):1283-1289.

FSD (Food Security Department). (1992). Comprehensive Food Security. DSM, Tanzania: Government of the United Republic of Tanzania, and the United Nations Food and Agriculture Organization (FAO). pp 15-31.

Geddes, A. W. (1990). The Relative Importance of Crop Pests in sub-Saharan Africa. *Natural Resources Institute Bulletin* 36: 66pp.

Genstat. 13.0 Commettee of the Statistics Dept. Rothamsted Experimental Station. (2013). Genstat 13 Reference Manual. Clarendon Press Oxford.

Guthrie, E. J. (1978). Measurement of yield losses caused by maize streak disease. *Plant Disease Reporter.* 62(10), 839-841.

Hanson, C. H., Robinson, H. F. and Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agronomy Journal*. 48:268- 272.

Hidayat, U., Iftikhar, H. K., Iltafullah, H., Hidayat-ur-Rahman, J. and Ibni, A. (2011). Genotype x Environment Interaction, Heritability and Selection Response for yield contributing traits in Mungbean. *African Journal of Biotechnology. 10(4): 475-483.*

Hilty, J. W., Hadden, C. H. and Garden, F. T. (1997). Response of maize hybrids and inbred lines to Gray Leaf Spot disease and its effects on yield in Tennessee. Plant. *Disease Reporter 63 (6): 515-518.*

Immanuel, S., Nagarajan, P., Thiyagarajan, K., Bharathi, M. and Rabindran, R. (2011). Genetic parameters of variability, correlation and path coefficient studies For grain yield and other yield attributes among rice blast disease Resistamt genotypes of rice *(Oriza sativa L.). African journal of biotechnology* .10(17): 3322-3334.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Estimation of genetic and Environmental Variability in soybeans. *Agronomy Journal,* 47: 314–318.

Hanson, C. H., Robinson, H. F. and Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agronomy Journal*. 48:268- 272.

Hidayat, U., Iftikhar, H. K., Iltafullah, H., Hidayat-ur-Rahman, J. and Ibni, A. (2011). Genotype x Environment Interaction, Heritability and Selection Response for yield contributing traits in Mungbean. *African Journal of Biotechnology. 10(4): 475-483.*

Hilty, J. W., Hadden, C. H. and Garden, F. T. (1997). Response of maize hybrids and inbred lines to Gray Leaf Spot disease and its effects on yield in Tennessee. Plant. *Disease Reporter 63 (6): 515-518.*

Immanuel, S., Nagarajan, P., Thiyagarajan, K., Bharathi, M. and Rabindran, R. (2011). Genetic parameters of variability, correlation and path coefficient studies For grain yield and other yield attributes among rice blast disease Resistamt genotypes of rice (*Oriza sativa L.). African journal of biotechnology*.10(17): 3322-3334.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Estimation of [illegible] and Environmental Variability in soybeans. *Agronomy Journal*, [illegible] 318.

Kaliba, A. R. M., Verkuijl, H., Mwangi, W., Moshi, A. J., Chilagane, A., Kaswende, J. S. and Anandajayasekeram, P. (1998). Adoption of maize production technologies in Eastern Tanzania. Mexico, D.F.: International Maize and Wheat Improvement Centre (CIMMYT), the United Republic of Tanzania and the Southern Africa Centre for Co-operation in Agricultural Research (SACCAR).

Kang, M. S. and Gorman, D. P. (1989). Genotype × environment interaction in maize. *Agronomy Journal.* 81(4): 662-664pp.

Kaswende, J. S. and Mbwaga, A. M. (1998). Maize annual progress report, ARI Ilonga. 1-12 pp.

Kimoone, G., Berga, L. and Adipala, E. (2005). Evaluation of selected elite potato Genotypes in eastern Uganda. Kampala, Uganda. *African crop science journal,* 13 (2):125-13.5.

Kim, S. K. and Brewbaker, J. L. (1977). Inheritance of general resistance in maize to *Puccinia sorghi. Crop Science*. 17: 456-461.

Lyimo, N., Temu, A, Gondwe, B., Nsemwa, L. T. A., Stathers, T., Lamboll, N. and Gibson, R. (2005). Southern Highlands Maize Innovation System Stakeholders Workshop. In: *Improving understanding and enhancing Access to Quality Seed and other products,* 9-10th November 2005 VETA Mbeya, Tanzania, 42-104pp.

Lyimo, N. G. (2006). Improvement of farmers' access to and management disease resistant cultivars in the Southern Highlands of Tanzania. Final technical report for DFID project R84061 Uyole, Mbeya, Tanzania pp 62.

Manal, H. (2011). Genetic parameters and path analysis of yield and its components in corn inbred Lines (*Zea mays L.*) at different sowing dates. *Asian Journal of Crop Science,* 3: 106-117.

Magenya, O. E., Mueke, J. and Omwega, C. (2008). Significance and transmission of maize streak virus disease in Africa and option for management. *African Journal of Biotechnology*. 7 (25): 4897-4910.

Markham, P. G., Pinner, M. S. and Boulton, M. I. (1984). The transmission of maize streak virus by leafhoppers, a new look at host adaptation. *Bulletin of Social Entomology*. 57(4): 431-432.

Mduruma, Z. O. and Ngowi, P. S. (1997). The need for genetic and management solution of limitations imposed by drought and low N on maize in Tanzania. In: proceeding of symposium on developing Drought and low-N tolerant maize (edited by Edmeades, G.O et al) 25-29 March1996, El batan, Mexico, pp 79-82.

Mesfin, T., Hollander, J. D. and Markham, P. G. (1995). Feeding activities of Cicadulina mbila *(Hemiptera: Cicadellidae)* on different host-plants. *Bulletin of Entomology and Research.* 85(3): 387-396.

Mesfin, T. and Bosque-Pe′rez, N. A. (1998). Feeding behaviour of *Cicadulina storey China* (Homoptera: Cicadellidae) on maize varieties susceptible or resistant to maize streak virus. *African Entomology*. 6: 185-191pp.

Moshi, A. J., Anandajayasekeram, P., Kariba, A., Martella, D., Mwangi, W. and Shao F. M. (1987). *Economic impact of maize research in Tanzania.* pp76.

Mruthunjaya, C.W., Salmath, P. M., Prashanth, M. and Harlapur, S. I. (2006). Studies on character association as influenced by yield, starch and oil in maize (*Zea mays L.*). *Karnataka Journal of Agriculture Science.* 19 (4): 932-935.

Najeeb, S., Rather, A. G., Parray, G. A., Sheikh, F. A. and Razvi, S. M. (2009). Studies on genetic variability, genotypic correlation and path coefficient analysis in maize under the high temperate condition of Kashmir. Maize genetic cooperation newsletter No. 83. pp46.

Ngowi, P. M. S. (2002). Effect of genotype × environment interaction and interrelationship of yield and yield components of 18 maize (*Zea mays L.*) genotypes in the low lands maize growing area of Tanzania. Dissertation for award of Msc. Degree at Sokoine University of Agriculture, Morogoro, Tanzania. 133pp.

Okoth, V. A. O., Dabrowski, Z. T., Thottappilly, G. and Emden, H. F. (1987). Comparative analysis some parameters affecting maize streak virus (MSV) transmission of various *Cicadulina spp.* populations. Insect Science and Application. 8(3): 295-300.

Olakojo, S. A. and Iken, J. E. (2001). Yield performance and stability of some improved maize (Zea mays L.) varieties. *Moor Journal of Agriculture Research.* 2: 21- 24pp.

Olaoye, G. (2009). Evaluation of new generation maize steak virus (MSV) resistant maize varieties for adaptation to southern guinea savanna ecology of Nigeria. African journal of biotechnology. 8(19): 4906-4910, (http:// www.academic journal.org/AJB) site visited on 4/11/2013.

Onwueme, I. C. and Sinha, T. D. (1991). Field Crop Production in Tropical Africa: Principle and Practice. Centre for tropical Agriculture.Ede.pp.159-175.

Pixley, R. and Banziger, M. (2004). Open-pollinated maize varieties:A backward step or valuable options for farmers? In Frisen, D. R. and A. F. E. Palmer (editorial). Integrated approaches to higher maize productivity in the new millennium. Proceeding, of the seventh Eastern and Southern Africa Regional Maize conference.5-11 February 2002. Nairobi, Kenya. CIMMYT and Kari. pp22-28.

Randle, W. M., Davis, D. W. and Groth, J. V. (1989). Improvement and genetic control of partial resistance in sweet corn to leaf rust. *Journal of American. Society of Horticulture. Science.* 109: 777-781.Rafique, M., Hussain, A. and Sanwar,M.(2008). Evaluation of 3 way crosses through genetic Variability, broad sense heritability, characters association and path analysis. *Journal of Agriculture. Research 46*(1): 39-45.

Rose, D. J.W. (1978). Epidemiology of Maize Streak Disease. *Entomology*. 23: 259 - 82.

Salasya, B. D. S., Mwangi, W., Verkuijl, H., Odendo, M. A. and Odenya, J. O. (1998). An assessment of the adoption of seed and fertilizer package and role of credit in smallholder maize production in Kakamega and Vihiga districts, Kenya. Mexico, CIMMYT and KARI. pp.36.

Shepherd, D. N., Mangwende, T., Martin, D. P., Bezuidenhout, M., Rybicki, E. P. and Thomson, J. A. (in press) Maize streak virus-resistant transgenic maize: a first for Africa. *Plant Biotech. Journal.*

Smith, M.C., Page, W. W., Holt, J. and Kyetere, D. (2000). Spatial dynamics of maize streak virus disease epidemic development in maize fields. *International journal of pest management.* 46(1): 55-66.

Steel, R. G. D. and Torrie, J. H. (1980). Principles and Procedures of Statistics. A Biometrical Approach. 2nd Edition. McGraw Hill Book. New York.pp. 580.

Sibiya, J. (2009). Breeding for resistance to phaeosphaeria leaf spot and other important foliar disease and a study of yield stability in African maize germplasm. Thesis for award of Phd at University of Kwazulu Natal South Africa, pp 94-102.

Thottappilly, G., Bosque-P'erez, N. A. and Rossel, H. W. (1993). Viruses and virus diseases of maize in tropical Africa. *Plant Pathology*. 42: 494-509.

Vianney, M. C. and Efren, E. M. (2008). Usefulness of improved open-pollinated varieties in the development of top cross white maize hybrids, *USM R & D* 16(2): 97-103.

Vivek, B., Pixley, K., Odongo, O., Njuguna, J., Imanywoha, J. B., Bigirwa, G. and Diallo, A. (2004). Regional Disease Nursery (REGNUR): *An Opportunity for Developing Multiple Disease Resistance*. In: Friesen, D. K. and Palmer, A. F. E. (eds). *Integrate Approaches to Higher Maize Productivity in the New Millennium*: Proceedings of the Seventh Eastern and Southern Africa Regional Maize Conference. 5 -11 Feb 2002, Nairobi, Kenya. CIMMYT and KARI. Pp 66 – 68.

Western, J. H. (1971). Disease of crop plant. Macmillan press Ltd, London. 20pp.

Woyengo, V. W., Odongo, O. M. and Ajanga, S. I. (2010). Combining ability analysis of 72 maize inbred lines and development of top cross hybrids resistant to foliar diseases. In: *Proceedings of the 12th KARI biennial scientific conference.* Nov 2010, Nairobi, Kenya. pp 308-311.

Yadav, S. K., Suresh, B. G., Praveen, P. and Binod, K. (2010). Assessment of genetic variability, correlation and path association in rice (oryza sativa l.). *Journal of bio-science.* 18: 1-8pp.

APPENDICES

Appendix 1: ANOVA summary showing mean squares for traits studied at Ilonga the 2012/2013 growing season

No	Characters	Replication (df = 2)	Genotype (df = 15)	Error (df = 30)	Total (df =47)
		Source of variation			
1	Grain yield (t/ha)	5.64***	2.63***	0.48	8.75
2	Days to 50% tasselling	0.06	16.93***	3.84	20.83
3	Days to 50% silking	16.08	23.42*	8.75	48.25
4	Plant height (cm)	321.8	918.5*	351.4	1591.7
5	Ear height (cm)	16.4	741.3***	192.5	950.2
6	No of ears/ plant	0.01	0.03	0.02	0.06
7	Lodging plants	881.5	464.1	496.4	1842
8	MSV incidence (%)	161.65	138.58**	0.48	300.71
9	MSV severity (1-5)	1.19***	0.56***	0.16	1.91
10	No of grain/ ear	5541	21227**	6190	32958
11	No of grain/ row	6.14	37.03*	14.72	57.89
12	Weight of 100 seed	111.61***	16.16	8.57	136.34
13	Ear girth (cm)	7.88**	1.87	1.29	11.04
14	Ear length (cm)	3.33	5.23**	1.826	10.386
15	Physiological maturity	2.58	5.12*	2.38	10.08
16	No of row /ear	0.02	4.69***	0.56	5.27

* = Significance difference at P= 0.05, ** = Significance difference at P = 0.01 and *** = Significance at P= 0.001

Appendix 2: ANOVA summary showing mean squares for traits studied at Kwamsanga during the 2012/2013 growing season

		Source of variation			
No	Characters	Replication (df = 2)	Genotype (df = 15)	Error (df = 30)	Total (df =47)
1	Grain yield (t/ha)	0.42	1.43***	0.34	2.19
2	Days to 50% tasselling	3.27	1.12	3.07	7.46
3	Days to 50% silking	3.27	1.85	4.14	9.26
4	Plant height (cm)	302.8	381.1	202.9	886.8
5	Ear height (cm)	262.9	598.5**	178.3	1039.7
6	No of ears/ plant	0.03	0.03	0.02	0.08
7	Lodging plants	55.4	417.3	225.4	698.1
8	MSV incidence (%)	76.02	180.37***	42.69	299.08
9	MSV severity (1-5)	0.2	0.99***	0.12	1.31
10	No of grain/ ear	23319*	16032*	6551	45902
11	No of grain/ row	30.43	64.05*	24.53	119.01
12	Weight of 100 seed	12.6	12.72*	5.46	30.78
13	Ear girth (cm)	0.37	1.83	0.96	3.16
14	Ear length (cm)	1.86	6.20*	2.77	10.83
15	Physiological maturity	1.90	3.02	2.45	7.37
16	No of row /ear	4.68*	2.37*	1.15	8.19

* = Significance difference at P= 0.05, ** = Significance difference at P = 0.01 and

*** = Significance at P= 0.001

Appendix 3: ANOVA summary showing mean squares for traits studied at Dakawa During the 2012/2013 growing season

		Source of variation			
No	Characters	Replication (df=2)	Genotype (df=15)	Error (df=30)	Total (df=47)
1	Grain yield (t/ha)	0.59	5.62***	0.76	2.32
2	Days to 50% tasselling	9.25	6.39*	2.98	6.21
3	Days to 50% silking	5.06*	3.91**	1.42	3.46
4	Plant height (cm)	160.2	1513.8***	399.4	2073.4
5	Ear height (cm)	18.8	1202.1***	187.9	1408.8
6	No of ears/ plant	0.01	0.09***	0.02	0.12
7	Lodging plants	289.88*	220.35**	77.13	587.36
8	MSV incidence (%)	81.39	465.66***	53.37	600.42
9	MSV severity (1-5)	0.14	0.78***	0.1	1.02
10	No of grain/ ear	3276	32576***	5621	41473
11	No of grain/ row	16.77	123.17***	26.05	165.99
12	Weight of 100 seed	2.14	23.14	17.62	42.9
13	Ear girth (cm)	1.28	7.09***	0.88	9.25
14	Ear length (cm)	0.38	13.21***	3.12	16.7
15	Physiological maturity	1.396	2.121	1.129	4.65
16	No of row /ear	1.008	5.916***	1.123	8.047

* = Significance difference at P= 0.05, ** = Significance difference at P = 0.01 and *** = Significance at P= 0.001

Appendix 4: ANOVA summary showing mean squares for traits in combining Analysis during the 2012/2013 growing season

No	Characters	Replication (df=2)	Location	Source of variation Genotype (df=15)	G × E (df=30)	Error (df=94)	Total (df=141)
1	Grain yield (t/ha)	2.33*	44.89***	7.11***	1.28**	0.6	53.88
2	Days to 50% tasselling	7.19	77.34***	13.3***	5.57*	3.27	99.48
3	Days to 50% silking	0.4	41.65***	14.86***	7.16	5.08	68.75
4	Plant height (cm)	54.64	29967.7***	1871.7***	470.9	319.9	32630.2
5	Ear height (cm)	109.52	1794.7***	2017.8***	262.1	182.3	4256.9
6	No of ears/ plant	0.02	0.02*	0.11***	0.02	0.02	0.17
7	Lodging plants	961.40*	10404.3***	825.3***	138.2	260.6	11628.4
8	MSV incidence (%)	91.35	3198.65***	581.77***	101.42**	52.53	3634.37
9	MSV severity (1-5)	0.47	15.53***	1.78***	0.28**	0.13	17.72
10	No of grain/ ear	8320.21	55760***	51468***	9184	6367	122779
11	No of grain/ row	23.59	287.48***	166.76***	28.74	21.47	504.45
12	Weight of 100 seed	34.65	1176.86***	22.73*	14.64	12.05	1226.28
13	Ear girth (cm)	0.66	60.52***	7.79***	1.5*	1.19	71.00
14	Ear length (cm)	0.42	111.46***	17.98***	3.33	2.57	135.34
15	Physiological maturity	0.19	7.34*	4.1*	3.081	2.024	16.55
16	No of row /ear	1.29	0.4	8.87***	2.05**	1.00	12.32

- = Significance difference at P= 0.05, ** = Significance difference at P = 0.01 and

*** = Significance at P= 0.001

Appendix 5: Equation coefficients for path analysis

1st Equation

r_1=1, r_2= -0.215, r_3= 0.599, r_4= 0.454, r_5= 0.016, r_6= -0.29, r_7= 0.146, r_8= 0.353, r_9= 0.281, X_1= 0.16

2nd Equation

r_1=-0.215, r_2=1, r_3= -0.326, r_4= -0.265, r_5= 0.403, r_6= 0.739, r_7= -0.364, r_8= -0.233 r_9= -0.347, X_1= -0.416

3rd Equation

r_1= 0.599, r_2= , r_3 =-0.326 , r_4= 1, r_5= -0.155 , r_6= -0.287 , r_7= 0.459, r_8= 0.506, r_9= 0.433, X_1= 0.751

4th Equation

r_1= 0.454, r_2=-0.265, r_3= 0.657, r_4= 1, r_5= -0.091, r_6= -0.288, r_7= 0.177 , r_8=0.683, r_9= 0.474 , X_1= 0.580

5th Equation

r_1=0.016, r_2=0.403, r_3= -0.155, r_4= -0.091, r_5= 1, r_6= 0.459, r_7= -0.105, r_8= 0.145, r_9=-0.104, X_1= -0.089

6^{th} Equation
r_1= -0.290, r_2= 0.739 , r_3=-0.287 , r_4=-0.288, r_5= 0.459 , r_6= 1, r_7= -0.195, r_8=-0.247
r_9= -0.234, X_1= -0.390
7^{th} Equation
r_1= 0.146, r_2= -0.364 , r_3 = 0.459, r_4= 0.177, r_5= -0.105, r_6= -0.195 , r_7= 1 , r_8=0.108,
r_9=0.221, X_1= 0.540
8^{th} Equation
r_1= 0.353, r_2= -0.233, r_3 = 0.506, r_4= 0.683, r_5= -0.145, r_6= -0.247, r_7= 0.108, r_8= 1
r_9= 0.410, X_1= 0.475
9^{th} Equation
r_1= 0.281, r_2= -0.347, r_3 = 0.433, r_4= 0.474, r_5= -0.104, r_6= 0.234 , r_7= 0.221, r_8=4100
r_9= 1, X_1= 0.524

Appendix 6: Solutions to the 9 simultaneous equations

P1 =0.264
P2 =0.08
P3 =0.274
P4 =0.058
P5 =0.077
P6 = - 0.139
P7= 0.3
P8 =0.074
P_9 =0.185
Calculated residual 'P' =0.5099241

Appendix 7: Direct and indirect effects

P_1	P_2	P_3	P_4	P_5	P_6	P_7	P_8	P_9
0.264	-0.002	0.164	0.026	0.001	0.04	0.044	0.026	0.052
-0.057	0.008	-0.089	-0.015	0.031	-0.103	-0.109	-0.017	-0.064
0.158	-0.003	0.274	0.038	-0.012	0.04	0.138	0.037	0.08
0.120	-0.002	0.18	0.058	-0.007	0.04	0.053	0.051	0.088
0.004	0.003	-0.042	-0.005	0.077	-0.064	-0.032	-0.011	-0.019
-0.077	0.006	-0.079	-0.017	0.035	-0.139	-0.058	-0.018	-0.043
0.039	-0.003	0.126	0.01	-0.008	0.027	0.3	0.008	0.041
0.093	-0.002	0.139	0.04	-0.011	0.034	0.032	0.074	0.076
0.074	-0.003	0.119	0.027	-0.008	0.033	0.066	0.03	0.185

The direct effects appear in the diagonal as P's, each colum is labeled as P_1, P_2, P_3......P_n
The sum of the rows total = direct and indirect effects is equal to the corresponding overall correlation coefficients