INFLUENCE OF GENOTYPE X ENVIRONMENT INTERACTION ON PERFORMANCE OF SELECTED MAIZE *(Zea mays* L.) HYBRIDS IN SOUTHERN HIGHLANDS OF TANZANIA

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ABSTRACT

A field experiment was conducted during the 2010/2011 cropping season in four locations of the Southern Highlands of Tanzania viz. Inyala, Mbimba, Uyole and Seatondale. The main objective of the study was to assess the response of selected maize genotypes across different growing environments for yield and adaptability and their interaction on yield and yield components whereas the specific objectives were to evaluate stability variables, interrelations and genetic parameters for traits in the studied maize hybrids. A randomized complete block design laid in a split-plot experiment with three replications at each location was used. The data collected include plant growth parameters, maize yield components and yield. The study shows that locations and weeding regimes were important for most variables, including grain yield while genotypes were important for ear height and number of kernel rows per cob. Location x weeding regimes was also important for most traits including grain yield; genotype x weeding regimes was important for number of leaves per plant while genotype x environment interaction was important for number of kernel rows per cob and days to maturity. Estimation of genetic parameters revealed high heritability coupled with high genetic advance for days to first tasselling, 50% tasselling, 50% pollen shed, first silking and ear height pointing out that these traits were under the control of additive genetic effects and that selection of these traits can be done in early generations of the breeding programme. Phenotypic Coefficient of Variation (PCV) was moderate for most traits including grain yield whereas Genetic Coefficient of Variation (GCV) was low for all traits. Path coefficient analysis singled out number of leaves per plant, plant height, days to 50% silking, 50% pollen shed and maturity as most important traits to consider during selection for grain yield improvements among the studied genotypes. It is recommended that genotype EH-2 (FH5160) can be carried further for national performance trial or possible release while UHS 5350 (EH3) and UH6303 can be used in the breeding programme.

DECLARATION

I, JUMA MATONYA, do hereby declare to the Senate of Sokoine University of Agriculture, that this dissertation is my original work and that it has neither been submitted nor being concurrently submitted for degree award in any other institution.

_____ _____

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The above declaration is confirmed.

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Last but not least thanks to all people who assisted me during preparation of the experimental sites, collection of data, analysis, typing and hard binding of my dissertation work.

DEDICATION

To my beloved Mom Mary Mboyi Kahema and my Lovely wife Neema Matonya, I pray that the Almightily God be with them for the rest of their lives.

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LIST OF ABBREVIATIONS

FAOSTAT	Food and Agriculture Organization of the United Nations, the Statistics Division
URT	United Republic of Tanzania

CHAPTER ONE

1.0 INTRODUCTION

Maize (*Zea mays* L.) is one of the major cereals in the world together with rice and wheat. It is an important staple food in many tropical, subtropical and warm temperate countries (Kutua, 2008). About half of the global crop is produced in North America. China is the second largest producer followed by Brazil, Mexico and Argentina (Winch, 2006). The global production was 784 786 580 metric tons in 2007 (FAOSTAT, 2010).

In Tanzania maize is the first priority staple food followed by rice, wheat and sorghum (URT, 2006). It accounts for 60% of the dietary calories, 50% of utilizable proteins for the majority of the rural population and covers about 45% of the area under annual crop cultivation (Lyimo, 2006).

The growth period of maize averages 90 – 120 days at low altitudes and 180 – 240 days at approximately 2500m above sea level (Winch, 2006). The optimum temperature for germination is 18 – 21^{o}C. It is very slow at 13^{o}C and does not germinate at temperatures below 10 ^{o}C. The ideal temperature at tasseling is 21-30^{o}C (Winch, 2006). In temperate or subtropical regions, a rainfall of 450 – 600mm during the growth period is enough while in the tropics it needs 600 – 900mm. A very dry spell just before or during tasselling reduces yields. Maize can grow from 0 to above 1500m a.s.l. To produce good yield, it requires fertile soils, high organic matter content and exchangeable bases, well drained, loam soils and careful management (Winch, 2006).

Despite maize being an important crop in Tanzania particularly in the southern highlands, it is faced with a number of problems. Among the problems include diseases like downy

mildew, rust, leaf blight, stalk and ear rots, maize streak virus and Grey Leaf Spot (GLS). Periodic drought caused by irregular rainfall distribution, limited use of nitrogenous fertilizers and the declining soil fertility, insect pests such as stem and ear borers, armyworms, cutworms, grain moths, beetles, weevils, grain borers, rootworms and witchweed (Striga) are also a great threat to the survival of maize (IITA, 2009).

1.2 Problem Statement and Justification

Genotype x Environment interaction is of fundamental importance to the plant breeder for development of new cultivars (Eberhart and Russell, 1966). The phenomenon is almost unanimously considered to be among the major factors limiting response to selection and it is considered a hindrance to crop improvement and production environments (Kang, 1998). Such effects may contribute together with purely environmental effects to the temporal and spatial instability of crop yields. Temporal and spatial instability in particular have a negative effect on farmers' income and in the case of staple crops, contributes to food insecurity at national and household levels. Genotype x Environment interaction due to different responses of genotypes in diverse environments makes choosing of superior genotypes difficult in plant breeding programs (Ilker *et al*., 2009). Genotype x Environment interaction makes it difficult to select the best performing and most stable genotypes and is an important consideration in plant breeding programs because it reduces the progress from selection in any one environment (Hill, 1975; Yau, 1995). The large Genotype x Environment interaction variation usually impairs the accuracy of yield estimation and reduces the relationship between genotypic and phenotypic values (Nachit *et al*., 1992).

Growing awareness of the importance of Genotype x Environment interactions has led to crop genotypes being assessed in multi-environments, regional trials for cultivar

recommendations or during final stages of elite breeding materials selection (Ndimbo, 2008). Studies on Genotype x Environment effects enable exploration of the potential opportunities for production over wide specific areas (Ndimbo, 2008). Studies on Genotype x Environment also reveal the response of genotypes to variable production levels among environments thereby providing an understanding of their stability of performance. The information gained helps to define, if necessary, a strategy to successfully cope with the effects of interactions (Annicchiarico, 2002). Evaluation of genotypic performance in a number of environments provides useful information to identify their adaptation and stability (Crossa, 1990). Multi-environment yield trials are used commonly to release superior genotypes for target sites in plant breeding programs (Ilker *et al*., 2009). Genotype x Environment interaction is a universal phenomenon when different genotypes are tested in a number of environments.

On the other hand, Genotype x Environment interaction reveals the need for development of genotypes that should be tested and selected for specific growing environments (Fehr, 1987). Evaluation of genotypes in multiple locations reduces the impacts of Genotype x Environment on crop performance. Limited work on Genotype x Environment interaction has been done on maize for yield and yield components in the Southern Highlands of Tanzania. The experiments which have been conducted are insufficient and not representative of most available genotypes under the existing environmental conditions. Since new and promising breeding materials are still coming out, it is necessary to test and evaluate them in various maize growing environments. This will assist in selecting and recommending them according to their yield performance and yield component characteristics.

1.3 Objectives

1.3.1 Overall objective

To assess the response of selected maize genotypes across different growing environments for yield and adaptability and their interaction on yield and yield components.

1.3.2 Specific objectives

(i) To evaluate the response and stability of five selected maize genotypes under four different maize growing environments.

(ii) To determine paths of influence among various yield components of maize and their contribution to grain yield.

(iii) To estimate the genetic parameters; genotypic and phenotypic coefficients of variation, heritability and genetic advance

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin and Distribution of Maize

The likeliest primary center of origin of maize is considered by most authorities to be Central America and Mexico, where many diverse types of maize are found (Leonard and Martin, 1989). Maize comes in five phenotypes (sweet, pop, floury, dent, and flint) all its forms derive from a single ancestor domesticated in central Mexico around 7000 years ago (McCann, 2005). According to Leonard and Martin (1989) its relative teosinte and several species of tripsacum also are found in this region. The discovery of fossil corn pollen and other archaeological evidences in Mexico points to Mexico as an early center of domestication. The cultivation of maize probably started in this region about the beginning of the Christian era (Wolfe and Kipps, 1959). A possible secondary center of origin of maize is South America in the Andean region of Bolivia, Ecuador and Peru (Leonard and Martin 1989). From these areas it rapidly spread to other countries including Tanzania.

2.2 Genotype x Environment Interaction

The environment under which the crop is grown modifies the phenotypic expression of traits to an individual cultivar. When cultivars are compared in different environments, their performance relative to each other may not be the same (Kibanda, 2001). Changes in relative performance of genotypes across environments are referred to as Genotype x Environment interactions (Fehr, 1987). Bernardo (2002) stipulated that, in the study of Genotype x Environment interaction, the term ‘genotype’ usually refers to individuals (e.g. families, recombinant inbreds, testcrosses or hybrids) that differ in their genotypes at many loci than those at a single locus. Chaudhary (1984) referred to environment as the

sum total of external conditions which affect growth and development of an organism. In this study interaction refers to the influence of environment upon the genotypes and response of genotypes upon the environment. Genotype x Environment interaction causes fluctuations of yield across environments. In other words, Genotype x Environment interaction is a differential genotypic expression across environments (Basford and Cooper, 1998).

The phenotype of an individual is determined by the effects of its genotype and the environment surrounding it. The effects of genotype and environment on phenotype may not be always independent. The phenotypic response to change in environment is not the same for all genotypes, the consequences of variation in phenotype depend upon the environment (Issa, 2009). Very often breeders encounter situations where the relative rankings of varieties change from location to location and/or from year to year. Genotype x Environment interaction is of major importance to breeders in the process of developing improved varieties. When varieties are grown at several locations for testing their performance, their relative rankings usually do not remain the same. This causes difficulty in demonstrating significant superiority of any genotype. Genotype x Environment interaction is present whether varieties are pure lines, single crosses, double crosses, top-crosses or any other material with which the breeder is working (Dabholkar, 1999).

An understanding of environmental and genotypic causes of Genotype x Environment interaction is important at all stages of plant breeding, including ideotype design, parent selection based on traits and selection based on yield (Jackson *et al.*, 1998; Yan and Hunt, 1998). Understanding of the causes of Genotype x Environment interaction can be used to establish breeding objectives, to identify ideal test conditions and to formulate

recommendations for areas of optimal cultivar adaptation (Issa, 2009). The presence of a large Genotype x Environment interaction may necessitate establishment of additional testing sites, thus increasing the cost of developing commercially important varieties (Kang, 1998). The potential need for unique cultivars in different geographical areas and the need to develop cultivars for specific purposes are determined by understanding of the interaction of genotypes with predictable environmental factors.

The objective in many plant breeding programs is to select genotypes that are consistently high yielding over the range of environments that occur in the target region (Abdulai *et al.,* 2007). However, selection is often inefficient due to Genotype by Environment interactions i.e. when genotypes fail to have the same relative performance in different environments (Knight, 1970). Since the relative rankings usually differ across environments, demonstrating the superiority of any single genotype becomes difficult if not impossible. The basic causes of Genotype x Environment interaction are believed to be due to biochemical pathways of certain physiological processes taking place in plants (Abdulai *et al.*, 2007). Genotype x Environment continues to challenge plant breeders by complicating the selection of genotypes evaluated in diverse environments by reducing the correlation between phenotypic and genotypic values (Kang and Gorman, 1989). When Genotype x Environment interaction are present, one of the options open to the breeder is to use stability analyses to identify the most high yielding and stable genotype (Abdulai *et al.*, 2007). Thus, several statistical methods have been proposed and used to study the adaptation and stability of varieties to varying environments as summarized by Lin *et al*. (1986).

2.2.1 Genes and environment

Organisms are determined either by their genes or by their environment; they are the consequence of the interaction of genes and environment (Suzuki *et al*., 1981). Genotype describes a complete set of genes inherited by an individual that is important for the expression of a trait under investigation. Phenotype describes all aspects of the individual's morphology, physiology and ecological relationships. The genotype is essentially a fixed character of the organism; it remains constant throughout life and is unchanged by environmental effects (Issa, 2009). The phenotype changes continually and the direction of that change is a function of the sequence of environments that the individual experiences (Suzuki *et al*., 1981).

The sum total of external conditions that influence expression of genes of an individual is known as the environment. The individuals or populations of plants do not live in a vacuum but are surrounded and influenced by these factors. Environmental variables can be classified as either predictable or unpredictable environments (Allard and Bradshaw, 1964). The predictable environments are those that occur in a systematic manner or under human control. They include the regular and more or less permanent features of the environment such as climate as determined by its longitude and latitude, soil type, rainfall and day length.

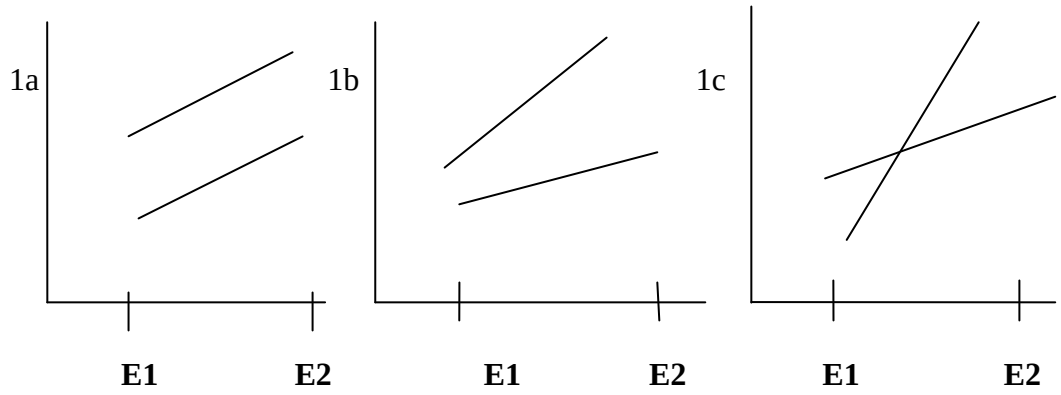
It also includes what are called controllable variables (Perkins and Jinks, 1971) e.g. the level of fertilizer applied, sowing date and sowing density, amount of irrigation and others that can be artificially created. The unpredictable or uncontrollable environments, on the other hand, include weather fluctuations such as differences between seasons in terms of amount and distribution of rainfall and the prevailing temperature during the crop growth. The absence or low level of interaction will be useful for uncontrollable variables,

whereas for the controllable variables a high level of interaction in the favourable direction is desirable to obtain maximal performance (Chahal and Gosal, 2002).

2.2.2 Classification of genotype x environment interaction

Genotype by Environment interaction occurs when differences between genotypes are not the same in all locations within and across years (Edmeades *et al*., 1989). It is the inconsistency of relative performance of genotypes over environments (Hill *et al*., 1998). If two genotypes, A and B are evaluated in two environments 1 and 2, Genotype x Environment interaction occurs when:

A1-B1 ≠ A2- B2 or A1-B1-(A2-B2) ≠0 where, A1 is the performance of genotype A in environment 1, A2 is the performance of genotype A in environment 2, B1 is the performance of genotype B in environment 1, B2 is the performance of genotype B in environment 2 (Issa, 2009). When two genotypes A and B are grown in two different environments E1 and E2, six types of interactions, some of which are crossovers and others non-crossovers are possible (Allard and Bradshaw, 1964). The two varieties may show similar behaviour i.e. parallel lines when grown in two environments (Fig. 1a) which indicates independence in the performance of genotype and environment. The presence of Genotype x Environment interaction leads to non-parallel response curves of varieties without intersecting each other (Fig. 1b) or with interaction (Fig. 1c).



Source: Issa (2009),

Figure 1: Different types of Genotype x Environment interactions shown by two varieties grown in two environments

The existence of non-intersecting but non-parallel lines suggests the relative ranking of varieties remains the same, though their absolute differences vary with the environment. The Genotype x Environment interaction is considered as crossover or qualitative if it leads to change in relative ranking of genotypes in different environments. The non-crossover or quantitative Genotype x Environment interaction, on the other hand results in differential change of mean but not of ranking of different genotypes.

Crossover interactions are of interest in plant breeding because these affect the genotypes to be selected in a given environment. Such interactions also suggest that genotypes are specifically adapted to environments. The non-crossover interaction on the other hand, influences the nature and magnitude of components of genetic variances and other related parameters like heritability and genetic advance. Changes in relative ranking appear to be the inevitable consequence of growing a set of plant genotypes in even a few locations and seasons. This is especially true in tropical regions where not only environmental fluctuations are greater, but crops also lack the protection conferred by purchased inputs.

Thus, for plant breeders large Genotype x Environment interaction impedes progress from selection and has important implications for testing and cultivar release (Issa, 2009).

Genotype x Environment interaction reduces association between phenotypic values and may cause promising selections from one environment to perform poorly in another, forcing plant breeders to examine genotypic adaptation (Romagosa and Fox, 1993). Its measurement is also important to determine an optimum breeding strategy for releasing genotypes with adaptation to target environments.

Performance tests over a series of environments give information on Genotype x Environment interaction at population level, but from a practical point of view, it is important to measure the stability of the performance of an individual genotype (Eberhart and Russell, 1966).

2.3 Stability of Genotype Performance

The term "stability of genotypes" is central to all types of analyses of Genotype x Environment interactions especially with reference to plant breeding. Stability in common usage connotes consistency in performance that would mean minimum variation among environments for a particular genotype (Chahal and Gosal, 2002). Lin *et al*. (1986) identified three concepts of stability:

Type 1: A genotype is considered to be stable if its variance among environment is small (Rahman, *et al.,* 2010). Becker and Léon (1988) called this stability a static, or a biological concept of stability. A stable genotype possesses an unchanged performance regardless of any variation of the environmental conditions. This concept of stability is useful for quality traits, disease resistance, or for stress characters like winter hardiness.

Parameters used to describe this type of stability are coefficient of variability (*CVi*) used by Francis and Kannenburg (1978) for each genotype as a stability parameter and the genotypic variances across environments (*Si2*).

Type 2: A genotype is considered to be stable if its response to environments is parallel to the mean response of all genotypes in the trial. Becker and Léon (1988) called this stability the dynamic or agronomic concept of stability. A stable genotype has no deviations from the general response to environments and thus permits a predictable response to environments. A regression coefficient (*bi*) (Finlay and Wilkinson, 1963) and Shukla (1972) stability variance (S^2i) can be used to measure type 2 stability.

Type 3: A genotype is considered to be stable if the residual mean square from the regression model on the environmental index is small. The environmental index implicates the mean yield of all the genotypes in each location minus the grand mean of all the genotypes in all locations. Type 3 is also part of the dynamic or agronomic stability concept according to Becker and Léon (1988).

Breeders are primarily concerned with high yielding and stable cultivars as much as possible since cultivar development is a time consuming endeavor. A successfully developed new cultivar should have a stable performance and broad adaptation over a wide range of environments in addition to high yielding potential (Fikere *et al.*, 2008). Evaluating stability of performance and range of adaptation has become increasingly important for breeding programs. Hence, if cultivars are being selected for a large group of environments, stability and mean yield across all environments are important than yield for specific environments (Piepho, 1998). In breeding for wide adaptation, the aim is to

obtain a genotype, which performs well in nearly all environments (Cooper and De-Lacy, 1994).

High yielding maize hybrids can differ in yield stability and that yield stability and high grain yield are not mutually exclusive (Tollenaar and Lee, 2002). There are two obvious general ways in which a cultivar can achieve stability (Lewontin, 1959). First, the genotype can be made of a number of genotypes each adapted to somewhat different range of environments. Second, the individual themselves may be well buffered so that each member of the population is well adapted to the range of environments.

Genetically, homogeneous populations such as pure line varieties or single crosses obviously depend on individual buffering to stabilize productivity whereas both paths are open to genetically heterogeneous populations (Ngowi, 2002). The term ‘individual buffering’ and ‘population buffering’ are adopted to describe these two methods of stabilizing yield (Ngowi, 2002).

Individual buffering- In out-breeding species there is a good deal of work which indicates that buffering is conspicuously a property of heterozygotes (Ngowi, 2002). Jones (1958) argues that ‘adaptedness’, the attribute of individual to be fit in the Darwinian sense to their immediate environment, is mediated by heterogeneous advantage in buffering ability. The situation seems much the same in out-breeding plants. According to Lewontin (1959), in inbreeding species there is evidence that buffering can be a property of specific genotypes not associated with heterozygosity. Cereal breeders for example, have considerable practical experience to indicate that there are varietal differences in degrees of buffering. An example in barley is the comparison between Atlas and Vaughn. Altlas is widely distributed throughout California and yields

satisfactorily in contrasting seasons. Vaughn, although superior in yields to Atlas under optimal cultural conditions, is otherwise an erratic producer (Allard and Bradshaw, 1964).

Population buffering–This refers to buffering above and beyond that of individual constituents of populations, i.e. buffering which arise in interaction among different coexisting genotypes (Ngowi, 2002). Like individual buffering, it is measurable in terms of Genotype x Environment interaction. The most precise information on population buffering comes from comparison between pure line varieties grown singly and in mixture (Ngowi, 2002). Mixed populations are nearly always stable in yield than their components (Simmonds, 1962). In wheat for example, coefficients of variability over seasons were about two-thirds as large for mixtures (7.3%) as for homogeneous populations (11.6%). There was suggestion that the stabilizing effect was much greater for some combinations than for others. On the other hand, information on population buffering in heterozygous materials comes primarily from comparisons of single crosses of corn (Ngowi, 2002). The analysis conducted by Jones (1958) on extensive yield trials revealed that coefficient of variability was smaller for double crosses (12.3%) than for single crosses (21.4%).

On the other hand, all living things can make physiological adjustments which permit them to cope with fluctuations in their immediate environment (Issa, 2009). These adjustments themselves are known as adaptations. Adaptation is the property of a genotype which permits its survival under selection. An adapted genotype or population is simply one which performs better than the standard under comparison (Dabholkar, 1999). Simmonds (1962) stipulated that adaptation has four separable aspects. These are:

(i) Specific genotypic adaptation: is close to adaptation of the corresponding genotypes to a limited environment.

(ii) General genotypic adaptation: is the capacity of a genotype to produce a range of phenotypes adapted to different environments.

(iii) Specific population adaptation: is analogous to 1 above and is the aspect of specific adaptation of heterogeneous population that is attributable to interaction between components rather than to the adaptations of components themselves.

(iv) General population adaptation: is analogous to general genotypic adaptation and is the capacity of a heterogeneous population to adapt to diverse environments.

2.4 Methods for Analysis of Genotype x Environment Interaction

Several methods have been proposed to analyze Genotype x Environment interaction or phenotypic stability (Lin *et al.,* 1986; Becker and Leon 1988; Piepho, 1998; Truberg and Huhn, 2000). These methods can be divided into two major groups, univariate and multivariate stability statistics (Lin *et al*., 1986). Joint regression is the most popular among univaraite methods because of its simplicity of calculation and application (Becker and Leon, 1988). Joint regression analysis was first proposed by Yates and Cochran (1938) and then widely used and reviewed by various authors (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Perkins and Jinks, 1968; Freeman and Perkins, 1971; Shukla, 1972; Freeman, 1973; Hill, 1975; Lin *et al*., 1986; Becker and Léon, 1988; Baker, 1988; Crossa, 1990; Hohls, 1995). Joint regression provides a conceptual model for genotypic stability (Becker and Leon, 1988; Romagosa and Fox, 1993). The Genotype x Environment interaction from analysis of variance is partitioned into heterogeneity of regression coefficients (bi) and the sum of deviation (ΣS^2di) from regressions. Finlay and Wilkinson (1963) defined a genotype with coefficient of regression equal to zero (bi= 0) as stable while Eberhart and Russell (1966) defined a genotype with high mean value, with regression coefficient of 1.0 and deviation from regression of 0 to be stable. Such a genotype would have increased performance as the

productivity of environment improves (Rahman *et al.*, 2010). Most biometricians consider S^2di as stability parameter rather than bi (Eberhart and Russell, 1966; Becker and Leon, 1988). Wricke (1962) suggested using Genotype x Environment interaction for each genotype as a stability measure, which he termed as ecovalance (*Wi*2). Shukla (1972) developed an unbiased estimate using stability variance (σ2*i)* of genotypes and a method to test the significance of (σ2*i*) for determining stability of a genotype. Francis and Kannenburg (1978) used the environmental variance (*S*2*i*) and the coefficient of variation (*CVi*) to define stable genotype.

On the other hand, Additive Main Effect and Multiplicative Interaction (AMMI) is gaining popularity and is currently the main alternative multivariate approach to the joint regression analysis in many breeding programs (Annicchiarico, 1997). AMMI was first introduced in social science as a multiplicative interaction model (Crossa, 1990) and was later adapted to the agricultural context as AMMI (Piepho, 1998). This model was considered appropriate if one is interested in predicting genotypic yields in specific environments (Annicchiarico, 1997). It combines the analysis for the genotype and environment main effect with several graphically represented interactions for principal component analysis (IPCAs) (Crossa, 1990; Abamu and Alluri, 1998). Thus, it helps in summarizing the pattern and relationship of genotypes, environment and their interaction (Gauch and Zobel, 1996). The genotype main effect plus Genotype x Environment interaction (GGE) biplot method, which is always close to the best AMMI models in most cases (Ma *et al.*, 2004), was recently developed to use some of the functions of these methods jointly. It allows visual examination of the relationships among the test environments, genotypes and the genotype by environment interactions (Ding *et al.*, 2007). The differences of the two methods, GGE biplot analysis is based on environment

centered PCA, whereas AMMI analysis is referred to double centered PCA (Kroonenberg, 1997; Ding *et al.*, 2007).

Both AMMI and GGE biplot methods are based on singular value decomposition (SVD) or principal component analysis and considered to be effective tool to diagnose Genotype x Environment interaction patterns graphically (Yan and Kang, 2003; Admassu *et al.*, 2008). Crossa (1990) indicated that the AMMI model can be used to analyze the Genotype x Environment interaction and to identify the superior hybrid maize genotypes. Also, he pointed out that it can be used in the selection of the best test environments for hybrid maize genotype evaluation. Fan *et al.* (2007) stipulated that the GGE biplot methodology was a useful tool for identifying locations that optimized hybrid genotypes performance and for making better use of limited resources available for the maize testing programs.

2.5 Yield and Yield Components

Studies on yield and yield components of maize have been done by different scholars. An example is that of Ngowi (2002) who noted a significant ($P \leq 0.05$) variation on number of leaves per plant for genotypes and Genotype x Environment interaction. The Genotype x Environment interaction was significant ($P \leq 0.01$) for plant height, days to 50% silking, 50% anthesis and anthesis silking interval (ASI) but not for yield. This implies that in this study the environment played a major role in influencing the traits/variables measured. Genotype x Environment Interaction was significant ($P \leq 0.05$) for yield, 100 grain weight, plant height and days to 50% pollen shedding. Broccoli and Burak (2004) found significant Genotype x Environment interaction on yield after evaluating fourteen commercial popcorn maize hybrids in three locations for two years with the aim of introducing this crop into a region of the Buenos Aires province, Argentina.

Singh *et al.* (2009) found high significant differences among the genotypes and environments for data on 10 yield components studied (days to maturity, plant height, ears/plant, ear length, ear girth, kernel rows/ear, kernels/row, 100 kernels weight, grain yield/plant and biological yield/plant.

The study done by Rahman *et al.* (2010) revealed that mean square values for days to 50 % silking, days to 50% anthesis and ASI, plant height, ear height, grain moisture (%) at harvest and grain yield showed high significant variation across three locations for these parameters. Similarly, highly significant differences were observed among hybrids across the three locations for days to 50% silking and days to 50% anthesis while non significant differences were observed for anthesis silking interval (ASI), plant and ear heights, grain moisture at harvest and grain yield in kg ha^{-1}. The interaction between hybrids and locations were also highly significant for days to 50% silking, days to 50% anthesis, ASI, grain moisture at harvest and grain yield revealing that these parameters were considerably influenced by the environmental variations encountered across the three locations. However, Hybrid x location interaction was non-significant for plant height and ear height, indicating stability of these two parameters across the tested environments, during their study.

2.6 Path Coefficient Analysis

Path coefficient analysis is defined as a standard partial regression coefficient that measures the direct influence of one variable upon another and permits the separation of the correlation coefficient into components of direct and indirect effects. The use of the method requires a cause and effects situation among variables and the direction must be assigned in the causal system based upon a priori grounds or experimental evidence (Dewey and Lu, 1959). In agriculture, path analysis has been used by plant breeders to

assist in identifying traits that are useful as selection criteria to improve crop yield (Dewey and Lu, 1959).

Different scholars have studied path coefficient analysis in maize. Ahmed and Hassanein (2001) found that ears per plant exerted negative direct and indirect effects through ear height on grain yield. Plant height had positive direct effect on grain yield per plant but indirect negative effect through ear height. The study done by Venugopal *et al.* (2003) found that number of seeds per row followed by 100 seed weight, days to 50% tasselling, ear girth and plant height contributed directly towards grain yield per plant. Number of seed rows per ear had a direct positive contribution towards grain yield. Ear length, 100 seed weight and number of seeds per row had an indirect negative influence on grain yield. Singh *et al.* (2003) observed that ear leaf area had the highest positive direct effect on green fodder yield per plant at genotypic and phenotypic levels followed by dry matter yield per plant, ear length and days to 50% silking. Ear length had the maximum direct effect on grain yield followed by 500-kernel weight and ear leaf area.

On the other hand, Heping *et al.* (2004) observed that maize yield was mainly influenced by ear length, followed by number of kernels per row, ear width, number of rows per ear, growth period and 1000 seed weight. Srivas and Singh (2004) found that plant height, days to 50% silking, stem girth, leaf length, leaf width and number of leaves per plant had positive direct effect on dry fodder yield at phenotypic levels.

Path analysis by Patel *et al.* (2005) revealed that dry matter yield per plant, number of leaves per plant, days to 50% silking and plant height had positive direct effects on green fodder yield. Shelake *et al.* (2005) observed high magnitude of direct effects for all characters at the genotypic level. The number of days to 50% tasseling, number of days

to 50% silking and harvesting index showed higher genotypic direct effect. Biological yield per plant had the highest negative genotypic direct effect on grain yield.

Kumar *et al.* (2006) reported that days to 50% tasselling, ASI, ear height and 100 seed weight had highest direct effect on grain yield. The days to 50% silking showed negative direct effect on grain yield. Dachum (2006) stipulated that kernel weight per ear mainly affected by ear length and ear diameter and the ear length with bearing kernel played an important role on kernel weight per ear in high yielding combinations.

Saleem *et al.* (2007) revealed that plant height had maximum positive direct effect on grain yield followed by number of rows per cob, cob height, flag leaf area and days to 50% silking while number of grains per cob had maximum negative direct effect on grain yield followed by biomass per plant. Days to 50% tasselling, silking and biomass per plant had maximum positive indirect effects through number of grains per cob on grain yield, while cob height, number of rows per cob and number of grains per cob had maximum indirect effects through biomass per plant on grain yield. Number of grains per cob had negative direct effect but had positive indirect effects through biomass per plant and plant height on grain yield. The 1000 grain weight and biomass per plant had negative direct effects but positive indirect effects through number of grains per cob and plant height on grain yield.

Shakoor *et al.* (2007) noticed that plant height exerted positive direct effect on grain yield per plant but indirect negative effect through ear height and days to 50% silking while ear per plant had negative direct and indirect effects through ear height on grain yield. Saleem *et al.* (2007) found that plant height under irrigated maize had maximum positive direct effect on grain yield followed by number of rows per cob and cob height.

Thus these traits may be given more emphasis during selecting high yielding maize genotypes under irrigated conditions. However, under drought stress conditions, days to 50 % silking had maximum direct effect on grain yield followed by cob height and flag leaf area. Hence these characters will be considered for yield improvement under drought conditions.

On the other hand, Jayakumar *et al.* (2007) showed that grains per row recorded maximum positive direct effect on grain yield followed by ear length, ear girth, days to tasselling, total sugars and plant height. The maximum negative direct effect on grain yield was recorded for kernel rows followed by 50% days to silking, crude protein, grain weight, days to maturity, shelling percentage and leaves above upper most ears. Sofi and Rather (2007) observed that 100 seed weight had the greatest direct effect on grain yield followed by number of kernels per row, number of kernel rows per ear, ear length and ear diameter. Xie-Zhen *et al.* (2007) showed that kernels per plant was arranged for the top position among the many agronomic traits that contributed to the yield enhancement of a single plant and was followed by kernels per row, 1000 kernel weight of maize and leaf orientation value. Mohammad *et al.* (2008) showed that all traits exerted positive direct effect on grain yield per plant except days to 50% silking.

Path analysis in maize by Rafiq *et al.* (2010) revealed that highest direct effect on grain yield was exhibited by 100 grain weight followed by grains per row, kernel rows per ear, ear length and ear diameter. Most of the traits exerted their positive indirect effects through 100 seed weight, kernel rows per ear and grains per row.

2.7 Genetic Variability, Heritability and Genetic Advance

Possibility of achieving improvement in any crop plants depends heavily on the magnitude of genetic variability. Phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and phenotypic components. The genotypic components being the heritable part of the total variability, its magnitude for yield and its component characters influences the selection strategies to be adopted by breeders.

Mohammad *et al.* (2008) found that Phenotypic Coefficient of Variation (PCV) was 1.94% whereas Genotypic Coefficient of Variation (GCV) was 1.98% and heritability in broad sense (h^2_b) was 95.4% for days to 50% tasselling. On the other hand, the authors found that PCV was 2.34% whereas GCV was 2.43% and h^2_b was 92.6% for days to 50% silking. Furthermore, a study by Prakash *et al.* (2006) revealed that plant height had 16.09% (PCV), 98.7% (GCV) and h^2 was 33.6 whereas ear height had 29% (PCV), 93.4% (GCV) and 40.71 (h^2). The study also found that number of kernel rows per cob was 12.44% (PCV), 85% (GCV) and 23.51 (h^2). On the other hand, Sumathi *et al.* (2005) reported that grain yield per plant had 10.58% (PCV), 99.15% (GCV) and 27.8% (h^2) while 100 grain weight had 13.92% (PCV), 88.08% (PCV) and 34.49% (h^2).

2.8 Comparative Studies on Genotype x Environment Interaction in other Crops

The study done by Kibanda (2001) on effects of Genotype x Environment interaction on yield of rice (*Oryza sativa* L.) revealed that there were significant varietal differences, environmental effects and Genotype x Environment interaction for days to 50 % flowering, plant height and panicle length. Results also showed that regression coefficient and the deviation from regression indicated that most of the entries performed

significantly ($P \leq 0.05$) stable for all the traits across environments except M55 for days to 50% flowering.

Kilic, *et al*. (2009) in their study on estimates of Genotype x Environment interactions and heritability of Black Point in Durum Wheat, found that genotype x location interactions, year x location interactions, locations, years and genotypes were highly significant ($P \leq 0.01$), while the genotype x location x year interaction was also important ($P \leq 0.05$). The presence of genotype x location interactions indicates that particular genotypes tended to rank differently in black point rate at different locations. The result of combined analysis over the years and locations indicated that there were significant ($P \leq 0.005$ levels) differences between varieties on genotype x location interaction in wheat.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Description of the Study Area

The experiment was conducted at four locations: Uyole, Mbimba, Inyala and Seatondale. Uyole is located at 08^0 56'S and 033^0 06'E at an elevation of 1795 meters above sea level whereas Mbimba is located at 08^0 57'S and 033^0 13'E at 1241 meters above sea level. Inyala is located at 08^0 51'S and 033^0 38' E at an elevation of 1505 meters above sea level whereas Seatondale is located at 07^0 45' S and 35^0 39' E at an elevation of 1693 meters above sea level. Uyole, Mbimba and Inyala are villages found in Mbeya Region whereas Seatondale is the village found in Iringa Region.

3.2 Experimental Design and Treatment Application

A randomized complete block design (RCBD) laid in a split plot experiment with three replications at each location was used. Three weeding regimes (No weeding, weeding once and weeding twice) as main plot (Factor a) and five genotypes (two way cross hybrids) (Factor b) from Agricultural Research Institute (ARI) Uyole were used. The description of maize genotypes is as shown in Table 1.

Table 1: Maize genotypes tested across four locations

Entry Number	Entry Code
1	EH-1
2	EH-2 (FH 5160)
3	UHS 5350 (EH-3)
4	EH-4
5	UH 6303 (Check)

The subplot size was 3.0 m x 2.8 m with 4 rows each and one plant per hill placed at a spacing of 70 cm x 30 cm and the main plot size was 14.25 m x 3 m. The gross plot size was 42.75 m x 9 m whereas the net plot size per each subplot was 1.4 m x 3 m (area data were collected). Uniform fertilizer rate of 25.3 kg P/ha and 22.5 kg N/ha as basal application was applied at each site. First top dressing of 12 kg S/ha and 56.5 kg N/ha was done followed by second top dress of 21 kg N/ha and 14.2 kg Ca/ha.

3.3 Cultural Practices

Plants were weeded once for weeding once treatment, twice for weeding twice treatment and not weeded for none weeding treatment. The first weeding was done at two weeks after planting and second one was done after 35 days from planting. Other agronomic practices were done as per recommendations.

3.4 Data Collection

3.4.1 Physical and chemical characteristics of the soil

Soil samples were taken from four sites, namely, Seatondale (Iringa), Inyala (Mbeya Rural), Uyole (Mbeya) and Mbimba (Mbozi). For each site, four random sub-samples were taken and mixed thoroughly from which a composite sample was obtained. Samples were taken using hand hoe, shovel and/or soil auger at a depth of 0 – 30 cm. Collected samples were submitted to ARI-Uyole soil chemistry laboratory for analysis.

The physical characteristics of soil recorded from each site included textural classes of sand, silt and clay (%) determined by Hydrometer method while the chemical soil characteristics were soil pH (1:2.5) (HO_2) by using pH meter, total Nitrogen% (TN%) by semi macro Kjeldahl, organic carbon% (OC%) by Walkley and Black, available P (mg/kg), cation exchange capacity (CEC) (cmol/kg) by using neutral ammonium

acetate soak and KCl percolation, sulphur (S) (mg/kg) and exchangeable bases viz. calcium (Ca^{+}), magnesium (Mg^{+}), and potasium (K^{+}) (cmol/kg).

3.4.2 Rainfall (mm) and temperature data (^{0}C)

Daily temperature ^{0}C (minimum and maximum) and rainfall (mm) were recorded from weather station present at each experimental site.

3.4.3 Plant height (cm)

Plant height was collected from six randomly selected plants from the net plot (4.2 m^2 of each subplot). The height of the plant was from ground level up to the base of fully opened flag leaf was measured in centimeters and average recorded. Plant height was measured after anthesis (Abadassi and Herv´e, 2000).

3.4.4 Ear height (cm)

Ear height was collected from six randomly selected plants from the net plot. The height from ground level up to the base of the upper most cob bearing internodes was measured as ear height in centimeters and average recorded.

3.4.5 Number of leaves per plant

Number of leaves per plant was collected from six randomly selected plants from the net plot. The total number of leaves per each plant was counted and average was recorded as number of leaves per plant.

3.4.6 Number of leaves below the ear

Number of leaves below the ear was collected from six randomly selected plants from the net plot. The total number of leaves below the upper most cob bearing the internodes was counted and average was recorded as number of leaves below the ear.

3.4.7 Number of leaves above the ear

Number of leaves above the ear was collected from six randomly selected plants from the net plot. The total number of leaves above the upper most cobs bearing the internodes was counted and average was recorded as number of leaves above the ear.

3.4.8 Ratio of leaves below and above the ear

The ratio of leaves below and above the ear was calculated by taking the total number of leaves below the ear dividing by total number of leaves above the ear and the value obtained was averaged and recorded as the ratio of leaves below and above the ear.

3.4.9 Days to first tasselling

The number of days from sowing up to the day when plants showed tassel emergence was recorded as days to first tasselling.

3.4.10 Days to 50% tasselling

The number of days from sowing up to the day when 50% of plants showed tassel emergence was recorded as days to 50% tasselling.

3.4.11 Days to 50% pollen shed

The number of days from sowing up to the day when 50% of plants shed their pollens was recorded as days to 50% pollen shed.

3.4.12 Days to first silking

The number of days from sowing up to the day when plants showed the first silk emergence was recorded as days to first silking.

3.4.13 Days to 50% silking

The number of days from sowing up to the day when 50% of plants showed silk emergence was recorded as days to 50% silking.

3.4.14 Anthesis silking interval (ASI)

ASI was recorded by taking the value of the difference in number of days between anthesis and silking in each plot.

3.4.15 Days to maturity

The number of days from sowing up to the day on which plants reached physiological maturity was recorded as days to maturity in each plot. Date of maturity was defined as the first day when grain of at least 50% of plants in a plot attained black layer (Tollenaar *et al.*, 2004).

3.4.16 Ear diameter (cm)

Ear diameter was measured from the ear of six randomly selected plants from the net plot. Then the diameter of each ear was measured using a vernier caliper and average recorded in centimeters as ear diameter.

3.4.17 Cob length (cm)

Cob length was measured from the cobs of six randomly selected plants from the net plot. It was measured from base to the tip of the cob and average recorded in centimeters.

3.4.18 Shelling percent (%)

Shelling percent was calculated from the ear of six randomly selected plants from the net plot. Then the following formula was used to compute this variable. Shelling percent = Weight of seed/weight of cobs x 100.

3.4.19 Number of kernel rows per cob

Number of kernel rows per cob was obtained by randomly taking six cobs from each net plot and thereafter the number of kernel rows for each cob was counted and average recorded as number of kernel rows per cob.

3.4.20 Number of cobs per plant

Number of cobs from each plant of net plot was counted, averaged and recorded as number of cobs per plant.

3.4.21 Hundred grain weight (g)

Hundred grain weights was obtained by taking at random total number of 100 grains from each net plot and their weight was recorded as 100 grain weight in each plot.

3.4.22 Grain moisture at harvest (%)

Grain moisture at harvest was collected by taking six ears from each net plot and then shelling the selected ears. The grains from the six ears were mixed together to form a bulk sample which was used to measure grain moisture using a moisture meter.

3.4.23 Grain yield per plant (g)

Grain yield per plant was obtained by weighing the grains obtained after shelling of cobs from individual plants of the net plot. The weight of grains from each plant of the net plot was averaged and recorded as grain weight per plant.

3.4.24 Husk cover score

Husk cover scores was scored using a scale of 1-5, where 1 = husk tightly covering ear tip and extends beyond it while 5 = poor husk cover, tip clearly exposed (Abadassi and Herv´e, 2000).

3.4.25 Harvest index (HI)

Harvest index was obtained from six randomly selected plants of the net plot. The grain and biological yields of the six plants were measured and averaged. Then HI was calculated by taking the average of grain weight dividing by average of biological yield and the value obtained was recorded as harvest index.

3.4.26 Weed species assessment

The dominant weed species per site was identified by placing a one meter square (1 m^2) quadrat in the plots at random followed by counting the number of plants for each species inside the quadrat. Thereafter the weed species that were larger in number at each site was recorded as the dominant weed species in that site.

3.4.27 Diseases severity score (Grey Leaf Spot, Rust and Blight)

In each plot, diseases score was done using a scale of 1-5, where 1= good or resistant and 5 = bad or susceptible (Vivek *et al.*, 2001).

3.4.28 Maize streak count incidence

Maize streak virus count incidence was done at flowering by counting the number of infected plants with maize streak virus disease in the plot and dividing by total number of plants in a plot times hundred to get percent of plants infected.

3.5 Estimation of Genetic Parameters

Genetic parameters were estimated for different traits on maize genotypes as described below.

3.5.1 Genotypic and phenotypic coefficient of variation

The genotypic and phenotypic coefficients of variation were computed according to Burton and Devane (1953) and expressed as percentage.

Genotypic coefficient of variation (GCV) = (δ_g /X) x100

Phenotypic coefficient of variation (PCV) = (δ_p/X) x100

Where,

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

X =general mean of the character

PCV and GCV values were categorized as low, moderate and high values as indicated by Sivasubramanian and Menon (1973) as follows:

0-10 %: Low

10-20%: Moderate

>20%: High

3.5.2 Heritability (h^2b)

Heritability in broad sense was estimated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage (Hanson *et al.*, 1956).

Heritability (h^2_b) = (Vg/Vp) x 100

Where,

Vg= Genotypic variance

Vp = Phenotypic variance

The heritability percentage was categorized as low, moderate and high as coined by Robinson *et al*. (1949) as follows:

0-30%: Low

30-60%: Moderate

>60%: High

3.5.3 Genetic advance

The extent of genetic advance to be expected by selecting five per cent of the superior progeny was calculated by using the following formula given by Robinson *et al*., (1949).

$GA = I\ \delta_p\ (h^2_b)$.

Where,

I = efficacy of selection which is 2.06 at 5% selection intensity

δ_p = Phenotypic standard deviation.

(h^2_b) = Heritability in broad sense.

3.5.4 Genetic advance (GA) as per cent of mean

GA as per cent of mean = (GA/X) x 100

Where,

GA = Genetic advance

X = General mean of character

The GA as per cent of mean was categorized as low, moderate and high according to Johnson *et al.,* (1955).

0-10 %: Low

10-20%: Moderate

20% and above: High

3.5.5 Association analysis

The correlation coefficients were calculated to determine the degree of association of characters with yield and also among the yield components themselves of each environment and combined analysis. Phenotypic correlations were computed using the formula given by Webber and Moorty (1952).

rp = Cov xyp / (Var xp x Var yp)1/2

Where,

rp = Phenotypic correlation

Cov xyp =Phenotypic covariance between the characters x and y.

Var xp and Var yp = Phenotypic variance of the characters x and y respectively.

rg = Cov xyg/ (Var xg x Var yg)1/2

Where;

rg = Genotypic correlation

Cov xyg = Genotypic covariance between the characters x and y.

g = genotypes, e = error, r = number of replications,

Var xg and Var yg = Genotypic variance of the characters x and y respectively.

From the table of combined site analysis, different variance components were estimated using a method given by Al-Jibouri *et al.* (1958). The expected mean squares (EMS) were used to calculate the variance due to genotype, environment and genotype x environment interaction. The analysis of variance table from which the estimates of components of variance were calculated is as shown in Table 2.

Table 2: Analysis of variance for analytical model

Sources of Variation	Degree of freedom	Mean square	Expected Mean Squares
Locations (a)	$(\lambda-1)$	M1	$\delta^2\varepsilon + \rho\delta^2_{\gamma\lambda} + \gamma\delta^2_{\rho} + \rho\gamma\delta^2_{\varepsilon}$
Replication	$(\rho-1)$	M2	$\delta^2\varepsilon + \rho\delta^2$
Error (a)	$\nu(\rho-1)$	M3	$\delta^2\varepsilon + \gamma\delta^2_{\rho/\varepsilon}$
Weeding regimes (b)	$(\omega-1)$	M4	$\delta^2\varepsilon + \rho\delta^2_{\gamma\omega} + \gamma\delta^2_{\rho} + \rho\gamma\delta^2_{\varepsilon}$
Locations x Weeding regimes	$(\lambda-1)(\omega-1)$	M5	$\delta^2\varepsilon + \rho\delta^2_{\gamma\lambda\omega} + \rho\gamma\delta^2_{\lambda\omega}$
Error (b)	$(\rho-1)(\lambda-1)(\omega-1)$	M6	$\delta^2\varepsilon + \gamma\delta^2_{\lambda\omega\,\rho/\varepsilon}$
Genotypes (c)	$(\gamma-1)$	M7	$\delta^2\varepsilon + \rho\delta^2_{\gamma\lambda\omega} + \rho\omega\delta^2_{\gamma\lambda} + \rho\lambda\delta^2_{\gamma\omega} + \rho\lambda\omega\delta^2_{\gamma}$
x location	$(\gamma-1)(\lambda-1)$	M8	$\delta^2\varepsilon + \rho\delta^2_{\gamma\lambda\omega} + \rho\omega\delta^2_{\gamma\lambda}$
Genotype x weeding regimes	$(\gamma-1)(\omega-1)$	M9	$\delta^2\varepsilon + \rho\delta^2_{\gamma\lambda\omega} + \rho\lambda\delta^2_{\gamma\lambda}$
Locations x weeding regimes x Genotype	$(\lambda-1)(\omega-1)(\gamma-1)$	M10	$\delta^2\varepsilon + \delta^2\varepsilon + \rho\delta^2_{\gamma\lambda\omega}$
Error (c)	$\lambda\omega\gamma(\lambda-1)(\omega-1)(\gamma-1)$	M11	$\delta^2\varepsilon$

3.5.6 Stability analysis

Estimation of genotypic means, deviation from regression line (s^2d) and the regression coefficient (b) was done to measure the stability of genotypes. A linear regression analysis for genotype performance assessed across environments was performed according to the method proposed by Eberhart and Russell (1966).

The regression model was given as $Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$

Where,

Y_{ij} = genotype mean of the i^{th} genotype at the j^{th} environment (i = 1, 2.., v, j= 1, 2 …n).

μ_i = the i^{th} genotype mean over all environments.

β_i = regression coefficient that measures the response of the i^{th} genotype to varying environments

I_j = environmental index obtained as the mean of all varieties at the j^{th} environment, minus grand mean

δ_{ij} = the standard deviation of deviation from regression of the i^{th} genotype at the j^{th} environment.

A genotype with high mean performance, regression coefficient equal to unity (b=1) and the variance of deviation from regression (s^2d) approaching zero was considered to be a good and stable genotype (Eberhart and Russell, 1966).

3.5.7 Relationships between regression coefficients, variance of deviation from regression (s2d) and means of genotypes for yield and yield components

The relationships between regression coefficients, variance of deviation from regression (s^2d) and means of genotypes for the variables studied are plotted in the scatter diagrams.

3.5.8 Path coefficient analysis

Path coefficient analysis was performed following the method outlined by Elazar (1982). The analysis was done to determine the direct and indirect effects of independent variables viz. plant height, number of kernel rows per cob, number of leaves per plant, number of leaves below the ear/plant, days to 50% pollen shed, days to 50% silking and days to maturity on the grain yield.

The method involved solving unknowns (path coefficients) from a series of simultaneous equations. Computation was done using the following formula: -

1. $r_{18} = P_{18} + r_{12}P_{28} + r_{13}P_{38} + r_{14}P_{48} + r_{15}P_{58} + r_{16}P_{68} + r_{17}P_{78}$
2. $r_{28} = P_{28} + r_{12}P_{18} + r_{23}P_{38} + r_{24}P_{48} + r_{25}P_{58} + r_{26}P_{68} + r_{27}P_{78}$
3. $r_{38} = P_{38} + r_{13}P_{18} + r_{23}P_{28} + r_{34}P_{48} + r_{35}P_{58} + r_{36}P_{68} + r_{37}P_{78}$
4. $r_{48} = P_{48} + r_{14}P_{18} + r_{24}P_{28} + r_{34}P_{38} + r_{45}P_{58} + r_{46}P_{68} + r_{47}P_{78}$
5. $r_{58} = P_{58} + r_{15}P_{18} + r_{25}P_{28} + r_{35}P_{38} + r_{45}P_{48} + r_{56}P_{68} + r_{57}P_{78}$
6. $r_{68} = P_{68} + r_{16}P_{18} + r_{26}P_{28} + r_{36}P_{38} + r_{46}P_{48} + r_{56}P_{58} + r_{67}P_{78}$
7. $r_{78} = P_{78} + r_{17}P_{18} + r_{27}P_{28} + r_{37}P_{38} + r_{47}P_{48} + r_{57}P_{58} + r_{67}P_{68}$
8. $1 = P^2_{x8} + P^2_{18} + P^2_{28} + P^2_{38} + P^2_{48} + P^2_{58} + P^2_{68} + P^2_{78} + 2P_{18}r_{12}P_{28} + 2P_{18}r_{13}P_{38} + 2P_{18}r_{14}P_{48} + 2P_{18}r_{15}P_{58} + 2P_{18}r_{16}P_{68} + 2P_{18}r_{17}P_{78} + 2P_{28}r_{23}P_{38} + 2P_{28}r_{24}P_{48} + 2P_{28}r_{25}P_{58} + 2P_{28}r_{26}P_{68} + 2P_{28}r_{27}P_{78} + 2P_{38}r_{34}P_{48} + 2P_{38}r_{35}P_{58} + 2P_{38}r_{36}P_{68} + 2P_{38}r_{37}P_{78} + 2P_{48}r_{45}P_{58} + 2P_{48}r_{46}P_{68} + 2P_{48}r_{47}P_{78} + 2P_{58}r_{56}P_{68} + 2P_{58}r_{57}P_{78} + 2P_{68}r_{67}P_{78}$

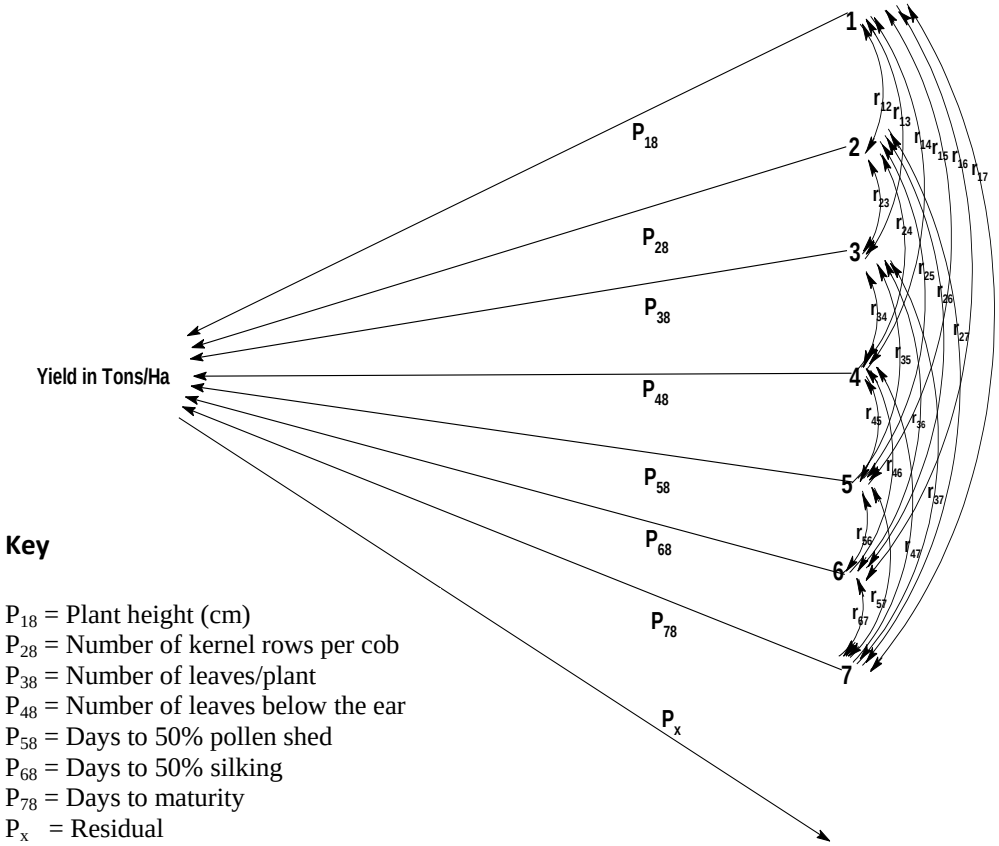


Figure 2: **Path diagram showing the nature of causal system.**

3.6 Data Analysis

Single site and combined sites analysis and covariance analyses (phenotypic and genotypic) between the two traits was done using PROC GLM of SAS version 8.2. Regression analysis was also done for assessment of stability of genotype performance across environments while path coefficient analysis was done to identify factors that influence yield directly and indirectly. Turkey's test was used for mean comparisons. The statistical model used for single site analysis was

$$Y_{ijkl} = \mu + R_j + W_k + \varepsilon_{ijk} + G_i + WG_{(ik)} + \varepsilon_{ijkl}$$

Where;

Y_{ijk} = the measurement obtained for the unit in i^{th} genotype of the j^{th} replication of the k^{th} weeding regime and l^{th} plot; μ = experimental mean, R_j = j^{th} replication effect, W_k = k^{th} weeding regime effect, ε_{ijk}= Error a, Gi= i^{th} genotype effect, $WG_{(ki)}$ = interaction effect of k^{th} and i^{th} weeding regime and ε_{ijkl} = Error b.

The statistical model used for combined sites analysis was;

$$Y_{ijklm} = \mu + R_{j(l)} + L_l + \varepsilon_{ijk} + W_k + LW_{(lk)} + \varepsilon_{ijkl} + G_i + GL_{(il)} + GW_{(ik)} + GLW_{(ilk)} + \varepsilon_{ijklm}$$

Where;

Y_{ijkl} = the measurement obtained for the unit in i^{th} genotype of the j^{th} replication of the k^{th} weeding regime of the l^{th} location and m^{th} plot, μ = experimental mean, $R_{j(l)}$ = j^{th} replication effect within l^{th} location effect, L_l = l^{th} location effect, ε_{ijk} = Error a, W_k = k^{th} weeding regime effect, $LW_{(lk)}$ = interaction effect of l^{th} location effect and k^{th} weeding regime effect, ε_{ijkl} = Error b, G_i = i^{th} genotype effect, $GL_{(il)}$= interaction effect of i^{th} genotype effect and l^{th} location effect, $GW_{(ik)}$ = interaction effect of i^{th} genotype effect and k^{th} weeding regime effect, $GLW_{(ilk)}$= interaction effect of i^{th} genotype effect, l^{th} location effect and k^{th} weeding regime effect and ε_{ijklm} = Error c

CHAPTER FOUR

4.0 RESULTS

4.1 Soils and Climatic Conditions

Soil characteristics varied across locations (environments). Mbimba had silt clay loam, Uyole recorded silt loam and Seatondale had sandy loam whereas Inyala had loam soils. All other three sites were slightly acidic but Mbimba was strongly acidic whereas all four sites had medium CEC and Mg^{2+} (Appendices 1, 2 and 3).

On the other hand Mbimba and Uyole had medium K while Seatondale and Inyala had high K and all sites had low S, Ca^{2+} and Ca: Mg ratio. Mbimba had medium TN and OC while all other three locations had low TN. However, Seatondale and Inyala had low OC but Uyole had very low OC. Furthermore, Mbimba, Seatondale, and Inyala had medium available phosphorous (P) while Uyole had high available P (Appendices 3, 4, 5, 6).

The highest rainfall was recorded during January and April at Uyole; March and April at Mbimba; March and April at Seatondale and January and April at Uyole. Mbimba received very high rainfall compared to other sites and well distributed rainfall across months was recorded at Mbimba and Uyole (Appendices 7, 8, 9 and 10).

Nevertheless the highest maximum temperatures for 2010/2011 cropping season was recorded during February and March at Uyole; May and June at Mbimba; December and January at Seatondale and December, April and May at Inyala. The highest maximum temperatures ranged from 23.1-29.4 (^{0}C) across locations while the minimum temperatures ranged from 10.46 – 15.20 (^{0}C) across environments (Appendices 7, 8, 9 and 10).

4.2 Effect of Weeding Regimes and Genotypes on Yield and Yield Components at Different Locations

There were different effects of weeding regimes and genotypes on maize growth parameters, yield and yield components for the locations.

4.2.1 Plant height (cm) and ear height (cm)

There were significant differences ($P \leq 0.001$) among the weeding regimes for plant and ear height at Inyala (Table 3). The highest mean values recorded were 209.21cm and 101.87cm for plant height and ear height respectively, which did not differ significantly from weeding once for plant height (196.95 cm) and ear height (95.3 cm). The shortest plants were from no weeding. The genotypes were significantly different from each other for ear height but not for plant height. Genotype EH-4 had the tallest ear height plants (92.82 cm), which did not differ significantly from EH-2 (FH 5160) (88.03 cm) and UH 6303 (88.32 cm), the shortest plants were from EH-1 (76.57 cm).

Table 3: Effect of weeding regimes and genotypes on maize yield components and yield at Inyala

Treatments	Plant height (cm)	Ear height (cm)	No. of leaves per plant	Number of leaves below the ear	No. of leaves above the ear	Leaves below /leaves above the ear	Days to first tasselling	Days to 50% tasselling	Days to 50% pollen shed	Days to first silking	Days to 50% silking	Anthesis silking interval	Days to maturity
Weeding regimes													
No weeding	132.45[b]*	59.20[b]	12.95[b]	8.13[a]	4.60[b]	1.87[a]	70.33[a]	79.46[a]	83.80[a]	80.73[a]	87.13[a]	4.60[a]	141.73[a]
Weeding once	196.95[a]	95.37[a]	13.39[ab]	7.81[a]	5.77[a]	1.40[b]	65.73[b]	74.93[b]	78.40[b]	76.20[b]	79.73[b]	3.00[a]	137.40[b]
Weeding twice	209.21[a]	101.87[a]	13.87[a]	8.30[a]	5.56[a]	1.56[b]	66.20[b]	74.87[b]	78.93[b]	76.26[b]	79.33[b]	4.60[a]	137.27[b]
SE±	5.59	2.10	0.16	0.17	0.13	0.06	1.09	0.83	0.67	0.74	0.57	0.74	0.74
Genotypes													
EH-1	163.04[a]	76.57[b]	12.57[b]	7.58[b]	5.29[a]	1.61[a]	68.44[a]	76.89[a]	81.44[a]	79.56[a]	83.44[a]	4.00[a]	140.56[a]
EH-2 (FH 5160)	177.97[a]	88.03[a]	13.72[a]	8.24[ab]	5.20[a]	1.66[a]	67.33[a]	75.11[a]	79.22[a]	75.67[a]	79.89[b]	3.89[a]	136.78[a]
UHS 5350 (EH-3)	188.56[a]	82.00[ab]	13.54[a]	8.03[ab]	5.47[a]	1.52[a]	66.33[a]	76.11[a]	79.11[a]	78.00[a]	83.56[a]	2.00[a]	139.11[a]
EH-4	190.83[a]	92.48[a]	13.78[a]	8.61[a]	5.14[a]	1.71[a]	68.22[a]	77.22[a]	80.89[a]	78.11[a]	81.89[ab]	3.22[a]	139.22[a]
UH 6303	177.27[a]	88.32[a]	13.40[ab]	7.94[ab]	5.44[a]	1.54[a]	66.78[a]	76.79[a]	81.22[a]	77.33[a]	83.56[a]	4.33[a]	138.33[a]
SE±	7.23	2.71	0.21	0.23	0.17	0.08	1.41	1.07	0.86	0.95	0.74	0.95	0.95
CV (%)	12.08	9.51	4.60	8.37	9.64	15.18	6.25	4.22	3.21	3.67	2.71	3.49	2.06
Grand Mean	179.53	2.72	13.40	8.08	5.31	1.61	67.42	76.42	80.38	77.73	82.06	81.99	138.80

Means within the same column followed by the same letter (s) are not significantly different from each other according to Turkey at 5% level, * superscript

Results from Mbimba show that the weeding regimes were significantly affected for plant and ear heights ($P \leq 0.05$) (Table 4). Tallest plants (200.69 cm) with highest ear height (104.22 cm) were recorded for weeding once, which did not differ significantly from weeding once for plant height (200.51 cm) whereas plants with shortest plants (169.00 cm) and ear height (90.24 cm) were recorded from weeding once. Genotypes did not differ significantly for plant height and were significantly different for ear height. Plants with highest ear height were from EH-4 (107.14 cm), which did not differ significantly from UH 6303 (104.20 cm). Plants with shortest ear heights were from EH-1 (85.58 cm).

Table 4: Effect of weeding regimes and genotypes on maize yield components and yield at Mbimba

Treatments	Plant height (cm)	Ear height (cm)	Number of leaves/ plant	Number of leaves below the ear	Number of leaves above the ear	Leaves below /leaves above the ear	Days to first tasselling	Days to 50% tasselling	Days to 50% pollen shed	Days to first silking	Days to 50% silking	Anthesis silking interval	Days to maturity
Weeding regimes													
No weeding	169.00[b*]	90.24[b]	11.39[b]	5.37[b]	6.03[b]	0.90[a]	79.26[a]	84.47[a]	89.47[a]	86.33[a]	93.33[a]	5.27[a]	149.53[a]
Weeding once	200.69[a]	104.22[a]	12.61[a]	6.00[a]	6.65[a]	0.91[a]	77.40[a]	83.26[ab]	87.60[b]	82.60[b]	86.47[b]	5.33[a]	148.00[a]
Weeding twice	200.51[a]	98.77[ab]	12.18[a]	5.82[ab]	6.15[b]	0.92[a]	77.87a	81.87[b]	86.33[b]	81.27[b]	85.33[b]	5.07[a]	148.26[a]
SE±	8.25	3.45	0.18	0.14	0.12	0.02	0.62	0.52	0.42	0.78	1.18	0.59	0.61
Genotypes													
EH-1	168.00[a]	85.58[b]	11.77[a]	5.50[a]	6.18[a]	0.88[a]	77.78[a]	84.44[a]	88.67[a]	83.89[a]	88.44[a]	5.44[a]	148.22[ab]
EH-2 (FH 5160)	190.41[a]	95.56[ab]	12.09[a]	5.77[a]	6.26[a]	0.91[a]	77.22[a]	81.78[a]	86.22[b]	82.56[a]	85.56[a]	4.11[a]	148.11[ab]
UHS 5350 (EH-3)	195.98[a]	96.23[ab]	12.16[a]	5.71[a]	6.47[a]	0.90[a]	77.00[a]	82.44[a]	87.44[a]b	82.33[a]	87.33[a]	4.67[a]	146.44[b]
EH-4	194.11[a]	107.14[a]	12.26[a]	5.89[a]	6.27[a]	0.93[a]	80.00[a]	82.89[a]	87.56[ab]	84.89[a]	90.00[a]	5.44[a]	151.22[a]
UH 6303	201.84[a]	104.20[a]	12.04[a]	5.78[a]	6.21[a]	0.93[a]	78.89[a]	84.45[a]	89.11[a]	83.33[a]	90.55[a]	6.44[a]	149.00[ab]
SE±	10.65	4.46	0.23	0.18	0.15	0.03	0.79	0.68	0.55	1.01	1.52	0.76	0.79
CV (%)	16.81	13.68	5.76	9.27	7.24	9.38	3.05	2.44	1.87	3.64	5.18	43.68	1.60
Grand Mean	190.06	97.74	12.06	5.73	6.28	0.91	78.18	83.20	87.80	83.40	88.38	5.22	148.60

Means within the same column followed by the same letter (s) are not significantly different from each other according to Turkey at 5% level, *****superscript

There were significant differences ($P \leq 0.001$) between weeding regimes for plant height and ear height but the genotypes were not significantly different for these variables at Seatondale site (Table 5). Weeding twice produced tallest plants (204.11 cm) and ear heights (101.27 cm) while no weeding resulted into shortest plants (131.27 cm) and shortest ear height (73.77 cm), which did not differ significantly from weeding once for ear height (74.75 cm). The mean values of genotypes ranged from 159.23 – 167.42 cm and 82.20 – 85.38 cm for plant height and ear height respectively.

Table 5: Effect of weeding regimes and genotypes on maize yield components and yield at Seatondale

Treatments	Plant height (cm)	Ear height (cm)	Number of leaves/plant	Number of leaves below the ear	Number of leaves above the ear	Leaves below /leaves above the ear	Days to first tasselling	Days to 50% tasselling	Days to 50% pollen shed	Days to first silking	Days to 50% silking	Anthesis silking interval	Days to maturity
Weeding regimes													
No weeding	131.27^{c*}	73.77^{b}	16.41^{a}	9.62^{a}	6.04^{b}	1.45^{a}	69.66^{a}	74.60^{a}	77.07^{a}	73.40^{a}	83.86^{a}	4.13^{a}	135.00^{a}
Weeding once	153.45^{b}	74.75^{b}	15.37^{b}	9.27^{a}	6.45^{ab}	1.56^{a}	68.53^{ab}	72.60^{b}	75.47^{a}	71.86^{ab}	78.40^{b}	3.53^{ab}	134.47^{a}
Weeding twice	204.11^{a}	101.27^{a}	16.26^{a}	9.88^{a}	6.91^{a}	1.52^{a}	67.13^{b}	70.40^{c}	72.67^{b}	70.13^{b}	75.33^{c}	2.40^{b}	132.73^{a}
SE±	5.04	2.42	0.21	0.22	0.24	0.08	0.56	0.45	0.47	0.50	0.62	0.42	0.80
Genotypes													
EH-1	163.28^{a}	82.22^{a}	15.92^{a}	9.78^{a}	6.21^{a}	1.58^{a}	68.00^{a}	72.33^{a}	74.88^{a}	71.56^{a}	78.22^{a}	3.33^{a}	133.22^{a}
EH-2 (FH 5160)	159.23^{a}	85.38^{a}	16.30^{a}	9.78^{a}	6.37^{a}	1.49^{a}	69.22^{a}	72.78^{a}	75.44^{a}	72.67^{a}	79.89^{a}	3.00^{a}	135.22^{a}
UHS 5350 (EH-3)	165.29^{a}	82.78^{a}	16.06^{a}	9.27^{a}	6.47^{a}	1.42^{a}	67.56^{a}	72.33^{a}	75.00^{a}	71.00a	79.78a	4.00a	133.22a
EH-4	159.50a	82.20a	15.67a	9.47a	6.77a	1.52a	69.33a	73.11a	75.56^{a}	72.56^{a}	79.67^{a}	3.44^{a}	135.33^{a}
UH 6303	167.42a	83.74a	16.14a	9.66a	6.50a	1.55a	68.11a	72.11a	74.44^{a}	71.22^{a}	78.44^{a}	3.00^{a}	133.33^{a}
SE±	6.51	3.11	0.27	0.28	0.31	0.10	0.72	0.58	0.61	0.64	0.79	0.54	1.03
CV	11.98	11.23	5.16	9.03	14.55	19.45	3.15	2.41	2.44	2.67	3.01	47.91	2.31
Grand Mean	162.94	83.26	16.01	9.59	6.46	1.51	68.44	72.53	75.07	71.80	79.20	3.36	134.06

Means within the same column followed by the same letter (s) are not significantly different from each other according to Turkey at 5% level
*Superscript

Results from Uyole site revealed that both genotypes and weeding regimes were not significantly different for plant height but were significantly different for ear height (Table 6). No weeding recorded the tallest plants (236.67 cm), which did not differ significantly from weeding once and weeding twice whereas plants with highest ear height was observed from no weeding (142.77 cm). The mean values of genotypes on plant height ranged from 223.94 – 237.17 cm and the highest ear height was recorded from EH-4 (138.70 cm), which did not differ significantly from UH 6303 (138.23 cm) or EH-2 (FH 5160) (223.94 cm).

Table 6: Effect of weeding regimes and genotypes on maize yield components and yield at Uyole

Treatments	Plant height (cm)	Ear height (cm)	Number of leaves/ plant	Number of leaves below the ear	Number of leaves above the ear	Leaves below /leaves above the ear	Days to first tasselling	Days to 50% tasselling	Days to 50% pollen shed	Days to first silking	Days to 50% silking	Anthesis silking interval	Days to maturity
Weeding regimes													
No weeding	236.67^{a*}	142.77^{a}	7.34^{b}	5.82^{a}	1.29^{b}	1.27^{b}	84.13^{a}	91.13^{a}	94.06^{a}	87.93^{a}	98.20^{a}	6.13^{a}	165.20^{a}
Weeding once	232.46^{a}	127.65^{b}	8.17^{a}	5.80^{a}	1.43^{a}	1.41^{a}	77.93^{b}	85.33^{b}	87.93^{b}	81.40^{b}	90.06^{b}	6.40^{a}	157.06^{b}
Weeding twice	229.04^{a}	117.79^{b}	8.01^{a}	5.91^{a}	1.31^{b}	1.35^{a}	78.73^{b}	84.53^{b}	87.60^{b}	81.80^{b}	88.13^{b}	5.80^{a}	155.13^{b}
SE±	6.30	2.94	0.11	0.08	0.03	0.02	0.58	0.42	0.49	0.72	0.65	0.86	0.65
Genotypes													
EH-1	237.17^{a}	122.16^{b}	7.38^{b}	5.73^{a}	1.28^{ab}	1.28^{bc}	81.11^{ab}	88.11^{ab}	91.67^{a}	85.22^{ab}	94.33^{a}	6.44^{a}	161.33^{a}
EH-2 (FH 5160)	223.94^{a}	126.58^{ab}	8.14^{a}	5.71^{a}	1.40^{a}	1.44^{a}	79.11^{b}	85.44^{c}	88.22^{b}	82.33^{b}	88.89^{b}	5.88^{a}	155.89^{b}
UHS 5350 (EH-3)	232.97^{a}	121.37^{b}	7.47^{b}	6.04^{a}	1.24^{b}	1.22^{c}	78.67^{b}	85.67^{c}	88.22^{b}	81.44^{b}	91.11^{ab}	6.55^{a}	158.11^{ab}
EH-4	236.19^{a}	138.70^{a}	8.32^{a}	5.92^{a}	1.42^{a}	1.43^{a}	82.89^{a}	89.55^{a}	92.22^{a}	86.44^{a}	93.56^{a}	5.78^{a}	160.56^{a}
UH 6303	233.36^{a}	138.23^{a}	7.87^{ab}	5.82^{a}	1.36^{ab}	1.36^{ab}	79.56^{b}	86.22^{bc}	89.00^{b}	83.11^{ab}	92.78^{a}	5.89^{a}	159.78^{a}
SE±	8.14	3.79	0.14	0.11	0.04	0.02	0.76	0.55	0.63	0.93	0.85	1.12	0.85
CV	10.49	8.79	5.53	5.41	7.93	5.28	2.82	1.90	2.10	2.78	2.77	54.96	1.60
Grand Mean	232.72	129.41	7.84	5.85	1.34	1.35	80.27	87.00	89.87	83.71	92.13	6.11	159.13

Means within the same column followed by the same letter (s) are not significantly different from each other according to Turkey at 5% level, ***s**uperscript

Results from combined site analysis showed that there were significant ($P \leq 0.001$) differences amongst the four locations and the weeding regimes for plant height and ear height (Table 7). However, genotypes were significantly different only for ear height. Uyole produced the tallest plants (232.72 cm) with highest ear height (129.40 cm) and Seatondale produced the shortest plants (162.94 cm) with shortest ear height (83.26 cm). Weeding once resulted into tallest plants (210.71 cm) while weeding twice had the highest ear height (104.93 cm), which did not differ significantly from weeding once (100.50 cm). The shortest plants (166.30 cm) with shortest ear height (91.50 cm) were recorded for no weeding. Plants with tallest ear heights were recorded from EH-4 (105.13 cm) but EH-1 produced plants with shortest ear heights (91.63 cm).

Table 7: Effect of location, weeding regimes and genotypes on maize growth parameters

Treatment	Plant height (cm)	Ear height (cm)	No. leaves/ plant	No. leaves below the ear	No. of leaves above the ear	Leaves below /leaves above the ear	Days to first tasselling	Days to 50% tasselling	Days to 50% pollen shed	Days to first silking	Days to 50% silking	Anthesis silking interval	Days to maturity
Locations													
Inyala	179.53^{c*}	85.48^{c}	13.40^{b}	8.08^{b}	5.31^{b}	1.61^{a}	67.42^{c}	76.42^{c}	80.38^{c}	77.80^{b}	82.06c	3.42^{b}	138.80^{c}
Mbimba	190.07^{b}	97.74^{b}	12.06^{c}	5.73^{c}	6.28^{a}	0.91^{c}	78.18^{b}	83.20^{b}	87.80^{b}	83.40^{a}	88.38b	5.22^{a}	148.60^{b}
Uyole	232.72^{a}	129.40^{a}	7.83^{d}	5.85^{c}	1.34^{c}	1.35^{b}	80.27^{a}	87.00^{a}	89.86^{a}	83.71^{a}	92.13a	6.11^{a}	159.13^{a}
Seatondale	162.94^{d}	83.26^{c}	16.01^{a}	9.58^{a}	6.46^{a}	1.51^{a}	68.44^{c}	72.53^{d}	75.06^{d}	71.80	79.20d	3.36^{b}	134.07^{d}
SE±	3.68	1.68	0.11	0.09	0.09	0.03	0.45	0.36	0.35	0.43	0.47	0.42	0.41
Weeding regimes													
No weeding	166.30^{c}	91.50^{b}	12.02^{b}	7.24^{a}	4.71^{b}	1.38^{a}	75.85^{a}	82.42^{a}	86.10^{a}	82.10^{a}	90.63^{a}	5.03^{a}	147.87^{a}
Weeding once	210.71^{b}	100.50^{a}	12.38^{a}	7.22^{a}	4.97^{a}	1.32^{a}	72.48^{b}	79.03^{b}	82.35^{b}	78.07^{b}	83.66^{b}	4.52^{a}	144.23^{b}
Weeding twice	196.94^{a}	104.93^{a}	12.58^{a}	7.48^{a}	4.87^{ab}	1.34^{a}	72.40^{b}	77.92^{c}	81.38^{b}	77.37^{b}	82.03^{c}	4.03^{a}	143.35^{b}
SE±	3.18	1.46	0.09	0.08	0.08	0.03	0.39	0.31	0.31	0.37	0.40	0.36	0.36
Genotypes													
EH-1	182.87^{a}	91.63^{b}	11.91^{b}	7.15^{a}	4.73^{a}	1.34^{ab}	73.83^{ab}	80.44^{a}	84.17^{a}	80.06^{ab}	86.11^{a}	4.81^{a}	145.83^{ab}
EH-2 (FH 5160)	187.89^{a}	98.87^{ab}	12.56^{a}	7.38^{a}	4.81^{a}	1.38^{ab}	73.22^{ab}	78.77^{b}	82.28^{b}	78.33^{b}	83.56^{b}	4.19^{a}	144.00^{c}
UHS 5350 (EH-3)	195.70^{a}	95.59^{b}	12.31^{ab}	7.26^{a}	4.92^{a}	1.27^{b}	72.39^{b}	79.14^{ab}	82.44^{b}	78.22^{b}	85.03ab	4.28^{a}	144.22b^{c}
EH-4	195.16^{a}	105.13^{a}	12.51^{a}	7.47^{a}	4.90^{a}	1.40^{a}	75.11^{a}	80.69^{a}	84.06^{a}	80.52^{a}	86.69^{a}	4.44^{a}	146.58^{a}
UH 6303	194.97^{a}	103.63^{a}	12.37^{ab}	7.30^{a}	4.88^{a}	1.35^{ab}	73.33^{ab}	79.88^{ab}	83.44^{a} b	78.75^{ab}	85.83^{a}	4.92^{a}	145.11^{abc}
SE±	0.03	1.88	0.12	0.11	0.10	0.03	0.50	0.41	0.39	0.48	0.53	0.47	0.46
CV	12.89	11.40	5.76	8.71	12.42	14.81	4.09	3.04	2.83	3.61	3.70	61.90	1.92
Grand Mean	191.31	98.97	12.33	7.31	4.85	1.35	73.58	79.79	83.28	79.18	85.44	4.52	145.15

Means within the same column followed by the same letter (s) are not significantly different from each other according to Turkey at 5% level, *superscript

4.2.2 Number of leaves per plant and number of leaves below the ear

At Inyala results show that, the weeding regimes significantly ($P \leq 0.05$) affected number of leaves per plant (Table 3). Weeding twice had the highest mean values for number of leaves per plant (13.87) but the lowest number of leaves below the ear (7.81) was recorded from weeding once, which did not differ significantly from weeding twice and no weeding. Genotypes differed significantly ($P \leq 0.05$) in number of leaves per plant and number of leaves below the ear. Genotype EH-4 recorded the highest number of leaves per plant (13.78) whereas the lowest number of leaves below the ear (7.58) was from EH-1.

There were significant ($P \leq 0.05$) differences between the weeding regimes for number of leaves per plant and number of leaves below the ear at Mbimba (Table 4). Weeding once produced plants with largest number of leaves (12.61), which did not differ significantly from weeding twice (12.18) and lowest number of leaves below the ear (5.37) was observed from no weeding treatment**.** The genotypes did not differ significantly differences for both number of leaves per plant and number of leaves below the ear. However, genotype EH-4 had the highest number of leaves (12.26) per plant whereas Genotype EH-1 recorded the least number of leaves below the ear (5.50).

No significant differences were observed among genotypes for number of leaves per plant and number of leaves below the ear at Seatondale. However, weeding regimes showed significant differences among them on number of leaves per plant (Table 5). The mean values for genotypes on number of leaves per plant ranged from 15.67 to 16.30 and 9.27 to 9.78 on number of leaves below the ear.

Results also show that at Uyole, there were significant differences ($P \leq 0.001$) among the genotypes and weeding regimes on number of leaves per plant but did not differ significantly on number of leaves below the ear (Table 6). The highest number of leaves per plant (8.32) was observed from genotype EH-4, which did not differ significantly from EH-2 (FH 5160) (8.14). On the other hand, the least number of leaves per plant were observed from EH-1 (7.38), which did not differ significantly from UHS 5350 (EH-3) (7.47). The least number of leaves below the ear were from EH-2 (FH 5160) (5.71) whereas the highest (6.04) were recorded from UHS 5350 (EH-3). Nevertheless weeding once gave the highest number of leaves per plant (8.17) which did not differ significantly from weeding twice (8.01).

Combined site analysis revealed significant ($P \leq 0.001$) differences across locations for number of leaves per plant and number of leaves below the ear. On the other hand, genotypes showed significant ($P \leq 0.05$) differences in number of leaves per plant but not number of leaves below the ear (Table 7). Weeding regimes were significantly affected number of leaves per plant ($P \leq 0.001$) but not number of leaves below the ear ($P \leq 0.05$). Seatondale recorded the highest number of leaves per plant (16.01) and number of leaves below the ear (9.58) whereas the least number of leaves per plant was recorded at Uyole (7.83). The least number of leaves below the ear was from Mbimba (5.73), which did not differ significantly from Uyole (5.85). Weeding twice recorded highest number of leaves per plant **(**12.58) but did not differ significantly from weeding once (12.38). Genotype EH-2 (FH 5160) produced the highest number of leaves per plant across locations (12.56). However, differences were not significant from EH-4 (12.51). Genotype EH-1 had the least number of leaves per plant (11.91). The lowest number of leaves below the ear was from genotype EH-1 (7.15) and the highest number of leaves below the ear was recorded from EH-4 (7.47).

4.2.3 Number of leaves above the ear and ratio of leaves below to leaves above the ear

At Inyala, there were significant differences ($P \leq 0.001$) among the weeding regimes for number of leaves above the ear and for the ratio of number of leaves below the ear to number of leaves above the ear (Table 3). The highest number of leaves above the ear (5.77) was recorded from weeding once, which did not differ significantly from weeding twice (5.56). The lowest ratio of number of leaves below the ear to leaves above the ear (1.40) was recorded from weeding once treatment which did not differ significantly from weeding twice (1.56). Genotypes differed significantly in number of leaves below the ear; however, did not differ significantly on the ratio of number of leaves below to leaves above the ear. Genotype EH-1 recorded the lowest number of leaves below the ear (7.58) whereas EH-4 exhibited the highest number of leaves below the ear (Table 3).

At Mbimba genotypes did not show significant differences for both number of leaves above and below the ear and the ratio of leaves below the ear to leaves above the ear (Table 4). Weeding regimes significantly ($P \leq 0.05$) affected number of leaves above and below the ear. However they were not significantly different on the ratio of leaves below to leaves above the ear. Weeding once produced plants with the highest mean for number of leaves above the ear (6.65). On the other hand, no weeding treatment was the least in performance (6.03) and did not differ significantly from weeding twice (6.15).

At Seatondale, there were no significant differences among genotypes on number of leaves above the ear and the ratio of leaves below to leaves above the ear (Table 5). On the other hand, weeding regimes showed significant differences ($P \leq 0.05$) among them for number of leaves above the ear. Highest number of leaves above the ear was recorded for weeding twice (6.91), which did not differ significantly from weeding once (6.45).

At Uyole, significant differences among genotypes and weeding regimes were observed ($P \leq 0.05$) on number of leaves above the ear and the ratio of leaves below to leaves above the ear ($P \leq 0.001$) (Table 6). Weeding once showed largest number of leaves above the ear (1.43) but genotype EH-4 recorded the highest number of leaves above the ear (1.42); however, did not differ significantly from genotype EH-2 (FH 5160) (1.40). On the other hand, genotype UHS 5350 (EH-3) recorded the least number of leaves above the ear (1.24) and the ratio of leaves below to leaves above the ear (1.22).

Results from combined sites analysis revealed that locations differed significantly ($P \leq 0.001$) on number of leaves above the ear and ratio of number of leaves below to leaves above the ear (Table7). Weeding regimes differed significantly on number of leaves above the ear but not on the ratio of leaves below to leaves above the ear. Unlike weeding regimes, the genotypes were significantly ($P \leq 0.001$) different on the ratio of leaves below to leaves above the ear and not number of leaves above the ear. The highest number of leaves above the ear was recorded at Seatondale (6.46), which did not differ significantly from those of Mbimba (6.28); Uyole recorded the lowest number of leaves above the ear (1.34). The lowest ratio of number of leaves below to leaves above the ear was observed at Mbimba (0.91) while the highest was from Inyala (1.61), which did not differ significantly from Seatondale (1.51). Weeding once gave the highest number of leaves above the ear (4.97) across sites and with no weeding had the least number of leaves above the ear (4.71). Despite the fact that genotypes did not differ significantly on the number of leaves above the ear, their overall mean performances were slightly different. The highest mean (4.92) and the lowest ratio of number of leaves below to leaves above the ear (1.27) was recorded from genotype UHS 5350 (EH-3) (4.92).

4.2.4 Days to first tasselling and days to first silking

Results of Inyala site showed significant differences among the weeding regimes for days to first tasselling ($P \leq 0.05$) and days to first silking ($P \leq 0.001$) (Table 3). The shortest periods to reach days to first tasselling (65.75 days) and days to first silking (76.20 days) were from weeding once; however, it was significantly different from weeding twice for days to first tasselling (66.20 days) and days to first silking (76.26 days). Non weeded plots took the longest time to tassel and silk with mean days of 70.33 and 80.73 respectively. There were no significant differences among the genotypes for days to first tasselling and days to first silking at this location. However, genotype EH-1 took many days to start tasselling (68.44 days) and silking (79.56 days) compared with the rest of the genotypes.

At Mbimba, no significant differences ($P \leq 0.05$) among the genotypes were observed with regard to first tasselling and days to first silking whereas weeding regimes significantly influenced days to first silking (Table 4). Genotype UHS 5350 (EH-3) tasseled earlier (77.00 days) than EH-4 was the latest to tassel (80.00 days). Plots weeded twice silked earliest (81.27 days) while non weeded ones silked latest (86.33 days).

The results at Seatondale showed that there were significant ($P \leq 0.05$) differences among the weeding regimes on days to first tasselling and days to silking whereas genotypes did not differ significantly in these variables (Table 5). Plants weeded twice took shortest period to attain days to first tasselling (67.13 days) and days to first silking (70.13 days). However, plants not weeded were the last to tassel (69.66 days) and to arrive at days to first silking (73.40 days). Days to first tasselling of genotypes studied ranged from 67.56 – 69.33 days and 71.00 – 72.67 days for days to fist silking.

At Uyole, significant differences among genotypes and weeding regimes were observed on days to first tasselling and days to first silking (Table 6). Genotype UHS 5350 (EH-3) attained days to first tasselling much earlier (78.67 days) than others and took the shortest period to start silking (81.44 days). Genotype EH-4 took the longest time to reach days to first tasselling (82.89 days) and days to first silking (86.44 days). However, weeding once attained days to first tasselling (77.93 days) and days to first silking (81.40 days) much earlier than other weeding regimes. On the other hand, no weeding was the last to reach days to first tasselling (84.13 days) and days to first silking (87.93 days). The former did not differ significantly from weeding twice on days to first tasselling (78.73 days) and days to first silking (81.80 days).

Results from combined site analysis revealed significant ($P \leq 0.001$) differences among the locations, weeding regimes and genotypes ($P \leq 0.05$) on days to first tasselling and days to first silking (Table 7). Earliest days to first tasselling and days to first silking were observed from Inyala (67.42 days) and Seatondale (71.80 days) respectively. Results show that plants at Uyole took the longest period to arrive at days to first tasselling (80.27 days) and days to first silking (83.71 days) than the rest of the locations. Weeding twice took shortest period to reach days to first tasselling (72.40 days) and days to first silking (77.37 days), which did not differ significantly from weeding once on days to first tasselling (72.48 days) and days to first silking (78.07 days). Genotype UHS 5350 (EH-3) took the shortest period to reach days to first tasselling (72.39 days) and days to first silking (78.22 days), which did not differ significantly from EH-2 (FH 5160) on days to first silking (78.33 days) whereas the longest period on days to first tasselling (72.39 days) and days to first silking (80.52 days) was from EH-4.

4.2.5 Days to 50% tasselling, days to 50% pollen shed and days to 50% silking

At Inyala, weeding regimes significantly ($P \leq 0.001$) affected days to 50% tasselling, days to 50% pollen shed and days to 50% silking (Table 3). The shortest period taken to reach days to 50% tasselling (74.87 days) and days to 50% silking (79.33 days) was recorded by weeding twice which did not differ significantly from weeding once for these variables. The longest period on days to 50% tasselling (79.46 days), days to 50% pollen shed (83.80 days) and days to 50% silking (87.13 days) was recorded on non weeded plots**.** The genotypes showed no significant differences among them on days to 50% tasselling and days to 50% pollen shed. However, the genotypes showed significant differences ($P \leq 0.01$) on days to 50% silking. Genotype EH-2 (FH 5160) took the shortest period to reach days to 50% silking (79.89 days) whereas UHS 5350 (EH-3) was the latest to reach at days to 50% silking (83.56 days), which did not differ significantly from EH-1 (83.44 days).

The results from Mbimba showed that weeding regimes significantly affected days to 50% tasselling ($P \leq 0.01$), days to 50% pollen shed and days to 50% silking ($P \leq 0.001$) while differences among genotypes were significant ($P \leq 0.01$) for days to 50% pollen shed (Table 4). Plants weeded twice took the shortest period to attain days to 50% tasselling (81.87 days), days to 50% pollen shed (86.33 days) and days to 50% silking (85.33 days), which did not differ significantly from weeding once for days to 50% pollen shed (87.60 days) and days to 50% silking (86.47 days). Genotype EH-2 (FH 5160) took the shortest period to reach days to 50% pollen shed (86.22 days) whereas genotype UH 6303 took longest time to reach at days to 50% pollen shed (89.11 days).

At Seatondale, no significant differences were observed among genotypes for days to 50% tasselling, 50% pollen shed and 50% silking (Table 5). However, weeding regimes

were significantly different ($P \leq 0.001$) on these traits. The shortest period on days to 50% tasselling (70.40 days), 50% pollen shed (72.67 days) and 50% silking (75.33 days) was from weeding twice while no weeding had the longest period taken to reach days to 50% tasselling (74.60 days), 50% pollen shed (77.07 days) and 50% silking (83.86 days). The mean values of genotypes on days to 50% tasselling ranged from 72.11 to 73.11 days, 74.44 to 75.56 on days to 50% pollen shed and 78.22 to 79.89 days for days to 50% silking.

Significant ($P \leq 0.01$) differences between weeding regimes and genotypes were observed at Uyole on days to 50% tasselling, 50% pollen shed and 50% silking (Table 6). The shortest period observed to attain days to 50% tasselling (84.53 days), 50% pollen shed (87.60 days) and 50% silking (88.13 days) was from weeded twice plants, which did not differ significantly from weeded once plants on days to 50% tasselling (85.33 days), 50% pollen shed (87.93 days) and 50% silking (90.06 days). Genotype EH-2 (FH 5160) took the shortest period to reach days to 50% tasselling (85.44 days), 50% pollen shed (88.22 days) and 50% silking (88.89 days), which did not differ significantly from UHS 5350 (EH-3) on days to 50% tasselling (85.67 days) and 50% pollen shed (88.22 days).

Table 7 indicates significant ($P \leq 0.01$) differences between locations and weeding regimes for days to 50% tasselling, 50% pollen shed and 50% silking. Also, differences among genotypes were significant ($P \leq 0.001$) on days to 50% pollen shed and 50% silking as well as days to 50% tasselling ($P \leq 0.05$). At Seatondale plants took the shortest period to attain days to 50% tasselling (72.53 days), 50% pollen shed (75.06 days) and 50% silking (79.20 days). However, at Uyole plants took the longest days to reach days to 50% tasselling (87.00 days), 50% pollen shed (89.86 days) and 50% silking (92.13 days). Weeded twice plots resulted into earliest realization of days to 50% tasselling

(77.92 days), 50% pollen shed (81.38 days) and 50% silking (82.03 days) whereas no weeding took the longest period to reach days to 50% tasselling (82.42 days), 50% pollen shed (86.10 days) and 50% silking (90.63 days). Genotype EH-2 (FH 5160) reached days to 50% tasselling (78.77 days), 50% pollen shed (82.28 days) and 50% silking (83.56 days) much earlier than other genotypes. Genotype EH-4 took the longest period to reach days to 50% tasselling (80.69 days) and 50% silking (86.69) whereas genotype EH-1 took the longest days to reach 50% pollen shed (84.17 days).

4.2.6 Anthesis silking interval and days to maturity

At Inyala, there were no significant differences among the weeding regimes for anthesis silking interval but were significantly ($P \leq 0.001$) different for days to maturity (Table 3). Plants weeded twice matured earlier (137.27 days), though did not differ significantly from those weeded once (137.40 days). Also there were no significant differences among the genotypes for anthesis silking interval and days to maturity. Days to maturity ranged from 136.78 – 140.56 days for genotypes studied.

Table 4 indicates that weeding regimes were not significantly different for anthesis silking interval and days to maturity at Mbimba. The genotypes did not show significant difference among them for anthesis silking interval and were significantly ($P \leq 0.05$) different for days to maturity. The earliest maturing genotype at Mbimba was UHS 5350 (EH-3) (146.44 days) and the latest was EH-4 (151.22 days).

At Seatondale there were no significant differences among genotypes on anthesis silking interval and days to maturity. However, significant ($P \leq 0.05$) differences were observed among the weeding regimes on anthesis silking interval but did not differ significantly on days to maturity (Table 5). Weeded twice plants gave the shortest anthesis silking interval (2.40) whereas the longest interval was recorded from no weeding (4.13 days).

The mean values of genotypes on anthesis silking interval ranged from 3.00 – 4.00 days and that of days to maturity ranged from 133.22 – 135.33 days.

There were significant differences ($P \leq 0.001$) between the genotypes and weeding regimes for days to maturity at Uyole but did not differ significantly for anthesis silking interval (Table 6). The mean values on anthesis silking interval ranged from 5.78 – 6.55 days and 5.80 – 6.40 days for genotypes and weeding regimes respectively. Genotype EH-2 (FH 5160) attained maturity much earlier (155.89 days) than others whereas genotype EH-1 was the late maturing (161.33 days), which did not differ significantly from EH-4 (160.56 days) and UH 6303 (159.78 days).

The results from combined site analysis revealed significant ($P \leq 0.001$) differences among the locations on anthesis silking interval and days to maturity whereas differences among weeding regimes and genotypes were significant ($P \leq 0.001$) on days to maturity (Table 7). Seatondale had the lowest anthesis silking interval (3.36 days), which did not differ significantly from Inyala (3.42 days). However, Uyole had the longest anthesis silking interval (6.11 days), which did not differ significantly from Mbimba (5.22 days). Plants at Seatondale took the shortest period to reach days to maturity (134.07 days) but the longest period was from Uyole (159.13 days). The overall mean values for anthesis silking interval ranged from 4.03 – 5.03 days for weeding regimes and 4.19 – 4.92 days for the studied genotypes. The earliest maturing genotype (144.00 days) was genotype EH-2 (FH 5160) whereas EH-4 was the latest to mature (146.58 days).

4.2.7 Ear diameter (cm) and Number of cobs per plant

At Inyala, there were significant ($P \leq 0.001$) differences among the weeding regimes. On the other hand, genotypes were significantly ($P \leq 0.05$) different on ear diameter but did

not differ significantly on number of cobs per plant. The highest mean on ear diameter (5.27 cm) was from weeded twice plants while the least values (3.54 cm) was from non weeded plants. Genotype UHS 5350 (EH-3) gave the highest mean (4.79 cm) and the least value was recorded for EH-1 (4.40 cm).

Table 8: Effect of weeding regimes and genotypes on maize yield components and yield at Inyala

Treatments	Ear diameter (cm)	Number of cobs/plant	Cob length (cm)	Number of rows/cob	Grain weight/plant (g)	Ear weight/plant (gm)	Shelling percent (%)	Biological yield/plant (g)	Harvest index (%)	100 grain weight (g)	Husk cover score (1-5)	Yield/ha (t)
Weeding regimes												
No weeding	3.54^{b*}	1.01^{a}	9.38^{b}	10.69^{b}	56.77^{c}	75.41^{c}	73.57^{b}	127.92^{c}	46.13^{b}	25.60^{b}	1.01^{a}	2.43^{c}
Weeding once	5.09^{a}	1.01^{a}	19.65^{a}	15.25^{a}	210.33^{b}	258.56^{b}	80.20^{ab}	390.57^{b}	54.07^{a}	44.40^{a}	1.00^{a}	9.00^{b}
Weeding twice	5.27^{a}	1.01^{a}	20.72^{a}	14.87^{a}	258.33^{a}	312.22^{a}	83.11^{a}	448.33^{a}	57.20^{a}	45.53^{a}	1.00^{a}	11.03^{a}
SE±	0.07	0.01	0.35	0.34	7.55	9.97	2.44	10.95	0.02	1.35	0.004	0.33
Genotypes												
EH-1	4.40^{b}	1.01^{a}	14.73^{b}	12.82^{b}	157.64^{a}	204.31^{a}	75.16^{a}	286.80^{b}	54.78^{a}	40.00^{a}	1.00^{a}	6.72^{a}
EH-2 (FH 5160)	4.68^{ab}	1.00^{a}	17.38^{a}	13.36^{ab}	183.82^{a}	215.28^{a}	82.20^{a}	321.77^{ab}	54.89^{a}	37.44^{a}	1.00^{a}	7.99^{a}
UHS 5350 (EH-3)	4.79^{a}	1.01^{a}	16.18^{ab}	14.92^{a}	182.10^{a}	223.79^{a}	80.53^{a}	324.72^{ab}	53.22^{a}	35.56^{a}	1.00^{a}	7.69^{a}
EH-4	4.74^{ab}	1.01^{a}	17.50^{a}	12.93^{b}	177.33^{a}	223.61^{a}	79.79^{a}	356.94^{a}	48.44^{a}	40.44^{a}	1.01^{a}	7.60^{a}
UH 6303	4.56^{ab}	1.00^{a}	17.13^{a}	13.98^{ab}	174.83^{a}	210.00^{a}	77.13^{a}	321.12^{ab}	51.00^{a}	39.11^{a}	1.00^{a}	7.43^{a}
SE±	0.09	0.01	0.45	0.43	9.74	12.88	3.15	14.13	0.02	1.74	0.005	0.42
CV (%)	5.81	2.56	8.15	9.58	16.69	17.94	11.97	13.15	13.41	13.59	1.49	16.99
Grand Mean	4.64	1.01	16.59	13.60	175.15	215.39	78.96	322.27	0.52	38.51	1.00	7.48

Means within the same column followed by the same letter (s) are not significantly different from each other according to Turkey at 5% level, *superscript

Results from Mbimba show no significant differences among the genotypes on ear diameter and number of cobs per plant while weeding regimes showed significant ($P \leq 0.001$) differences on ear diameter but not on number of cobs per plant (Table 9). Weeding twice had the highest mean on ear diameter (5.15 cm) but the least mean was from no weeding treatment (4.10 cm).

Table 9: Effect of weeding regimes and genotypes on maize yield components and yield at Mbimba

Treatments	Ear diameter (cm)	No. of cobs/ plant	Cob length (cm)	No. of rows/ cob	Grain weight/ plant (g)	Ear weight/plant (gm)	Shelling percent (%)	Biological yield /plant (g)	Harvest index (%)	100 grain weight (g)	Husk cover score (1-5)	Yield (t/ha)
Weeding regimes												
No weeding	4.10^{b*}	1.00^{a}	10.34^{a}	12.34^{b}	58.45^{b}	93.94^{b}	59.13^{a}	157.87^{b}	35.33^{b}	29.00^{b}	1.00^{a}	2.48^{b}
Weeding once	4.93^{a}	1.00^{a}	15.89^{a}	14.13^{a}	152.99^{a}	219.35^{a}	71.39^{a}	360.54^{a}	42.00^{ab}	36.66^{a}	1.00^{a}	6.36^{a}
Weeding twice	5.15^{a}	1.00^{a}	14.81^{a}	14.24^{a}	177.06^{a}	252.20^{a}	71.77^{a}	385.06^{a}	47.33^{a}	42.00^{a}	1.07^{a}	7.47^{a}
SE±	0.09	0.00	0.82	0.31	9.09	11.08	3.69	15.73	0.02	1.98	0.04	0.38
Genotypes												
EH-1	4.64^{a}	1.00^{a}	12.43^{a}	13.48^{ab}	122.56^{a}	178.56^{a}	71.17^{a}	277.97^{a}	44.11^{a}	36.11^{a}	1.00^{a}	5.11^{a}
EH-2 (FH 5160)	4.80^{a}	1.00^{a}	14.87^{a}	13.58^{ab}	142.87^{a}	199.64^{a}	69.48^{a}	308.90^{a}	45.11^{a}	38.89^{a}	1.00^{a}	6.12^{a}
UHS 5350 (EH-3)	4.94^{a}	1.00^{a}	13.04^{a}	14.68^{a}	141.49^{a}	201.53^{a}	70.99^{a}	315.27^{a}	42.22^{a}	36.11^{a}	1.00^{a}	5.85^{a}
EH-4	4.54^{a}	1.00^{a}	13.76^{a}	12.50^{b}	123.33^{a}	185.00^{a}	62.17^{a}	320.00^{a}	35.33^{a}	34.44^{a}	1.11^{a}	5.19^{a}
UH 6303	4.70^{a}	1.00^{a}	14.31^{a}	13.58^{ab}	117.27^{a}	177.74^{a}	63.33^{a}	283.66^{a}	41.00^{a}	33.89^{a}	1.00^{a}	4.89^{a}
SE±	0.12	0.00	1.06	0.40	11.74	14.31	4.76	20.31	0.03	2.55	0.05	0.49
CV (%)	7.77	0	23.25	8.81	27.19	22.77	21.17	20.23	21.07	21.34	14.58	27.31
Grand Mean	4.73	1.00	13.68	13.57	129.50	188.50	67.43	301.16	0.42	35.89	1.02	5.44

Means within the same column followed by the same letter (s) are not significantly different from each other according to Turkey at 5% level, *superscript

At Seatondale significant differences were observed among the weeding regimes on ear diameter ($P \leq 0.001$) and number of cobs per plant ($P \leq 0.05$) whereas the genotypes were not significantly different on these traits (Table 10). The highest mean on ear diameter was from weeding twice (5.21cm) but the least mean was recorded by no weeding treatment (3.95 cm). Weeding twice had the highest number of cobs per plant (1.18) but the least number was from no weeding treatment (1.00). The mean values of genotypes ranged from 4.47 – 4.70 cm for ear diameter and 1.04 – 1.14 for number of cobs per plant.

Table 10: Effect of weeding regimes and genotypes on maize yield components and yield at Seatondale

Treatments	Ear diameter (cm)	Number of cobs/plant	Cob length (cm)	Number of rows/cob	Grain weight/ plant (g)	Ear weight /plant (gm)	Shelling percent (%)	Biological yield/plant (g)	Harvest index (%)	100 grain weight (g)	Husk cover score (1-5)	Yield/ha (t)
Weeding regimes												
No weeding	3.95^{c*}	1.00^{b}	15.07^{a}	12.28^{b}	72.05^{c}	85.55^{c}	75.25^{a}	177.14^{c}	39.47^{a}	26.89^{c}	1.33^{b}	3.11^{c}
Weeding once	4.53^{b}	1.10^{ab}	29.00^{a}	12.40^{b}	118.95^{b}	165.27^{b}	75.59^{a}	332.83^{b}	39.07^{a}	32.87^{b}	1.40^{ab}	4.92^{b}
Weeding twice	5.21^{a}	1.18^{a}	20.64^{a}	14.76^{a}	208.95^{a}	291.79^{a}	78.87^{a}	580.83^{a}	38.00^{a}	37.41^{a}	1.93^{a}	8.99^{a}
SE±	0.09	0.03	6.71	0.29	10.31	10.42	1.73	20.96	0.02	0.88	0.16	0.49
Genotypes												
EH-1	4.59^{a}	1.14^{a}	19.56^{a}	13.32^{a}	158.27^{a}	175.74^{a}	76.66^{a}	352.78^{a}	42.33^{a}	33.60^{a}	1.56^{a}	6.81^{a}
EH-2 (FH 5160)	4.53^{a}	1.10^{a}	17.63^{a}	12.66^{a}	130.04^{a}	181.82^{a}	77.46^{a}	347.32^{a}	39.78^{a}	32.17^{a}	1.66^{a}	5.64^{a}
UHS 5350 (EH-3)	4.47^{a}	1.06^{a}	18.30^{a}	12.73^{a}	137.36^{a}	173.17^{a}	72.76^{a}	359.99^{a}	34.78^{a}	31.26^{a}	1.66^{a}	5.65^{a}
EH-4	4.70^{a}	1.12^{a}	16.73^{a}	13.97^{a}	128.83^{a}	183.14^{a}	78.90^{a}	382.82^{a}	37.89^{a}	30.32^{a}	1.33^{a}	5.89^{a}
UH 6303 (Check)	4.53^{a}	1.04^{a}	16.52^{a}	13.06^{a}	112.08^{a}	190.47^{a}	77.09^{a}	375.10^{a}	39.44^{a}	34.61^{a}	1.56^{a}	5.19^{a}
SE±	0.11	0.04	8.66	0.37	13.31	13.46	2.23	27.07	0.03	1.13	0.21	0.63
CV (%)	7.31	11.77	12.63	8.44	29.97	22.32	8.75	22.33	21.73	10.50	40.81	33.69
Grand Mean	4.56	1.09	21.57	13.15	133.32	180.87	76.57	363.60	0.39	32.39	1.56	5.68

Means within the same column followed by the same letter (s) are not significantly different from each other according to Turkey at 5% level, *superscript

At Uyole, there were no significant differences among the genotypes on ear diameter and number of cobs per plant (Table 11). Unlike genotypes, the weeding regimes showed significant differences ($P \leq 0.05$) among them on ear diameter and number of cobs per plant. Weeding twice recorded the highest mean on ear diameter (5.03 cm) and number of cobs per plant (1.15) while no weeding performed poorly on ear diameter (4.61 cm) and number of cobs per plant (1.00). The latter did not differ significantly from weeding once on ear diameter (4.72 cm).

Table 11: Effect of weeding regimes and genotypes on maize yield components and yield at Uyole

Treatments	Ear diameter (cm)	Number of cobs/plant	Cob length (cm)	Number of rows/ cob	Grain weight/plant (g)	Ear weight /plant (gm)	Shelling percent (%)	Biological yield /plant (g)	Harvest index (%)	100 grain weight (g)	Husk cover score (1-5)	Yield/ ha (t)
Weeding regimes												
No weeding	4.61^{b*}	1.00^{b}	14.65^{c}	13.92^{a}	107.04^{c}	147.69^{c}	73.43^{a}	339.34^{c}	32.56^{a}	32.88^{b}	1.00^{a}	4.65^{c}
Weeding once	4.72^{b}	1.07^{ab}	17.85^{b}	14.52^{a}	145.95^{b}	186.08^{b}	77.23^{a}	483.43^{b}	30.60^{a}	33.94^{b}	1.00^{a}	6.41^{b}
Weeding twice	5.03^{a}	1.15^{a}	19.73^{a}	14.39^{a}	201.64^{a}	254.12^{a}	77.47^{a}	579.86^{a}	73.73^{a}	38.68^{a}	1.00^{a}	8.79^{a}
SE±	0.08	0.02	0.46	0.19	6.35	7.07	1.91	15.29	0.15	0.81	0.00	0.27
Genotypes												
EH-1	4.71^{a}	1.03^{a}	17.32^{a}b	14.34^{a}b	145.79^{a}	193.13^{a}	74.36^{a}	477.77^{a}	31.11^{a}	36.81^{ab}	1.00^{a}	6.31^{a}
EH-2 (FH 5160)	4.81^{a}	1.14^{a}	18.68^{a}	13.78^{bc}	165.49^{a}	197.92^{a}	80.32^{a}	449.73^{a}	37.56^{a}	37.74^{a}	1.00^{a}	7.35^{a}
UHS 5350 (EH-3)	4.80^{a}	1.06^{a}	16.19^{b}	15.11^{a}	143.44^{a}	191.54^{a}	75.21^{a}	449.74^{a}	63.00^{a}	32.40^{c}	1.00^{a}	6.23^{a}
EH-4	4.67^{a}	1.08^{a}	17.26^{ab}	13.06^{c}	158.42^{a}	205.34^{a}	76.40^{a}	478.42^{a}	66.86^{a}	36.22^{abc}	1.00^{a}	6.93^{a}
UH 6303	4.93^{a}	1.06^{a}	17.60^{ab}	15.11^{a}	144.58^{a}	191.88^{a}	73.92^{a}	489.14^{a}	29.59^{a}	32.65^{bc}	1.00^{a}	6.29^{a}
SE±	0.09	0.04	0.59	0.24	8.20	9.13	2.46	19.74	0.20	1.04	0.00	0.35
CV (%)	6.21	10.21	10.21	5.17	16.23	13.98	9.71	12.67	18.39	8.89	0.00	15.99
Grand Mean	4.78	1.07	17.41	14.28	151.55	195.96	76.04	467.54	0.46	35.17	1.00	6.62

Means within the same column followed by the same letter (s) are not significantly different from each other according to Turkey at 5% level, *superscript

Combined analysis of the four locations showed significant differences among the locations on ear diameter ($P \leq 0.05$) and number of cobs per plant and ($P \leq 0.001$) (Table 12). Uyole showed the highest mean on ear diameter (4.78 cm) but the highest mean for number of cobs per plant was observed at Seatondale (1.09), which did not differ significantly from Uyole (1.07). Weeding regimes were significantly ($P \leq 0.001$) different among them on ear diameter and number of cobs per plant. Weeding twice resulted into highest mean of ear diameter (5.16 cm) and number of cobs per plant (1.08) while no weeding treatment gave the least mean on ear diameter (4.05 cm) and number of cobs per plant (1.00). Genotypes did not differ significantly on ear diameter and number of cobs per plant and had values ranging from 4.59cm – 4.75 cm on ear diameter, 1.03 – 1.06 on number of cobs per plant.

Table 12: Effect of location, weeding regimes and genotypes on maize yield and yield components

Treatments	Ear diameter (cm)	Number of cobs/plant	Cob length (cm)	Number of rows/cob	Grain weight/plant (g)	Ear weight/ plant (gm)	Shelling percent (%)	Biological yield/plant (g)	Harvest index (%)	100 grain weight (g)	Husk cover score (1-5)	Yield/ha (t)
Locations												
Inyala	4.64^{ab*}	1.00^{b}	16.59^{ab}	13.60^{b}	175.15^{a}	215.40^{a}	78.96^{a}	322.27^{c}	52.47^{a}	38.51^{a}	1.00^{b}	7.48^{a}
Mbimba	4.73^{ab}	1.00^{b}	13.68^{b}	13.57^{b}	129.50^{c}	188.50^{b}	67.43^{b}	301.16^{c}	41.56^{a}	35.89^{ab}	1.02^{b}	5.44^{c}
Uyole	4.78^{a}	1.07^{a}	17.41^{ab}	14.28^{a}	151.54^{b}	195.96^{ab}	76.04^{a}	467.54^{a}	45.62^{a}	35.16^{bc}	1.00^{b}	6.62^{b}
Seatondale	4.56^{b}	1.09^{a}	21.56^{a}	13.14^{b}	133.31^{cb}	180.87^{b}	76.57^{a}	363.60^{b}	38.84^{a}	32.39^{c}	1.56^{a}	5.67^{c}
SE±	0.05	0.013	2.19	0.16	5.03	5.96	1.51	10.38	0.05	0.79	0.05	0.22
Weeding regimes												
No weeding	4.05^{c}	1.00^{c}	12.36^{b}	12.31^{c}	73.58^{c}	100.65^{c}	70.35^{b}	200.57^{c}	38.37^{b}	28.59^{c}	1.08^{b}	3.16^{c}
Weeding once	4.82^{b}	1.04^{b}	18.98^{a}	14.07^{b}	157.06^{b}	207.32^{b}	76.92^{a}	391.84^{b}	41.44^{ab}	36.97^{b}	1.10^{b}	6.67^{b}
Weeding twice	5.16^{a}	1.08^{a}	20.60^{a}	14.57^{a}	211.50^{a}	277.58^{a}	76.98^{a}	498.52^{a}	54.07^{a}	40.91^{a}	1.25^{a}	9.07^{a}
SE±	0.04	0.011	1.69	0.14	4.35	5.16	1.31	8.99	0.04	0.68	0.04	0.19
Genotypes												
EH-1	4.59^{a}	1.04^{a}	16.01^{a}	13.49^{bc}	146.06^{a}	187.93^{a}	74.33^{a}	348.83^{a}	43.08^{a}	36.63^{a}	1.14^{a}	6.24^{a}
EH-2 (FH 5160)	4.71^{a}	1.06^{a}	17.14^{a}	13.34^{bc}	155.56^{a}	198.67^{a}	77.36^{a}	356.93^{a}	44.33^{a}	36.56^{a}	1.17^{a}	6.78^{a}
UHS 5350 (EH-3)	4.75^{a}	1.03^{a}	20.71^{a}	14.36^{a}	151.10^{a}	197.51^{a}	74.87^{a}	360.66^{a}	48.31^{a}	33.83^{a}	1.17^{a}	6.41^{a}
EH-4	4.66^{a}	1.05^{a}	16.31^{a}	13.11^{c}	146.98^{a}	199.28^{a}	74.31^{a}	384.55^{a}	47.14^{a}	35.36^{a}	1.11^{a}	6.23^{a}
UH 6303	4.68^{a}	1.03^{a}	16.39^{a}	13.93^{ab}	137.19^{a}	192.52^{a}	72.87^{a}	367.26^{a}	40.25^{a}	35.07^{a}	1.14^{a}	5.86^{a}
SE±	0.06	0.01	2.19	0.18	5.62	6.67	1.69	11.61	0.05	0.88	0.05	0.25
CV (%)	7.12	8.10	14.00	8.01	22.90	20.49	13.53	19.15	18.56	14.89	27.81	23.81
Grand Mean	4.68	1.04	17.31	13.65	147.38	195.18	74.75	363.64	0.45	35.49	1.14	6.30

Means within the same column followed by the same letter (s) are not significantly different from each other according to Turkey at 5% level, *superscript

4.2.8 Cob length (cm) and number of kernel rows per cob

At Inyala, there were significant ($P \leq 0.001$) differences among the weeding regimes on cob length and number of kernel rows per cob (Table 8). The genotypes were also significantly ($P \leq 0.001$) different on cob length and number of kernel rows per cob ($P \leq 0.05$). The highest mean for cob length (20.72 cm) was from weeding twice, which did not differ significantly from weeding once (19.65cm) and the least mean (9.36 cm) was from no weeding treatment. On the other hand, weeding once recorded the largest number of kernel rows per cob (15.25), which did not differ significantly from weeding twice (14.87). Genotype EH-4 recorded highest mean for cob length (17.50 cm), which did not differ significantly from UH 6303 (17.13 cm) and EH-2 (FH 5160) (17.38 cm) but the least mean was from EH-1 (14.73 cm). The highest mean for number of kernel rows per cob was recorded from UHS 5350 (EH-3) (14.92) and the lowest were observed from EH-1 (12.82).

At Mbimba, weeding regimes were significantly different ($P \leq 0.001$) on number of kernel rows per cob but not for cob length (Table 9**).** The highest mean number of kernel rows per cob was recorded from weeding twice (14.24) but did not differ significantly from weeding once (14.13). Genotypes showed significant differences ($P \leq 0.05$) among them for number of kernel rows per cob but not on cob length. Genotype UHS 5350 (EH-3) had the highest mean number of kernel rows per cob (14.68cm) and the least mean was shown by EH-4 (12.50 cm).

There were no significant differences among the genotypes on cob length and number of kernel rows per cob at Seatondale. The length of cobs ranged from 16.52 cm to 19.56 cm whereas the number of kernel rows per cob ranged from 12.66 – 13.97 cm (Table 10). Weeding regimes differed significantly ($P \leq 0.001$) for number of kernel rows per cob but

not on cob length. The highest mean number of kernel rows per cob was recorded for weeding twice (14.76) and the least mean was from no weeding (12.28), which did not differ significantly from weeding once (12.40).

The results from Uyole show significant differences among the genotypes on cob length and number of kernel rows per cob while weeding regimes differed significantly ($P \leq 0.001$) on cob length (Table 11). Genotype EH-2 (FH 5160) had the longest cobs (18.68 cm) but the shortest cobs were observed from genotype UHS 5350 (EH-3) (16.19 cm). The highest number of kernel rows per cob were recorded from UHS 5350 (EH-3) and UH 6303 (15.11) whereas the lowest number was from EH-4 (13.06). Weeding twice recorded the longest cobs (19.73cm) whereas no weeding exhibited the shortest cobs (14.65 cm).

Results from combined site analysis indicates significant ($P \leq 0.001$) differences amongst the locations and weeding regimes on cob length and number of rows per cob while genotypes were significantly different ($P \leq 0.001$) among them on number of rows per cob but not on cob length (Table 12). Seatondale location recorded the longest cobs (21.56 cm) but the shortest cobs were from Mbimba (13.68 cm). However, Uyole recorded the highest number of kernel rows per cob amongst the locations (14.28) whereas the least number was from Seatondale (13.14), which did not differ significantly from Mbimba (13.57) and Inyala (13.60). Weeding once resulted into longest cobs (20.60 cm), which did not differ significantly from weeding twice (18.98 cm) whereas the highest number of kernel rows per cob (14.57) was recorded for weeding twice. Furthermore UHS 5350 (EH-3) genotype recorded the longest cobs (20.71 cm) and highest number of kernel rows per cob (14.36) across environments. Genotypes EH-1

gave the shortest cob length (16.01 cm) and the least number of kernel rows per cob (13.1 1) was recorded from genotype EH-4.

4.2.9 Grain weight per plant (g) and ear weight (g)

Significant differences ($P \leq 0.001$) were observed at Inyala among the weeding regimes on grain weight per plant and ear weight per plant but non significant differences were observed among genotypes on the same variables (Table 8). The highest mean was from weeding twice for grain weight per plant (258.33 g) and ear weight per plant (312.22 g). The least mean on grain weight per plant (56.77 g) and ear weight per plant (75.41) was recorded for non weeded plants. The mean values of genotypes for grain weight and ear weight ranged from 157.64 – 183.82 g and 204.31 – 223.79 g respectively.

Genotypes were not significantly different from each other on grain and ear weights per plant at Mbimba (Table 9). The mean values of genotypes on grain weight ranged from 117.27 – 142.87 g and 177.74 – 201.53 g for ear weight. Weeding regimes showed significant ($P \leq 0.001$) differences among them on grain weight and ear weight per plant. Weeding twice recorded the highest grain weight (177.06 g) and ear weight (252.20 g) different from no weeding which had the lowest grain weight per plant (58.45 g) and ear weight (93.94 g).

Significant differences ($P \leq 0.001$) were observed between weeding regimes for grain weight and ear weight per plant at Seatondale (Table 10). Weeding twice had the highest mean on grain weight per plant (208.95 g) and ear weight (291.79 g) whereas no weeding recorded the least grain weight per plant (72.05 g) and ear weight (85.55 g). Genotype EH-1 had the highest grain weight (158.27 g) though differences were not significant from the rest of genotypes.

Table 11 shows that at Uyole there were significant differences ($P \leq 0.001$) among the weeding regimes on grain weight per plant and ear weight but genotypes did not differ significantly from each other on these variables. Weeded twice plants gave the highest grain weight per plant (201.64 g) and ear weight (254.12 g) and non weeded plants had the least grain weight per plant (107.04 g) and ear weight (147.69 g). The mean values of genotypes for grain weight ranged from 143.44 – 165.49 g and 191.54 – 205.34 g for ear weight.

Results from combined analysis showed that weeding regimes and locations differed significantly ($P \leq 0.001$) on grain weight per plant and ear weight (Table 12). Unlike weeding regimes and locations, genotypes were not significantly different from each other on these traits. Inyala location had the highest mean on grain weight (175.15 g) and ear weight (215.40 g) among the locations while Seatondale performed poorly on ear weight (180.87 g), which did not differ significantly from Mbimba (188.50 g) on this trait. Weeding twice exhibited the highest grain weight per plant (211.50g) and ear weight (277.58 g) and no weeding performed poorly for grain weight per plant (73.58 g) and ear weight per plant (100.65 g) across the sites. The mean values of genotypes for grain weight and ear weight ranged from 137.19 – 155.56 g and 187.93 – 199.28 g respectively.

4.2.10 Shelling percent (%) and biological yield (g)

The weeding regimes showed significant differences between them at Inyala on shelling percent ($P \leq 0.05$) and biological yield ($P \leq 0.001$) (Table 8). The highest shelling percent (83.11%) and biological yield (448.33 g) were observed for weeding twice and no weeding had lowest shelling percent (73.57%) and biological yield (127.92 g). The genotypes were significantly ($P \leq 0.001$) different for biological yield and not for

shelling percent. The highest mean for biological yield was observed for genotype EH-4 (356.94 g) and genotype EH-1 had the least biological yield (286.80 g).

Table 9 indicates that there were no significant differences among the weeding regimes for shelling percent; however, were significantly different from each other for biological yield ($P \leq 0.001$) at Mbimba. On the other hand, genotypes did not show significant difference amongst them on these variables. Weeding twice had highest biological yield (385.06 g) and no weeding produced the least biological yield (157.87 g). Though genotypes did not differ significantly amongst themselves, EH-4 gave more biological yield (320.00 g) than other genotypes.

The results at Seatondale show that there were no significant differences among the genotypes on shelling percent and biological yield whereas the weeding regimes differed significantly ($P \leq 0.001$) on biological yield (Table 10). The mean values of genotypes for shelling percent ranged from 72.76 – 78.90% and 347.32 – 382.82 g for biological yield.

There were no significant differences between genotypes for shelling percent and biological yield at Uyole while weeding regimes showed significant ($P \leq 0.001$) differences among them for biological yield (Table 11). Weeding regime values for shelling percent ranged from 73.43 - 77.47%. Weeding twice recorded the highest mean on biological yield per plant (579.86 g) and no weeding had the least biological yield per plant (339.34 g). Genotypes values ranged from 73.92 – 80.32% for shelling percent and 449.73 - 489.14 g for biological yield.

Results from combined site analysis showed significant ($P \leq 0.001$) differences between locations and weeding regimes for shelling percent and biological yield but genotypes did

not differ significantly among themselves on these traits (Table 12). The highest shelling percent (78.96%) were recorded at Inyala and the biological yield per plant (467.5 g) at Uyole whereas the lowest shelling percent (67.43%) and biological yield per plant (301.16 g) were recorded from Mbimba. Inyala did not differ significantly from Uyole and Seatondale on shelling percent. Weeding twice recorded the highest shelling percent (76.98%) and biological yield (498.52 g), which did not differ significantly from weeding once on shelling percent whereas no weeding had the least means across locations for shelling percent (70.35%) and biological yield (200.57 g). The values of genotypes ranged from 72.87 - 77.36% for shelling percent and 348.83-384.55 g for biological yield.

4.2.11 Harvest index (%), 100 grain weight (g) and husk cover score.

Results from Inyala site showed no significant differences among the weeding regimes on husk cover score and were significantly ($P \leq 0.001$) different on harvest index and 100 kernels weight while genotypes did not differ significantly for both traits (Table 8). The highest harvest index (57.20%) and 100 grain weight (45.53 g) were recorded for weeding twice and no weeding had lowest mean for harvest index (46.13%) and 100 grain weight per plant (25.60 g).

Results also showed no significant differences among the genotypes on harvest index and 100 grain weight at Mbimba while the weeding regimes showed significant ($P \leq 0.001$) differences between them for harvest index and 100 grain weight (Table 9). Weeding twice had the highest mean for harvest index (47.33%) and 100 kernels weight (42.00 g), which did not differ significantly from weeding once for 100 grain weight and the least mean was shown by no weeding for harvest index (35.33%) and 100 grain weight (29.00 g). The mean values of genotypes for harvest index ranged from 35.33- 45.11% and 33.89 – 38.895 g for 100 grain weight.

At Seatondale, there were significant differences among the weeding regimes for husk cover score ($P \leq 0.05$) and 100 grain weight ($P \leq 0.001$) (Table 10). The highest mean on 100 grain weight (37.41 g) and husk cover score (1.93) was recorded from weeding twice and the lowest mean on 100 grain weight (26.89 g) and husk cover score was from no weeding. Genotypes did not differ significantly from each other on these traits and had values ranging from 30.32 – 34.61 g for 100 grain weight and 1.33-1.66 for husk cover scores.

No significant differences were observed between the weeding regimes and genotype on harvest index and husk cover score at Uyole; however, there were significant differences among the weeding regimes ($P \leq 0.001$) and genotypes ($P \leq 0.05$) on 100 grain weight (Table 11). Weeding twice recorded highest 100 grain weight (38.68 g) and no weeding had the least 100 grain weight (32.88 g), which did not differ significantly from weeding once. Genotype EH-2 (FH 5160) had the highest mean on 100 grain weight (37.74 g) and the lowest mean was from UHS 5350 (EH-3) (32.40 g).

Results from combined sites analysis revealed no significant differences among the genotypes for harvest index, 100 grain weight and husk cover scores across sites. However there were significant differences ($P \leq 0.001$) between the locations on 100 grain weight and husk cover scores but not for harvest index. Weeding regimes differed significantly on 100 grain weight ($P \leq 0.001$), harvest index ($P \leq 0.05$) and husk cover scores (Table 12). The mean values of genotypes ranged from 43.08 – 48.31% for harvest index, 33.83 – 36.63 g for 100 grain weight and 1.11 – 1.17 for husk cover scores. Inyala had the highest mean on harvest index (52.47%) and 100 grain weight (38.51 g) among the locations. Seatondale recorded the least mean on harvest index (38.84) and 100 grain weight (32.39 g). Weeding twice recorded the highest mean on harvest index (54.07%),

100 grain weight (40.91 g) and husk cover scores (1.25) and no weeding performed poorly for all the variables.

4.2.12 Yield (t ha^{-1})

Weeding regimes showed significant differences ($P \leq 0.001$) amongst them for yield while the genotypes did not show significant differences among them at Inyala (Table 8). The highest mean performance was observed for weeding twice (11.0 t ha^{-1}) and poor performance was recorded from no weeding (2.4 t ha^{-1}). Although genotypes did not show significant differences among them, EH-2 (FH 5160) gave the highest yield (7.99 t ha^{-1}) and genotype EH-1 had lowest yield (6.72 t ha^{-1}).

No significant differences were observed among the genotypes on yield at Mbimba (Table 9). Unlike genotypes, the weeding regimes showed significant ($P \leq 0.001$) differences among them. Weeding twice resulted into highest yield (7.47 t ha^{-1}) although differences were not significantly different from weeding once (6.36 t ha^{-1}). The mean values of genotypes for this trait ranged from 4.89 – 6.12 t ha^{-1}.

Table 10 indicates no significant differences among the genotypes for yield at Seatondale and had values ranging from 5.19 – 6.81 t ha^{-1}. Weeding regimes were significantly different from each other on this trait. The highest mean was recorded from weeding twice (8.99 t/ha) and the least mean was from no weeding (3.11 t ha^{-1}). At Uyole differences among weeding regimes were significant ($P \leq 0.001$) on yield. However differences among genotypes were not significant on this trait at Uyole (Table 11). The highest mean was recorded from weeding twice (8.79 t ha^{-1}) and the least mean was from no weeding (4.65 t ha^{-1}).

The results from combined sites analysis indicate significant differences ($P \leq 0.001$) among the locations and weeding regimes on yield whereas genotypes were not significantly different from each other on this trait (Table 12). Inyala had the highest mean on yield (7.48 t ha^{-1}) amongst the locations while Mbimba had the least mean on this variable (5.44 t ha^{-1}), which did not differ significantly from Seatondale (5.67 t ha^{-1}). Weeding twice resulted into highest mean (9.07 t ha^{-1}) among the weeding regimes across the environments and no weeding had the least yield (3.16 t ha^{-1}). The mean values of genotypes on this trait ranged from 5.86 - 6.78 t ha^{-1}.

4.3 Interaction Among the Treatments

Results for interaction between locations and genotypes for number of kernel rows per cob are shown in Table 13. The highest number of kernel rows per cob was from genotypes UH 6303 (15.11) and UHS 5350 (EH-3) (15.11) at Uyole whereas the lowest number of kernel rows per cob (12.50) were shown by genotype EH-4 at Mbimba.

Table 13: Location x genotype interaction on number of kernel rows per cob

Locations / Genotypes	Inyala	Mbimba	Uyole	Seatondale	$\bar{x}$ ± 0.182
EH-1	12.82	13.49	14.34	13.32	13.49
EH-2 (FH 5160)	13.36	13.59	13.78	12.66	13.34
UHS 5350 (EH-3)	14.92	14.69	15.11	12.73	14.36
EH-4	12.93	12.50	13.06	13.97	13.11
UH 6303	13.99	13.58	15.11	13.06	13.93
$\bar{x}$ ± 0.163	13.60	13.57	14.28	13.15	13.65

Results show that the interaction between locations and weeding regimes resulted to no weeding regimes at Uyole having plants taking longest days to reach days to 50% pollen shed (94.07 days) (Table 14). Shortest days to 50% pollen shed (72.67 days) were shown by weeding twice at Seatondale.

Table 14: Location x weeding regimes interaction on days to 50% pollen shed

Weeding regimes / Locations	No weeding	Weeding once	Weeding twice	$\bar{x}$ ± 0.352
Inyala	83.80	78.40	78.93	80.38
Mbimba	89.47	87.60	86.33	87.80
Uyole	94.07	87.93	87.60	89.87
Seatondale	77.07	75.47	72.67	75.07
± 0.305	86.10	82.35	81.38	83.28

Table 15 indicates that the interaction between location and weeding regimes resulted to weeding twice at Seatondale having plants taking shortest days to 50% tasselling (70.40 days). Longest period taken by plants to reach days to 50% tasselling was from no weeding (91 days) at Uyole location.

Table 15: Location x weeding regimes interaction on days to 50% tasselling

Weeding regimes / Locations	No weeding	Weeding once	Weeding twice	$\bar{x}$ ± 0.314
Inyala	79.47	74.93	74.87	76.42
Mbimba	84.47	83.27	81.87	83.20
Uyole	91.13	85.33	84.53	87.00
Seatondale	74.60	72.60	70.40	72.53
$\bar{x}$ ± 0.362	82.42	79.03	77.92	79.79

Results of location x weeding regimes interaction for days to maturity is indicated in Table 16 and shows that the shortest period taken by plants to reach days to maturity (132.73 days) occurred at Seatondale for weeding twice treatment. However, the longest period taken for plants to attain days to maturity (165.2 days) was recorded at Uyole from no weeding treatment.

Table 16: Location x weeding regimes interaction on days to maturity

Weeding regimes / Locations	No weeding	Weeding once	Weeding twice	$\bar{x}$ ± 0.414
Inyala	141.73	137.40	137.27	138.80
Mbimba	149.53	148.00	148.27	148.60
Uyole	165.20	157.07	155.13	159.13
Seatondale	135.00	134.47	132.73	134.07
$\bar{x}$ ± 0.359	147.87	144.23	143.35	145.15

Results show that the highest number of cobs per plant (1.18) was shown by weeding twice treatment at Seatondale location whereas the least (1.0) was from all locations for no weeding treatment (Table 17). Similarly Inyala and Mbimba had the least number of cobs on weeding once and weeding twice treatments.

Table 17: Location x weeding regimes interaction on number of cobs per plant

Weeding regimes / Locations	No weeding	Weeding once	Weeding twice	$\bar{x}$ ± 0.012
Inyala	1.00	1.00	1.00	1.00
Mbimba	1.00	1.00	1.00	1.00
Uyole	1.00	1.07	1.15	1.07
Seatondale	1.00	1.10	1.18	1.09
$\bar{x}$ ± 0.010	1.00	1.04	1.08	1.04

The highest mean for grain weight per plant (258.33 g) was observed from Inyala location on weeding twice treatment whereas the least grain weight per plant (56.77 g) was shown by no weeding (Table 18) at Inyala.

Table 18: Location x weeding regimes interaction on grain weight per plant (g)

Weeding regimes / Locations	No weeding	Weeding once	Weeding twice	$\bar{x}$ ± 5.030
Inyala	56.77	210.33	258.33	175.15
Mbimba	58.45	152.99	177.06	129.50
Uyole	107.04	145.95	201.64	151.55
Seatondale	72.05	118.95	208.95	133.32
$\bar{x}$ ± 4.357	73.58	157.06	211.50	147.38

Table 19 shows that Inyala location recorded the highest ear weight (312.22 g) from weeding twice treatment and the least weight (75.41 g) was from no weeding treatment.

Table 19: Location x weeding regimes interaction on ear weight per plant (g)

Weeding regimes / Locations	No weeding	Weeding once	Weeding twice	$\bar{x}$ ± 5.963
Inyala	75.41	258.56	312.22	215.40
Mbimba	93.94	219.35	252.20	188.50
Uyole	147.69	186.08	254.12	195.96
Seatondale	85.55	165.27	291.79	180.87
$\bar{x}$ ± 5.164	100.65	207.32	277.58	195.18

Table 20 indicates that the highest hundred kernels weight (45.53 g) was recorded from Inyala by weeding twice. However, the least hundred kernels weight (25.6 g) was observed from Inyala on non weeded plants.

Table 20: **Location x weeding regimes interaction on hundred kernels weight (g)**

Weeding regimes / Locations	No weeding	Weeding once	Weeding twice	$\bar{x}$ ± 0.788
Inyala	25.60	44.40	45.53	38.51
Mbimba	29.00	36.67	42.00	35.89
Uyole	32.88	33.94	38.68	35.17
Seatondale	26.89	32.87	37.41	32.39
$\bar{x}$ ± 0.682	28.59	36.97	40.91	35.49

Results show that the highest grain yield (11.03 g) was observed from Inyala for weeding twice treatment followed by that of Seatondale (9.00 g) for weeding twice. However, the least grain yield (2.43 g) was from Inyala on no weeding treatment (Table 21).

Table 21: **Location x weeding regimes interaction on grain yield (g)**

Weeding regimes / Locations	No weeding	Weeding once	Weeding twice	$\bar{x}$ ± 0.223
Inyala	2.43	9.00	11.03	7.48
Mbimba	2.48	6.36	7.47	5.44
Uyole	4.65	6.41	8.80	6.62
Seatondale	3.11	4.92	9.00	5.68
$\bar{x}$ ± 0.194	3.17	6.67	9.07	6.30

Table 22 shows that genotypes EH-1 and UHS 5350 (EH-3) took the shortest period (133.22 days) to reach days to maturity at Seatondale whereas the longest period (161.33 days) was observed from Uyole on genotype EH-1.

Table 22: **Location x genotype interaction on number of days to maturity**

Locations / Genotypes	Inyala	Mbimba	Uyole	Seatondale	$\bar{x}$ ± 0.464
EH-1	140.56	148.22	161.33	133.22	145.83
EH-2 (FH 5160)	136.78	148.11	155.89	135.22	144.00
UHS 5350 (EH-3)	139.11	146.44	158.11	133.22	144.22
EH-4	139.22	151.22	160.56	135.33	146.58
UH 6303	138.33	149.00	159.78	133.33	145.11
$\bar{x}$ ± 0.414	138.80	148.60	159.13	134.07	193.53

Table 23 shows that the least number of leaves per plant (7.38) was recorded from Uyole for genotype EH-1 whereas the largest number (16.30) was from Seatondale on genotype EH-2 (FH 5160).

Table 23: Location x genotype interaction on number of leaves per plant

Locations / Genotypes	Inyala	Mbimba	Uyole	Seatondale	$\bar{x}$ ± 0.118
EH-1	12.57	11.77	7.38	15.92	11.91
EH-2 (FH 5160)	13.72	12.09	8.14	16.30	12.56
UHS 5350 (EH-3)	13.54	12.16	7.47	16.06	12.31
EH-4	13.78	12.26	8.32	15.67	12.51
UH 6303	13.40	12.04	7.88	16.14	12.37
$\bar{x}$ ± 0.106	13.40	12.06	7.84	16.02	12.33

The largest number of leaves above the ear (6.45) was recorded from Seatondale for weeding twice treatment while the least number of leaves above the ear (1.29) was recorded at Uyole from no weeding treatment (Table 24).

Table 24: Location x weeding regimes interaction on number of leaves above the ear

Weeding regimes / Locations	No weeding	Weeding once	Weeding twice	$\bar{x}$ ± 0.090
Inyala	4.60	5.77	5.56	5.31
Mbimba	6.03	6.35	6.15	6.18
Uyole	1.29	1.43	1.31	1.34
Seatondale	6.91	6.04	6.45	6.46
$\bar{x}$ ± 0.078	4.71	4.90	4.87	4.82

Results indicate that the highest biological yield per plant (580.83 g) was recorded from Seatondale for weeding twice treatment. However, the least biological yield per plant (177.14g) was observed at Seatondale from no weeding treatment (Table 25).

Table 25: Location x weeding regimes interaction on biological yield (g)

Weeding regimes / Locations	No weeding	Weeding once	Weeding twice	$\bar{x}$ ± 10.382
Inyala	127.92	390.57	448.33	322.27
Mbimba	157.87	360.54	385.06	301.16
Uyole	339.34	483.43	579.86	467.54
Seatondale	177.14	332.83	580.83	363.60
$\bar{x}$ ± 8.991	200.57	391.84	498.52	363.64

Results indicate that the largest ear diameter (5.27 cm) was observed from Inyala for weeding twice but the least ear diameter (3.54 cm) was recorded from Inyala on non weeded plants (Table 26).

Table 26: Location x weeding regimes interaction on ear diameter

Weeding regimes / Locations	No weeding	Weeding once	Weeding twice	$\bar{x}$ ± 0.049
Inyala	3.54	5.09	5.27	4.64
Mbimba	4.10	4.93	5.15	4.73
Uyole	4.61	4.72	5.03	4.78
Seatondale	3.95	4.53	5.21	4.56
$\bar{x}$ ± 0.042	4.05	4.82	5.16	4.68

4.4 Estimation of Variance Components and Genetic Parameters

The variance components and genetic parameters for yield components and yield of selected maize genotypes combined from four locations are shown in Tables 27 and 28. Results indicate high broad sense heritability for ear height, number of leaves per plant, days to first tasselling, days to 50% tasselling, days to 50% pollen shed and days to first silking. High genetic advance was recorded for number of leaves above the ear, plant height, ear height, number of kernel rows per cob, grain weight, ear weight, shelling percent and number of leaves per plant. Other traits where genetic advance was high include days to first tasselling, days to 50% tasselling, days to 50% pollen shed, days to first silking, days to 50% silking, days to maturity, hundred kernel weight, grain yield and the ratio of number of leaves below to number of leaves above the ear. Low genotypic coefficient of variation (GCV) was observed to most of characters and low to moderate phenotypic coefficient of variation (PCV) was recorded. However ear height had the highest GCV followed by biological yield. Moderate PCV was exhibited by ear height, biological yield, grain weight, ear weight, harvest index, anthesis silking interval and grain yield.

Table 27: Variance components, heritability (broad sense), expected genetic advance (EGA), genotypic and phenotypic coefficients of variation for some growth parameters, yield and yield components

Variables	δ^2_g	δ^2_{gl}	δ^2_{ph}	h^2	EGA(% of mean)	GVC (%)	PCV (%)
Plant height	47.481	0.000	148.418	31.99	419.650	3.602	6.368
Ear height	78.805	0.000	103.515	76.13	1612.207	8.97	10.280
Biological yield	320.421	0.000	2,258.431	14.19	382.016	4.923	13.070
Ear diameter	0.000	0.000	0.035	0.00	0.000	0.000	3.980
Number of cobs per plant	0.000	0.000	0.001	1.63	9.132	0.000	2.720
Cob length	0.000	0.000	1.396	0.00	0.000	0.000	6.825
Number of kernel rows per cob	0.390	0.390	0.746	52.31	681.941	4.575	6.328
Grain weight	29.955	0.000	484.349	6.18	190.106	3.714	14.93
Ear weight	23.217	0.000	720.988	3.22	91.254	2.469	13.760
Shelling percent	1.104	0.000	9.892	11.16	96.729	1.406	4.208
Number of leaves per plant	0.140	0.006	0.199	70.33	524.169	3.035	3.618
Number of leaves above the ear	0.002	0.000	0.039	4.41	36.991	0.850	4.072
Number of leaves below the ear	0.001	0.033	0.044	1.80	10.688	0.433	2.883

δ^2_g = genetic variance, δ^2_{ph} = phenotypic variance, δ^2_{gl} = genotype x location variance, h^2 = heritability (broad sense), EGA = expected genetic advance

Table 28: Variance components, heritability (broad sense) and expected genetic advance (EGA) of some growth parameters, yield and yield components

Variables	δ^2_g	δ^2_{gl}	δ^2_{ph}	h^2	EGA (% of mean)	GVC	PCV
Number of leaves below the ear	0.002	0.000	0.039	4.410	36.991	0.922	4.072
Number of leaves below the ear/number of leaves above the ear	0.005	0.000	0.010	52.74	788.514	5.238	7.258
Harvest index	0.000	0.000	0.008	0.00	0.000	0.000	20.000
Days to first tasselling	2.512	0.000	3.493	71.92	376.309	2.154	2.540
Days to 50% tasselling	1.342	0.000	2.154	62.29	236.021	1.452	1.839
Days to 50% pollen shed	1.495	0.091	2.338	63.96	241.912	1.468	1.836
Days to first silking	2.435	0.000	3.453	70.51	340.870	1.971	2.347
Anthesis siliking interval	0.000	0.000	0.564	0.00	0.00	0.000	16.610
Days to 50% silking	2.963	0.000	5.078	58.35	317.034	2.015	2.638
Days to maturity	1.989	1.198	3.530	56.34	150.221	0.972	1.294
Hundred kernel weight	1.161	0.000	6.455	17.98	265.150	3.036	7.159
Husk cover score	0.000	0.000	0.010	0.000	0.000	0.000	8.550
Grain yield	0.112	0.000	0.957	11.70	374.178	5.312	15.52

□□□□□□□□□□□□□□□□□□□□δ^2_g = genetic variance, □□□□□δ^2_{ph} = phenotypic variance, δ^2_{gl} = genotype x location variance, h^2 = □heritability (broad sense), EGA = expected genetic advance

4.5 Association Analysis

Genotypic and phenotypic correlations for yield and yield components of maize genotypes for combined data over four locations are presented in Tables 29, 30 and 31. High significant positive genotypic and phenotypic correlations were found between ear height and plant height, biological yield and plant height. Ear heights and ear diameter had significant positive genotypic and phenotypic correlations with all of the mentioned variables. Also, cob length had significant positive genotypic and phenotypic correlations with plant height, ear diameter, ear height and biological yield. It was positively correlated with number of cobs per plant at genotypic level, whereas the number of kernel rows per cob had similar relationships with these traits and cob length except for number of cobs per plant. Grain weight per plant had significant positive genotypic and phenotypic correlation with plant height, biological yield and ear height; number of cobs per plant, cob length and number of kernel rows per cob.

Table 29: Genotypic (top) and Phenotypic (parentheses) correlation of yield and yield components from Maize genotypes combined from Uyole, Inyala, Seatondale and Mbimba

	1	2	3	4	5	6	7	8	9	10	11	12	13
1.Plant height	1.00												
2. Ear height	0.829*** (0.815)***	1.00											
3. Biological yield	0.645*** (0.676)***	0.589*** (0.531)***	1.00										
4. Ear diameter	0.479*** (0.610)***	0.470*** (0.467)***	0.501*** (0.763)***	1.00									
5. Number of cobs per plant	-0.003 (0.139)	0.033 (0.096)	0.234* (0.466)***	-0.035 (0.213)**	1.00								
6. Cob length	0.302*** (0.478)***	0.277*** (0.367)***	0.513*** (0.763)***	0.475*** (0.704)***	0.074 (0.328)***	1.00							
7. Number of kernel rows per cob	0.403*** (0.530)***	0.403*** (0.439)***	0.422*** (0.601)***	0.698*** (0.781)***	-0.066 (0.110)	0.362*** (0.549)***	1.00						
8. Grain weight per plant	0.345*** (0.535)***	0.316*** (0.349)***	0.584*** (0.787)***	0.556*** (0.807)***	0.168* (0.286)***	0.769*** (0.811)***	0.373*** (0.601)***	1.00					
9. Ear weight	0.406*** (0.557)***	0.380*** (0.364)***	0.674*** (0.837)***	0.697*** (0.867)***	0.111 (0.289)***	0.648*** (0.763)***	0.471*** (0.646)***	0.766*** (0.925)***	1.00				
10. Shelling percent	0.061 (0.170)	0.012 (0.087)	0.255** (0.332)***	0.268*** (0.358)***	0.054 (0.100)	0.304*** (0.380)***	0.190* (0.279)***	0.436*** (0.425)***	0.227** (0.303)***	1.00			
11. Number of leaves per plant	0.610*** (0.520)***	0.652*** (0.608)***	0.424*** (-0.172)*	-0.123 (-0.032)	-0.068 (0.017)	0.070 (0.125)	-0.214** (-0.152)	0.039 (0.061)	0.032 (0.060)	0.105 (0.128)	1.00		
12. Leaves below the ear	-0.486*** (-0.405)***	-0.507*** (-0.436)***	-0.207* (-0.011)	-0.165 (-0.075)	0.034 0.167*	0.244** (0.266)***	-0.206* (-0.154)	0.170* (0.09)	0.078 (0.051)	0.281*** (0.272)***	0.818*** (0.813)***	1.00	
13. Leaves above the ear	-0546*** (-0.478)***	-0.608*** (-0.597)***	-0.497*** (-0.294)***	-0.052 (-0.009)	-0.085 (-0.099)	-0.086 (-0.056)	-0.143 (-0.06)	-0.077 (-0.012)	0.007 (0.033)	-0.087 (-0.059)	0.854*** (0.833)***	0.492*** (0.443)***	1.00

*Significant at 5%, ** Significant at 1%, *** significant at 0.1%

Table 30: Genotypic (top) and Phenotypic (parentheses) correlations of yield and yield components from Maize genotypes combined from Uyole, Inyala, Seatondale and Mbimba

	Plant height	Ear height	Biological yield	Ear diameter	Number of cobs per plant	Cob length	Number of kernel rows per cob	Grain weight	Ear weight	Shelling percent	Number of leaves per plant	Leaves above the ear
14. Leaves below/leaves above the ear	-0.253*** (-0.251)***	-0.209** (-0.215)**	0.003 (-0.018)	-0.287*** (-0.228)**	0.185* (0.173)*	0.204** (0.131)	-0.250*** (-0.237)***	0.090 (0.019)	-0.071 -(0.072)	0.304*** (0.262)***	0.242*** (0.237)***	0.680*** (0.656)***
15. Harvest index	-0.068 (0.037)	-0.015 (0.024)	-0.062 (0.089)	0.009 (0.163)	-0.116 (-0.096)	0.037 (0.136)	-0.019 (0.092)	0.012 (0.179)*	-0.022 (0.169)*	0.088 (0.155)	-0.013 -0.099	0.035 (0.003)
16. Days to first tasselling	0.446*** (0.302)***	0.562*** (0.500)***	0.218** (0.015)	0.142 (-0.060)	-0.042 (-0.072)	-0.252*** (-0.072)	0.094 (-0.297)***	-0.146 (-0.030)	-0.065 (-0.261)***	-0.231** (-0.218)**	-0.721*** (-0.257)***	-0.766*** (-0,698)***
17. Days to 50% tasselling	0.506*** (0.316)**	0.623*** (0.503)***	0.3000*** (-0.078)	0.154 (-0.103)	-0.052 (-0.196)*	-0.201** (-0.344)***	0.161 (-0.008)	-0.100 (-0.258)***	-0.060 (-0.253)***	-0.131 (-0.172)*	0.836*** (0.820)***	0.793*** (0.774)***
18. Days to 50% pollen shed	0.486*** (0.293)***	0.490*** (0.453)***	0.245*** (-0.131)	0.149 (0.106)	-0.066 (-0.245)***	-0.223** (-0.374)***	0.127 (-0.034)	-0.117 (-0.253)***	-0.074 (-0.249)***	-0.160* (-0.196)**	-0.815*** (-0.797)***	-0.823*** (-0.814)***
19. Days to first silking	0.428*** (0.215)**	0.560*** (0.385)***	0.250*** (-0.179)*	0.087 (-0.172)*	-0.023 (-0.253)***	-0.261*** (-0.438)***	0.061 (-0.102)	-0.126 (-0.265)***	-0.059 (-0.254)***	-0.252*** (-0.293)***	-0.732*** (-0.710)***	-0.739*** (-0.742)***
20. Anthesis Silking interval	0.215** (0.131)	0.199* (0.165)*	0.047 (-0.080)	0.055 (-0.065)	-0.070 (-0.107)	-0.088 (-0.144)	-0.078 (0.001)	-0.082 (-0.164)*	0.009 (-0.170)*	-0.381*** (0.002)	-0.400*** (-0.375)***	0.309*** (0.378)***
21. Days to 50% silking	0.448*** (0.136)	0.536*** (0.333)***	0.224** (-0.285)***	0.039 (-0.337)***	-0.093 (-0.267)***	-0.229** (-0.473)***	0.114 (-0.166)	-0.164* (-0.459)***	-0.131 (-0.467)***	-0.269*** (0.324)***	-0.783*** (-0.717)***	-0.750*** (-0.673)***
22. Days to maturity	0.642*** (0.495)***	0.721*** (0.652)***	0.398*** (0.087)	0.184* (0.005)	-0.021 (-0.101)	-0.129 (-0.211)**	0.186* (0.068)	-0.041 (-0.159)*	-.002 (-0.149)	-0.153 (-0.168)*	-0.896*** (-0.884)***	-0.789*** (-0.761)***
23. Hundred Kernel weight	0.243*** (0.449)***	0.238*** (0.294)***	0.296*** (0.566)***	0.349*** (0.649)***	-0.060 (0.060)	0.355*** (0.546)***	0.193* (0.458)***	0.423*** (0.718)***	0.490*** (0.751)***	0.116 (0.228)**	-0.036 (-0.011)	-0.010 (-0.049)
24. Yield	0.352*** (0.398)***	0.329*** (0.361)***	0.596*** (0.792)***	0.532*** (0.797)***	0.196* (0.302)***	0.760*** (0.812)***	0.757*** (0.888)***	0.989*** ().996)***	0.760*** (0.918)***	0.421*** (0.420)***	-0.008 (-0.041)	0.148 (0.089)

*Significant at 5%, ** Significant at 1%, *** significant at 0.1**%**

Table 31: Genotypic (top) and Phenotypic (parentheses) correlations of yield and yield components from Maize genotypes combined from Uyole, Inyala, Seatondale and Mbimba

	14	15	16	17	18	19	20	21	22	23	24	25
14. Leaves below/leaves above the ear	1.000											
15. Harvest index	0.112 0.079	1.000										
16. Days to first tasselling	-0.417*** (-0.394)***	-0.030 (0.078)	1.000									
17. Days to 50% tasselling	-0.349*** (-0.330)***	0.029 (-0.003)	0.896*** (0.875)***	1.000								
18. Days to 50% pollen shed	-0.414*** (-0.388)***	0.016 (-0.001)	0.897*** (0.852)***	0.970*** (0.969)***	1.000							
19. Days to first silking	-0.395*** -(0.353)***	-0.012 (0-030)	0.899*** (0.818)***	0.851*** (0.853)***	0.845*** (0.864)***	1.000						
20. Anthesis Silking interval	-0.167* (-0.166)	0.048 (0.029)	0.300*** (0.321)***	0.474*** (0.485)***	0.543*** (0.538)***	0.106 (0.131)	1.000					
21. Days to 50% silking	-0.357*** -0.298***	-0.017 (-0.094)	0.803*** (0.773)***	0.867*** (0.864)***	0.873*** (0.863)***	0.821*** (0.815)***	0.400*** (0.414)***	1.000				
22. Days to maturity	-0.320*** (-0.315)***	-0.015 (-0.033)	0.865*** (0.861)***	0.914*** (0.970)***	0.897*** (0.881)***	0.853*** (0.814)***	0.360*** (0.379)***	0.860*** (0.824)***	1.000			
23. Hundred Kernel weight	-0.062 (-0.084)	-0.003 (0.164)	-0.025 (-0.169)*	-0.015 (-0.149)	-0.023 (-0.130)	-0.008 (-0.120)	-0.047 (-0.124)	-0.095 (-0.346)***	0.017 (-0.085)	1.000		
24. Husk cover score	0.179* (0.173)*	-0.066 (-0.086)	-0.332*** (-0.277)***	-0.369*** (-0.417)***	-0.378*** (-0.462)***	-0.315*** (-0.450)***	-0.218** (-0.201)**	-0.335*** (-0.373)***	-0.376*** (-0.371)***	-0.044 (-0.047)	1.000	
25. Yield	0.095 (0.023)	0.013 (0.179)*	-0.132 (-0.252)***	-0.085 (-0.248)***	0.247** (0.265)***	-0.108 (-0.257)***	-0.082 (-0.165)	-0.140 (-0.446)***	-0.018 (-0.146)	0.421*** (0.714)***	0.059 (0.094)	1.000

*Significant at 5%, ** Significant at 1%, *** significant at 0.1%

Also, the results show that ear weight had significant positive genotypic and phenotypic correlations with plant height, ear diameter, ear height, biological yield and grain weight. Shelling percent had significant positive genotypic and phenotypic correlations with ear diameter, cob length and grain weight, biological yield and ear weight.

There were significant positive genotypic and phenotypic correlations between number of leaves per plant with plant height and ear height. Number of leaves below the ear had significant negative genotypic and phenotypic correlations with plant and ear height while it had significant positive genotypic and phenotypic correlations with number of leaves per plant and shelling percent.

Number of leaves above the ear had significant negative genotypic and phenotypic correlations with plant height, ear height and biological yield and significant positive genotypic and phenotypic correlations with number of leaves per plant and leaves below the ear.

The ratio of leaves below to leaves above the ear had significant positive genotypic and phenotypic correlations with shelling percent, number of leaves per plant and leaves above the ear. It had significant negative genotypic and phenotypic correlations with number of kernel rows per cob, ear diameter, ear height and plant height (Table 30).

Days to first tasselling had significant positive genotypic and phenotypic correlations with plant height and ear height and had significant negative genotypic and phenotypic correlations with number of leaves per plant, shelling percent and number of leaves above the ear. Days to 50% tasselling had significant positive genotypic and phenotypic correlations with number of leaves per plant, leaves above, plant height and ear height.

Significant positive genotypic and phenotypic correlations was recorded between 50% pollen shed and plant and ear height. Furthermore, there were significant negative genotypic and phenotypic correlations between days to 50% pollen shed and number of leaves per plant and leaves above the ear. Days to first silking had significant positive genotypic and phenotypic correlations with plant height and ear height while it had significant negative genotypic and phenotypic correlations with number of leaves per plant, leaves above the ear, shelling percent and cob length.

Results show that days to maturity had significant positive genotypic and phenotypic correlations with plant height and ear height and biological yield at genotypic level. It had also significant positive genotypic and phenotypic correlations with days to first tasselling, days to 50% tasselling, days to 50% pollen shed, days to first silking and days to 50% silking. Days to maturity had significant negative genotypic and phenotypic correlations with number of leaves per plant and leaves above the ear.

Hundred kernel weights had significant positive genotypic and phenotypic correlations with plant height, ear height, ear diameter, biological yield, ear weight and grain weight whereas days to 50% tasselling and days to first tasselling were significantly positive correlated at genotypic and phenotypic levels. High significant positive genotypic and phenotypic correlations was recorded between days to first silking and days to first tasselling, days to 50% tasselling and days to 50% pollen shed. Anthesis silking interval had significant positive genotypic and phenotypic correlations with days to 50% tasselling and days to 50% pollen shed.

Results also show significant positive genotypic and phenotypic correlations between days to 50% silking and days to first tasselling, days to 50% tasselling, days to 50%

pollen shed, days to first silking and anthesis silking interval. Yield had significant positive genotypic and phenotypic correlations with plant height, ear height, ear diameter, biological yield, ear weight and grain weight, cob length, number of kernel rows per cob, shelling percent and hundred kernel weight. Non significant negative genotypic and phenotypic correlations between days to maturity and grain yield were recorded.

4.6 Stability Analysis

Stability parameters of yield components and yield for studied genotypes combined across the four locations are presented in Tables 32 - 40. The genotypes showed different stabilities on various variables as explained below.

4.6.1 Plant height

Results show that all genotypes studied responded on average with changing environment; that is the regression coefficients did not differ significantly from value of 1 (b = 1) (Table 32). The lowest value of b was recorded from EH-2 (FH5160) and the highest value of variance of deviation from regression (s^2d) was from EH-1.

Table 32: Estimates of stability parameters for plant height, ear height and biological yield for five genotypes averaged in four combined locations (Inyala, Mbimba, Seatondale and Uyole)

Genotypes	Plant height (cm)	b	b-1	s^2d	Ear height (cm)	b	b-1	s^2d	Biological yield (g)	b	b-1	s^2d
EH-1	182.87	1.15	0.15	217.27	91.63	0.95	-0.05	30.91	348.83	1.24	0.24	87.42
EH-2 (FH5160)	187.89	0.91	-0.09	12.32	98.89	0.89	-0.11	3.46	356.93	0.86	-0.014	68.06
UHS 5350 (EH-3)	195.70	0.94	-0.06	17.14	95.59	0.86	-0.14	3.76	360.66	0.78	-0.22	12.96
EH-4	195.16	1.04	0.04	52.42	105.13	1.14	0.14	22.75	384.55	0.91	-0.09	81.72
UH 6303	194.97	0.97	-0.03	53.88	103.63	1.16	0.16	3.69	367.26	1.21	0.21	77.97

b= regression coefficient, s^2d= variance of deviation from regression

4.6.2 Ear height (cm)

Results show that the regression coefficients did not differ significantly from value of 1 (b = 1) for this trait (Table 32). Genotype EH-2 (FH 5160) had medium mean performance and b-values approaching to unit value coupled with the least variance of deviation from regression EH-2 (FH 5160). Genotype EH-4 had the highest mean performance but it had b values above the unit value.

4.6.3 Biological yield (g)

Results show that UHS 5350 (EH-3) recorded medium biological yield and possessed lowest value of variance of deviation from regression though its b values did not approach the unit value (Table 32).

4.6.4 Ear diameter (cm)

Table 33 shows that all genotypes studied except EH-4 had the regression coefficients which did not differ significantly from value of 1 (b = 1) on ear diameter. Genotype EH-4 responded significantly less than average. The lowest value of variance of deviation from regression was recorded from EH-2 (FH5160).

Table 33: Estimates of stability parameters for ear diameter, number of cobs/plant and cob length for five genotypes averaged in four combined locations (Inyala, Mbimba, Seatondale and Uyole)

Genotypes	Ear diameter	b	b-1	s^2d	No. of cobs/plant	b	b-1	s^2d	Cob length	b	b-1	s^2d
EH-1	4.59	0.84	-0.16	0.017	1.04	1.19	0.19	0.002	16.1	1.52	0.52	2.50
EH-2 (FH5160)	4.71	1.29	0.29	0.002	1.06	1.36	0.36	0.002	17.14	0.82	-0.18	0.45
UHS 5350 (EH-3)	4.75	1.60	0.60	0.023	1.03	0.65	-0.35	0.000	15.93	1.11	0.11	0.76
EH-4	4.66	-0.46*	-1.46*	0.008	1.05	1.23	0.23	0.000	16.31	0.85	-0.15	0.83
UH 6303	4.68	1.74	0.74	0.006	1.03	1.19	0.19	0.002	16.39	0.70	-0.30	0.66

* Significant at 5% level, b= regression coefficient, s^2d= variance of deviation from regression

4.6.5 Number of cobs per plant

The results show that the genotypes genotype UHS 5350 (EH-3) recorded relatively lower values of b coupled with the lowest value of variance of deviation from regression which was similar to EH-4 (Table 33). The other genotypes had b values above unity.

4.6.6 Cob length

Findings indicate that, the regression coefficients did not differ significantly from value of 1 on this trait (Table 33). They also show that, none of the genotypes had b-values closer to unity although genotype EH-2 (FH 5160) gave the lowest value of variance of deviation from regression.

4.6.7 Number of kernel rows per cob

Table 34 shows that all genotypes studied except EH-4 had b values which did not differ significantly from value of 1 (b = 1) on this trait. Genotype EH-4 responded significantly less than average. The lowest value of variance of deviation from regression was recorded for UH 6303.

Table 34: Estimates of stability parameters for plant number of kernel rows/cob, grain weight and ear weight for five genotypes averaged in four combined locations (Inyala, Mbimba, Seatondale and Uyole)

Genotypes	Number of kernel rows/cob	b	b-1	s^2d	Grain weight	b	b-1	s^2d	Ear weight	b	b-1	s^2d
EH-1	13.49	0.99	-0.01	0.28	146.06	0.44	-0.56	293.78	187.94	0.87	-0.13	17.31
EH-2 (FH5160)	13.34	0.91	-0.09	0.09	155.56	1.08	0.08	91.39	198.67	0.86	-0.14	34.22
UHS 5350 (EH-3)	14.36	1.88	0.88	0.66	151.10	0.91	-0.09	104.45	197.51	1.29	0.29	121.66
EH-4	13.11	-0.62	-1.62*	0.45	146.98	1.20	0.20	28.41	199.28	1.25	0.25	32.49
UH 6303	13.93	1.84	0.84	0.03	137.19	1.37	0.37	29.05	192.52	0.73	-0.27	88.55

* Significant at 5% level, b= regression coefficient, s^2d= variance of deviation from regression

4.6.8 Grain weight

Results indicate that genotype EH-2 (FH5160) had b values closer to unity (b=1) and EH-4 had the lowest value of variance of deviation from regression (Table 34).

4.6.9 Ear weight

Results reveal that genotype EH-1 had b values closer to unity (b=1) and had the lowest value of variance of deviation from regression on ear weight (Table 34).

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4.6.10 Shelling percent

The findings indicate that the genotypes had b values which did not differ significantly from value of 1 (b = 1) on this trait (Table 35). Genotype EH-2 (FH 5160) had b values closer to unity (b=1) and the lowest value of variance of deviation from regression was exhibited by EH-1.

Table 35: Estimates of stability parameters for shelling percent, number of leaves/plant and number of leaves below the ear for five genotypes averaged in four combined locations (Inyala, Mbimba, Seatondale and Uyole)

Genotypes	Shelling percent	b	b-1	s^2d	Number of leaves/ plant	b	b-1	s^2d	No. of leaves below the ear	b	b-1	s^2d
EH-1	74.33	0.40	-0.60	1.79	11.91	1.03	0.03	0.14	7.15	1.05	.05	0.11
EH-2 (FH5160)	77.36	1.08	0.08	3.03	12.56	1.00	0.00	0.04	7.38	1.07	0.07	0.01
UHS 5350 (EH-3)	74.87	0.64	-0.36	10.24	12.31	1.06	0.06	0.03	7.26	0.90	-0.10	0.02
EH-4	74.31	1.61	0.61	2.28	12.51	0.91	-0.09	0.07	7.47	0.98	-0.02	0.11
UH 6303	72.87	1.27	0.27	2.59	12.37	1.01	0.01	0.01	7.30	1.00	0.00	0.01

b= regression coefficient, s^2d= variance of deviation from regression

4.6.11 Number of leaves per plant

Table 35 shows that genotype EH-2 (FH 5160) recorded b value equal to unity for number of leaves per plant and the lowest value of variance of deviation from regression was from UH 6303.

4.6.12 Number of leaves below the ear

Results show that the regression coefficients of studied genotypes did not differ significantly from value of 1 (b = 1) on number of leaves below the ear (Table 35). Genotype UH 6303 exhibited the b value equal to unity and had the least value of variance of deviation from regression.

4.6.13. Number of leaves above the ear

Data indicate that genotype UH 6303 had b value equal to unity (b=1) on number of leaves above the ear. The lowest value of variance of deviation from regression for this variable was recorded from EH-2 (FH 5160).

Table 36: Estimates of stability parameters for number of leaves above the ear, number of leaves below/leaves above the ear and harvest index for five genotypes averaged in four combined locations (Inyala, Mbimba, Seatondale and Uyole)

Genotypes	No. of leaves above the ear	b	b-1	s^2d	No. of leaves below the ear/no. of leaves above the ear	b	b-1	s^2d	Harvest index	b	b-1	s^2d
EH-1	4.74	0.98	-0.02	0.011	1.34	1.09	0.09	0.004	0.43	0.77	-0.23	0.010
EH-2 (FH 5160)	4.81	0.97	-0.03	0.004	1.38	1.03	0.03	0.005	0.44	0.95	-0.05	0.004
UHS 5350 (EH-3)	4.92	1.04	0.4	0.012	1.27	0.89	-0.11	0.003	0.48	1.42	0.42	0.012
EH-4	4.90	1.01	0.01	0.058	1.40	1.07	0.07	0.003	0.47	1.14	0.14	0.026
UH 6303	4.88	1.00	0.00	0.010	1.35	0.93	-0.07	0.003	0.40	0.72	-0.28	0.008

b= regression coefficient, s^2d= variance of deviation from regression

4.6.14 Number of leaves below the ear per number of leaves above the ear

Table 36 reveals that genotype EH-2 (FH 5160) had b value close to unity (b = 1) on the ratio of number of leaves below and leaves above the ear whereas genotypes UHS 5350 (EH-3), EH-4 and UH 6303 recorded the least values of variance of deviation from regression on this variable.

4.6.15 Harvest index

Findings show that the genotypes studied gave b value which did not differ significantly from value of 1 (b = 1) on harvest index (Table 36). Genotype EH-2 (FH 5160) had b values closer to unity (b=1) and recorded the least values of variance of deviation from regression for this variable.

4.6.16 Days to first tasselling

Results reveal that genotype EH-1 had b value equal to unity (b=1) whereas the least values of variance of deviation from regression was observed from UHS 5350 (EH-3) (Table 37).

Table 37: Estimates of stability parameters for days to first tasselling, 50% tasselling and 50% pollen shed for five genotypes averaged in four combined locations (Inyala, Mbimba, Seatondale and Uyole)

Genotypes	Days to first tasseling	b	b-1	s^2d	Days to 50% tasseling	b	b-1	s^2d	Days to 50% pollen shed	b	b-1	s^2d
EH-1	73.83	1.00	0.00	0.92	80.44	1.10	0.10	0.08	84.17	1.10	-0.10	0.28
EH-2 (FH 5160)	73.22	0.88	-0.12	0.25	78.78	0.89	-0.11	0.36	82.28	0.87	-0.13	0.21
UHS 5350 (EH-3)	72.39	0.96	-0.04	0.04	79.14	0.92	-0.08	0.03	82.44	0.94	-0.06	0.59
EH-4	75.11	1.13	0.13	0.07	80.69	1.08	0.08	1.74	84.06	1.06	0.06	1.56
UH 6303	73.33	1.03	0.03	0.58	79.89	1.00	0.00	1.21	83.44	1.02	0.02	1.69

b= regression coefficient, s^2d= variance of deviation from regression

4.6.17 Days to 50% tasselling

Table 37 indicates that genotype UH 6303 had b value equal to unity (b=1) whereas the least value of variance of deviation from regression was observed from genotype UHS 5350 (EH-3). The deviations from regression were not statistically significant for all genotypes.

4.6.18 Days to 50% pollen shed

Results show that genotype UH 6303 had b value closer to unity (b=1) on days to 50% pollen shed but the least values of variance of deviation from regression was observed from genotype EH-2 (FH 5160) (Table 37). However the highest values were recorded from genotype UH 6303.

4.6.19 Days to first silking

Results indicate that genotype UH 6303 gave b value which was closer to unity (b=1) and showed the lowest value of variance of deviation from regression while genotype EH-2 (FH 5160) recorded the highest.

Table 38: Estimates of stability parameters for plant days to first silking, anthesis silking interval and days to 50% silking for five genotypes averaged in four combined locations (Inyala, Mbimba, Seatondale and Uyole)

Genotypes	Days to first silking	b	b-1	s^2d	Anthesis silking interval	b	b-1	s^2d	Days to 50% silking	b	b-1	s^2d
EH-1	80.06	1.09	0.09	0.92	4.81	1.01	0.01	0.09	86.11	1.16	0.16	1.66
EH-2 (FH 5160)	78.33	0.86	-0.04	1.35	4.19	0.80	-0.20	0.44	83.56	0.74	-0.26	1.23
UHS 5350 (EH-3)	78.22	0.90	-0.10	1.23	4.28	1.23	0.23	1.37	85.03	0.88	-0.22	0.10
EH-4	80.53	1.13	0.13	0.74	4.44	0.98	-0.02	0.12	86.69	1.06	0.06	0.23
UH 6303	78.75	1.02	0.02	0.07	4.92	0.98	-0.02	0.94	85.83	1.17	0.17	1.28

b= regression coefficient, s^2d= variance of deviation from regression

4.6.20 Anthesis Silking interval

Results show that the genotypes studied gave b value which did not differ significantly from value of 1 (b = 1) on ASI (Table 38). Genotype EH-1 had b value very close to unity (b=1) and had the least value of s^2d whereas UHS 5350 (EH-3) recorded the highest value.

4.6.21 Days to 50% silking

Table 38 reveals that genotype EH-4 gave b value closer to unity (b=1) but the least value s^2d was from genotype UHS 5350 (EH-3). On the other hand, the highest value recorded by EH-1. The deviations from regression were not statistically significant for all genotypes.

4.6.22 Days to maturity

Findings show that the studied genotypes had b value which was not significantly different from unity on days to maturity (Table 39). However genotype EH-4 had b value closer to unity (b=1) whereas the least value of s^2d was from UH 6303 but the highest value was from EH-2 (FH 5160).

Table 39: Estimates of stability parameters for days to maturity, hundred kernel weights and husk cover for five genotypes averaged in four combined locations (Inyala, Mbimba, Seatondale and Uyole)

Genotypes	Days to maturity	b	b-1	s^2d	Hundred kernels weight (g)	b	b-1	s^2d	Husk cover score (1-5 scale)	b	b-1	s^2d
EH-1	145.83	1.07	0.07	2.43	36.63	1.02	0.02	0.61	1.14	1.01	0.01	0.0001
EH-2 (FH 5160)	144.00	0.87	-0.13	2.46	36.56	0.89	-0.11	6.00	1.17	1.21	0.21	0.0004
UHS 5350 (EH-3)	144.22	0.96	-0.04	1.25	33.83	0.77	-0.23	2.86	1.17	1.21	0.21	0.0004
EH-4	146.58	1.03	0.03	1.04	33.83	1.60	0.60	2.19	1.11	0.55	-0.45	0.0036
UH 6303	145.11	1.06	0.06	0.04	35.07	0.73	-0.27	6.76	1.14	0.97	-0.03	0.0001

b= regression coefficient, s^2d= variance of deviation from regression

4.6.23 Hundred kernels weight (g)

Results indicate that genotype EH-1 had b value closer to unity (b=1) and recorded the least value of s^2d (Table 39). On the other hand, genotype UH 6303 recorded the highest value of s^2d.

4.6.24 Husk covers score (1-5 scale)

Results show that all genotypes studied responded on average with changing environment Genotype EH-1 had b value closer to unity (b=1) and gave the lowest value of s^2d while EH-4 recorded the highest on this trait. However, genotype (EH-4) which had the lowest mean value for this trait.

4.6.25 Yield (g)

Table 40 shows that genotype EH-2 (FH 5160) had b value closer to unity (b=1) while UH 6303 recorded the highest b value. The least value of variance of deviation from regression was from UH 6303 whereas the highest was recorded from genotype EH-1.

Table 40: Estimates of stability parameters for grain yield for five genotypes averaged in four combined locations (Inyala, Mbimba, Seatondale and Uyole)

Genotypes	Yield (g)	b	b-1	s^2d
EH-1	6.24	0.46	-0.54	0.64
EH-2 (FH 5160)	6.78	1.09	0.09	0.17
UHS 5350 (EH-3)	6.41	0.86	-0.14	0.16
EH-4	6.23	1.28	0.28	0.08
UH 6303	5.86	1.31	0.31	0.03

4.7 Relationships between Regression Coefficients and Means of Genotypes for Yield and Yield Components

The relationships between regression coefficients, variance of deviation from regression (s^2d) and means of genotypes viz; G1 (EH-1), G2 (EH-2 (FH 5160), G3 (UHS 5350 (EH-3), G4 (EH-4) and G5 (UH 6303) (Check) for the variables studied are as shown in the scatter diagrams.

4.7.1 Ear height

Fig.3 indicates the relationship between regression coefficients and means for ear height. None of the genotypes had optimum ear height (taller plants) with b-values approaching unity; however G1, had b-values approaching 1 although it had short plants.

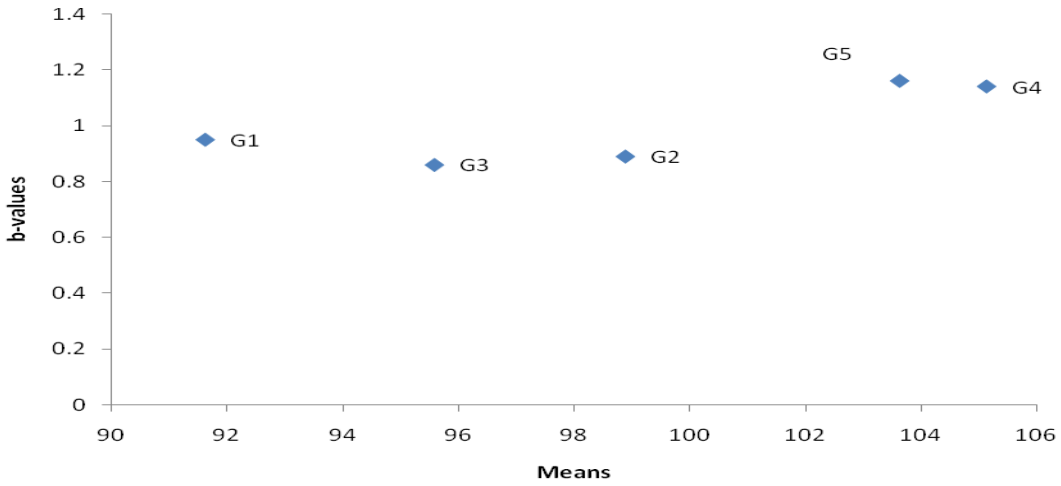


Figure 3: Scatter diagram of b-values against means for ear height

4.7.2 Biological yield

The relationship between regression coefficients and means for biological yield is shown in Fig. 4. The scatter diagram indicates that G4 had highest mean value for biological yield and had b-values approaching unit value (b = 1).

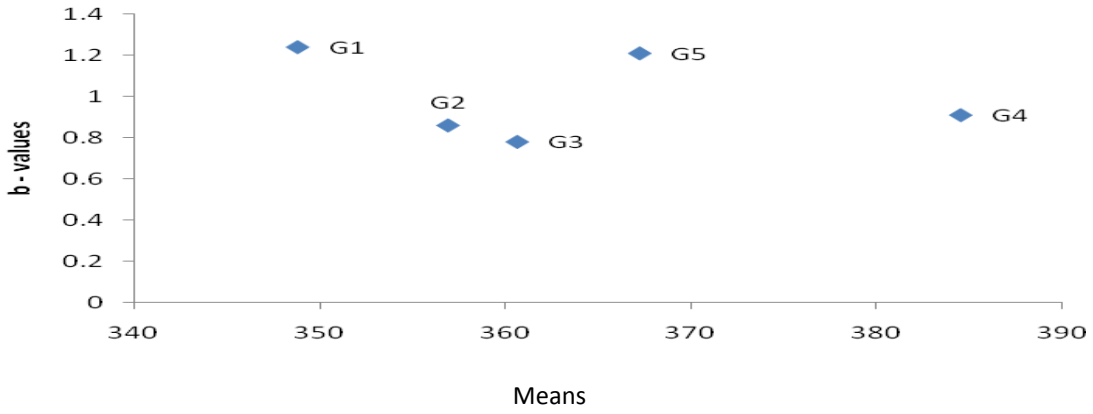


Figure 4: Scatter diagram of b-values against means for biological yield

4.7.3 Plant height

The relationship between regression coefficients and means for plant height is depicted in the scatter diagram in Fig. 5 in which G3, G4 and G5 produced taller plants and had b-value approaching unity (b = 1).

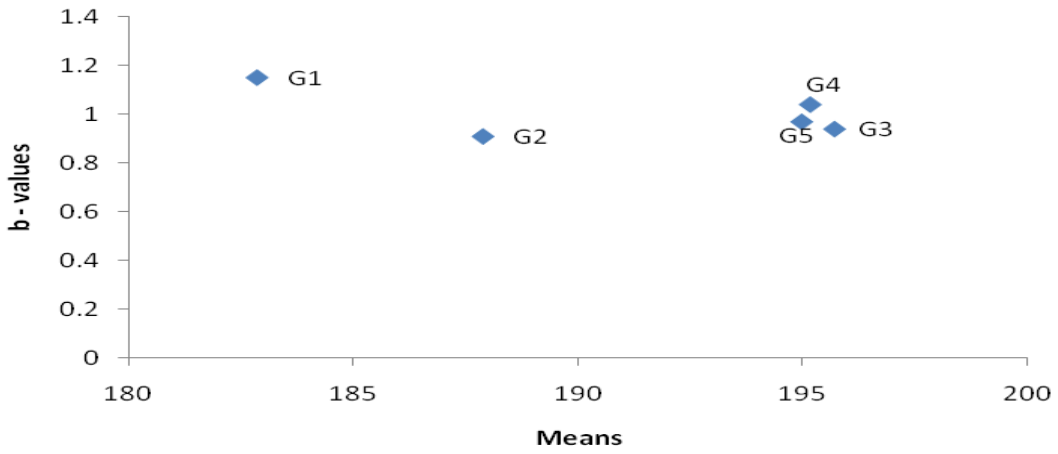


Figure 5: Scatter diagram of b-values against means for plant height

4.7.4 Ear diameter

Fig.6 indicates the relationship between regression coefficients and means for ear diameter. The scatter diagram indicates that none of the genotypes had optimum ear diameter with b-values approaching unity. However G1 had b-value approaching the unity (b =1) and had medium ear diameter.

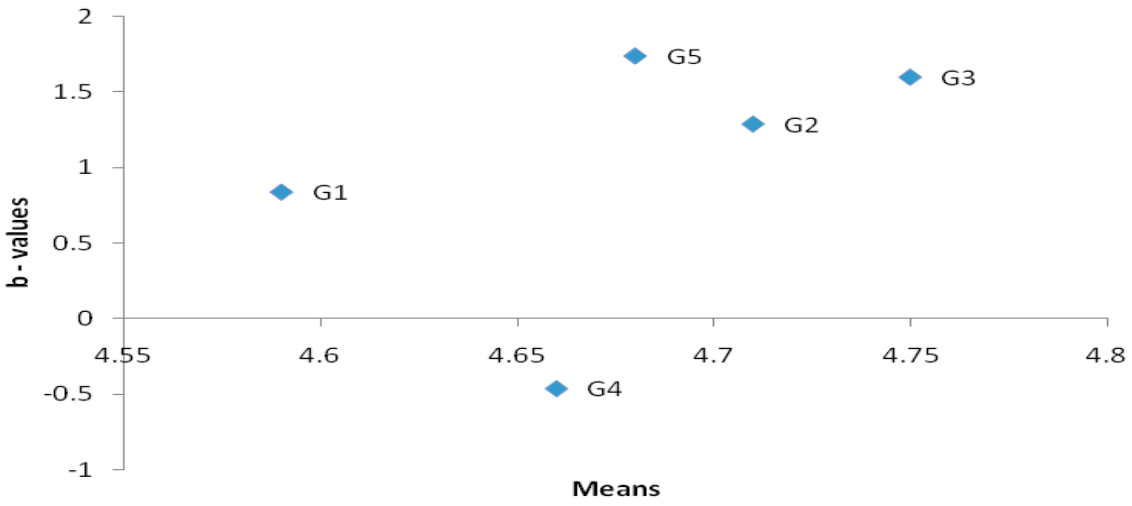


Figure 6: Scatter diagram of b-values against means for ear diameter

4.7.5 Number of cobs per plant

The relationship between regression coefficients and means for number of cobs per plant is illustrated in the scatter diagram in Fig. 7. None of the genotypes had b value closer to unity; however G2 recorded the highest number of cobs per plant.

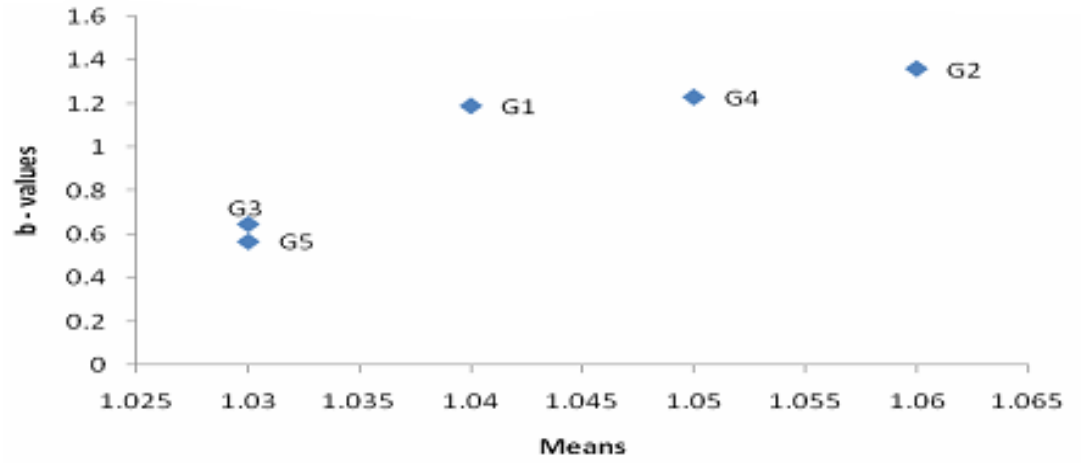


Figure 7: Scatter diagram of b-values against means for number of cobs per plant

4.7.6 Cob length

The relationship between regression coefficients and means for cob length is shown in the scatter diagram in Fig. 8. It reveals that G3 had b-value closer to unit y (b = 1).

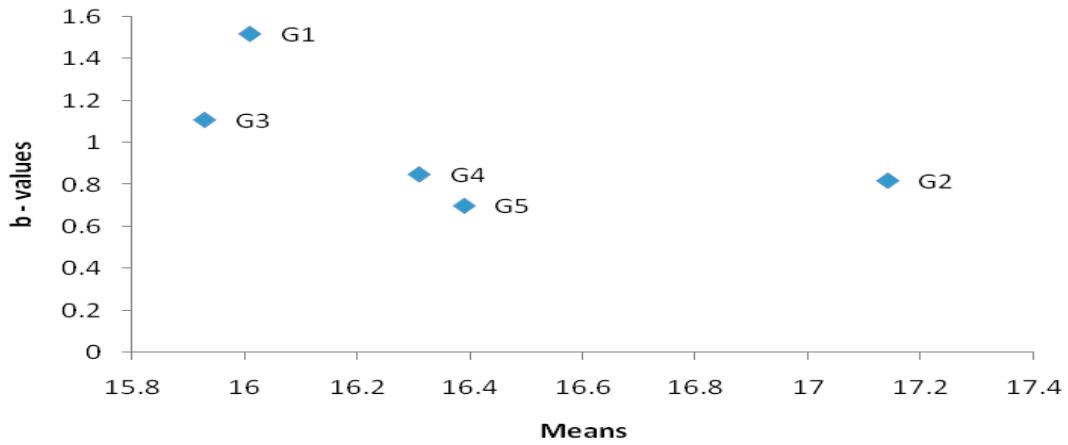


Figure 8: Scatter diagram of b-values against means for cob length

4.7.7 Number of kernel rows per cob

The relationship between regression coefficients and means for number of kernel rows per cob is shown in the scatter diagram in Fig. 9. It indicates that G1 recorded higher mean value compared to G2 and had b-value very close to 1 (b =1). Other genotypes (G3, G5) had higher mean value for this trait but their b-values were higher than the unit value.

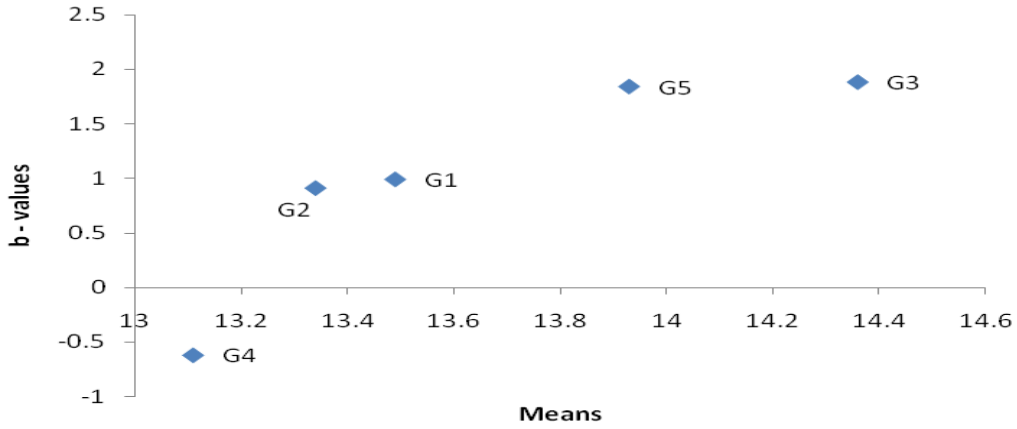


Figure 9: Scatter diagram of b-values against means for number of kernel rows per cob

4.7.8 Grain weight

The relationship between regression coefficients and means for grain weight is indicated in the scatter diagram in Fig. 10. G2 had the highest mean for grain weight and had b value closer to unity.

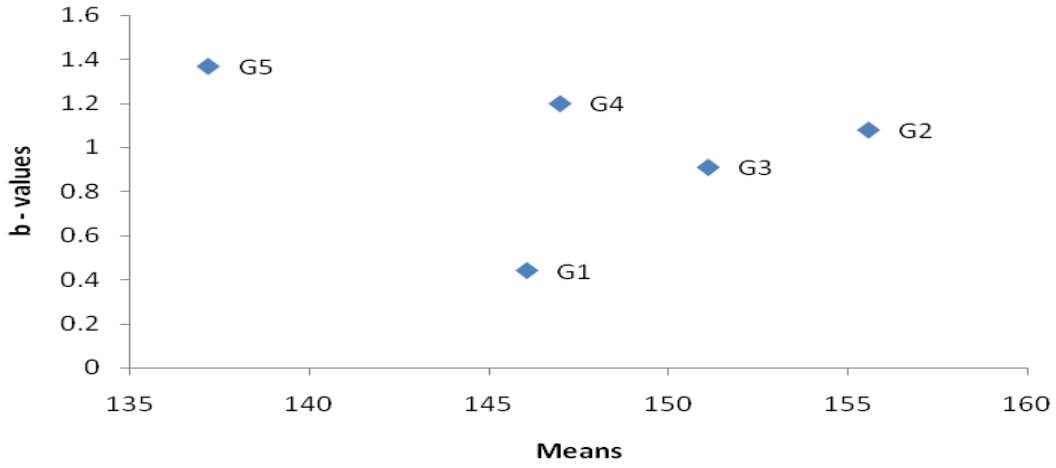


Figure 10: Scatter diagram of b-values against means for grain weight

4.7.9 Ear weight

The relationship between regression coefficients and means for ear weight is shown in the scatter diagram in Fig. 11. None of the genotypes had b-value approaching 1 although G4, G2 and G2 had heavier weights.

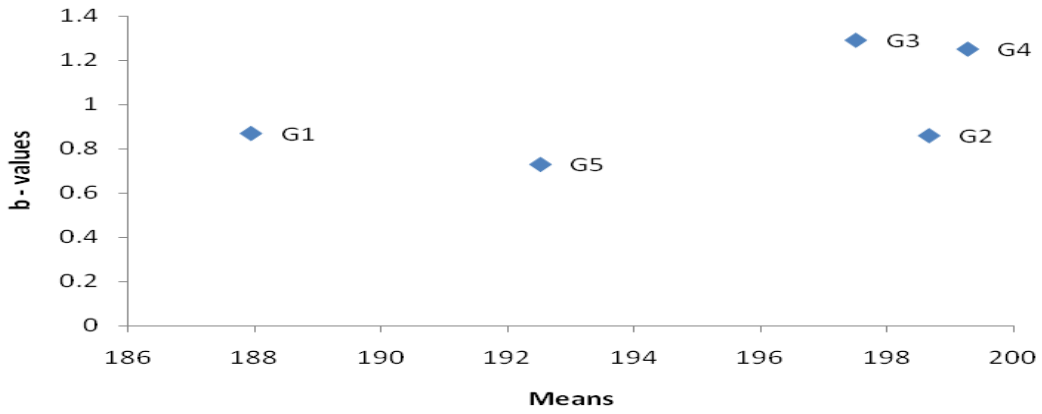


Figure 11: Scatter diagram of b-values against means for ear weight

4.7.10 Shelling percent

The relationship between regression coefficients and means for shelling percent is shown in the scatter diagram in Fig. 12. G2 recorded the highest mean with b value approaching unity whereas G4 had the highest b value and medium mean for this variable.

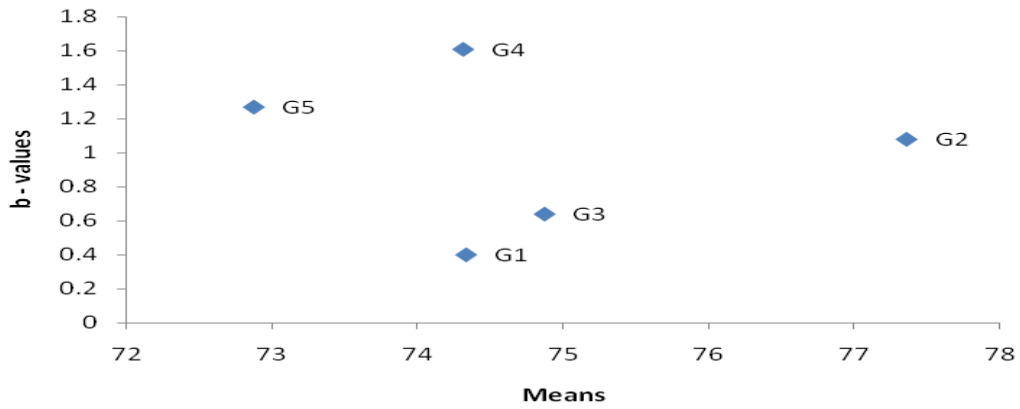


Figure 12: Scatter diagram of b-values against means for shelling percent

4.7.11 Number of leaves per plant

The relationship between regression coefficients and means for number of leaves per plant is shown in the scatter diagram in Fig. 13. The b-values of G1 was slightly higher than unity and had the least number of leaves per plant while G2 had b-values equal to unity (b = 1) and recorded the highest mean values for this trait. G5 had b-value closer to unit value and the numbers of leaves were relatively high.

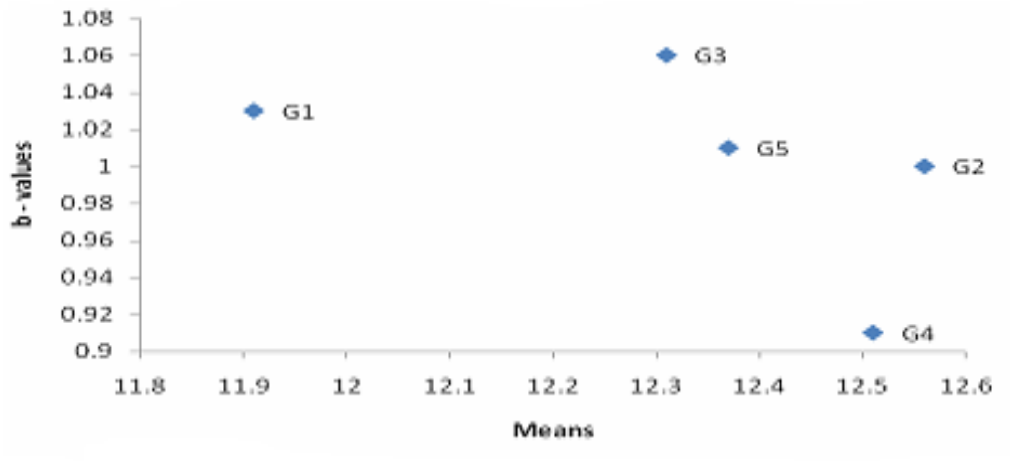


Figure 13: Scatter diagram of b-values against means for number of leaves per plant

4.7.12 Number of leaves below the ear

The relationship between regression coefficients and means for number of leaves below the ear is shown in the scatter diagram in Fig. 14. G4 had highest number of leaves below the ear and had b-values approaching unity (b = 1). G5 had b value closest to 1 with medium number of leaves below the ear.

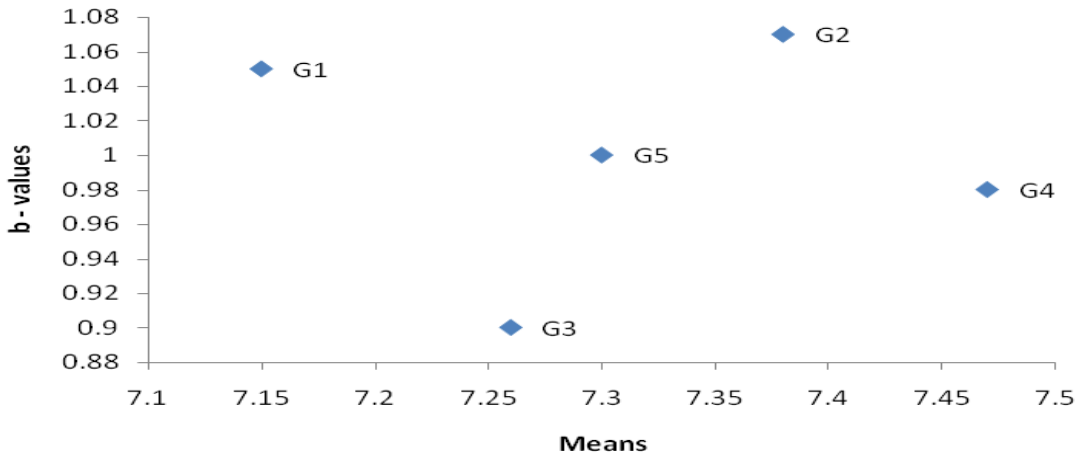


Figure 14: Scatter diagram of b-values against means for number of leaves below the ear

4.7.13 Number of leaves above the ear

The relationship between regression coefficients and means for number of leaves above the ear is illustrated in the scatter diagram in Fig. 15. G5 had b-values equal to unit value (b = 1) though it had slightly lower number of leaves above the ear compared to G4 and G3 which had higher b-values.

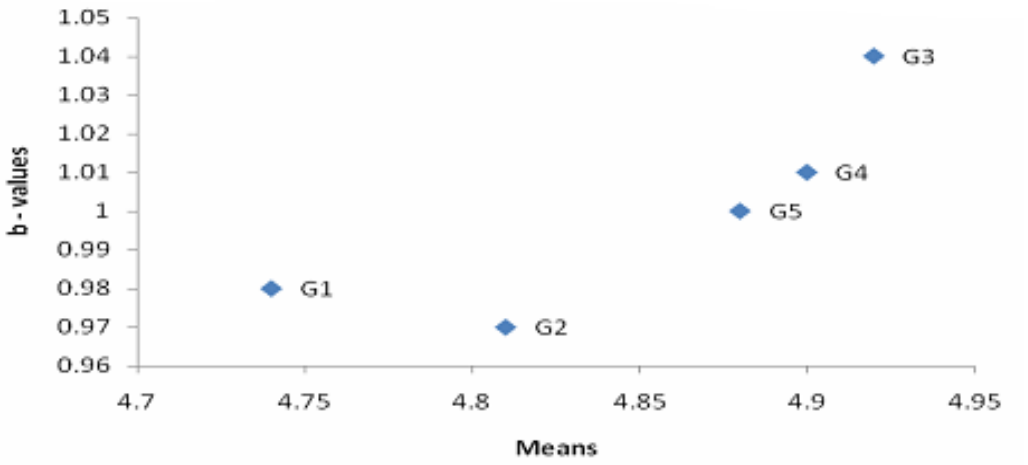


Figure 15: Scatter diagram of b-values against means for number of leaves above the ear

4.7.14 Number of leaves below the ear per number of leaves above the ear

The relationship between regression coefficients and means for number of leaves below the ear per number of leaves above the ear is shown in the scatter diagram in Fig. 16. G3 had lowest ratio of number of leaves below to number of leaves above the ear whereas G1 and G5 had medium mean with b-values not deviating much from unity.

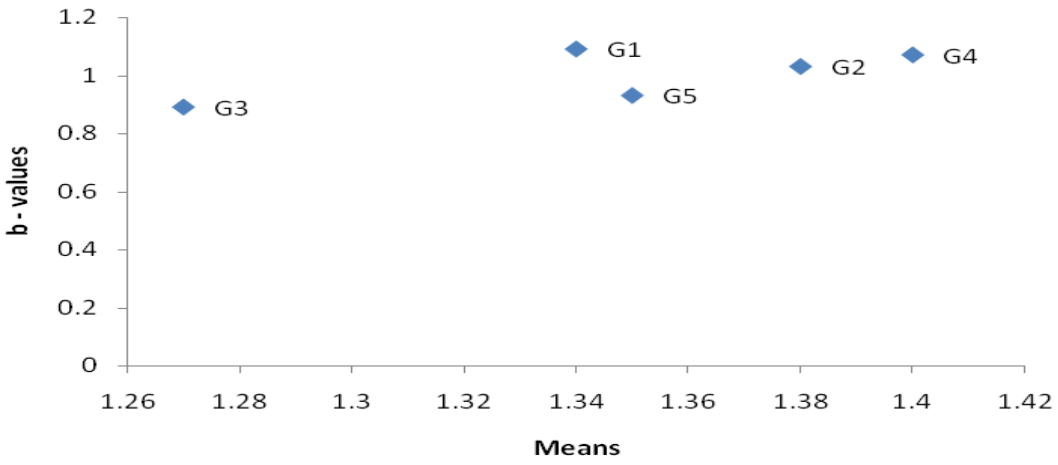


Figure 16: Scatter diagram of b-values against means for number of leaves below the ear per number of leaves above the ear

4.7.15 Harvest index

The relationship between regression coefficients and means for harvest index is indicated in the scatter diagram in Fig. 17. G2 and had b-value approaching unity.

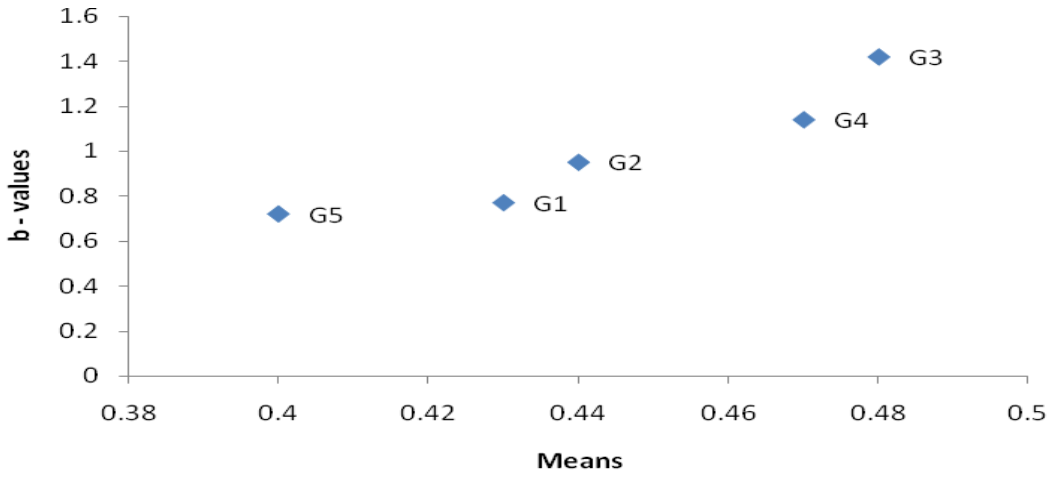


Figure 17: Scatter diagram of b-values against means for harvest index

4.7.16 Days to first tasselling

The relationship between regression coefficients and means for days to first tasselling is shown in the scatter diagram in Fig. 18. G3 had b-value approaching unity (b=1) and was the earliest genotype to silk whereas G4 took the longest period to silk with the highest b-values.

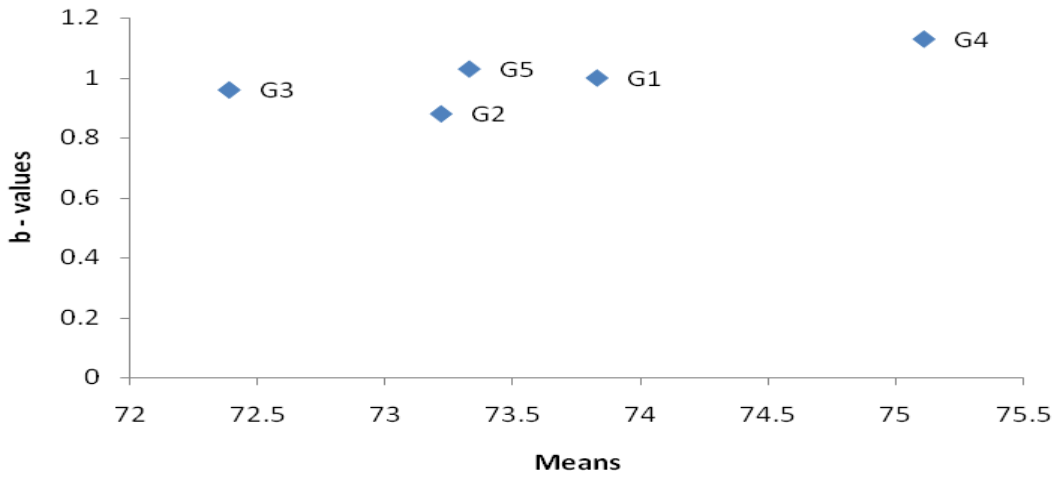


Figure 18: Scatter diagram of b-values against means for days to first tasselling

4.7.17 Days to 50% tasselling

The relationship between regression coefficients and means for days to 50% tasselling is illustrated in the scatter diagram in Fig. 19. G2 and G3 had b-values approaching unity (b =1) and took shorter period to reach days to 50% tasselling whereas G5 had b-value equal to unity (b = 1) but it took medium period to attain days to 50% tasselling.

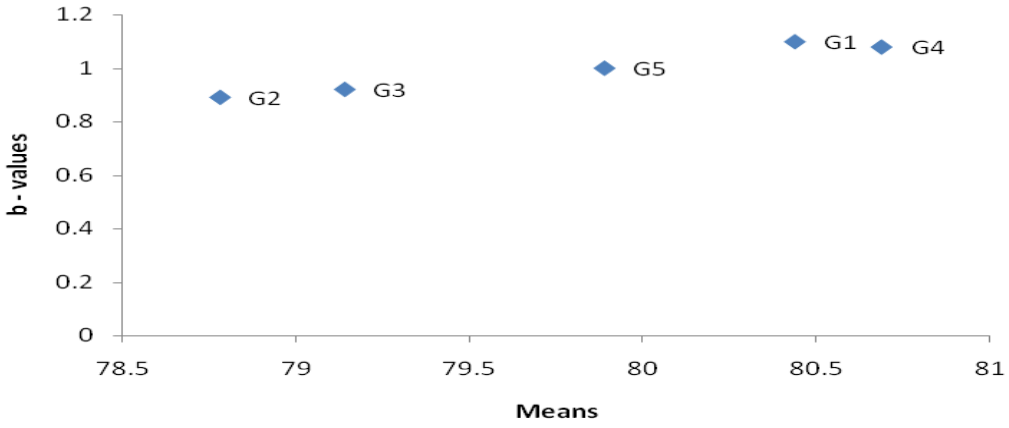


Figure 19: Scatter diagram of b-values against means for days to 50% tasselling

4.7.18 Days to 50% pollen shed

The relationship between regression coefficients and means for days to 50% pollen shed is indicated in the scatter diagram in Fig. 20. G3 and G2 were earliest although G3 was closer to unity. Similarly G5 responded on average (b=1) and was intermediate on days to 50% pollen shed.

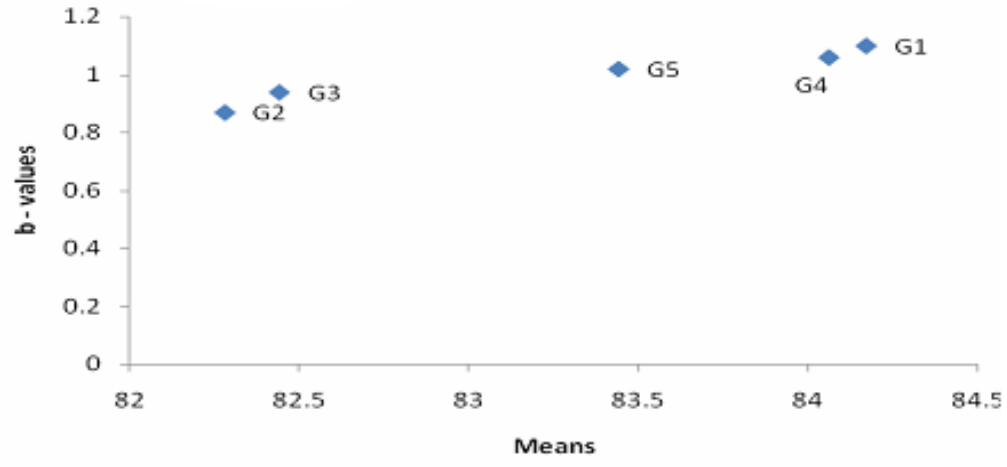


Figure 20: Scatter diagram of b-values against means for days to 50% pollen shed

4.7.19 Days to first silking

The relationship between regression coefficients and means for days to first silk is shown in the scatter diagram in Fig. 21. G3 had b-value approaching unity and took shortest period to reach days to first silking whereas G4 had the highest b-values and took the longest time to arrive at days to first silking. G5 had regression coefficient closest to unit value and had relatively short days to first silking.

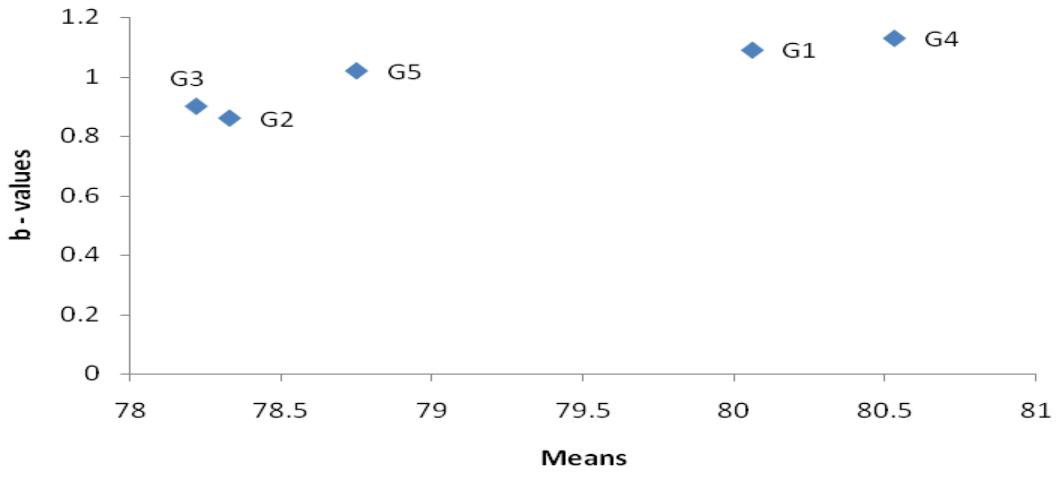


Figure 21: Scatter diagram of b-values against means for days to first silking

4.7.20 Anthesis silking interval

The relationship between regression coefficients and means for anthesis silking interval is indicated in the scatter diagram in Fig. 22. G2 and G3 recorded shortest silking intervals with b-values not approaching unit value whereas G5 and G1 had b-values approaching unit value but exhibited longest anthesis silking intervals. G4 had the closest b-value to unity with intermediate anthesis silking interval.

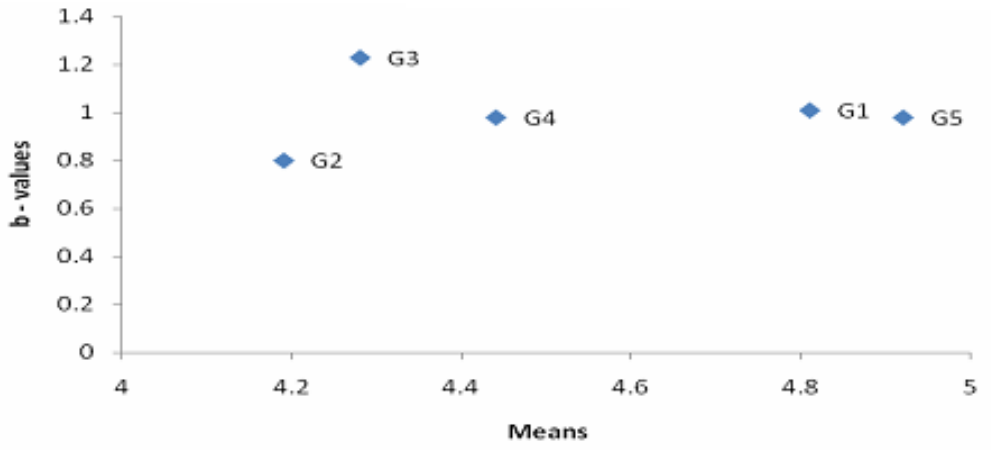


Figure 22: Scatter diagram of b-values against means for anthesis silking interval

4.7.21 Days to 50% silking

The relationship between regression coefficients and days to 50% silking is presented in the scatter diagram in Fig. 23. G2 had b-value not approaching unity but took shortest period to reach days to 50% silking. On the other hand, G4 responded on average (b-value closer to 1) but took longest period to reach days to 50% silking.

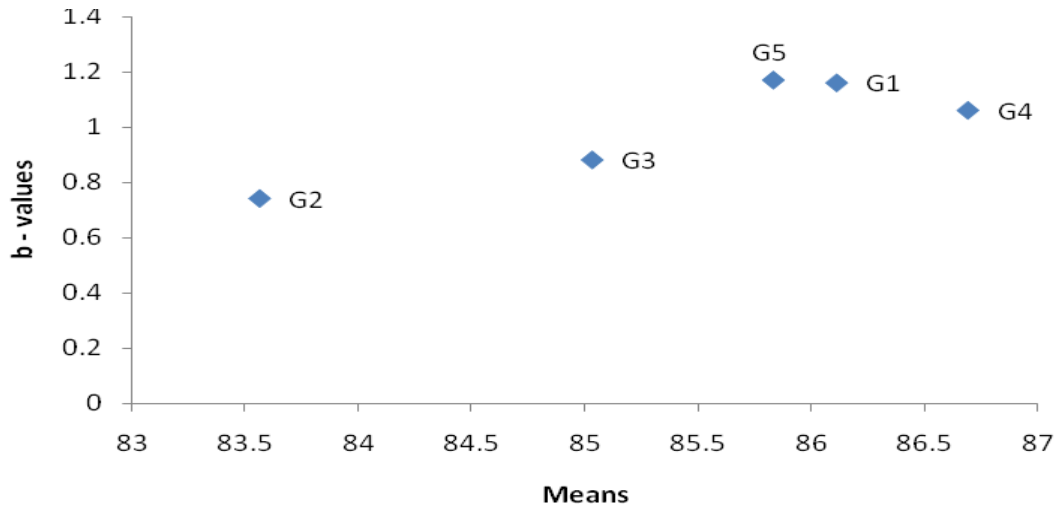


Figure 23: Scatter diagram of b-values against means for days to 50% silking

4.7.22 Days to maturity

The relationship between regression coefficients and means for days to maturity is indicated in the scatter diagram in Fig. 24. G2 was an early maturing genotype with b-value approaching unity (b=1) while G4 was the late maturing genotype with b value approaching unit value as well. All genotypes had b values approaching unity in this variable.

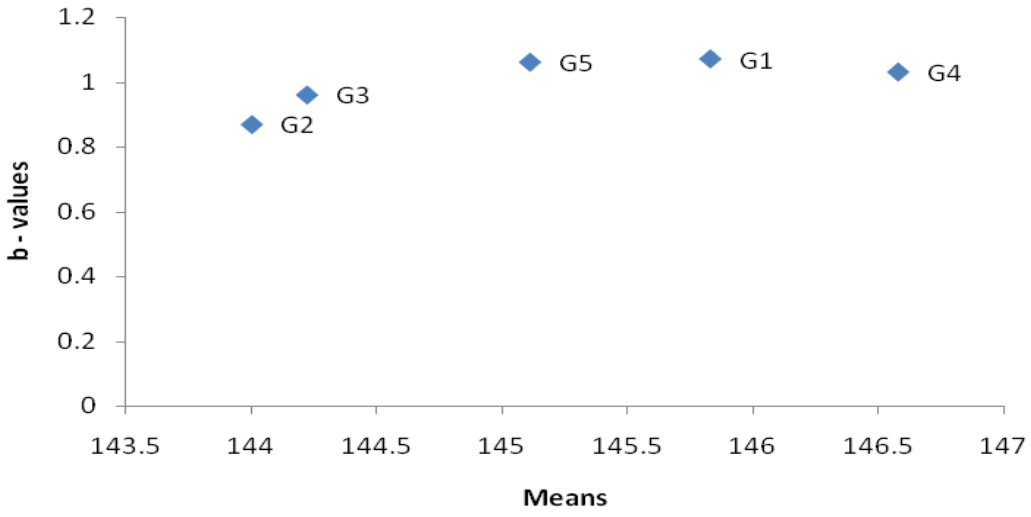


Figure 24: Scatter diagram of b-values against means for days to maturity

4.7.23 Hundred kernel weight

Fig. 25 indicates that the relationship between regression coefficients and means for hundred kernel weight**.** The scatter diagram shows that G1 and G2 had highest 100 kernel weights with b-value approaching unit value.

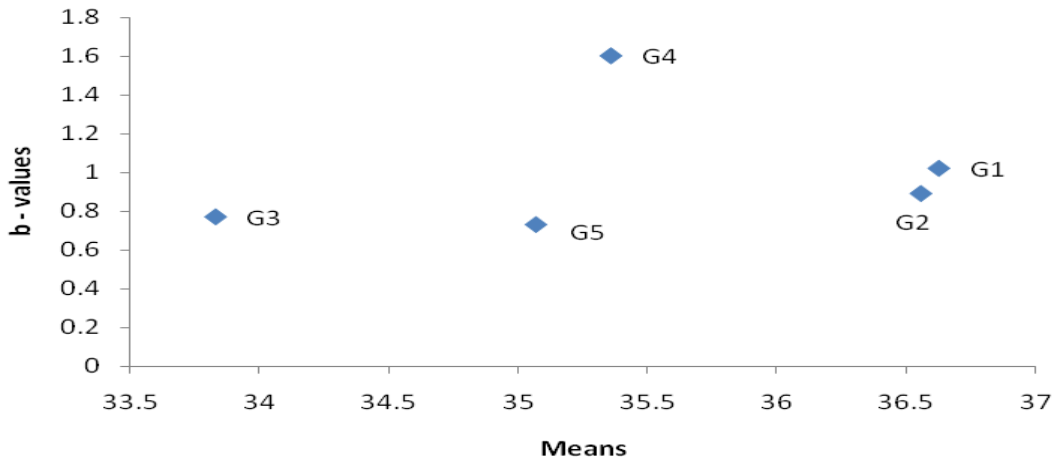


Figure 25: Scatter diagram of b-values against means for hundred kernel weight

4.7.24 Husk cover scores

Fig. 26 shows the relationship between regression coefficients and means for husk cover score. The scatter diagram indicates that none of the genotypes had higher mean values for this trait with b-value approaching or equal to unit. However G4 had b-value less than the unit value though its mean value was low.

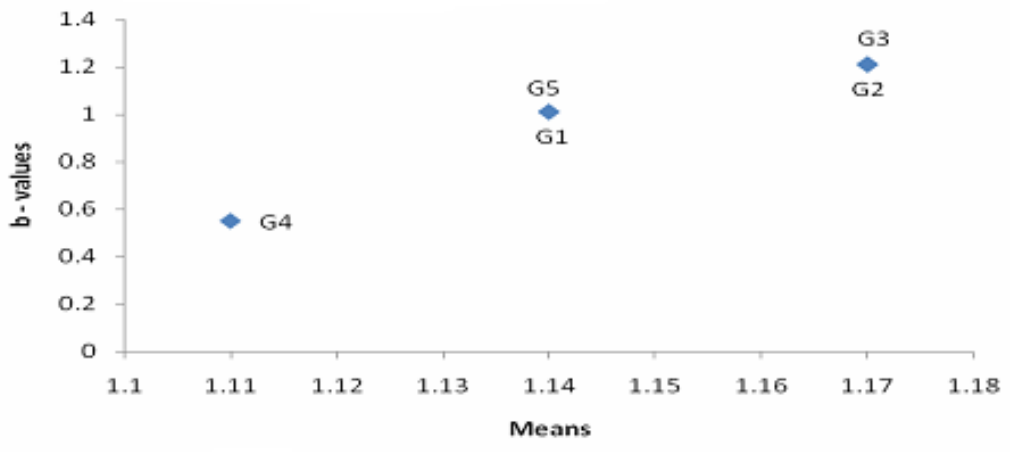


Figure 26: Scatter diagram of b-values against means for husk cover score

4.7.25 Grain yield

The relationship between regression coefficients and means for yield is shown in the scatter diagram in Fig. 27. G2 had b-value approaching unit value and yielded highest.

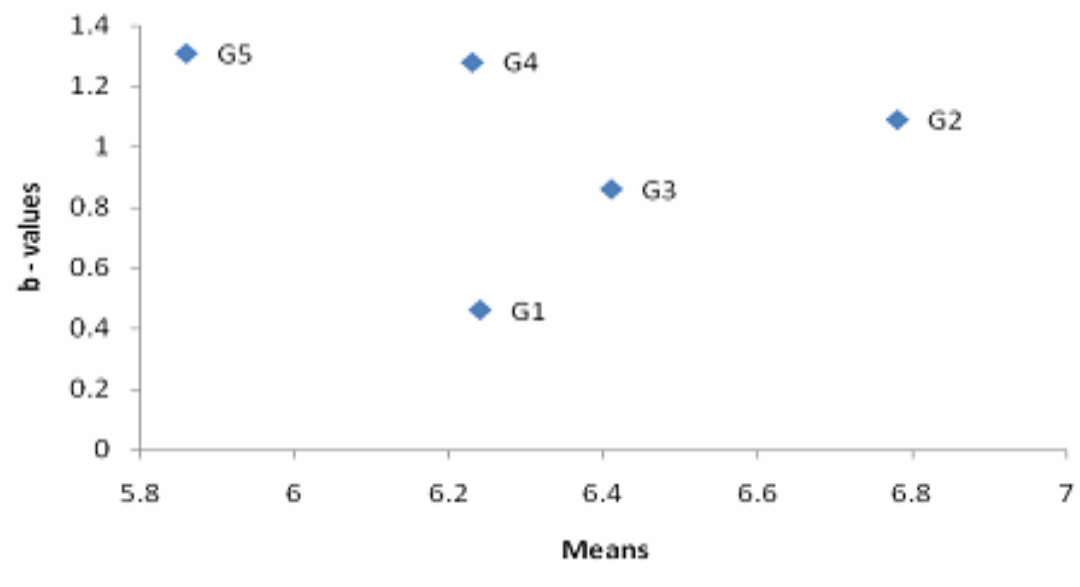


Figure 27: Scatter diagram of b-values against means for yield

4.8 Relationships between variance of deviation from regression (s2d) and means of genotypes for yield and yield components

The relationships between the variance of deviation from regression (s^2d) and means of genotypes viz; G1 (EH-1), G2 (EH-2 (FH 5160), G3 (UHS 5350 (EH-3), G4 (EH-4) and G5 (UH 6303) (Check) for the variables studied are as shown in the scatter diagrams (Fig. 28 – 51).

4.8.1 Plant height

The relationship between variance of deviation from regression and means of plant height is shown in the scatter diagram in Fig. 28. G3 produced tallest plants and G2 had the

least variance of deviation from regression whereas G1 produced shortest plants coupled with the highest variance of deviation.

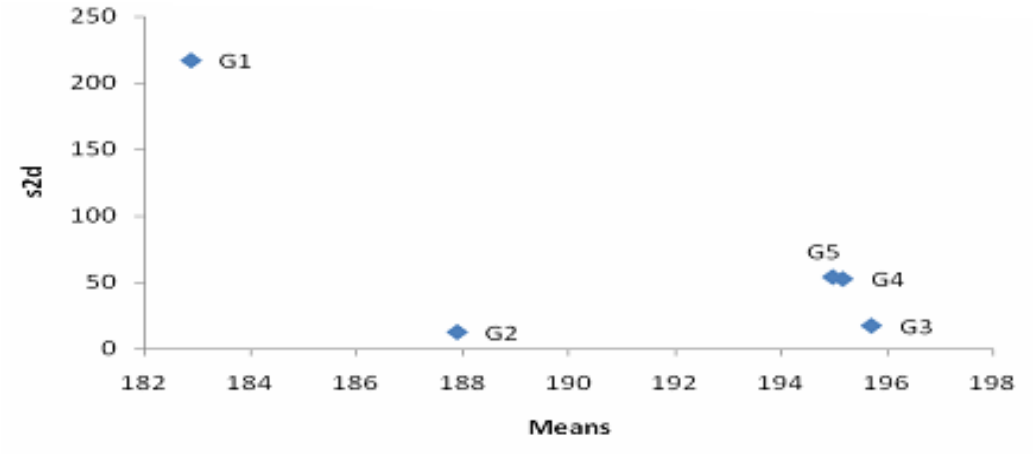


Figure 28: Scatter diagram of s^2d values against means of plant height

4.8.2 Ear height

Fig. 29 illustrates the relationship between variance of deviation from regression and means of ear height. G5 had the least value of variance of deviation from regression and had optimum ear height plants.

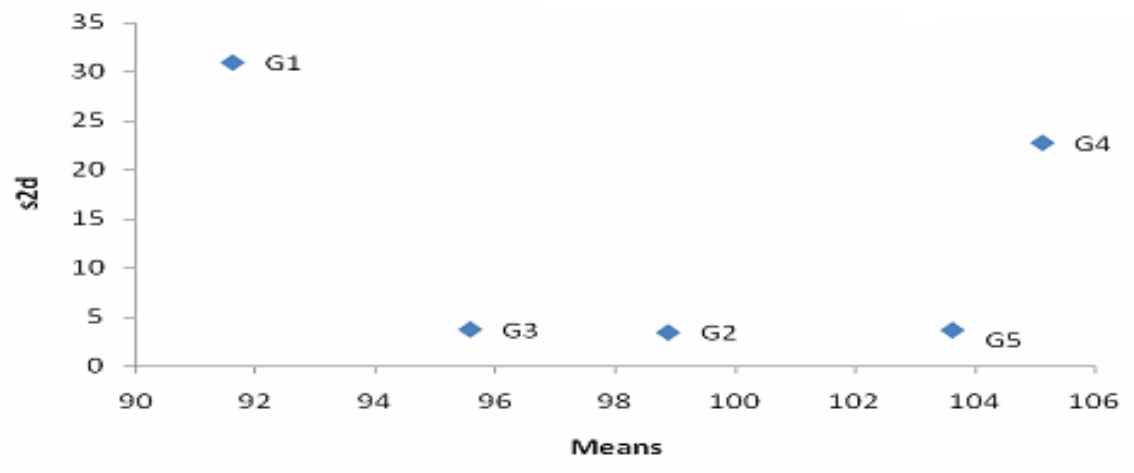


Figure 29: Scatter diagram of s^2d values against means of ear height

4.8.3 Biological yield

The relationship between variance of deviation from regression and means of biological yield is shown in the scatter diagram in Fig. 30. None of the genotypes had low variance of deviation from regression coupled with high biological yield.

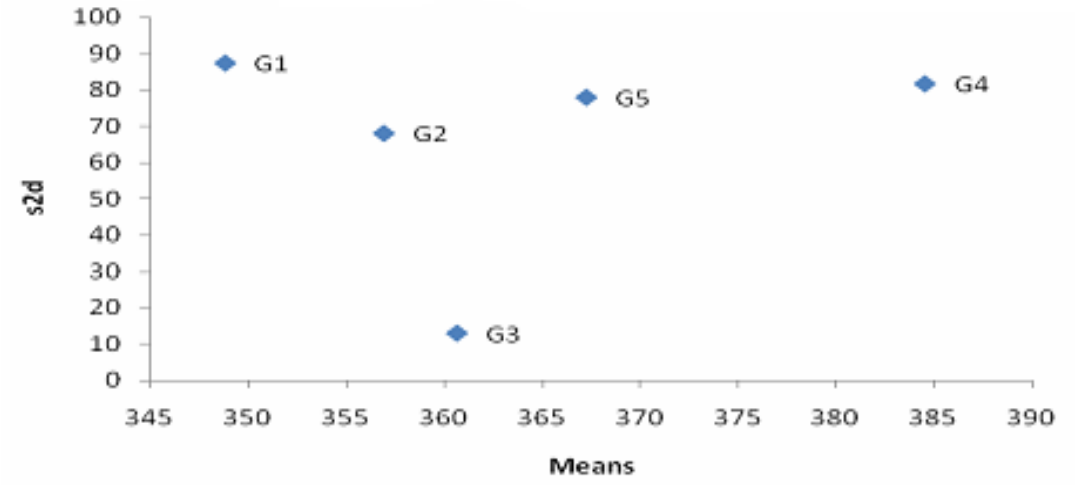


Figure 30: Scatter diagram of s^2d values against means of biological yield

4.8.4 Ear diameter

Fig. 31 indicates the relationship between variance of deviation from regression and means of ear diameter. The scatter diagram shows that G2 had the lowest variance of deviation from regression although it had medium ear diameter whereas G3 had the highest variance of deviation from regression with the largest ear diameter.

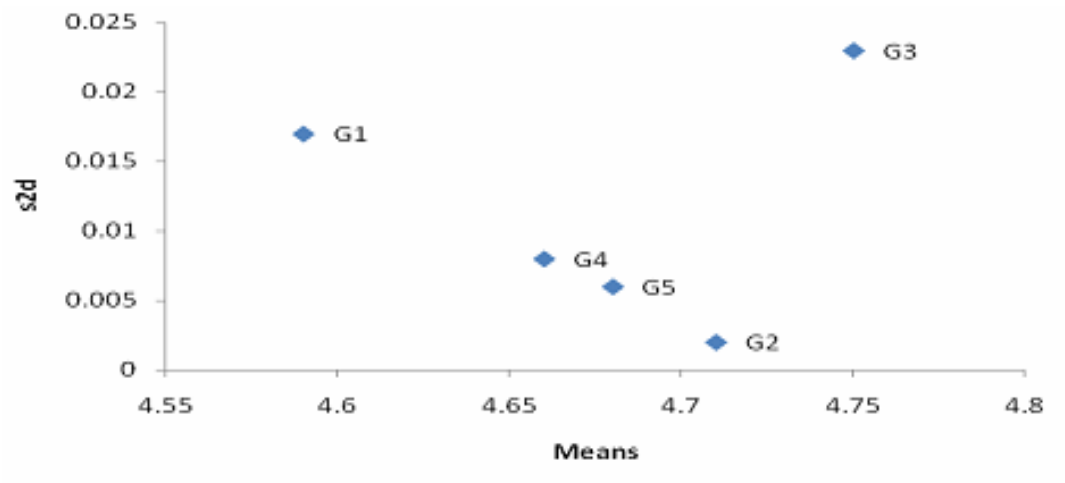


Figure 31: Scatter diagram of s^2d values against means of ear diameter

4.8.5 Number of cobs per plant

The relationship between variance of deviation from regression and means of number of cobs per plant is illustrated in the scatter diagram in Fig. 32. The scatter diagram shows G4 had slightly higher number of cobs per plant than most of the genotypes studied and recorded the lowest value of variance of deviation from regression which was similar to G3. G2 had the highest number of cobs per plant but had highest variance of deviation from regression.

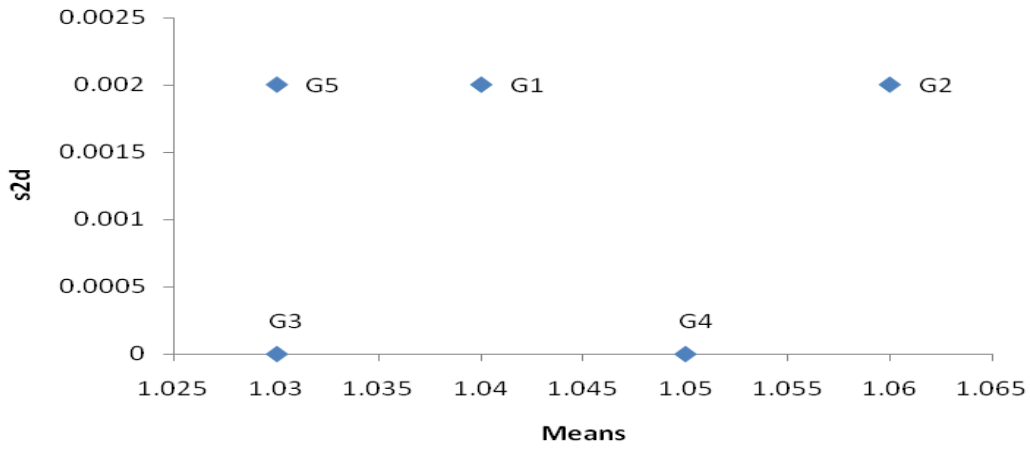


Figure 32: Scatter diagram of s^2d values against means of number of cobs per plant

4.8.6 Number of kernel rows per cob

Fig. 33 shows the relationship between variance of deviation from regression and means of number of kernel rows per cob. G5 had higher number of kernel rows per cob than most of the genotypes studied and exhibited the least value of variance of deviation from regression. G3 had the highest value of deviation from regression with most rows per cob.

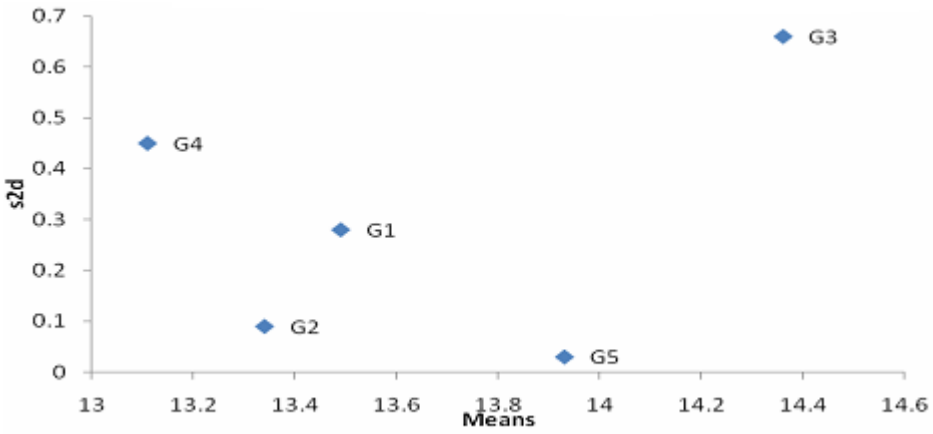


Figure 33: Scatter diagram of s^2d values against means of number of kernel rows per cob

4.8.7 Grain weight per plant (g)

The relationship between variance of deviation from regression and means of grain weight per plant is shown in the scatter diagram in Fig. 34. None of the genotypes studied recorded the least value of variance of deviation from regression coupled with highest grain weight. G5 had the least variance of deviation from regression and grain weight per plant whereas G2 and G3 recorded higher grain weights and relatively lower variance of deviation from regression.

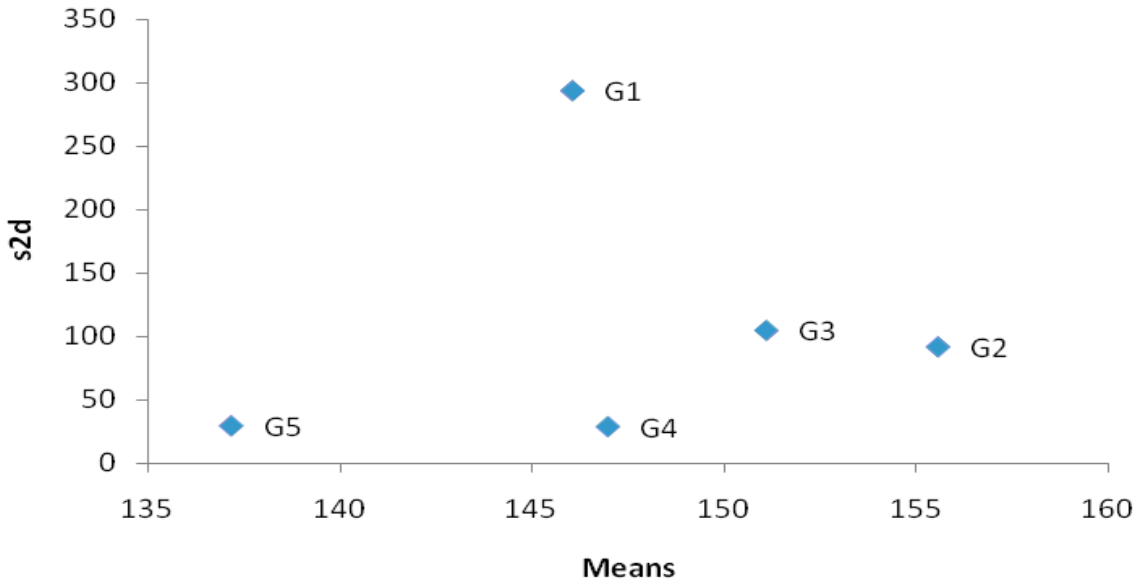


Figure 34: Scatter diagram of s^2d values against means of grain weight per plant

4.8.8 Ear weight (g)

Fig.35 illustrates the relationship between variance of deviation from regression and means of ear weight per plant. None of the genotypes studied recorded the least value of variance of deviation from regression coupled with highest ear weight. G1 had the least variance of deviation from regression although it recorded the least ear weight among the genotypes studied. G2 and G4 recorded heaviest ear weights and relatively low variance of deviation from regression.

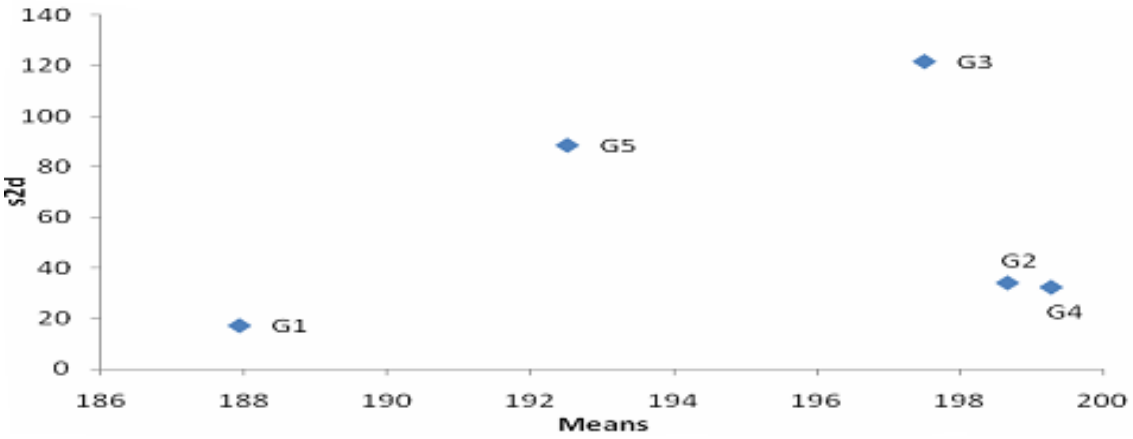


Figure 35: Scatter diagram of s^2d values against means of ear weight per plant

4.8.9 Shelling percent (%)

The relationship between variance of deviation from regression and means of shelling percent is illustrated in the scatter diagram in Fig. 36. G1 and G4 recorded medium shelling percent amongst the genotypes studied and had the least value of variance of deviation from regression while G2 had the highest shelling percent with relatively low variance.

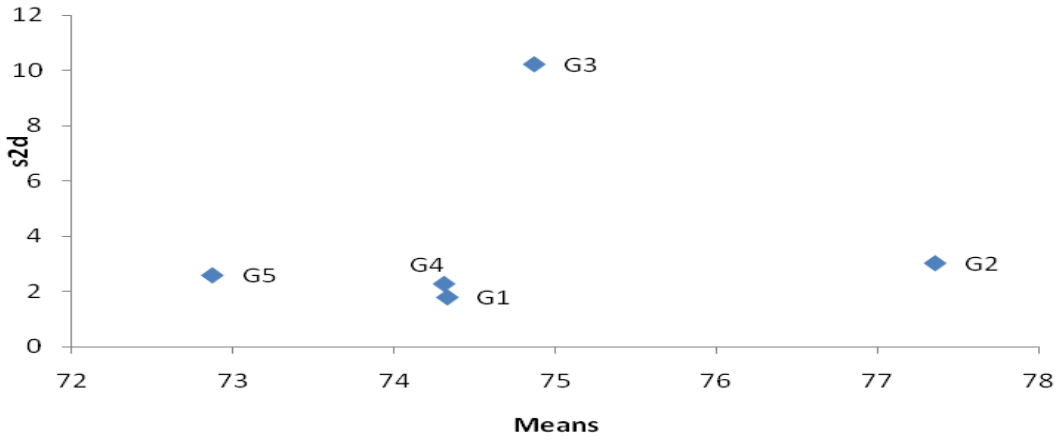


Figure 36 Scatter diagram of s^2d values against means of shelling percent

4.8.10 Number of leaves per plant

The relationship between variance of deviation from regression and means of number of leaves per plant is indicated in the scatter diagram in Fig. 37. G1 had the least number of leaves per plant but recorded the highest variance of deviation from regression while G5 recorded the least values of variance of deviation from regression with higher number of leaves per plant than G1 and G3.

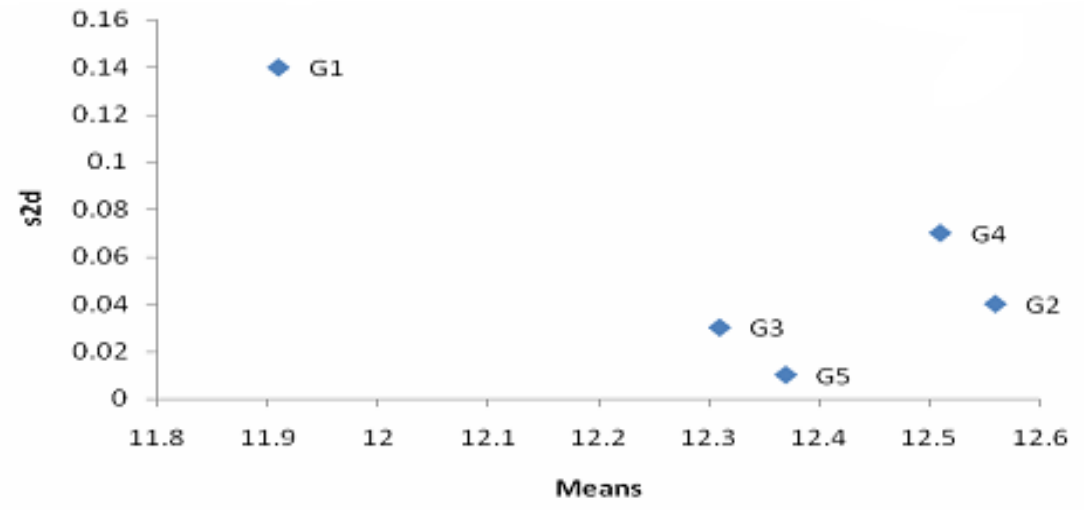


Figure 37: Scatter diagram of s^2d values against means of number of leaves per plant

4.8.11 Number of leaves below the ear

Fig. 38 indicates the relationship between variance of deviation from regression and means of number of leaves below the ear. G1 had the least number of leaves below the ear but recorded the highest variance of deviation from regression. G3, G5 and G2 had relatively low variance of deviation from regression with medium number of leaves below the ear.

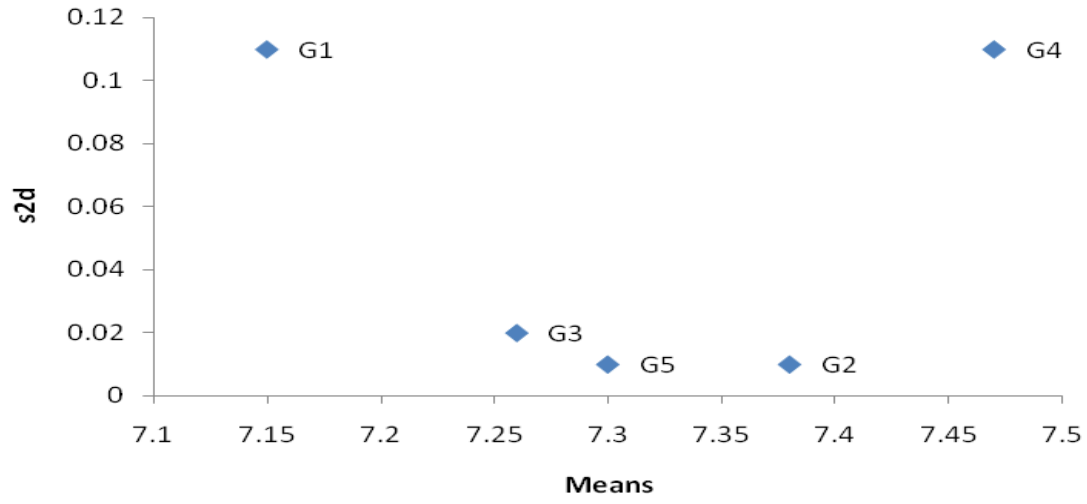


Figure 38: Scatter diagram of s^2d values against means of number of leaves below the ear

4.8.12 Number of leaves above the ear

Fig. 39 shows the relationship between variance of deviation from regression and means of number of leaves above the ear. G2 had medium number of leaves above the ear and had the least value of variance of deviation from regression while G3 and G5 had relatively more leaves above the ear and low variance of deviation from regression.

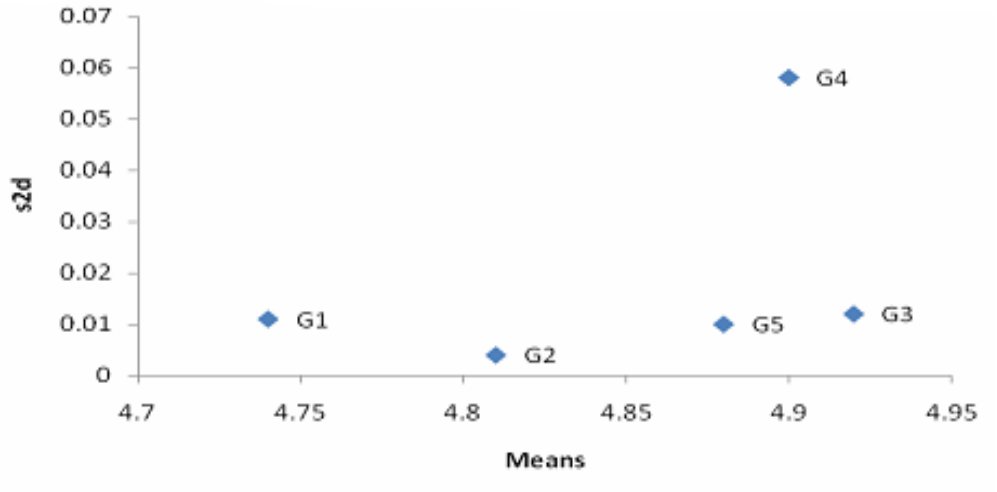


Figure 39: Scatter diagram of s^2d values against means of number of leaves above the ear

4.8.13 Number of leaves below the ear per number of leaves above the ear

The relationship between variance of deviation from regression and means of number of leaves below the ear per number of leaves above the ear is indicated in the scatter diagram in Fig. 40. G3 had the least ratio of number of leaves below to number of leaves above the ear and had the least value of variance of deviation from regression. G5 and G4 had variance of deviation from regression similar to G3 but they had relatively higher values for this ratio.

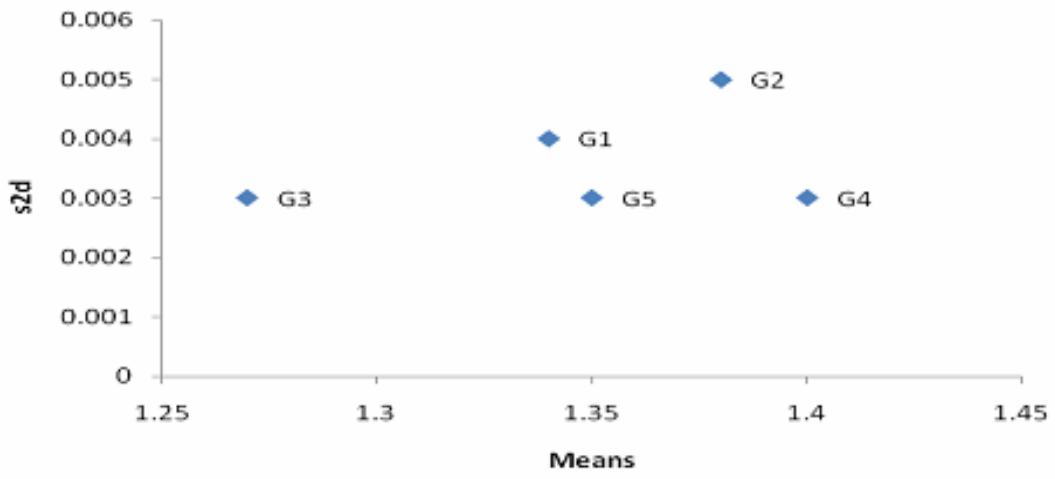


Figure 40: Scatter diagram of s^2d values against means of number of leaves below the ear per number of leaves above the ear

4.8.14 Harvest index (%)

Fig. 41 indicates the relationship between variance of deviation from regression and means of harvest index. It reveals that G2 recorded the least value of variance of deviation from regression although its mean value for this trait was slightly lower compared to G3 and G4. The highest value of variance of deviation from regression was from G4 which had relatively high mean.

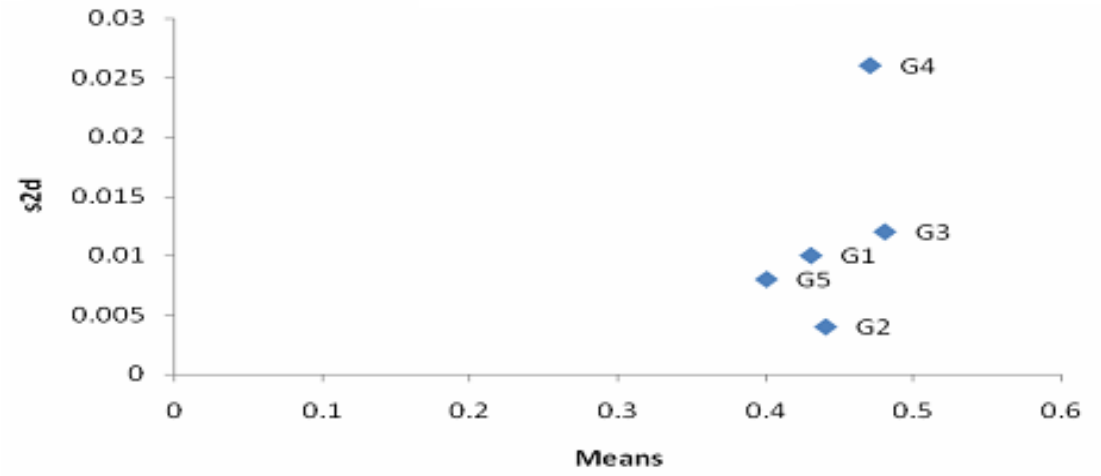


Figure 41: Scatter diagram of s^2d values against means of harvest index

4.8.15 Days to first tasselling

The relationship between variance of deviation from regression and means of days to first tasselling is illustrated in the scatter diagram in Fig. 42. G3 produced plants which gave tassels earliest and recorded the least value of variance of deviation from regression. G4 was the latest but also had low variance.

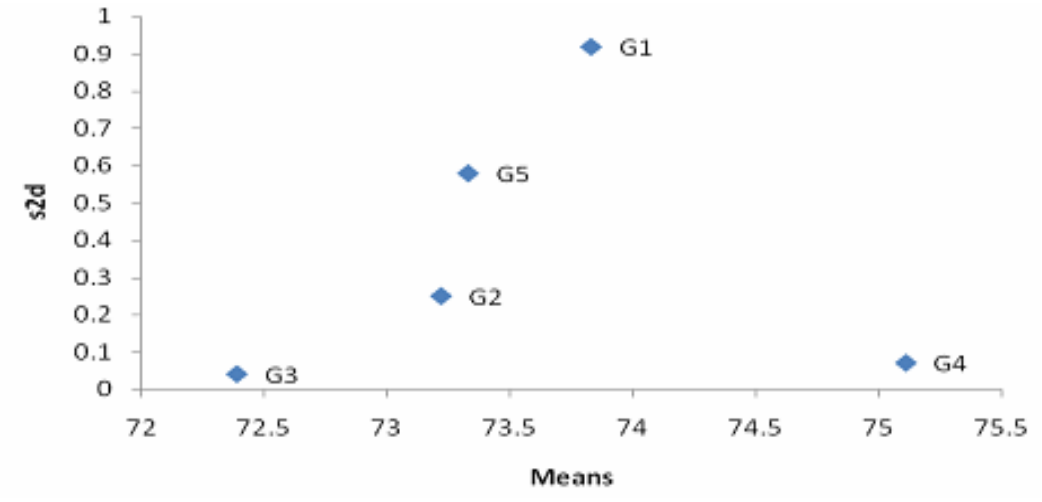


Figure 42: Scatter diagram of s^2d values against means of days to first tasselling

4.8.16 Days to 50% tasselling

Fig.43 illustrates the relationship between variance of deviation from regression and means of days to 50% tasselling. It shows that G2 and G3 were earlier and their variances of deviation were relatively low. On the other hand G1 had low variance with relatively longer days to 50% tasselling.

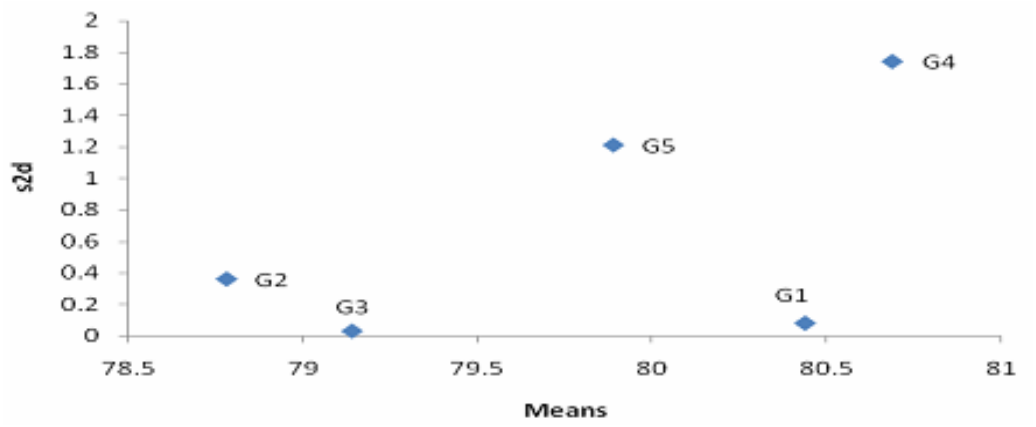


Figure 43: Scatter diagram of s^2d values against means of days to 50% tasselling.

4.8.17 Days to first silking

The relationship between variance of deviation from regression and means of days to first silking is indicated in the scatter diagram in Fig. 44. None of the studied genotypes had lowest value of variance of deviation from regression coupled with shortest period taken to reach days to first silking. However genotype G5 had relatively shorter period used to attain days to first silking and recorded the least value of variance of deviation from regression. The longest period to reach days to days to first silking was recorded for G4 with higher variance. G2 and G3 had relatively shorter period to silking but with highest variances.

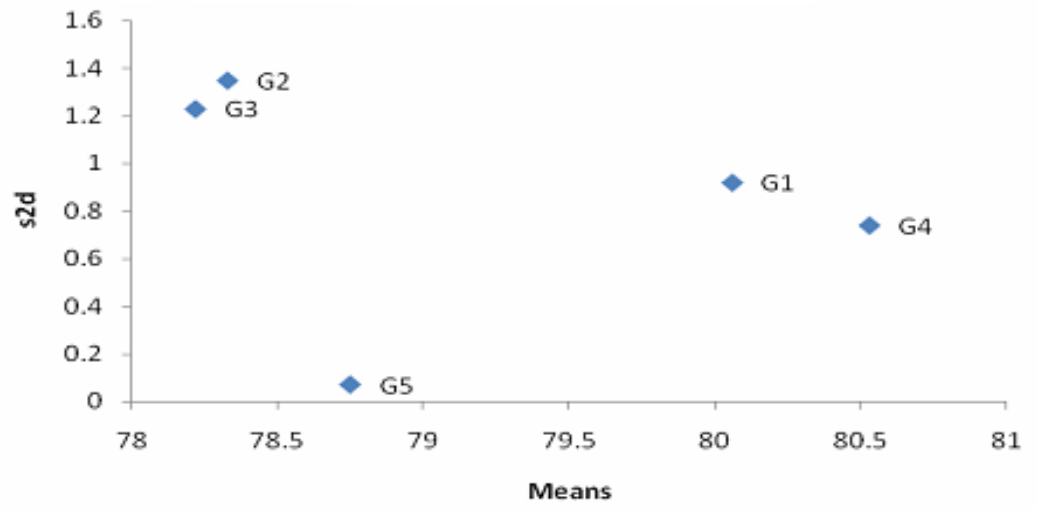


Figure 44: Scatter diagram of s^2d values against means of days to first silking

4.8.18 Anthesis silking interval

The relationship between variance of deviation from regression and means of anthesis silking interval is indicated in the scatter diagram in Fig. 45. Genotype G2 recorded the shortest mean value for this variable with variance of deviation from regression that was relatively higher than that of G4 and G1. G4 and G1 had lower variances with medium to higher mean values.

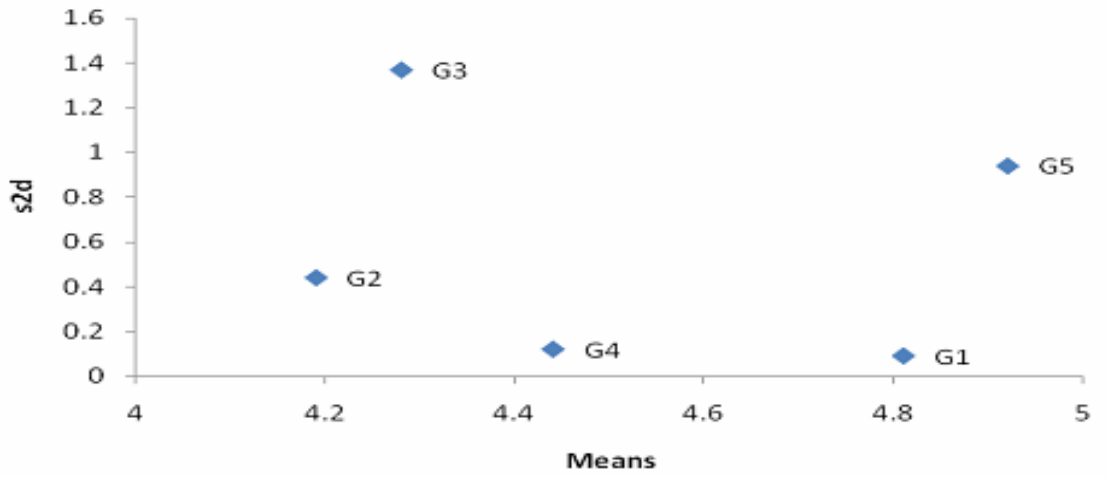


Figure 45: Scatter diagram of s^2d values against means of anthesis silking interval

4.8.19 Days to 50% pollen shed

Fig. 46 indicates the relationship between variance of deviation from regression and means of days to 50% pollen shed. G1 took longest time to reach days to 50% pollen with relatively low variance of deviation from regression. G2 had the least value of variance of deviation from regression and produced plants which attained days to 50% pollen shed earlier than the rest of the genotypes studied.

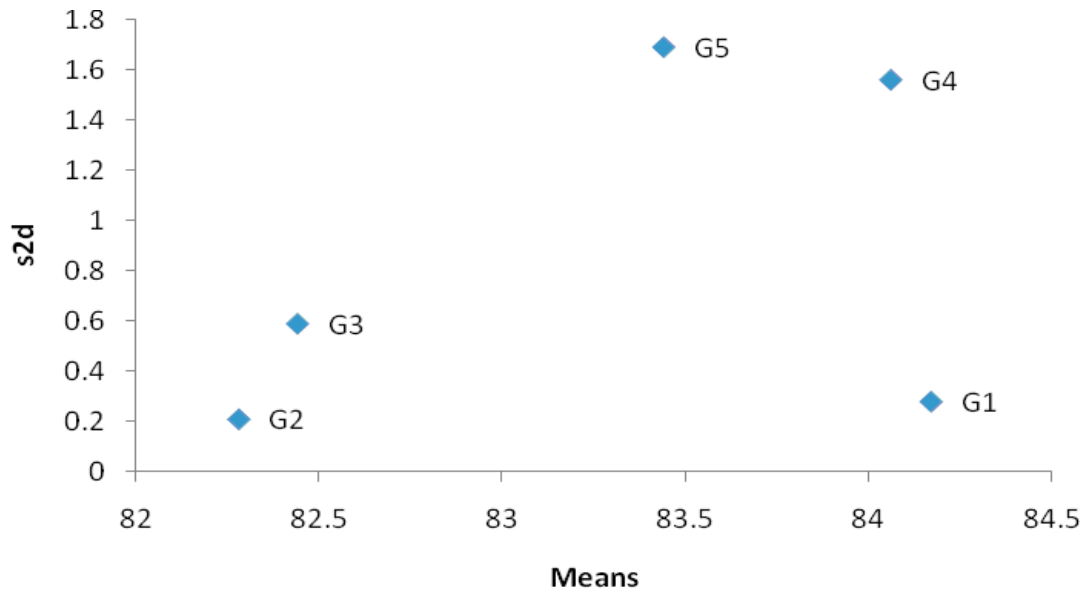


Figure 46: Scatter diagram of s^2d values against means of days to 50% pollen shed

4.8.20 Days to 50% silking

The relationship between variance of deviation from regression and means of days to 50% silking is indicated in the scatter diagram in Fig. 47. None of the studied genotypes had lowest value of variance of deviation from regression coupled with shortest period taken to reach days to 50% silking. However genotype G3 had medium period used to attain days to 50% silking and recorded the least values of variance of deviation from regression. G4 was the latest with relatively low variance whereas G2 was the earliest with relatively higher variance.

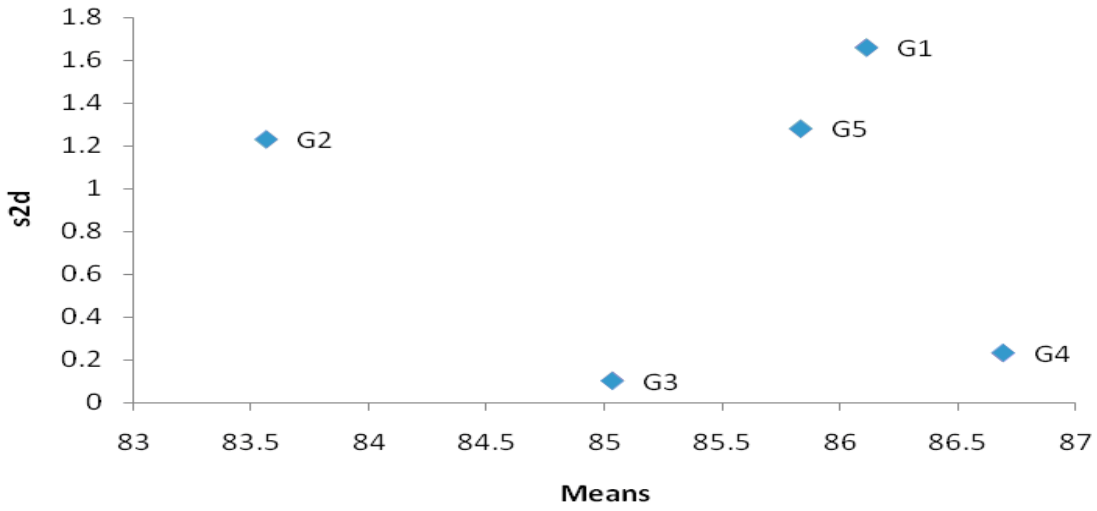


Figure 47: Scatter diagram of s^2d values against means of days to 50% silking

4.8.21 Days to maturity

Fig.48 illustrates the relationship between variance of deviation from regression and means of days to maturity. None of the early maturing genotypes recorded the least value of variance of deviation from regression. However G5 recorded the least value of variance of deviation from regression with medium period to reach days to maturity compared with G2 which matured early. G4 was the latest with slightly lower variance while G3 was earlier. G2 was the earliest but with highest variance.

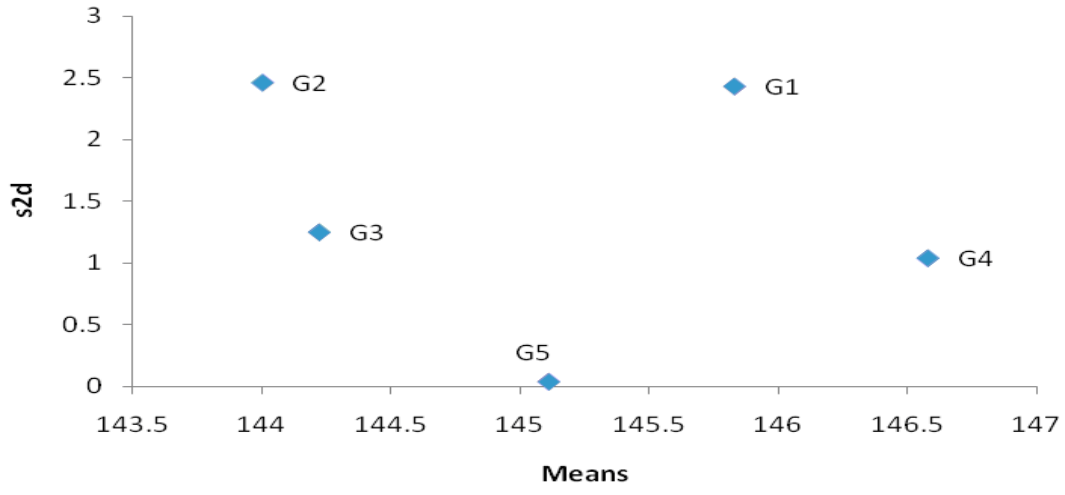


Figure 48: Scatter diagram of s^2d values against means of days to maturity

4.8.22 Hundred kernel weight (g)

The relationship between variance of deviation from regression and means of hundred kernels weight is shown in the scatter diagram in Fig. 49. G1 had the least values of variance of deviation from regression and recorded the highest mean values for hundred kernels weight.

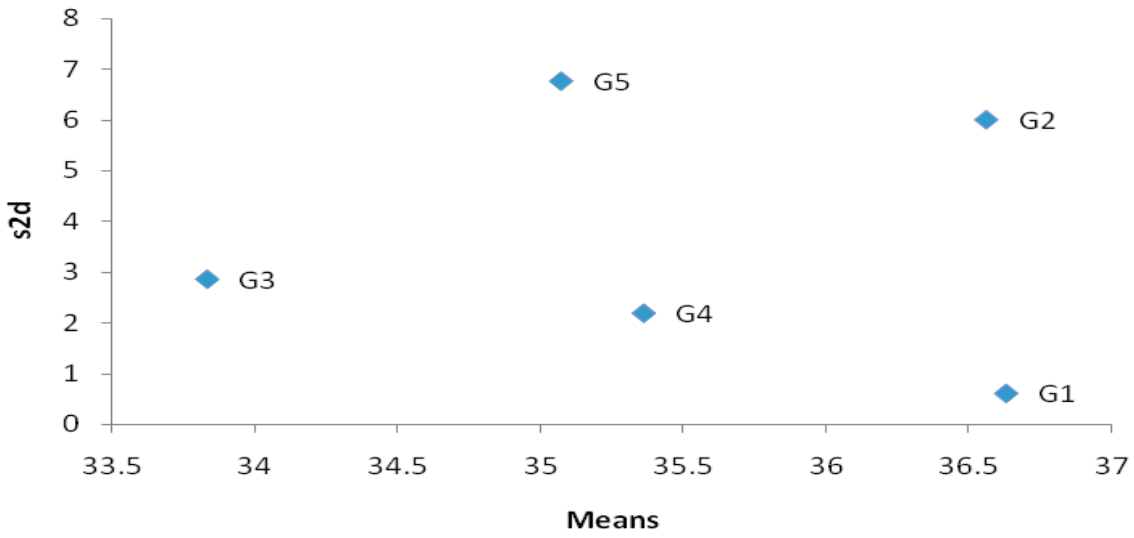


Figure 49: Scatter diagram of s^2d values against means of hundred kernel weight

4.8.23 Husk covers score

The relationship between variance of deviation from regression and means of husk covers score is illustrated in the scatter diagram in Fig. 50. G5 and G1 recorded the lowest and similar values of variance of deviation from regression with medium husk cover. G2 and G3 recorded higher mean values for this variable with also relatively higher values of variance of deviation from regression. G4 had the least cover score but highest variance.

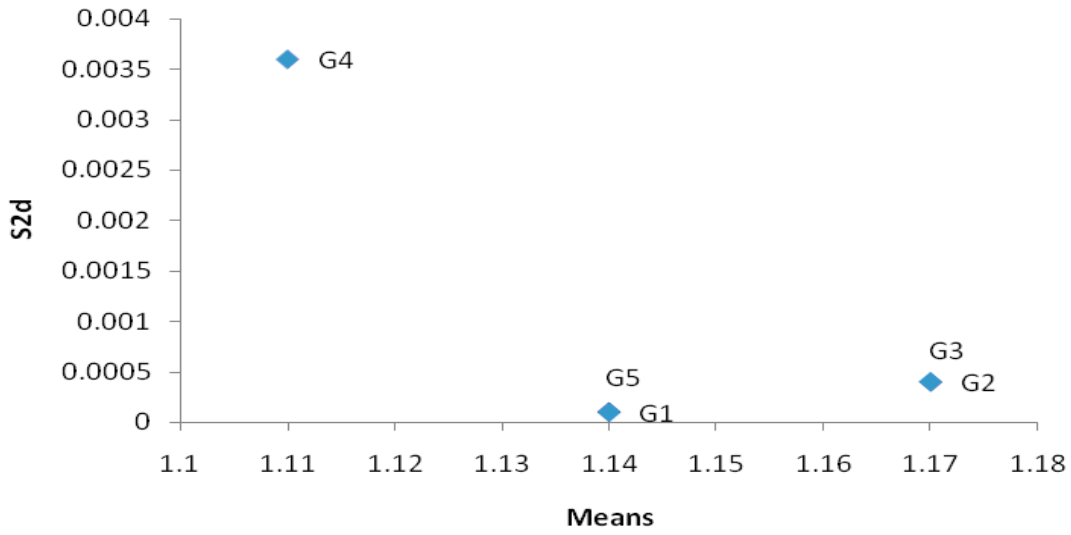


Figure 50: Scatter diagram of s^2d values against means of husk covers score

4.8.24 Grain yield (g)

Fig. 51 indicates the relationship between variance of deviation from regression and means of yield. The scatter diagram shows that G2 had the highest grain yield with relatively lower value of variance of deviation from regression. G5 recorded the least value of variance of deviation from regression coupled with the least grain yield production. G4 had low variance of deviation with medium grain yield.

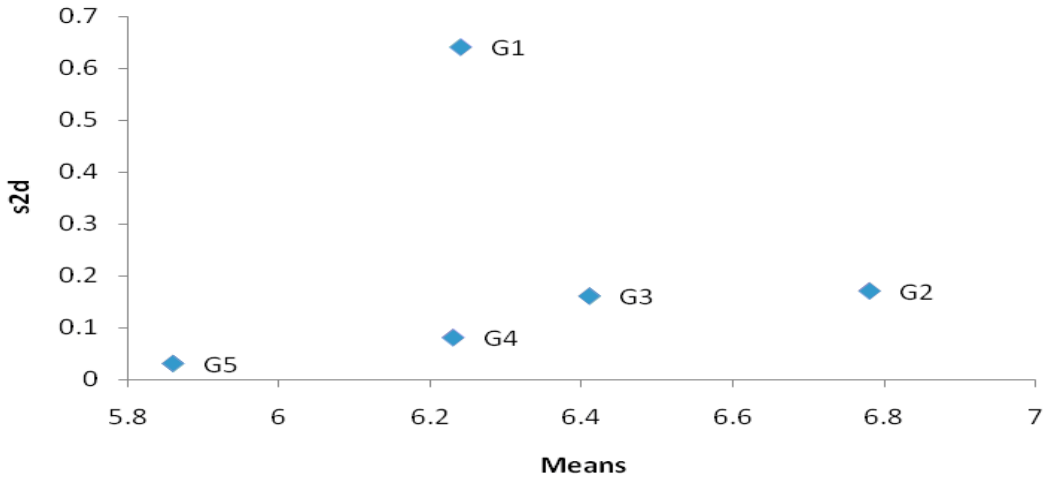
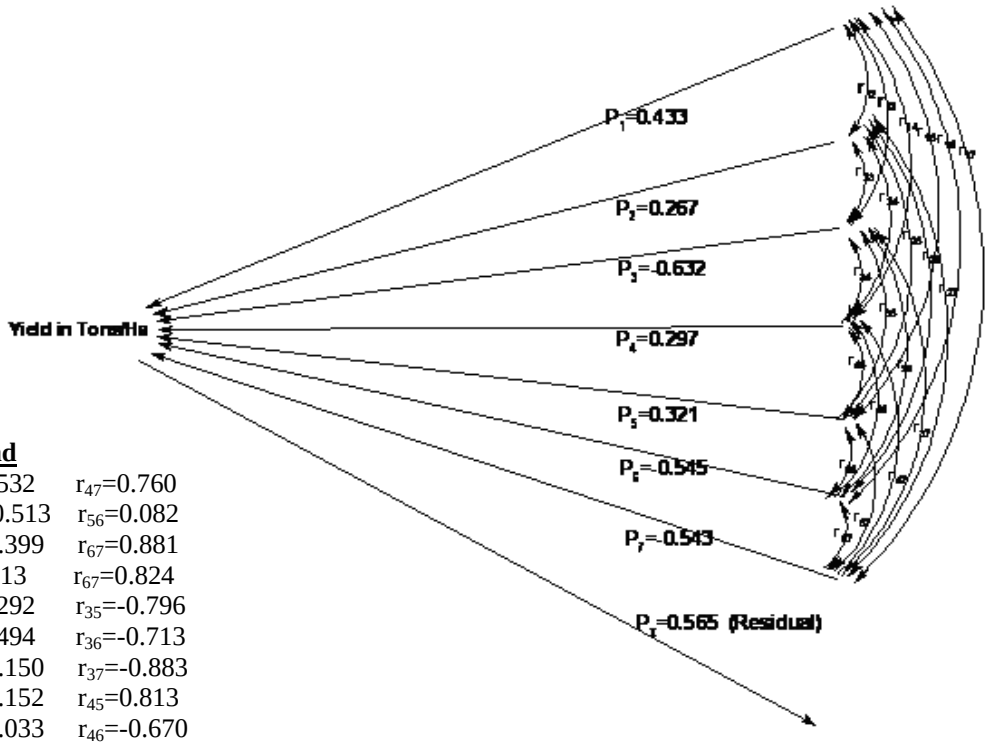


Figure 51: Scatter diagram of s^2d values against means of yield

4.9 Path coefficient analysis over four locations (Inyala, Mbimba, Seatondale and Uyole) for yield and yield components

Path coefficient analysis results on yield and yield components are shown on Appendix 12. The results show that many of the traits had positive direct effects on yield. The highest positive direct effect (0.433) on yield was from plant height followed by days to 50% pollen shed (0.321). The least positive direct effect was depicted by number of kernel rows per cob. On the other hand, the strongest negative direct effect was shown by number of leaves per plant (-0.632) followed by 50% silking (-0.545) and days to maturity (-0.543). The direct effect on yield observed for plant height was however reduced to a low and positive non significant correlation (0.398) predominantly by the negative indirect effect through days to maturity (-0.268). This was in turn attributed to the negative direct effect of days to maturity on yield. The strongest negative direct effect on yield observed for days to 50% silking was largely contributed by the negative indirect effect through days to maturity. However this was reduced to a low and negative non significant correlation (-0.446) predominantly by positive indirect effect through number of leaves per plant. On the other hand, the positive direct effect on yield that was revealed for number of kernel rows per cob was largely contributed by positive indirect effect through days to 50% silking and was reduced predominantly by negative indirect effect through number of leaves below the ear. Furthermore, the strongest negative direct effect on yield exhibited by days to maturity was mainly contributed by negative indirect effect through days to 50% silking. This was in turn reduced to a low and negative non significant correlation (-0.146) predominantly by positive indirect effect through number of leaves per plant.



Legend

R_{12}=0.532 r_{47}=0.760
R_{13}= -0.513 r_{56}=0.082
R_{14}=-0.399 r_{67}=0.881
r_{34}=0.913 r_{67}=0.824
R_{15}=0.292 r_{35}=-0.796
R_{17}=0.494 r_{36}=-0.713
R_{23}=-0.150 r_{37}=-0.883
R_{24}=-0.152 r_{45}=0.813
R_{25}=-0.033 r_{46}=-0.670
r_{26}=-0763 r_{27}=0.088

Direct effects

P_{18} = Plant height (cm)
P_{28} = Number of kernel rows per cob
P_{38} = Number of leaves/plant
P_{48} = Number of leaves below the ear
P_{58} = Days to 50% pollen shed
P_{68} = Days to 50% silking
P_{78} = Days to maturity
P_x = Residual

Figure 52: Path diagram showing the nature of causal system

4.10 Diseases Reactions

There were significant differences among the locations for diseases incidences of leaf blight (*Helminthosporium maydis*), rust (*Puccinia polysora*), grey leaf spot (*Cercospora zeae-maydis*) and maize streak virus (Table 42). Leaf blight disease was observed only at Mbimba site, rust at Mbimba and Uyole, grey leaf spot and maize streak virus at Mbimba However, the severity of the diseases observed was not very high. Weeding regimes were not significantly different from each for leaf blight, rust and maize streak virus except for grey leaf spot where weeding twice recorded high diseases incidences. The Genotypes did not differ significantly amongst them for both diseases across locations.

Table 41: Mean Blight, Rust and Grey Leaf Spot scores and Streak count of five genotypes evaluated at Inyala, Mbimba, Uyole and Seatondale

Treatments	Blight score (1-5)	Rust score (1-5)	Grey Leaf Spot (1-5)	Streak count
Locations				
Inyala	1.00[b*]	1.00[b]	1.00[b]	0.00[b]
Mbimba	2.11[a]	1.47[a]	1.58[a]	0.98[a]
Uyole	1.00[b]	1.37[a]	1.00[b]	0.00[b]
Seatondale	1.00[b]	1.00[b]	1.00[b]	0.00[b]
SE±	0.06	0.06	0.05	0.01
Weeding regimes				
No weeding	1.30[a]	1.15[a]	1.10[b]	0.23[a]
Weeding once	1.27[a]	1.27[a]	1.15[ab]	0.25[a]
Weeding twice	1.27[a]	1.22[a]	1.18[a]	0.25[a]
SE±	0.05	0.05	0.04	0.01
Genotypes				
EH-1	1.33[a]	1.17[a]	1.06[a]	0.25[a]
EH-2 (FH 5160)	1.31[a]	1.28[a]	1.11[a]	0.25[a]
UHS 5350 (EH-3)	1.33[a]	1.25[a]	1.11[a]	0.25[a]
EH-4	1.17[a]	1.22[a]	1.22[a]	0.25[a]
UH 6303	1.25[a]	1.14[a]	1.22[a]	0.22[a]
SE±	0.06	0.06	0.05	0.01
CV (%)	29.51	30.61	27.84	30.46
Grand Mean	1.28	1.21	1.44	0.24

Means within the same column followed by the same letter (s) are not significantly different from each other according to Turkey at 5% level.
*Superscript

CHAPTER FIVE

5.0 DISCUSSION

5.1 Yield and Yield Components

Very high and significant ($P \leq 0.001$) interaction observed between locations x weeding regimes for hundred kernels weight, ear diameter, number of cobs per plant, number of kernel rows per cob, grain weight, biological yield, ear weight, number of leaves per plant, number of leaves above the ear, grain yield, days to 50% pollen shed, 50% tasselling and days to maturity indicates that these traits were highly influenced by locations and weeding regimes and that their performance depended on location characteristics and weeding regimes across environments.

The influence of locations x weeding regimes was evidenced at Uyole for no weeding treatment where plants took the longest period to reach days to 50% pollen shed and at Seatondale for weeding twice treatment where shortest days to 50% pollen shed was recorded. The influence of locations x weeding regimes was also evidenced by performance of the plants for weeding twice treatment at Seatondale where they took shortest period to reach days to 50% tasselling and longest time at Uyole for no weeding treatment. The evidence of the influence of locations x weeding regimes was also clearly seen at Seatondale where days to maturity was shortest for weeding twice and the longest period was from Uyole for no weeding treatment.

On the other hand the influence of interaction effect of these factors was observed between Seatondale location and weeding twice which lead to highest number of cobs per plant whereas the least number of cobs per plant was exhibited by no weeding at all locations. Evidence of the influence of locations x weeding regimes was also seen at

Inyala for weeding twice treatment where there was highest grain weight, hundred kernel weights, ear weight and grain yield. The influence of location x weeding regimes on number of leaves above the ear was depicted by largest number of leaves above the ear at Seatondale for weeding twice treatment while the least number of leaves above the ear was recorded at Uyole for no weeding treatment. Furthermore, the influence of interaction effect of these factors for biological yield was clearly seen at Seatondale in the weeding twice treatment and the least biological yield was at the same location for no weeding. Ear diameter did not escape also from the interaction effect of locations and weeding regimes. This variable was highest at Inyala for weeding twice treatment and was least at the same location for no weeding.

Highly significant ($P \leq 0.001$) effect for location x genotype interaction for number of kernel rows per cob, days to maturity and number of leaves per plant implies that the influence of genotypes on the performance of these traits depended on locations. The influence of locations on performance of the studied genotypes for number of kernel rows per cob was evidenced by largest number of kernel rows per cob for genotype UH 6303 and UHS 5350 (EH-3) (15.11) at Uyole. The influence of locations x genotypes for days to maturity lead to differential number of days taken to reach days to maturity; for example the shortest period taken by plants to reach days to maturity was from Inyala on genotype EH-2 (FH 5160) (136.78 days) whereas the longest period was from Uyole on EH-1 (161.33 days).

The differences in soil types, rainfall amount and distribution, temperatures and altitudes existed in the four locations affected greatly these traits. The effect of temperature in reducing the length of the growth cycle for the studied genotypes was clearly observed at Seatondale where temperature was relatively higher than other sites. This lead to reduced

number of days to 50% tasselling, 50% pollen shed, days to first silking, days 50% silking and 100 grain weight. On the other hand the low temperature observed at Uyole had great impact on increasing number of days to attain these traits.

The influence of weeding regimes for these traits and others is clearly seen across locations. Weeding twice performed well almost for each variable measured. For example weeding twice produced plants with highest plant heights and ear heights across locations. Its performance was also high for ear diameter, biological yield, cob length, grain and ear weights and number of leaves per plant. Weeding twice also had plants which took short period to arrive at days to first tasseling, days to 50% pollen shed, days to first silking and days to maturity. Good performance for most measured variables and earliness for days to first tasseling, days to 50% pollen shed, days to first silking and days to maturity exhibited by weeded plants suggests presence of less competition among the plants.

In a mixture of crop and weeds, competition exists between plants for incident solar radiation, soil nutrients, and soil moisture (Tollenaar *et al*., 1993). Knezević *et al*. (2006) found that estimated maximum yield loss was more variable between locations and may reflect environmental variation and its effect on crop-weed competition. With this regard, plants in treatments with no weeding treatment were highly affected by weeds especially between week three and five from crop emergence. These resulted into poor performance for most measured variables across locations.

Highly significant differences ($P \leq 0.001$) between locations on number of leaves above the ear implies that this trait was affected by soil types and climatic conditions found in the four locations. High and significant ($P \leq 0.001$) effects among locations, weeding regimes and genotypes for days to first tasselling and days to first silking reveals that

these traits were highly influenced by locations, weeding regimes and were also affected by genetic variations existed between studied genotypes and that there is a scope for genetic improvement of the studied genotypes using these traits. Genotype UHS 5350 (EH-3) suited for days to first tasselling and days to first silking which did not differ significantly from EH-2 (FH 5160) for days to first silking.

The influence of weeds on performance of the genotypes is clearly seen amongst the weeding regimes for this trait; plants not weeded took longer period to arrive at days to first tasselling (75.85 days) and days to first silking (86.10 days) while those weeded twice took shorter period to reach at days to first tasselling (72.40 days) and days to first silking (77.37 days) across environments. These findings suggest that plants not weeded at all had high competition with weeds for incident solar radiation, soil nutrients and soil moisture. This situation may have retarded the rate of growth for the plants and hence delayed arrival at days to first tasselling and days to first silking. Maqbool *et al.* (2006) found that weed population and biomass in all weed-crop competition durations was significantly higher than weed free crop and resulted in a considerable reduction in crop growth and yield. Similarly, the maximum reduction in crop growth rate (38%), leaf area index (44%) and grain yield (51%) were recorded in full season weed-crop competition as compared with weed free crop.

High and significant ($P \leq 0.001$) effects of location and weeding regimes for days to 50% tasselling, days to 50% pollen shed and days to 50% silking shows that the performance of these traits was affected significantly by variations amongst the locations and weeding regimes. High and significant ($P \leq 0.001$) effects of genotypes for days to 50% pollen shed and days to 50% silking as well as days to 50% tasselling ($P \leq 0.05$) suggest that there is scope for genetic improvement and that selection can be exercised for better

genotypes to be used in breeding or used for production. According to the study, genotypes EH-4, EH-1 and UH 6303 suited for days to 50% pollen shed, days to 50% silking and days to 50% tasselling respectively.

Highly significant ($P \leq 0.001$) differences that were observed amongst the locations for anthesis silking interval (ASI) and days to maturity indicates that the locations played a great role in determining the period taken by plants to reach maturity. The differences in temperature, rainfall amount and distribution could have played a great role in these traits (Appendices 1-11). In a study by Saeed and Francis (1983) on Genotype × Environment interactions in grain sorghum, it was found that minimum temperature was more important than maximum temperature especially for late maturing genotypes. The influence of temperature suggests to have played a great role for Uyole location where plants matured very late and had highest mean for anthesis silking interval. Too long ASI will probably reduce grain number and further bring about yield loss (Edmeades *et al*., 1999). One of the effective ways to resolve this problem is to breed for short-ASI varieties. The optimum level of ASI for location x weeding regime was found at Seatondale for weeding twice treatment.

Highly significant ($P \leq 0.001$) effects of locations and weeding regimes for number of cobs per plant indicates that this variable was influenced by locations and weeding regimes and that the influence of weeding regimes for this trait depended on locations. Under this study the number of cobs per plant was relatively higher in areas with moderate rainfall and decreased with high increase in rainfall. Seatondale had highest number of cobs per plant (1.09) across locations. This suggests that there was better synchronization between pollen shed of the tassel and silk extrusion of the ears at this location. In addition, the number of cobs per plant increased with increase in weeding

frequency thus weeding twice exhibited more number of cobs per plant amongst the weeding regimes (Table 12 and Appendices 7-10). Buren *et al.* (1974) and Anderson *et al.* (1984) observed that prolific maize lines which produced multiple ears at low populations maintained higher kernel number than did single-eared lines under high Nitrogen regimes.

Highly significant ($P \leq 0.001$) differences between locations and weeding regimes for cob length and none significant differences amongst the genotypes for this trait implies that the performance of this variable was influenced by locations and weeding regimes and that the genotypes were homogeneous for this trait and cob length might be a stable variable. McDonald *et al* (2004) in their study of historical evidence for climatic influences on maize found that, variations in climate are widely recognized as central factors governing the competitive balance in mixed-species plant communities and that in agricultural systems weed densities vary according to different environmental conditions thereby reducing yield differently.

Highly significant ($P \leq 0.001$) effects of locations and weeding regimes for grain weight and ear weight suggests that the influence of variations among the locations and weeding regimes played a great role on the performance of genotypes for these traits. The weeding regimes for example had different performances amongst themselves for these traits suggesting that they had different influence on the traits. The optimum performance for these variables was recorded at Inyala on weeding twice. Non significant differences between the genotypes for grain and ear weights imply that the genotypes were homogeneous for this trait and that these traits might be stable.

High and significant differences ($P \leq 0.001$) between locations and weeding regimes for shelling percent and biological yield suggests that variations which existed across environments and weeding treatments applied affected shelling percent and biological yield differently. The differences in weed infestation, population density and competing ability of weeds suggest to have played a great role in shaping the performance of genotypes for these traits. The lowest shelling percent (67.43%) and biological yield (301.16g) exhibited at Mbimba could mean that competition for soil nutrients, solar radiation and soil moisture between the plants and weeds was high at this location hence low accumulation of biomass especially in none weeded plants. This could be supported by a large number of weeds species found at this site viz. wandering jew (*Tradescantia fluminensis)* which sends out roots at each nodal point allowing it to trail over the ground to form a thick carpet-like cover. *T. fluminensis* is considered an invasive species, noxious weed, or pest plant in many places and is consequently targeted for eradication (Wolff, 1999) and bracken fern *(Pteridium esculentum* Forst. F), which is known to produce phytotoxins that suppress the growth of other plant species (Adams and McHenry1978). Bracken forms a fine web of roots under the soil and is difficult to remove mechanically. Other weeds included finger grass, blackjack weeds, guinea fowl grass and kikuyu grass.

None significant differences among the genotypes for harvest index and 100 grain weight across environments reveals homogeneity of the studied genotypes on these traits. High and significant ($P \leq 0.001$) effects of locations and weeding regimes for 100 grain weight and grain yield suggests that the performance of these traits were highly influenced by location and weeding regimes variability across environments. Highly significant ($P \leq 0.001$) effects of locations, weeding regimes and location x weeding regimes for grain yield indicates that yield was highly affected by differential characteristics of

locations and weeding regime treatments and their interaction effects across environments.

5.2 Estimates of Variance Components

Partitioning of variance into its components permits an estimation of relative importance of various determinants of the phenotypes, in particular the role of heredity versus environment. The relative magnitude of these components determines genetic properties of any breeding population. When genotypic variance is high, heritability is simultaneously high with little environmental effect.

High heritability recorded for days to first tasselling, days to 50% tasselling, days to 50% pollen shed, days to first silking, ear height and number of leaves per plant indicates that these traits are more influenced by genes and that selection of these traits can be done in early generations. High heritability for days to first tasselling and days to first silking was also found by Bello *et al*. (2012). Swamy *et al.* (1971), Patil *et al*. (1972) and Singh and Chaudhary (1985) also reported similar findings for days to first tasselling. These findings were contrary to those of Olakojo and Olaoye (2011) who found lower heritability for days to 50% tasselling. Variables with moderate and lower heritability suggest that genes could be involved but traits are easily influenced by environmental changes.

High heritability coupled with high genetic advance for days to first tasselling, days to 50% tasselling, days to 50% pollen shed, days to first silking and ear height point out that these traits were under the control of additive genetic effects. Therefore provides better opportunities for selecting plant materials regarding these traits. Similar findings were obtained by Swamy *et al.* (1971), Afzal *et al.* (1997) and Singha *et al.* (2000). They also found high heritability and genetic advance for days to first tasselling and plant height.

Rafiq *et al*. (2010) also found higher genetic advance for plant and ear heights as well as grain weight. These findings are contrary to those of Chakraborty and Sah (2012) who found low genetic advances for plant height and days to 50% silking.

Low and medium estimates of phenotypic and low genotypic coefficients were observed in different plant traits. Phenotypic Coefficient of Variation (PCV) was moderate for harvesting index, anthesis silking interval, yield, grain and ear weights, biological yield and ear height. These results of moderate PCV are in conformity with those noticed by Robin and Subramanian (1994), Mani *et al.* (1996), Pradeep and Satyanarayana (2001), Sumathi *et al.* (2005) and Prakash *et al.* (2006). Low GCV was also found by Shakoor (2007) for number of cobs per plant, plant height, days to 50% tasselling, days to 50% silking and grain yield. Relatively higher estimates of GCV for ear height, number of leaves below the ear per number of leaves above the ear and yield among the traits measured suggest that the selection can be effective for these traits. Phenotypic coefficient of variability (PCV) was higher than the genotypic coefficient of variability (GCV) for all traits. This suggests that environmental effects constitute a major portion of the total phenotypic variation in all traits. Thus selection of superior genotypes based on such traits would not be effective. Similar findings were found by Rafiq *et al.* (2010) in their studies of heritability, correlation and path analysis in maize.

5.3 Relationship among Traits

High significant positive genotypic and phenotypic correlations that were found between ear height and plant height imply that the increase in plant height results into an increase in ear height and that these traits could be selected together for simultaneous improvement. These results are similar to findings by Yusuf and Bello (2010). Significant positive genotypic and phenotypic correlations that existed between biological yield with

plant height and ear height and between ear diameters with plant height implies that biological yield, plant and ear heights can be simultaneously selected for improvement of the studied genotypes and that ear diameter and plant height can also be used concurrently in improving the genotypes studied.

Highly significant positive genotypic and phenotypic correlations between cob length with plant height, ear diameter, ear height, biological yield and number of cobs per plant implies that these traits can be simultaneously improved and that the improvement of these traits would result into grain yield improvement because these traits were significantly and positively associated with grain yield at genotypic and phenotypic level. Grain weight per plant had significant positive genotypic and phenotypic correlation with plant and ear heights, biological yield, number of cobs per plant, cob length and number of kernel rows per cob. This implies that these variables can be selected together for improvement of the studied genotypes.

Significant positive genotypic and phenotypic correlations between ear weight with plant height, ear diameter, ear height, biological yield and grain weight and shelling percent with ear diameter, cob length, grain weight, biological yield and ear weight indicates these variables can be concurrently used in the breeding programme.

Significant positive genotypic and phenotypic correlations between number of leaves per plant with plant height and ear height implies that selection geared at greater height results in more number of leaves. Yusuf (2010) recorded similar relationships between number of leaves and ear height. Positive correlations between plant height and number of leaves were earlier recorded by Ji-hua *et al*. (2007). Significant positive genotypic and phenotypic correlations between number of leaves below the ear with number of leaves

per plant and shelling percent indicates that these variables were positively associated and that they can be concurrently utilized for breeding purposes.

Significant negative genotypic and phenotypic correlations between number of leaves below the ear with plant and ear height depicts that these variables cannot be selected simultaneously for improvement of the studied genotypes. Significant negative correlations that existed between numbers of leaves above the ear with plant height, ear height and biological yield at genotypic and phenotypic levels suggests that the variables are antagonistic.

Significant positive genotypic and phenotypic correlations between number of leaves above the ear with number of leaves per plant and leaves below the ear implies that the variables can be concurrently used in the improvement of the tested genotypes. Significant positive genotypic and phenotypic correlations that were found between the ratio of leaves below to leaves above the ear with shelling percent, number of leaves per plant and leaves above the ear suggests that there were positive relationship between the ratio and shelling percent, number of leaves per plant and leaves above the ear and that either one of these traits can be given attention for yield improvement except for number of leaves per plant which was negatively associated with grain yield.

Significant negative genotypic and phenotypic correlations that were observed between the ratio of leaves below to leaves above the ear with number of kernel rows per cob, ear diameter, ear height and plant height indicates that these traits behaved antagonistically with the ratio of leaves below to leaves above the ear.

Negative association that was observed between yield and anthesis silking interval were earlier reported by Saidaiah *et al.* (2008). Negative correlation of ASI with grain yield revealed that genotypes with short ASI are desirable for higher grain yield probably due to higher synchronization of pollen and silks with higher rate of pollinations and fertilization and grain production.

Significant negative phenotypic correlations between days to first tasselling, days to 50% tasselling and days to first silking with grain yield suggests yield decreased with an increase in time taken to reach tasselling, silking and days to 50% tasselling. Negative association that was observed between yield and these variables were earlier reported by Eleweanya, (2005), Hefny, (2011) and Maliki *et al.* (2005).

Significant positive genotypic and phenotypic correlation that was observed between days to first tasselling and plant height and ear height suggests that these traits had direct relationship to each other and that taller plants with higher ear heights took long period to reach days to first tasselling. Significant negative genotypic and phenotypic correlations between days to first tasselling with number of leaves per plant, leaves above the ear and shelling percent indicates that these traits had inverse relationships with days to first tasselling. The lesser number of leaves per plant and above the ear resulted into longest period to reach days to first tasselling. Negative association between days to first tasselling and shelling percent was also found by Iqbal *et al.* (2011).

Days to 50% tasselling had significant positive genotypic and phenotypic correlations with number of leaves per plant, leaves above the ear, plant height and ear height thereby revealing that these traits can be simultaneously be selected for crop improvement. Significant positive genotypic and phenotypic correlations that were observed between

days to 50% pollen shed and plant height and ear height indicates that these variables can be concurrently used for yield improvement because they were also positively associated with yield. Significant positive correlations between days to 50% pollen shed with plant height and ear height were also recorded by Betran and Hallauer (1996). However contrary findings were recorded by Eleweanya *et al*. (2005) who found negative association between days to 50% tasselling with number of leaves per plant and plant height thereby indicating that improvement of either one of these traits would sacrifice the others.

Significant negative genotypic and phenotypic correlations that were observed between days to 50% pollen shed and number of leaves per plant and leaves above the ear indicates that these traits had inverse relationship with days to 50% pollen shed. Significant positive genotypic and phenotypic correlations that existed between days to first silking with plant height and ear height and had negative correlations with number of leaves per plant, leaves above the ear, shelling percent and cob length suggests that days to first silking, plant and ear heights can simultaneously be selected for crop improvement and that days to first silking had antagonistic relationship with number of leaves per plant, leaves above the ear, shelling percent and cob length. These findings are in agreement with those by Malik *et al*. (2011) and Betran and Hallauer (1996) who found significant positive relationship between days to silking and plant and ear height. However, Yusuf (2010) obtained contrary findings in which there were none significant positive phenotypic correlation between days to first tasselling and number of leaves per plant. These results imply that the traits can be simultaneously selected for improvement.

Significant positive genotypic and phenotypic correlation that was observed between days to maturity with days to first tasselling, days to 50% tasselling, days to 50% pollen shed,

days to first silking and days to 50% silking, plant and ear height suggests that these traits can concurrently be selected for crop improvement.

Significant positive genotypic and phenotypic correlation that was recorded between 100 kernels weight and plant height, ear height, ear diameter, biological yield, ear weight, grain weight indicates that these traits can be simultaneously selected for yield improvement in the breeding programme due to the fact that they were positively associated with grain yield.

Highly significant positive genotypic and phenotypic correlations that was recorded between days to first silking with days to first tasselling, days to 50% tasselling with days to 50% pollen shed and between anthesis silking interval with days to 50% tasselling and days to 50% pollen shed suggests that these traits can be simultaneously selected for crop improvement. These findings are in conformity with those of Malik *et al*. (2011) who recorded significant positive genotypic and phenotypic correlations between anthesis silking interval and days to 50% pollen shed.

Grain yield had significant positive genotypic and phenotypic correlations with plant height, ear height, ear diameter, biological yield, ear weight and grain weight, cob length, number of kernel rows per cob, shelling percent and hundred kernel weight. Other scholars found similar findings (Rafiq *et al*., 2010, Hemavathy, 2008, Eleweanya, 2005, El-Kholy *et al*., 2005). These findings reveal that in order to improve yield of the studied genotypes one has to pay attention on these traits. That is improvement of one of these traits would lead to improvement of grain yield for the studied genotypes due to the fact that these traits were positively associated to each other and yield. These findings are contrary to those of Sreckov *et al.* (2011) who found negative genotypic correlation

between grain yields with plant height and those by Sreckov *et al.* (2010) who found negative association between grain yield and ear height. Akbar *et al.* (2008) also reported negative phenotypic correlation between grain yield and ear height in maize contrary to this study. Negative associations between grain yield with plant height that was found by Sreckov *et al.* (2011) and with ear height (Sreckov *et al.*, 2010, Akbar *et al.*, 2008) implies that these traits had antagonistic relationship with grain yield.

Non significant negative genotypic and phenotypic correlations between days to maturity and grain yield suggest that these variables were antagonistic to each other. These results are in agreement with those of Iqbal *et al*. (2011). These findings are contrary to those of Hammad *et al*. (2011) who recorded positive associations between days to maturity and grain yield thereby implying that improvement on days to maturity would improve yield.

In the present study, negative and positive associations existed between traits was either caused by genetic nature (pleiotropic effects, linked genes) or environmental factors. Phenotypic correlations were caused by both types of factors (genetic and environmental) and they can be seen by measuring the phenotype (Bocanski, 2009). Genetic correlations were caused only with genetic factors. They are very important in plant breeding, especially additive genetic correlations, because they give us information about level of relationship between two traits which is caused by additive, i.e. breeding value of individual, which can be changed during selection (Hallauer and Miranda, 1988). Miller and Rawling (1967) found that genetic correlations are the most important and are caused by linkage or pleiotropy or both. Adams (1967) however, believed that correlations may be developmental rather than genetic *per se* and are postulated to be due to genetically independent components developing in sequential patterns.

5.4 Path Coefficient Analysis

High and significant positive correlations recorded on plant height with grain yield was contributed largely by direct effect of plant height whereas that of days to 50% pollen shed was to a great extend contributed by direct effect of days to 50% pollen shed. Thus plant height and days to 50% pollen shed had important influence on grain yield.

Highly significant positive correlations exhibited by number of kernel rows per cob to grain yield was largely contributed by indirect effect via days to 50% silking whereas that of the effects of days to 50% pollen shed was largely contributed by indirect effect via number of leaves per plant. Thus kernel rows interact positively with days to 50% silking while days to 50% pollen shed interact well with number of leaves on their relations with grain yield.

Highly significant negative correlations exhibited by days to 50% silking to grain yield was mainly contributed by direct effect of days to 50% silking followed by indirect effect via days to maturity. Thus days to silking have adverse effects on grain yield while days to silking interact unfavourably with days to maturity in influencing yield. Had it not been the negative direct effect through number of leaves per plant, the relationship between yield and number of leaves per plant would be positive. Similarly the relationship between days to 50% silking and grain yield would be positive if the direct effect of days to 50% silking was positive. There would also be positive relationship between grain yield and days to maturity if the direct effect of days to maturity on grain yield would be positive.

The direct effects of plant height, days to 50% pollen shed, number of leaves per plant, days to 50% silking and days to maturity was also reflected in the overall r-value of each

trait. Therefore, the highest positive direct effects exerted by plant height followed by days to 50% pollen shed and the strongest negative direct effect exerted by number of leaves per plant, days to 50% silking and days to maturity implies that for improvement of the studied genotypes, one has to consider the improvement of these traits.

5.5 Stability Analysis of Genotypes

Scores for genotypes with b- value equal or approaching to unity and with desired mean for yield and yield components are indicated in Table 42- 48. Genotype EH-2 (FH 5160) was stable for plant height response with the available changing environments across locations (Table 42). Therefore EH-2 (FH 5160) had potential genes for tallness and stability for use in breeding programmes. However genotypes UHS 5350 (EH-3) and UH6303 had optimum performance for plant height and b values approaching unity except that they had higher values of variance of deviation from regression (s^2d). Inter-crossing these genotypes with EH-2 (FH 5160) following subsequent selection of segregants containing low variance of deviation from regression and other desired stability parameter would improve these genotypes. EH-2 (FH 5160) could be recommended for production based on height if other traits are desirable. Genotypes EH-2 (FH5160) and UHS 5350 (EH-3) were stable and optimum for ear height thereby implying the genotypes had potential genes for this variable. Thus they could be intercrossed with the other genotypes viz.EH-1, EH-4 and Uh 6303 to introgress into them genes for stability on this trait.

None of the studied genotypes had highest mean for biological yield coupled with all the required stability parameters. However the current genotypes may be used in breeding programme to select plants with highest biological yield with the desired stability parameters. EH-2 (FH 5160) and UHS 5350 (EH-3) or EH-4 and UHS 5350 (EH-3) can

be inter-crossed with possible segregants of high biological yield mean together with stability parameters required for a genotype release for farmers.

Table 42: Scores for genotypes with stability parameter scores for yield and yield components

Variables	Genotypes	Stability parameters					
		b significant or non significant	s^2d significant or non significant	Optimum performance	b approaching or equal to unit value	Low s^2d	Remarks
Plant height	EH-1	NS	NS				
	EH-2 (FH 5160)	NS	NS	YES	YES	YES	Stable
	UHS 5350 (EH-3)	NS	NS	YES	YES		
	EH-4	NS	NS	YES			
	UH 6303	NS	NS	YES	YES		
Ear height	EH-1	NS	NS				
	EH-2 (FH 5160)	NS	NS	YES	YES	YES	Stable
	UHS 5350 (EH-3)	NS	NS	YES	YES	YES	Stable
	EH-4	NS	NS	YES			
	UH 6303	NS	NS	YES			
Biological yield	EH-1	NS	NS				
	EH-2 (FH 5160)	NS	NS	YES	YES		
	UHS 5350 (EH-3)	NS	NS	YES		YES	
	EH-4	NS	NS	YES	YES		
	UH 6303	NS	NS	YES			
Ear diameter	EH-1	NS	NS		YES		
	EH-2 (FH 5160)	NS	NS	YES		YES	
	UHS 5350 (EH-3)	NS	NS	YES			
	EH-4	SG	NS	YES		YES	
	UH 6303	NS	NS	YES		YES	

b= regression coefficient, s^2d= variance of deviation from regression, NS= non significant, SG= significant ($P \leq 0.05$)

None of the studied genotypes recorded high mean for ear diameter together with all the stability parameters required. However the studied genotypes may be used in breeding programme to select plants with highest ear diameter with the desired stability parameters. The inter-crossing can be done between EH-1 with EH-2 (FH 5160) for this purpose with possible segregants containing highest mean for ear diameter and the desired stability parameters.

None of the studied genotypes had the desired mean for number of cobs per plant and required stability parameters (Table 43). EH-2 (FH 5160) and EH-4 genotypes had most of the required parameters except that they had b-values above the unit value. Further studies should find genotypes with desired stability parameters especially for average response (b=1) to be inter-crossed EH-2 (FH 5160) and EH-4 for improvement of stability characters and number of cobs per plant.

The desired mean and stability parameters for cob length were exhibited by EH-2 (FH 5160). However EH-4 recorded most of the desired stability parameters and attained the optimum performance for cob length although recorded higher variance of deviation from regression. There is a possibility of getting segregants containing the desired stability when inter-crossing is done between this genotype and EH-2 (FH 5160).

The stable genotype for number of kernel rows per cob was EH-2 (FH 5160) whereas UH 6303 fulfilled most of the desired mean and stability parameters for this trait except it had b-values above unity. Therefore there is possibility of getting sgregants with the desired stability parameters for this genotype if it is inter-crossed with EH-2 (FH 5160) in breeding programmes.

None of the genotypes studied fulfilled all the requirements for stability of grain weight. Genotypes containing desired stability parameters should be identified and then inter-crossed with UHS 5350 (EH-3) with subsequent selection of segregants containing backgrounds for higher grain weight and required stability.

Table 43: Scores for genotypes with stability parameter scores for yield and yield components

Variables	Genotype	Stability parameters					
		b significant or non significant	s^2d significant or non significant	Optimum performance	b approaching or equal to unit value	Low s^2d	Remarks
Number of cobs/plant	EH-1	NS	NS			YES	
	EH-2 (FH 5160)	NS	NS	YES		YES	
	UHS 5350 (EH-3)	NS	NS			YES	
	EH-4	NS	NS	YES		YES	
	UH 6303	NS	NS			YES	
Cob length	EH-1	NS	NS	YES			
	EH-2 (FH 5160)	NS	NS	YES	YES	YES	Stable
	UHS 5350 (EH-3)	NS	NS				
	EH-4	NS	NS	YES	YES		
	UH 6303	NS	NS	YES			
Number of kernel rows/cob	EH-1	NS	NS	YES	YES		
	EH-2 (FH 5160)	NS	NS	YES	YES	YES	Stable
	UHS 5350 (EH-3)	NS	NS	YES			
	EH-4	NS	NS	YES			
	UH 6303	NS	NS	YES		YES	
Grain weight	EH-1	NS	NS	YES			
	EH-2 (FH 5160)	NS	NS	YES			
	UHS 5350 (EH-3)	NS	NS	YES	YES		
	EH-4	SG	NS				
	UH 6303	NS	NS				

b= regression coefficient, s^2d= variance of deviation from regression, NS= non significant, SG= significant ($P \leq 0.05$)

The genotypes studied did not meet all the desired mean and stability parameters for ear weight (Table 44). However genotype EH-2 (FH 5160) attained most of the stability attributes and the desired mean for ear weight except that it had highest values of variance of deviation from regression. There is need therefore to find genotypes which contain the desired stability attributes so that it can be inter-crossed with EH-2 (FH 5160) with

subsequent selection of segregants containing backgrounds for higher ear weight and required stability attributes.

None of the genotypes studied met all the requirements for stability of shelling percent. There is no possibility for improvement of this trait using the current genotypes because genotypes had either very low or higher b values. The better option is to find genotypes elsewhere so as to inter-cross with EH-1 or EH-4 in the breeding programme following selection of segregants containing backgrounds for higher shelling percent and desired stability parameters.

All genotypes studied did not meet all the desired mean and stability attributes for number of leaves per plant. However there is an improvement possibility for this variable if EH-1 is inter-crossed with genotype EH-2 (FH 5160) or EH-4 in the breeding programme with subsequent selection of segregants containing backgrounds for desired mean and stability parameters of this variable.

In improving number of leaves below the ear, UHS 5350 (EH-3) and EH-2 (FH 5160) can be inter-crossed with other genotypes containing the desired stability in the breeding programme with subsequent selection of segregants containing backgrounds for desired mean and desired stability attributes.

Table 44: Scores for genotypes with stability parameter scores for yield and yield components

Variables	Genotypes	Stability parameters					
		b significant or non significant	s^2d significant or non significant	Optimum performance	b approaching or equal to unit value	Low s^2d	Remarks
Ear weight	EH-1	NS	NS		YES		
	EH-2 (FH 5160)	NS	NS	YES	YES		
	UHS 5350 (EH-3)	NS	NS	YES			
	EH-4	NS	NS	YES			
	UH 6303	NS	NS	YES			
Shelling percent	EH-1	NS	NS	YES		YES	
	EH-2 (FH 5160)	NS	NS	YES			
	UHS 5350 (EH-3)	NS	NS	YES			
	EH-4	NS	NS	YES		YES	
	UH 6303	NS	NS				
Number of leaves/ plant	EH-1	NS	NS	YES			
	EH-2 (FH 5160)	NS	NS		YES	YES	
	UHS 5350 (EH-3)	NS	NS			YES	
	EH-4	NS	NS		YES	YES	
	UH 6303	NS	NS			YES	
No. of leaves below the ear	EH-1	NS	SG	YES			
	EH-2 (FH 5160)	NS	SG	YES		YES	
	UHS 5350 (EH-3)	NS	SG	YES	YES	YES	
	EH-4	SG	SG	YES	YES		
	UH 6303	NS	SG	YES		YES	

b= regression coefficient, s^2d= variance of deviation from regression, NS= non significant, SG= significant ($P \leq 0.05$)

Genotypes EH-1, EH-2 (FH 5160) and UH 6303 were stable for number of leaves above the ear whereas UHS 5350 (EH-3) and UH 6303 were stable for the ratio of leaves below to leaves above the ear and EH-2 (FH 5160) was stable for harvest index trait (Table 45). The genotype that was stable for days to first tasselling and days to 50% tasselling was UHS 5350 (EH-3). The other genotypes could be intercrossed with UHS 5350 (EH-3) and UH 6303 for ratio of leaves below to above the ear, EH-2 (FH 5160) for harvest index

and UHS 5350 (EH-3) for days to first tasselling to improve mean performance and stability.

Table 45: Scores for genotypes with all stability parameter scores for yield and yield components

Variables	Genotypes	Stability parameters					
		b significant or non significant	s^2d significant or non significant	Optimum performance	b approaching or equal to unit value	Low s^2d	Remarks
No. of leaves above the ear	EH-1	NS	NS	YES	YES	YES	Stable
	EH-2 (FH 5160)	NS	NS	YES	YES	YES	Stable
	UHS 5350 (EH-3)	NS	NS	YES		YES	
	EH-4	NS	NS	YES		YES	
	UH 6303	NS	NS	YES	YES	YES	Stable
No. of leaves below the ear/no. of leaves above the ear	EH-1	NS	NS			YES	
	EH-2 (FH 5160)	NS	NS	YES		YES	
	UHS 5350 (EH-3)	NS	NS	YES	YES	YES	Stable
	EH-4	NS	NS	YES		YES	
	UH 6303	NS	NS	YES	YES	YES	Stable
Harvest index	EH-1	NS	NS	YES			
	EH-2 (FH 5160)	NS	NS	YES	YES	YES	Stable
	UHS 5350 (EH-3)	NS	NS	YES			
	EH-4	NS	NS	YES			
	UH 6303	NS	NS	YES		YES	
Days to first tasseling	EH-1	NS	NS		YES	YES	
	EH-2 (FH 5160)	NS	NS	YES	YES		
	UHS 5350 (EH-3)	NS	NS	YES	YES	YES	Stable
	EH-4	SG	NS			YES	
	UH 6303	NS	NS	YES			

b= regression coefficient, s^2d= variance of deviation from regression, NS= non significant, SG= significant ($P \leq 0.05$)

Genotype UHS 5350 (EH-3) was stable for days to 50% tasselling (Table 46). Inter-crossing can also be done between EH-2 (FH 5160) with EH-1, EH-1 with UHS 5350 (EH-3) and EH-2 (FH 5160) with UHS 5350 (EH-3) in the breeding programme with subsequent selection of segregants containing backgrounds for desired mean and desired stability attributes to obtain genotypes with desired stability parameters and mean performance.

None of the genotypes studied attained all the requirements for stability of days to 50% pollen shed. However there is possibility for improvement of this trait using the current genotypes. Genotypes EH-1 and EH-2 (FH 5160) can be inter-crossed in the breeding programme with subsequent selection of segregants containing backgrounds for desired mean and desired stability attributes.

All genotypes studied did not meet all the desired mean and stability attributes for number of days to first silking. Genotype EH-2 (FH 5160) and UHS 5350 (EH-3) met most of the required attributes but recorded higher values of variance of deviation from regression. However, inter-crossing these genotypes with UH 6303 in the breeding programme following selection of segregants containing backgrounds for desired mean and stability parameters of this variable to obtain genotypes with all desired stability attributes may result into stable genotypes for this variable.

None of the genotypes studied fulfilled all the requirements for stability of anthesis silking interval. However genotypes EH-2 (FH 5160) and EH-4 can be inter-crossed in the breeding programme with subsequent selection of segregants containing backgrounds for shortest anthesis silking interval and stability parameters to obtain genotypes with all desired stability parameters and mean performance.

Table 46: Scores for genotypes with stability parameter scores for yield and yield components

Variables	Genotypes	Stability parameters					
		b significant or non significant	s^2d significant or non significant	Optimum performance	b approaching or equal to unit value	Low s^2d	Remarks
Days to 50% tasseling	EH-1	NS	NS			YES	
	EH-2 (FH 5160)	NS	NS	YES	YES		
	UHS 5350 (EH-3)	NS	NS	YES	YES	YES	Stable
	EH-4	NS	NS				
	UH 6303	NS	NS		YES		
Days to 50% pollen shed	EH-1	NS	NS	YES			
	EH-2 (FH 5160)	NS	NS		YES	YES	
	UHS 5350 (EH-3)	NS	NS		YES		
	EH-4	NS	NS	YES			
	UH 6303	NS	NS				
Days to first silking	EH-1	NS	NS				
	EH-2 (FH 5160)	NS	NS	YES	YES		
	UHS 5350 (EH-3)	NS	NS	YES	YES		
	EH-4	NS	NS				
	UH 6303	NS	NS			YES	
Anthesis silking interval	EH-1	NS	NS			YES	
	EH-2 (FH 5160)	NS	NS	YES	YES		
	UHS 5350 (EH-3)	NS	NS				
	EH-4	SG	NS		YES	YES	
	UH 6303	NS	NS		YES		

b= regression coefficient, s^2d= variance of deviation from regression, NS= non significant, SG= significant ($P \leq 0.05$)

All genotypes studied did not attain the desired mean and stability attributes for number of days to 50% silking (Table 47). Genotype UHS 5350 (EH-3) met most of the required attributes but did not have optimum performance. Thus inter-crossing this genotype with

EH-2 (FH 5160) in the breeding programme with subsequent selection of segregants containing backgrounds for desired mean and stability may improve this trait.

None of the genotypes studied fulfilled all the requirements for stability of days to maturity. However, genotypes UHS 5350 (EH-3) and EH-2 (FH 5160) recorded most of the required attributes except they had highest values of variance of deviation from regression. These genotypes may be inter-crossed with UH 6303 in the breeding programme with subsequent selection of segregants containing backgrounds for desired mean and stability for days to maturity.

All genotypes studied did not get all the stability attributes required for hundred kernel weights. However if genotypes EH-1 and EH-2 (FH 5160) are inter-crossed following selection of segregants containing backgrounds for desired stability and mean performance for hundred kernel weights. Genotype UH 6303 was stable and optimum for husk cover scores.

Table 47: Scores for genotypes with stability parameter scores for yield and yield components

Variables	Genotypes	Stability parameters					
		b significant or non significant	s^2d significant or non significant	Optimum performance	b approaching or equal to unit value	Low s^2d	Remarks
Days to 50% silking	EH-1	NS	NS				
	EH-2 (FH 5160)	NS	NS	YES			
	UHS 5350 (EH-3)	NS	NS		YES	YES	
	EH-4	NS	NS				
	UH 6303	NS	NS				
Days to maturity	EH-1	NS	NS				
	EH-2 (FH 5160)	NS	NS	YES	YES		
	UHS 5350 (EH-3)	NS	NS	YES	YES		
	EH-4	NS	NS				
	UH 6303	NS	NS			YES	
Hundred kernels weight	EH-1	NS	NS	YES		YES	
	EH-2 (FH 5160)	NS	NS	YES	YES		
	UHS 5350 (EH-3)	NS	NS				
	EH-4	NS	NS				
	UH 6303	NS	NS				
Husk covers score	EH-1	NS	NS	YES		YES	
	EH-2 (FH 5160)	NS	NS	YES		YES	
	UHS 5350 (EH-3)	NS	NS	YES		YES	
	EH-4	SG	NS	YES		YES	
	UH 6303	NS	NS	YES	YES	YES	

b= regression coefficient, s^2d= variance of deviation from regression, NS= non significant, SG= significant ($P \leq 0.05$)

None of the genotypes had all the required parameters for grain yield stability (Table 48). However there is a possibility for inter-crossing the current genotypes with subsequent selection of segregants having backgrounds for high grain yield and stability parameters on grain yield. Inter-crossing can be done among genotypes EH-2 (FH 5160), EH-4 and

UHS 5350 (EH-3) to obtain segregants combining optimum performance and b-values approaching or equal to 1. Then these progenies have to be inter-crossed with UH 6303 to incorporate the attribute of low value of variance of deviation from regression to meet the required stability parameters for tested genotypes on grain yield.

Table 48: Scores for genotypes with stability parameter scores for yield and yield components

Variable	Genotypes	Stability parameters					
		b significant or non significant	s^2d significant or non significant	Optimum performance	b approaching or equal to unit value	Low s^2d	Remarks
Grain yield	EH-1	NS	NS				
	EH-2 (FH 5160)	NS	NS	YES			
	UHS 5350 (EH-3)	NS	NS		YES		
	EH-4	NS	NS			YES	
	UH 6303	NS	NS			YES	

b= regression coefficient, s^2d= variance of deviation from regression, NS= non significant,

5.6 Diseases Reactions

Significant differences amongst the locations for occurrence of diseases imply that locations, soil and climatic conditions might have played a great role in the occurrence of the diseases. Blight scores ranged from 1.00 – 2.11, 1.27 – 1.30 and 1.17 – 1.33 for studied locations, weeding regimes and genotypes respectively. This suggests that there was minimum or low natural occurrence of the disease in the 2010/2011 cropping season. The occurrence of the diseases at Mbimba only suggests that Mbimba had favourable environmental condition for the occurrence of the disease. This is evidenced by largest amount of rainfall and average daily temperature greater than 25°C recorded at Mbimba. Pelmus *et al*. (1986) reported that the incidence of *H. turcicum* on maize was favoured by relative humidity greater than 80 %, average daily temperature greater than 25°C, delayed sowing and high plant density. The lesions produced by the diseases may have interfered with photosynthesis process on leaves thus resulting into slight reduction of

photosynthasea (Mbwaga, 1990). This might be the cause for the low yield recorded at Mbimba amongst the sites.

Rust scores ranged from 1.00 – 1.47, 1.15 – 1.27 and 1.14 – 1.28 for studied locations, weeding regimes and genotypes respectively. This implies that the occurrence of the disease across locations was not high. The quality and quantity factors such as ear length, ear diameter, percentage of moisture and percent soluble solids in the kernel are affected by the disease whereas abundant moisture in the form of light rains or heavy dews and high humidity are factors which favour rust diseases (Babadoost, 1991). Under this study Mbimba and Uyole had most of these environmental conditions hence the occurrence of the disease.

Grey leaf spot (GLS) scores ranged from 1.00 – 1.58, 1.10 – 1.18 and 1.06 – 1.22 for studied locations, weeding regimes and genotypes respectively. This indicates that the severity or natural occurrence of the disease was low in the 2010/2011 cropping season. Significant differences amongst the locations and weeding regimes for grey leaf spot suggests that the weeding regimes and locations had different influence on the severity and occurrence of the disease. This is shown by the occurrence of grey leaf spot only at Mbimba and that weeding twice recorded relatively higher severity than other weeding regimes probably due to less shielding effect from spore interception in less denser canopies. Other authors also found that there was less disease per plant under high plant populations because of a 'shielding' effect from spore interception in denser canopies under high populations than in open canopies under lower plant populations; and found that under high inoculums level, there was increased disease with lower plant densities (CABI, 2012). Leaf lesions and discoloration (chlorosis) that occurred during late growth

stages of plants may have interfered the process of photosynthesis thereby reducing yield to a small extent at Mbimba.

The occurrence of maize streak with mean number of plants affected ranging from 0.00 – 0.98, 0.23 – 0.25 and 0.22 – 0.25 indicates that the natural occurrence of the disease was low in the 2010/2011 cropping season. Significant differences amongst the locations for maize streak virus suggest that location influenced the occurrence of the disease. Similar mean number of affected plants for all genotypes except UH 6303 for the disease suggests that the level of tolerance for these genotypes was similar. In addition slightly higher coefficient of variation for the studied diseases suggests that the spread of the diseases was not uniform across replications and locations.

CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

From the study, the following conclusions could be made:

(i) The four locations under which the study was conducted differed in rainfall amount, soil characteristics, altitudes and hence temperatures.

(ii) Environments (locations) and weeding regimes played an immense role in influencing the performance of maize genotypes evaluated across locations

(iii) Location x weeding regimes was important for biological yield, ear diameter, number of kernel rows per cob, grain and ear weights, number of leaves per plant, number of leaves above the ear, days to 50% tasselling, days to 50% pollen shed, number of cobs per plant, days to maturity, hundred kernel weight, plant height, ear height, husk cover score and yield.

(iv) Genotype x weeding regimes interaction was important for number of leaves per plant.

(v) Genotype x environment interaction was important for number of kernel rows per cob and days to maturity.

(vi) High heritability associated with high genetic advance that was recorded for days to first tasselling, days to 50% tasselling, days to 50% pollen shed, days to first silking and ear height indicates that selection of these traits can be done in early

generations. However the low heritability shown by number of leaves below and above the ear, biological yield, days to 50% silking and number of cobs per plant suggests that these traits can be selected in late stages of crop improvement.

(vii) Path coefficient analysis singled out number of leaves per plant, days to 50% silking, days to maturity, plant height and days to 50% pollen shed as most important traits to consider during selection for grain yield improvement in the studied genotypes.

(viii) Optimum performance, desired b-values and variance of deviation from regression revealed that EH-2 (FH 5160) was stable for plant height, ear height and cob length, number of kernel rows per cob, number of leaves above the ear and harvest index.

6.2 Recommendations

Based on the study conducted in the four locations, with regard to variations due to weeding regimes, locations, genotypes, location x weeding regimes and location x genotypes on yield and yield components of maize hybrid genotypes studied, the following are recommendations:

(i) Number of leaves per plant, days to 50% silking, days to maturity, plant height and days to 50% pollen shed should be given priority among other traits for a breeder to improve yield of the studied genotypes.

(ii) Genotype EH-2 (FH 5160) should be given priority in the breeding programme for plant height, ear height and cob length, number of kernel rows per cob, number of leaves above the ear and harvest index.

(iii) For grain yield improvement of the studied genotypes, intercrossing should be done between EH-2 (FH 5160) and UHS 5350 (EH-3) to obtain segregants combining optimum performance and b-values approaching or equal to 1. Then these progenies have to be inter-crossed with UH 6303 or EH-4 to incorporate the attribute of low value of variance of deviation from regression to meet the required stability parameters for tested genotypes on grain yield.

(iv) For growing genotypes with shortest days to maturity, high number of cobs per plant, number of leaves above the ear and biological yield, shortest days to 50% tasselling and 50% pollen shed one has to grow the genotypes at Seatondale and weed twice.

(v) Further study is needed to study the performance of the hybrids in more diverse environments and seasons to confirm their stability and proper records on disease reaction before they are released for farmers' use.

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APPENDICES

Appendix 1: Soil Texture

S/N	Site	Clay%	Silt%	Sand%	Texture
1.	Mbimba	36.60	43.00	20.40	Silty clay loam
2.	Uyole	19.60	56.80	23.60	Silt loam
3.	Seatondale	15.60	15.80	68.60	Sandy loam
4.	Inyala	28.40	33.00	48.60	Loam

Appendix 2: Soil pH

S/N	Site	pH	Interpretation	Remark
1.	Mbimba	5.17	Strongly acidic	Out of range for maize production
2.	Uyole	6.10	Slightly acidic	Within acceptable range for maize production
3.	Seatondale	6.20	Slightly acidic	Within acceptable range for maize production
4.	Inyala	5.54	Slightly acidic	Within acceptable range for maize production

Cut off point for maize production are pH = 5.5 – 7.5 ()

Appendix 3: CEC and K Concentrations (Cmol/kg)

S/N	Site	Concentration (Cmol/kg)			
		CEC	Interpretation	K	Interpretation
1.	Mbimba	16.65	Medium	0.58	Medium
2.	Uyole	17.68	Medium	0.59	Medium
3.	Seatondale	14.34	Medium	0.61	High
4.	Inyala	15.39	Medium	0.71	High

Appendix 4: Soil Ca and Mg Concentrations (Cmol/kg)

S/N	Site	Nutrient concentrations					
		Ca^{2+}	Interpretation	Mg^{2+}	Interpretation	Ca: Mg Ratio	Interpretation
1.	Mbimba	0.54	Low	0.81	Medium	0.67	Low
2.	Uyole	0.72	Low	0.72	Medium	1.00	Low
3.	Seatondale	0.86	Low	0.72	Medium	1.19	Low
4.	Inyala	0.77	Low	0.81	Medium	0.95	Low

Appendix 5: Soil Total Nitrogen (TN) and Organic Carbon (OC) (%)

S/N	Site	Concentrations (%)			
		TN	**Interpretation**	**OC**	**Interpretation**
1.	Mbimba	0.24	Medium	1.73	Medium
2.	Uyole	0.14	Low	0.17	Very low
3.	Seatondale	0.14	Low	0.73	Low
4.	Inyala	0.12	Low	0.84	Low

Appendix 6: Soil available P (mg/kg)

S/N	Site	P Conc. (mg/kg)	Interpretation
1.	Mbimba	14.63	Medium
2.	Uyole	25.03	High
3.	Seatondale	14.61	Medium
4.	Inyala	15.32	Medium

Appendix 7: Weather conditions during the 2010/2011 rain season at Uyole

Month	Max Temperature (^{0}C)	Min Temperature (^{0}C)	Rainfall (mm)
December	24.6	14.1	114
January	23.8	13.8	237.8
February	23.8	13.8	168.5
March	23.8	13.4	154.7
April	23.1	12.6	182.7
May	23.1	11.1	2.4
June	-	-	-

Source: Uyole Agro-meteorological Station

Appendix 8: Weather conditions during the 2010/2011 rain season at Mbimba

Month	Max Temperature (^{0}C)	Min Temperature (^{0}C)	Rainfall (mm)
December	25.6	14.9	228.7
January	25.4	15.04	131.2
February	24.7	14.9	193.4
March	25.9	14.81	297.0
April	25.31	14.10	269.7
May	25.95	12.70	54.0
June	25.93	10.46	-

Source: Mbimba Agro-meteorological Station

Appendix 9: Weather conditions during the 2010/2011 rain season at Seatondale

Month	Max Temperature (^{0}C)	Min Temperature (^{0}C)	Rainfall (mm)
December	29.4	15.0	115.1
January	29.0	14.8	99.5
February	28.5	15.2	74.9
March	28.2	15.0	126.9
April	28.0	15.3	102.3
May	27.6	14.8	1.5
June	26.9	14.0	-

Source: Iringa Agro-meteorological Station

Appendix 10: Weather conditions during the 2010/2011 rain season at Inyala

Month	Max Temperature (^{0}C)	Min Temperature (^{0}C)	Rainfall (mm)
December	28.2	14.7	162.9
January	26.8	14.3	273
February	26.8	15	105.8
March	26.5	14.1	163
April	27.6	13.8	255
May	27.6	12.3	-
June	27.2	11.5	-

Source: Inyala Agro-meteorological Station

Appendix 11: Soil S

S/N	Site	S	Interpretation
1.	Mbimba	0.10	Low
2.	Uyole	0.12	Low
3.	Seatondale	0.11	Low
4.	Inyala	0.08	Low

Appendix 12: Path coefficient analysis for yield and yield components of maize genotypes

1. Effect of plant height	$r_{18=}$		**0.398*** **
Direct effect		P_{18}	0.433
Indirect effect via number of kernel rows per cob		$r_{12}P_{28}$	-0.142
Indirect effect via number of leaves per plant		$r_{13}P_{38}$	0.324
Indirect effect via number of leaves below the ear		$r_{14}P_{48}$	-0.119
Indirect effect via days to 50% pollen shed		$r_{15}P_{58}$	0.094
Indirect effect via days to 50% silking		$r_{16}P_{68}$	0.076
Indirect effect via days to maturity		$r_{17}P_{78}$	-0.268
Total r			**0.398**
2. Effect of number of kernel rows per cob		r_{28}	**0.888*** **
Direct effect		P_{28}	0.267
Indirect effect via plant height		$r_{12}P_{18}$	0.230
Indirect effect via number of leaves per plant		$r_{23}P_{38}$	0.095
Indirect effect via number of leaves below the ear		$r_{24}P_{48}$	-0.045
Indirect effect via days to 50% pollen shed		$r_{25}P_{58}$	-0.011
Indirect effect via days to 50% silking		$r_{36}P_{68}$	0.389
Indirect effect via days to maturity		$r_{27}P_{78}$	-0.037
Total r			**0.888**
3. Effect of umber of leaves per plant		r_{38}	**-0.041**
Direct effect		P_{38}	-0.632
Indirect effect via plant height		$r_{13}P_{18}$	-0.222
Indirect effect via number of kernel rows per cob		$r_{23}P_{28}$	-0.040
Indirect effect via number of leaves below the ear		$r_{34}P_{48}$	0.241
Indirect effect via days to 50% pollen shed		$r_{35}P_{58}$	-0.256
Indirect effect via days to 50% silking		$r_{36}P_{68}$	0.389
Indirect effect via days to maturity		$r_{37}P_{78}$	0.479
Total r			**-0.041**
4. Effect of number of leaves below the ear		r_{48}	**0.114**
Direct effect		P_{48}	0.297
Indirect effect via plant height		$r_{14}P_{18}$	-0.173
Indirect effect via number of kernel rows per cob		$r_{24}P_{28}$	-0.241
Indirect effect via number of leaves per plant		$r_{34}P_{38}$	-0.514
Indirect effect via days to 50% pollen shed		$r_{45}P_{58}$	-0.261
Indirect effect via days to 50% silking		$r_{46}P_{68}$	0.365
Indirect effect via days to maturity		$r_{47}P_{78}$	0.413
Total r			**0.114**
5. Effect of days to 50% pollen shed		r_{58}	**0.265*** **
Direct effect		P_{58}	0.321
Indirect effect via plant height		$r_{15}P_{18}$	0.126
Indirect effect via number of kernel rows per cob		$r_{25}P_{28}$	-0.009
Indirect effect via number of leaves per plant		$r_{35}P_{38}$	0.503
Indirect effect via number of leaves below the ear		$r_{45}P_{48}$	0.241
Indirect effect via days to 50% silking		$r_{56}P_{68}$	-0.470
Indirect effect via days to maturity		$r_{67}P_{78}$	-0.447
Total r			**0.265**

6. Effect of days to 50% silking	r_{68}	**-0.446*** **
Direct effect	P_{68}	-0.545
Indirect effect via plant height	$r_{16}P_{18}$	0.061
Indirect effect via number of kernel rows per cob	$r_{26}P_{28}$	-0.044
Indirect effect via number of leaves per plant	$r_{36}P_{38}$	0.451
Indirect effect via number of leaves below the ear	$r_{46}P_{48}$	-0.199
Indirect effect via days to 50% pollen shed	$r_{56}P_{58}$	0.277
Indirect effect via days to maturity	$r_{67}P_{78}$	-0.447
Total r		**-0.446**
7. Effect of days to maturity	r_{78}	**-0.146**
Direct effect	P_{78}	-0.543
Indirect effect via plant height	$r_{17}P_{18}$	0.214
Indirect effect via number of kernel rows per cob	$r_{27}P_{28}$	0.018
Indirect effect via number of leaves per plant	$r_{37}P_{38}$	0.558
Indirect effect via number of leaves below the ear	$r_{47}P_{48}$	-0.226
Indirect effect via days to 50% pollen shed	$r_{57}P_{58}$	0.282
Indirect effect via days to 50% silking	$r_{67}P_{68}$	-0.449
Total r		**-0.146**

Px_8 = 0.565