GENOTYPE x ENVIRONMENT INTERACTION OF IMIADAZOLINONE RESISTANT MAIZE GENOTYPES FOR YIELD UNDER STRIGA INFESTATION

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BY

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ACRONYMS AND ABBREVIATIONS

AATF	-	African Agricultural Technology Foundation
AMMI	-	Additive Main Effects and Multiplicative Interaction
ANOVA	-	Analysis of variance
ASV	-	AMMI stability value
CIMMYT	-	International Maize and Wheat Improvement Center
CSA	-	Central Statistics Authority
CV	-	Coefficient of variation
DAP	-	Diammonium phosphate
DF	-	Degrees of freedom
EIAR	-	Ethiopian Institute of Agricultural Research
EIPCA	-	Environmental IPCA score
FAO	-	Food and Agricultural Organization
GEI	-	Genotype by environment interaction
GGE	-	Genotype + GEI
GIPCA	-	Genotypic IPCA score
ICRISAT	-	International Crop Research Institute for Semi-arid Tropics
IITA	-	International Institute of Tropical Agriculture
IPCA	-	Interaction principal component axis
IR	-	Imidazolinone (imazapyr) resistant
m.a.s.l.	-	Meters above sea level
mm	-	Millimeter
MS	-	Mean square
OPV	-	Open pollinated variety
PCA	-	Principal component analysis
Q/ha	-	Quintal per hectare
SAS	-	Statistical analysis system
SREG	-	Site regression
SS	-	Sum of squares
SVD	-	Singular value decomposition

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GENOTYPE x ENVIRONMENT INTERACTION OF IMIDAZOLINONE RESISTANT MAIZE GENOTYPES FOR YIELD UNDER STRIGA INFESTATION

ABSTRACT

Twenty-five imidazolinone resistant (IR) maize genotypes were laid down in 5x5 simple lattice design with 2 replications at six striga infested and five striga free environments during 2006/07 cropping season. The objectives of the study were to evaluate IR maize genotypes for grain yield and adaptability under striga infestation and free field conditions, to determine the magnitude of genotype-by-environment interaction (GEI) of IR maize genotypes for grain yield, to determine stability of yield performance among the IR maize genotypes and identify the stable genotype(s) and those with adaptation to specific environments and to study the correlation among various stability parameters. For trials where successful striga infestation was achieved, yield was reduced on average from 8.62 to 26.87 Q/ha. The average percent reduction in yield for all the IR maize genotypes was 40.40% whereas for the standard check, WH-403 it was 65.00%. The highest percent reduction due to striga infestation was observed on WH-403 at Alupe (79.00%) and Kibos (75.54%). Under striga free condition, WH-403 gave the highest mean yield of 42.28 Q/ha but with only 3.37% yield advantage over the highest yielding IR genotype, INTA/CML390/373 while under striga infested field the highest yielding IR genotype, CML445/390/373 had a yield advantage of 86.50% over WH-403 showing the superiority of IR maize genotypes under striga infestation. Combined ANOVA revealed highly significant effects of the environments, genotypes and GEI. The presence of significant GEI showed the inconsistency in performance of maize genotypes across the 11 environments. Six statistical methods were conducted to determine yield stability. Results of additive main effects and multiplicative interaction (AMMI) analysis showed that out of 11 interaction principal component axis (IPCAs) only the first two IPCAs were found to be highly significant and cumulatively contributed 58% of the total GEI while linear regression explained only 6% of the total GEI. Spearman's coefficient of rank correlation between mean yield and regression coefficient (β_i), stability variance

(σ^2_i), ecovalence (W_i) and deviation from regression ($\sigma^2_{d_i}$) was positive and significant, but there was non-significant correlation between mean yield and coefficient of variation (CV) and AMMI stability value (ASV). Since ASV explains interaction effects and provides agronomically meaningful insights into the data structure, it is better if used as stability measure for reliable selections of stable genotypes. Based on most of the stability parameters estimated, the three-way cross maize hybrid, CML78/390/202 and the late maturing maize OPV, ECA-144, were found to be the most stable.

Key Words: AMMI, ASV, GEI, Maize, IR, Stability, Striga

1. INTRODUCTION

Maize (*Zea mays* L.) originated in Central America and was introduced to West Africa in the early 1500s by Portuguese traders and then to Ethiopia during the 1600s and 1700s (Dowswell *et al*., 1996). Although of recent introduction to Ethiopia, today, maize is one of the most important food crops all over the country.

In terms of area, it is the second most important commodity following tef. According to CSA 2001/02 data, the average area planted for maize during 1997/98-2001/02 was about 1,497,300 hectares. This accounted for about 21.7% of the total area planted under cereal crops and 18.0% of total area under cereals, pulses and oil crops. It also ranks first in total production and productivity (yield per hectare) (CSA, 2001/02). The relatively high productivity of maize, favorable growing conditions and the technological advances over the last decade have contributed to its increased area of production in the country. Due to this, it has been selected as one of the national commodity crops to achieve food self-sufficiency as well as to feed the alarmingly increasing population of the country (Demissew *et al.*, 2002).

Though maize has high yield potential, the local varieties that Ethiopian farmers are using are low yielders, and are subjected to many biotic and abiotic stresses. The major maize production constraints include stresses, such as drought, nutrient deficiency, weeds, diseases and insect pests (Ransom *et al*., 1993). Among the biotic stresses, annual, perennial and noxious parasitic weed (*Striga* spp) are the most important limiting factors in maize production, particularly for small-scale farmers who cannot afford to use various control options (Sauerborn, 1991a). These weeds compete for moisture, light, nutrients and space.

The witchweeds *Striga hermonthica* (Del.) Benth and *Striga asiatica* (L.) Kunze decimate maize (*Zea mays* L.), millets (*Pennisetum spp.*), sorghum (*Sorghum bicolor* (L.) Moench) and upland rice (*Oryza sativa*) throughout sub-Saharan Africa (Kanampiu *et al*., 2003). From the high plateau of East Africa, where peasant farmers struggle to survive on

tiny fields of maize, to the arid savannas of northern Nigeria where they rely on sorghum, African farmers are fighting a losing battle against the spreading scourge of striga. Based on Food and Agricultural Organization (FAO) studies, over 100 million Africans lose half their crop production to these flowering, root-attaching parasites (Kanampiu *et al*., 2003).

The impact of striga on the host is very significant and highly damaging. Plant stunting, bleaching and wilting symptoms are observed on striga infested hosts, even before the striga shoots emerge. Striga is a metabolic sink for the host, diverting water, nutrients and carbohydrates from the host. In addition to draining photosynthates, minerals and water (Press and Graves, 1995), striga does most of its damage to its host, partly through phyto-toxins, before the weed emerges from the soil (Gurney *et al*., 1995). Above ground, the crop withers and grain production is reduced. Striga infestation reduces plant height, number of ears harvested, ear length, ear diameter and 1000-kernel weight and increases stalk lodging (Kim, 1991).

According to Rezene (1991) there are about 100 weed species in 66 genera and 24 plant families known to be problematic for maize in Ethiopia. Striga is considered to be one of the most serious pests that affect subsistence production of mainly maize, sorghum, and millet in vast areas of Ethiopia. Striga has recently been reported to extend to areas where it has not previously been present (Ahmed *et al*., 1987; Fasil and Parker, 1994). Hence, striga represents one of the largest single biological barriers to increased maize production in infested areas of Ethiopia and it has become an increasing challenge to breeders and agronomists.

In the last 100 years, *S. hermonthica* has established itself in Ethiopia and is the most limiting factor for maize production in some maize growing regions (Rezene *et al*., 1993). This could be due to the relatively recent intensification of agriculture in the country (Parker and Riches, 1993). It occurs in northern, western, central and eastern parts of the country (Yohannes *et al*., 1999).

Striga control in low external input farming systems depends on several components such as hand weeding, crop rotation, intercropping, soil fertility management, *etc*., which need to be combined in an integrated approach not only to reduce striga densities but also to improve soil fertility and eventually maize yields. One important approach in striga control is the maize crop and its tolerance/resistance to striga. Crop cultivars with resistance/tolerance to striga have long been proposed as a means of reducing losses due to striga and would be compatible with low-cost input requirements of small-scale farmers.

Varieties of sorghum and rice that are resistant to striga have been reported (Williams, 1959). Maize breeding at the International Institute of Tropical Agriculture (IITA) has reportedly produced varieties with some level of resistance to striga (Kim, 1994). However, these varieties are adapted to West African conditions and so far no resistant maize cultivar is commercially available in Eastern Africa (Ransom *et al.*, 1995). Nevertheless, considerable variability in resistance or tolerance has been reported in maize for *S. hermonthica* and *S. asiatica* (Ransom *et al*., 1990).

Use of imidazolinone (imazapyr) resistant (IR) maize genotypes is one of the few control options, which seem to be technically feasible and cost effective in small-scale holdings since it allows a very efficient and season-long control of striga emergence (Kanampiu *et al.*, 2003). Maize genotypes that possess gene for imidazolinone resistance have been found (Tan *et al.*, 2005). This novel approach is based upon inherited resistance of maize to a systemic herbicide (imazapyr), a mechanism widely referred to as imazapyr resistance (IR). Those maize genotypes, which possess the gene for imidazolinone resistance successfully, germinate after being coated with the herbicide. When IR maize seed is coated with the herbicide, germinated striga seeds attempting to parasitise the resulting maize plant are destroyed. Only 30 grams of imazapyr coated onto 25 kg of seed is sufficient to protect one hectare of maize from striga (Kanampiu *et al.*, 2003).

The response to resistance is variable under different growing conditions due to different intensity of the weed (Oswald and Ransom, 2004). Therefore, it is necessary to evaluate the genotype's differential response in multi-environment trials and assessing their genotype-by-environment interaction (GEI).

Genotypes' interaction with environmental factors (location, year of planting, soil type, level of technology used, *etc*.) is an important consideration for plant breeders. The effects that genotypes and environments exert on GEI are statistically non-additive, indicating that differences in yields among genotypes will depend on the environment (Yue *et al*., 1997). Consequently, selection procedures based on the mean yield of genotypes in a given environment are less efficient. Eberhart and Russel (1966) recommended growing of varieties in adequate number of environments, covering a full range of possible environmental conditions, so that useful information is available regarding stability.

Gelana *et al*. (2001) and Mosisa *et al*. (2001) studied GEI and stability of different maize cultivars at different locations in Ethiopia and found that genotypes significantly interact with the environments. But no published results and information concerning GEI for IR maize genotypes under striga infestation and striga free field conditions has been established to date in Ethiopia. Hence the present study was carried out with the objective to evaluate the performance of IR maize genotypes under striga infestation and to study their GEI and stability across environments.

2. LITERATURE REVIEW

2.1 The Striga Species

Striga is one of the very few flowering plants that are parasitic on other plants, dodder and mistletoe being other examples. Striga has been given the common name of "witchweed" because of the various debilitating effects inflicted upon its host in addition to attaching to the roots and robbing the host's water and nutrients (Robert, 2000). *Striga* spp. belong to a genus of obligate, root-parasitic flowering plants in the family Scrophulariaceae which comprises 41 species, most of which are found in Africa with greatest diversity in West and Central Africa (Raynal-Roques, 1994).

Although more than 30 species of striga have been described, Ramaiah *et al*. (1983) reported that only five are presently of economic importance in Africa. These are, in approximate order of economic importance in Africa, *S. hermonthica* (Del.) Benth., *S. asiatica* (L.) Kuntze, *S. gesnerioides* (Willd.) Vatke, *S. aspera* (Willd.) Benth., and *S. forbesii* Benth. All except *S. gesnerioides* are parasites of Africa's cereal crops sorghum, millet, maize, and rice. *S. gesnerioides* is a parasite on cowpea and other wild legumes. *S. hermonthica* (Del.) Benth. and *S. asiatica* (L.) Kuntze (Figure 1) are the two most widespread and economically important species, which parasitize food crops, such as maize, sorghum, millet and rice.

According to some authors, in Ethiopia, the most widespread species is *S. hermonthica* occurring in northern, western, central and eastern parts of the country (Fasil and Parker, 1994; Rezene *et al*., 1993; Parker and Riches, 1993; Yohannes *et al*., 1999). Wondimu and Rezene (1988) reported *S. hermonthica* as a production problem in the sorghum growing areas of Welo, Tigray, Gondar, Gojam (Abay Gorge and Bir Valley), Hararge, Welega and Central and Northern lowlands of Shewa. The second species, *S. asiatica*, was reported as a production problem in the sorghum and maize growing areas of Hararghe region in Habro and Babile weredas and Gumaide (Gamo Gofa) (Wondimu and Rezene, 1988). The third species is *S. aspera* reported on maize and wild grasses on two

state farms in upper Birr and Fincha (Ahmed *et al*., 1987). *S. latericea* is reported as a problem in sugarcane production in Metehara area (Wondimu and Rezene, 1988).

Figure 1. *Striga asiatica*(L.) Kuntze (left) and *Striga hermonthica* (Del.) Benth (right)

2.2 Crop Losses in Africa due to Striga Species

Different authors presented different levels of yield loss estimates in their studies. The extent of yield loss is related to the incidence and severity of attack, the host's susceptibility to striga, environmental factors (the soil nutritional status and agro-climatic conditions), the plant species, the genotype grown and the management level at which crops are produced. Stressed crops are more prone to serious damage.

Based on a report by Parkinson (1985), yield losses of 30-50% are common under typical field infestation; losses over the whole Africa may range from 5-15%. Striga reduces the yield of maize by up to 100% when infection occurs at an early stage (Parkinson, 1985). Losses range from 15% under more favorable conditions up to 100% when several stress factors affect the crop simultaneously (Parker, 1991). Estimated 21 million hectares of maize and sorghum are striga infested in Africa with yield loss of 4.1 million tons per year (Sauerborn, 1991b). Striga infestation can become severe to the extent that farmers abandon their fields.

Striga is a serious problem in all the countries of West and Central Africa. Few attempts have been made to estimate the yield losses caused by striga in farmers' fields. Sauerborn (1991b) observed the presence of striga on 40-75% of the visited cereal fields that were scattered over the whole of northern Ghana. In infested fields, 34% of the stands were parasitized. It was further estimated that the yield losses in maize, pearl millet and sorghum in these infested areas were 16%, 31% and 29% of the potential yield per hectare, respectively. Based on data available from six West African countries, the loss in total grain production was estimated to be 12% (Sauerborn, 1991b).

The growing severity of striga infestation in Africa results from the changes in farming systems through intensification of cereal production (mono-cropping), in an attempt to produce sufficient food for the burgeoning population (Doggett, 1984). In West Africa alone, it is estimated that about 40 million hectares in cereal production are severely infested with *Striga* spp., while nearly 70 million hectares have moderate levels of infestation (Lagoke *et al.*, 1991). Today about 20 million hectares of maize are affected in sub-Saharan Africa where yield losses range between 30-100%, obliging the rural population to abandoned their villages and to clear forests for new settlement and farming. As a result, annual yield losses due to all *Striga* spp. in the savannah region alone are estimated to impact the lives of over 300 million Africans (M'Boob, 1989).

The prevalence of striga soil infestation is steadily increasing as population pressures result in more continuous cultivation of cereal crops. In Ethiopia and elsewhere, land pressures cause farmers needing to feed their families to opt for continuous cropping of the higher yielding cereal crops without rotation or moving to other land. In the northern regions of Ethiopia, striga is favored by low soil fertility and soil moisture stress conditions (less shading by the poor growth of the host crop) (Robert, 2000).

2.3 Control Options

2.3.1 Integrated control methods

Striga is particularly difficult to control because of its prolonged germination period and reduction of yield potential before the parasite emerges from the soil (Berner, *et al*., 1997). Striga control methods have been researched in Africa for over 50 years and have focused on agronomic practices, host plant resistance and herbicide applications. Up to now, there is no single control option which can solve the problem of striga infestation on maize fields. Therefore, an integrated approach using several methods must be employed (Rowland, 1993). Among the integrated options that are used to control striga, use of resistant/tolerant maize varieties, biological control measures, crop rotation, timely sowing, intercropping with legumes, fallowing, optimizing plant population, use of trap and catch crops, hand pulling at flowering before seed setting, use of chemicals and natural fertilizers are some of the options available.

Though many of the striga control methods are effective, none of these are widely adopted by farmers for several reasons: (i) their benefits are seen only in the medium to long-term since effects build slowly over several seasons, (ii) they require an understanding of striga life-cycle which farmers usually lack, (iii) they require rotating land out of cereal crops like maize and sorghum while population pressure requires intensification of land use for food production, (iv) while host plant resistance exists, the gains are inadequate and ineffective under high levels of infestation, and (v) conventional 'over-the-top' herbicide applications are prohibitive in cost and ineffective since damage is done before striga emerges from the soil.

The research on control of striga in Eastern and Central Africa started in the 1930s (Parker, 1991). A number of control measures have been identified and each of them has one or more limitations that have led to low farmer adoption. There has been a call made by striga research scientists on the need for integrated striga management strategies encompassing two or more control options suitable for various agro-ecosystems.

In order to be effective, technologies must control striga before maize yields are affected and deplete the striga seed bank to control further yield losses. Therefore, methods that act before or during striga attachment will be the most effective in preventing the damaging effects of the weed. In the African small farmer's context, the method must also be inexpensive and fit well into the present cropping systems of the farmers including intercropping or rotations with non-host crops that stimulate striga seed germination.

2.3.2 The new approach: use of imidazolinone -resistant (IR) maize

The new herbicide seed coating technology, Imidazolinone-Resistant (IR) maize or the Clearfield® technology was launched in Kisumu, Kenya, on 5th July 2005 after eight years of research to counter the destructive striga weed in Kenyan maize fields. When IR-maize seed is coated with a systemic herbicide (imazapyr), germinating striga seeds attempting to parasitise the resulting maize plant are destroyed, and also the technology reduces the striga seed bank by destroying some of the remaining seeds (AATF, 2006).

The novel approach is based on inherited resistance of maize to a systemic herbicide (imazapyr) that was derived from a naturally occurring gene in maize originally identified by researchers at BASF, a multinational producer and supplier of chemicals and made available to International Maize and Wheat Improvement Center (CIMMYT) (Kanampiu *et al.*, 2003). The maize is not genetically modified. Plant breeders at CIMMYT in collaboration with Weizmann Institute of Science (Israel) and the Kenya Agricultural Research Institute, with support from the Rockefeller Foundation and BASF later incorporated the IR-gene into African maize varieties following conventional breeding methods and have developed the IR-maize (Clearfield®) seed coating technology, which involves using herbicide-resistant maize with low dosages of the imazapyr herbicide, giving almost season-long striga control (Kanampiu *et al.*, 2003). Three seed companies, Kenya Seed, Lagrotech and Western Seed are producing imazapyr coated IR- maize seeds for field testing and have extensive demonstration of the technology throughout western in Kenya (Kanampiu *et al.*, 2003).

According to a report by Kanampiu *et al.* (2003) and AATF (2006), the technology combines low-doses (as little as 30 grams per hectare) of a systemic acetolactate synthase (ALS) inhibiting herbicide such as imazapyr or pyrithiobac as a seed coating with imidazolinone-resistant (IR) maize seed. The treatment leaves a field virtually clear of emerging striga blooms season-long. Small quantities of imazapyr delivered in this manner act at the time of striga attachment to the maize root and so prevent the exertion of the phytotoxic effect of striga on the maize plant which usually occurs even before emergence of the striga from the soil. Additionally, imazapyr that is not absorbed by the maize seedling diffuses into the surrounding soil and kills ungerminated striga seeds. Higher rates may be necessary to achieve full season control using late maturing maize varieties or where the season is longer.

Kanampiu *et al.* (2003) underline on the added benefits of this technology for poor farmers because only minute amounts of the herbicide applied to the IR maize seeds brings the technology within the financial reach of poor farmers with little resources to invest in alternative control options. Low-dose herbicide seed dressing on IR-maize also controls striga without impacting sensitive intercrops when they are planted 12 centimeter or more from maize hills. This allows small-scale farmers to continue intercropping, at most with slight modification, while using maize seed treated to control striga. Since the maize seed is treated, there is no need or added cost for spraying equipment, no possibility of off-target application and little chance of damage to sensitive intercrops.

Furthermore, this technology delivers herbicide at rates of about 5% of those recommended for over-the-top herbicide applications, making it an affordable, low-cost solution for striga control. With effective striga control, the potential for returns on inputs such as fertilizers and other pest control products is greatly improved (Kanampiu *et al.*, 2003). Recent on-farm trials in Kenya and Tanzania indicate that seed dressing with Imazapyr and Pyrithiobac offers good striga control and increase maize yields (Kanampiu *et al*., 2004). As this technology is new, the response of IR maize genotypes to different agro-climatic conditions and hence their GEI has not been studied in detail.

2.4 Genotype x Environment Interaction (GEI) and Stability Analyses

When a series of cultivars are evaluated over a wide range of locations, the ranking of the cultivars will be different for each location. The changes in ranks (lack of correlation) and the differences in relative yields over a range of locations (heterogeneity of variances) can be defined statistically as the GEI. Because of the variation in environment from location to location and from year to year, the GEI must be considered in cultivar development.

Allard and Bradshaw (1964) classify environmental variation as either predictable or unpredictable. The former, which is normally subject to human control, includes factors like planting date, plant density and spatial arrangement, fertilizer rates and crop management practices. The unpredictable environmental factors include amounts and distribution of rainfall, temperature variations, *etc.*

Quantitative genetic theory states that an individual's phenotype is the product of the genetics of the individual, the environment that the individual is exposed to, and the interaction that occurs between the genotype of the individual and the environment (GEI). Large GEI effects tend to be viewed as problematic in breeding because the lack of a predictable response hinders progress from selection (Dudley and Moll, 1969). This idealized predictable response across multiple environments is generally referred to as stability. When stability concepts are applied to breeding; selection for increased grain yield, the idealized genotype is one that is capable of utilizing the resources available in higher yielding environments and has a mean performance that is above average in all environments. Yield stability is influenced in part by the genetic structure of the variety. More heterozygous varieties and more heterogeneous varieties are less affected by environmental differences (Allard and Bradshaw, 1964).

2.4.1 Significance and implication of GEI and stability studies for plant breeding

The development of cultivars or varieties, which can be adapted to a wide range of diversified environments, is the ultimate goal of plant breeders in a crop improvement program. The adaptability of a variety over diverse environments is usually tested by the degree of its interaction with different environments under which it is planted. A variety or genotype is considered to be more adaptive or stable if it has a high mean yield but a low degree of fluctuation in yielding ability when grown over diverse environments.

Stability and high yield will require evaluating maize genotypes in both stress and non-stress environments. Selection of genotypes in multi-location testing will minimize the effect of GEI, but it has been shown that genotypes differ significantly in the extent of their interactions (Russell and Eberhart, 1968). When genotypes are compared over a series of locations their relative rankings differ significantly, which makes it difficult to demonstrate the significant superiority of any one genotype over a broad range of environmental conditions. Only extensive testing can identify genotypes with the least interaction with the environment (Eberhart and Russell, 1966).

GEI reveals the inconsistent performance of a genotype in different environments and at the same time the information obtained from GEI offers opportunities, especially in the selection and adoption of genotypes showing stable performance across environments and those with specific adaptation (Annicchiarico, 2002). In countries such as Ethiopia, environmental variations are very high and unpredictable (Tesfaye *et al.,* 1998; Dugan and Labuschahne, 2002) and lead to significant GEI even within a small geographic area, making cultivar development and recommendation more difficult. Under such circumstances, evaluation of genotypic performance at several locations provides useful information to determine their adaptation and stability (Crossa, 1990). As a result it is not only average performance that is important in genotype evaluation programs but also the magnitude of the interactions (Fehr, 1992; Gauch and Zobel, 1997).

2.4.2 Strategies for reducing GEI

There are two possible strategies for developing cultivars with low GEI. The first is subdivision or stratification of a heterogeneous area into smaller, more homogeneous sub-regions, with breeding programs aimed at developing cultivars for specific sub-regions. However, even with this refinement, the level of interaction can remain high because it does not reduce the cultivar by year interaction within location. This approach is also costly. The second strategy for reducing GEI involves selecting cultivars with a better stability across a wide range of environments (Eberhart and Russell, 1966).

2.5 Statistical Methods of Analyzing GEI

A number of techniques for analyzing information in a GEI study are available (Hussein *et al*., 2000). A combined analysis of variance (ANOVA) procedure is the most common method used to identify the existence of GEI from replicated multi-location trials. If the GEI variance is found to be significant, one or more of the various methods for measuring the stability of genotypes can be used to identify the stable genotype(s) (Alberts, 2004).

Stability parameters for studying GEI have been reviewed extensively by Lin *et al.* (1986). Similarly, Liu and Sun (1993) evaluated 17 statistics for describing cultivar stability and favored the Eberhart and Russell (1966) regression model. These methods can be divided into two major groups, *i.e.* univariate and multivariate stability statistics. Joint linear regression is the most popular among the univariate methods because of its simplicity of calculation and application, where as 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).

Some of the analytical methods currently used in GEI and stability studies are explained as follows:

2.5.1 Francis and Kannenberg's (1978) coefficient of variation (CV)

In the static or biological concept of stability phenotypic stability is simply the variance of a genotype across environments (Hill *et al.,* 1998). This concept of stability is identical with type 1 stability as defined by Lin and Binns (1991) (Becker and Léon, 1988), who suggest that it is particularly useful if the environmental range is small. A modified version of the static concept, based upon the coefficient of variation, has been used by Francis and Kannenberg (Hill *et al.,* 1998).

The mean CV analysis introduced by Francis (1977) was designed to aid in studies on the physiological basis of yield stability. He introduced a simple graphical approach to assess performance and stability concurrently. It measures the performance and CV for each genotype over all environments and the mean yield plotted against the CV. It was found to characterize genotypes in groups rather than individually (Francis and Kannenberg, 1978).

2.5.2 Eberhart and Russel's joint linear regression model (β_i and $\sigma^2{}_{d_i}$)

Pooled analysis of variance combined with joint regression analysis proposed by Yates and Cochran (1938) cited in Francis and Kannenberg (1978), modified by Finlay and Wilkinson (1963) and made popular by Eberhart and Russell (1966) has been, and still is, a popular technique for studying GEI effects and stability. The Eberhart and Russel (1966) stability regression model involves the use of joint linear regression where the yield of each genotype in different environments is regressed on the environmental mean yield.

With this model, the sum of squares (SS) due to environments and GEI are partitioned into environments (linear), GEI (linear), and deviations from the regression sum of

squares. The method consists of a conventional analysis of variance and a combined regression for stability analysis. Zobel *et al.* (1988) cited in Alberts (2004) stated that the genotype's performance across environments is generally expressed in terms of three principal parameters namely: the mean yield ($\hat{Y}$), the regression coefficient (b_i), and the mean square deviation ($\sigma^2_{d_i}$) from the regression.

The β_i has been described as a measure of environmental response or adaptation of a particular cultivar to different environments (Paroda and Hayes, 1971; Adugna and Labuschagne, 2002), and $\sigma^2_{d_i}$ is the most suitable measure of stability (Paroda and Hayes, 1971; Becker and Leon, 1988). Eberhart and Russel (1966) proposed a model to test the stability of varieties under various environments. They defined a stable variety as having unit regression slope (β_i =1.00) and minimum deviation from the regression ($\sigma^2_{d_i}$ =0), whereas those significantly deviating from unity are either adapted to high yielding environments if β_i >1 or low yielding environments if β_i <1. Therefore, a variety with a high mean yield over the environments, unit regression coefficient (β_i =1) and deviation from regression as small as possible ($\sigma^2_{d_i}$ =0), will be a better choice as a stable variety.

In a GEI study on maize the GEI plus environmental linear effects were found to be significant for grain yield. Highly significant mean squares due to environments (linear) indicated differences between environments. The variance due to GEI (linear) was significant indicated that the stability parameter " β_i " estimated by linear response to change in environment was not the same for all genotypes (Gelana *et al*., 2001; Mosisa *et al*., 2001).

2.5.3 Lin and Binns' cultivar superiority (performance) measure (P_i)

Lin and Binns' (1988) methodology is a good alternative for the assessment of cultivar performance in GEI. Their method does not have limitations inherent to the use of

regression. It characterizes the genotypes with a single parameter (P_i) by associating stability and productivity, and defines a superior cultivar as one with a performance near the maximum in various environments (Lin and Binns, 1988). This definition of superiority is similar to the breeder's objective, since a superior cultivar should be among the most productive in the greatest possible number of environments (Farias *et al*., 1997).

The values estimated from Lin and Binns' (1988) cultivar superiority (performance) measure are the squares of the differences between an entry mean and the maximum mean at a location, summed and divided by twice the number of locations. Checks need not be common at all locations. Genotypes with the smallest values tend to have larger yields and also be more stable.

2.5.4 Wricke's ecovalence concept (W_i)

Wricke (1962) defined the concept of ecovalence as the contribution of each genotype to the GEI sum of squares. For this reason, genotypes with a low W_i value have smaller deviations from the mean across environments and are thus more stable (Alberts, 2004).

According to Becker and Léon (1988) ecovalence measures the contribution of a genotype to the GEI; a genotype with zero ecovalence is regarded as stable. Genotypes with, an average, small residues are preferred because they show more predictable variability. As the ecovalence value increases, the genotype's contribution to the total GEI sum of squares also increases (Zobel *et al.,* 1988).

2.5.5 Shukla's stability variance (σ^2)

Shukla (1972) defined the stability variance of genotype *i* as its variance across environments after the main effects of environmental means have been removed. Since

the genotype main effect is constant, the stability variance is thus based on the residual ($GEI_j + e_{ij}$) matrix in a two-way classification. A genotype is called stable if its stability variance (σ^2_i) is equal to the environmental variance (σ^2_e) which means that $\sigma^2_i = 0$. A relatively large value of (σ^2_i) will thus indicate greater instability of genotype *i*. With σ^2_i, a genotype has stable trait expression when its contribution to GEI is small. The σ^2_i encompasses both GEI pattern and residual or noise. As the stability variance is the difference between two sums of squares, it can be negative, but negative estimates of variances are common in variance component problems. Negative estimates of σ^2_i may be taken as equal to zero as usual (Shukla, 1972). The stability variance is a linear combination of the ecovalence, and therefore both W_i and σ^2_i are equivalent for ranking purposes (Lin *et al*., 1986; Sneller *et al*., 1997; Alberts, 2004).

2.5.6 Additive main effect and multiplicative interaction (AMMI) model

While regression analysis attempts to define the GEI by two parameters, the objective of most univariate stability statistics is to summarize the GEI using only one parameter. Multivariate statistical methods have been introduced to explore multi-directionality and to extract more information out of the GEI component of phenotypic variability (Hussein, 2000).

The AMMI model was developed in 1952 (Yau, 1995). It has been called bi-plot analysis, or considered simply as principal component analysis (PCA), and was used before the introduction of the term AMMI analysis. Lately AMMI analysis has been applied to different crops by different scientists (Zobel *et al.,* 1988; Crossa *et al.,* 1990). The AMMI method integrates ANOVA and PCA into a unified approach (Gauch, 1988). According to Zobel *et al*. (1988) and Crossa *et al.* (1990), it can be used to analyze multi-location trials.

Zobel *et al*. (1988) pointed out that, considering the three traditional models, ANOVA fails to detect a significant interaction component, PCA fails to identify and separate the significant genotype and environment main effects, linear regression models account for only a small portion of the interaction sum of squares. AMMI is ordinarily the model of first choice when main effects and interaction effects are both important, which is the most common case with yield trials (Mandel, 1971).

The AMMI model combines the ANOVA for the genotype and environment main effects with PCA of the GEI (Gauch, 1992; Kaya *et al*., 2002), leading to a more exhaustive data analysis, accurate yield estimates, and reliable selections of genotypes. The interaction is explained in the form of a bi-plot display where, IPCA scores are plotted against each other and provides visual inspection and interpretation of both main and interaction effects for both the genotypes and environments (Annicchiarico, 2002). Integrating bi-plot display and genotypic stability statistics enable genotypes to be grouped based on similarity of performance across diverse environments.

2.5.7 Site regression (SREG) model

Linear-bilinear models are useful tools for analyzing multi-environment trials and studying and interpreting GEI (Crossa and Cornelius, 1997). Useful linear-bilinear models, among others, are the AMMI model and the SREG model.

Yan *et al.* (2000a) presented standard biplots of the SREG model and proposed connecting the scores of the furthest cultivars in the biplot such that they are the corners of an external polygon and, for each side of the polygon, drawing a line segment perpendicular to that side that passes through the origin. These line segments subdivided the polygon into sectors involving different subsets of sites and cultivars. The genotype that is at the corner of one sector is the best performer in the sites included in that sector. Sites located far away from the origin discriminate the cultivars more than those near the origin (Yan *et al.*, 2000a).

In the AMMI model, only the GEI term is absorbed, whereas in the SREG model, the main effects of genotypes plus the GEI, which are the two sources of variation of SREG model, are absorbed and can be presented in a GGE graph. The biplot from the SREG model shows that ideal genotypes should have large primary effects (high mean yield) and near zero secondary effects (more stable) and the ideal sites should have large primary effects (high power to discriminate genotypes) and small secondary effects (Yan *et al.,* 2000b; Crossa *et al.,* 2001).

3. OBJECTIVES

The present study was carried out with the following objectives:

3.1 General Objectives

- To evaluate IR maize genotypes for grain yield and adaptability under striga infestation and striga free field conditions
- To determine the magnitude of GEI of IR maize genotypes for grain yield under striga infestation and striga free field conditions

3.2 Specific Objectives

- To determine stability of yield performance among the IR maize genotypes and identify stable genotype(s) and those with adaptation to a specific environment
- To study the correlation among various stability parameters

4. MATERIALS AND METHODS

4.1 Description of the Study Areas

The field experiments were conducted at four locations in north western (Pawe and Manbuk) and central (Shewa Robit and Ataye) parts of Ethiopia and two locations in western Kenya (Alupe and Kibos). These locations are characterized by high level of striga infestation. Some characteristics of these locations are given below.

i) Pawe

Pawe Agricultural Research Center is found in Pawe special wereda, which is located in Metekel zone of the Benishangul Gumuz National Regional State, in the lowlands of the north western part of Ethiopia, 570 kilometers from the capital city, Addis Ababa. It is geographically located at 11^0 09' North latitude and 36^0 03' East longitude (Pawe Research Center Agrometeorology Division). It has an altitude of 1000–1200 meters above sea level (m.a.s.l), thus belonging to the general classification of lowlands, *i.e.*, lands less than 1500 m.a.s.l..

It has a unimodal rainfall pattern, with an extended rainy season, from March to September. However, the peak rainy season is from July to August. According to records from 1987–2006, the mean annual rainfall is 1579.4 mm. The mean annual maximum temperature is 33.6 ^{0}C, and mean monthly values range from 27.7–37.6 ^{0}C. The mean annual minimum temperature is 13.4 ^{0}C, and mean monthly values range between 11.8–19.3 ^{0}C (Pawe Research Center Agrometeorology Division). The coldest months are December and January whereas March and April are the hottest months (Abayneh, 2003). The soils of Pawe are broadly categorized as vertisols (black clay soils), which account for 40–45% of the area; Nitisols (red or reddish-brown laterite soils), which account for 25–30%; and intermediate soils of a blackish brown color, which account for 25–30 %.

ii) Manbuk

Manbuk research site, which is under Pawe Research Center, is found in Dangur wereda located in Metekel zone of the Benishangul Gumuz National Regional State, in the north western part of Ethiopia, around 595 kilometers from the capital city, Addis Ababa. It has an altitude of 1165 m.a.s.l. It has a unimodal rainfall pattern, with an extended rainy season from May to October with mean annual rainfall of greater than 900mm. The woreda is dominated by black clay soil that covers 75% of the total area and the rest 20% red clay and 5% sandy soil (Dangur Wereda Bureau of Agriculture, Personal Communication).

iii) Shewa Robit

Shewa Robit is found in north Shewa zone of the Amhara Regional State, in the central part of Ethiopia, around 220 kilometers from the capital city, Addis Ababa. The study was conducted on research site of Melkasa Research Center, obtained temporarily from Shewa Robit detention center. According to records from 1997–2006, the mean annual rainfall of the area is 1076 mm. The mean annual maximum temperature is 31.20 ^{0}C, and mean monthly values range from 30.32–31.90 ^{0}C. The mean annual minimum temperature is 16.39 ^{0}C, and mean monthly values range between 14.40–17.5 ^{0}C (Robi Tobacco Farm Meteorological Station).

iv) Ataye

Ataye is found in Efrata and Gedim Woreda which is located in north Shewa zone of the Amhara Regional State, in the central part of Ethiopia, around 280 kilometers from the capital city, Addis Ababa. The study site was a farmer's field in Sar Amba village about 25km from Ataye town.

v) Alupe

The Alupe Research Sub-Station is located at Alupe, Busia district in western Kenya. It is geographically located at $0^0$29' North latitude and $34^0$08' East longitude. It has an elevation of 1190 m.a.s.l. with a maximum and minimum temperature of 28 ^oC and 16^oC, respectively and annual average rainfall of 1775 mm. The soils are ferro-orthic acrisols with a sandy clay texture, which are shallow to moderately deep and well drained (Oswald and Ransom, 2004).

vi) Kibos

The Kibos Research Sub-Station is located at Kibos, Kisumu district in western Kenya. It is geographically located at $0^0$02' South latitude and $34^0$48' East longitude. It has an elevation of 1240 m.a.s.l. with a maximum and minimum temperature of 32 ^oC and 20^oC, respectively and annual average rainfall of 1300 mm. The soil is of an alluvial origin and is classified as a vetroeutic planosol, which is moderately well drained with a loamy texture (Oswald and Ransom, 2004).

4.2 Details of Treatments

The treatments used in the experiment were composed of 25 genotypes including 23 Imidazolinone Resistant (IR) materials; out of which 19 were open pollinated varieties and the rest four were hybrids, one standard check and one local check. For Ethiopia Gibe Composite-1, for Alupe PHB3253 and for Kibos WS-909 were used as local checks. The details of the genotypes are given in Table 1. Except the standard and the local checks, all the IR maize seeds were treated with an imazapyr herbicide, which kills any ordinary maize without herbicide resistance. Therefore, to avoid cross-contamination of the herbicide, persons who planted the treated IR maize seeds were not the ones who planted the standard and the local checks.

Table 1. Name and origin of maize genotypes used in the experiments

Entry No	Code	Pedigree	Origin
1	ZM521	ZM521-IR-LATE OPV	CIMMYT
2	ZM421	ZM421-IR-LATE OPV	CIMMYT
3	ECA-20	ECAVL20-IR-LATE OPV	CIMMYT
4	ECA-17	ECAVL17-IR-LATE OPV	CIMMYT
5	ECA-18	ECAVL18-IR-LATE OPV	CIMMYT
6	Z97SYNGLS (A)	Z97SYNGLS (A)-IR-LATE OPV	CIMMYT
7	Z97SYNGLS (B)	Z97SYNGLS (B)-IR-LATE OPV	CIMMYT
8	ECA-102	ECA-STRIGAOFF-VL-102-#-LATE OPV	CIMMYT
9	ECA-125	ECA-STRIGAOFF-VL-125-#-LATE OPV	CIMMYT
10	ECA-131	ECA-STRIGAOFF-VL-131-#-LATE OPV	CIMMYT
11	ECA-140	ECA-STRIGAOFF-VL-140-#-LATE OPV	CIMMYT
12	ECA-144	ECA-STRIGAOFF-VL-144-#-LATE OPV	CIMMYT
13	ECA-203	ECA-STRIGAOFF-VL-203-#-LATE OPV	CIMMYT
14	ECA-206	ECA-STRIGAOFF-VL-206-#-LATE OPV	CIMMYT
15	ECA-208	ECA-STRIGAOFF-VL-208-#-LATE OPV	CIMMYT
16	ECA-209	ECA-STRIGAOFF-VL-209-#-LATE OPV	CIMMYT
17	ECA-210	ECA-STRIGAOFF-VL-210-#-LATE OPV	CIMMYT
18	ECA-216	ECA-STRIGAOFF-VL-216-#-LATE OPV	CIMMYT
19	ECA-E-IR	ECA-E-IR-EARLY OPV	CIMMYT
20	CML445/390/373	CML445-IR(BC3)F1-B-B-B/CML390-IR(BC3)F1-B-B/CML373-IR(BC3)F1-B-B-INT-3W	CIMMYT
21	INTA/CML390/373	INTA/INTB-B-140-B/CML390-IR(BC3)F1-B-B/CML373-IR(BC3)F1-B-B-INT-3W	CIMMYT
22	CML78/390/202	CML78-IR(BC3)F1-B-B/CML390-IR(BC3)F1-B-B//CML202-IR/CML204-IR-INT DC	CIMMYT
23	CML78/373/202	CML78-IR(BC3)F1-B-B/CML373-IR(BC3)F1-B-B//CML202-IR/CML204-IR-INT DC	CIMMYT
24	WH-403	WH403-STANDARD CHECK	CIMMYT
25	LOCAL CHECKS	-GIBE COMPOSITE-1 (ETHIOPIA) -PHB3253 (ALUPE) -WS909 (KIBOS)	ETHIOPIA and KENYA

4.3 Design and Description of the Experiment

The 25 maize genotypes were grown in a 5 x 5 simple lattice design with two replications. After thorough land preparation, planting was done by hand with 2-3 maize seeds per hill. On the striga infested fields each planting hole/hill was infested with two teaspoonfuls of sand-striga seeds inoculum before planting, which gives approximately 15 gram of the inoculum per hill (Appendix 7). In all the study areas *S. hermonthica* (Del.) Benth. is used as seed source for striga inoculation. Each entry was planted on a plot of two rows each 5.1m long, spaced 0.30m between plants and 0.75m between rows. Seedlings were thinned out fifteen days after sowing to maintain single seedling per hill, which corresponds to a plant population of 44,444 plants ha^{-1}.

For Ethiopian locations, 100 Kg/ha of urea and 100 Kg/ha of Diammonium Phosphate (DAP) was applied of which the entire dose of DAP was applied at planting while half of the urea was applied at planting and the remaining half was top dressed at 35 days after planting. All weeds except striga were removed before they became critical for nutrient competition. All cultural practices were followed according to recommendations.

4.4 Data Collection

1. **Number of days to Anthesis (pollen sheding):** It is the number of days from emergence to when 50% of the plants in the plot start pollen shedding from the central branch of tassels.
2. **Number of days to Silking (female flowering):** It is the number of days from emergence to when 50% of the plants in the plot show up silk of 2-3cm length.
3. **Number of days to Maturity:** It is the number of days from emergence to when 50% of the plants develop black layer at the attachment of the seed to the cob.
4. **Striga count:** Striga plants were counted from each plot at 6, 8, 10 and 12 weeks after planting.
5. **Root lodging:** The number of plants that were leaning 30 degree or more from the perpendicular at the base of the plant where root starts.

6. **Stem lodging:** The number of plants with stalk broken below the ears.
7. **Plant aspect:** It is over all desirability of the plants in a plot with regard to disease resistance, ear placement, and plant leaf orientation. It is recorded using scale of 1-5 where 1 is excellent; short plants with uniform and short ear placement and 5 is poor; tall plants with high ear placement.
8. **Plant height:** It is height in cm from the base to the point where the tassels start to branch. The average height of 10 randomly selected plants was used for analysis.
9. **Ear height:** It is height in cm from the base to the node bearing the upper most ear. Record was taken from the same 10 plants whose plant height was recorded.
10. **Number of ears harvested:** it is the total number of ears harvested. An ear is defined as a cob with at least one-grain.
11. **Ear aspect:** It was recorded after harvest before taking a sample for moisture determination. The ears were spread out in front of the plot and rated for overall desirability (diseases, insect damage, ear size, grain filling, uniformity of ears) on scale of 1-5 where 1 is nice and uniform cobs with preferred texture and 5 is ugly cobs with the undesired texture.
12. **Number of diseased ears:** The number of cobs rotten, molded or diseased was recorded per plot basis.
13. **Field weight:** All the unshelled ears were weighed in kilograms and then multiplied by shelling percent of 80 to get weight of shelled grain and then the values were converted to quintal per hectare (Q/ha).
14. **Moisture content at harvest:** Moisture content was recorded right after the field weight was taken using moisture tester by taking five to ten cobs and shelling at least two kernels from each cob.

4.5 Data Analysis

4.5.1 Analysis of variance (ANOVA)

The plot mean values were subjected to ANOVA of the simple lattice design for each environment. The relative efficiencies and coefficients of variation of simple lattice over RCBD were calculated as described by Gomez and Gomez (1984), when the values were comparable, analysis was done using RCBD. Genotypes were assumed fixed whereas locations as random effects. Homogeneity of error variances test between environments for the validity of the combined ANOVA was determined by using methods given by Gomez and Gomez (1984). A SAS statistical software program was used for the ANOVA of both individual environments and the combined analysis (Hussien *et al*., 2000). GEI was determined using combined ANOVA, which partitions the total variance into genotype, environment, GEI and error.

4.5.2 Stability analyses

Joint linear regression analysis proposed by Eberhart and Russell (1966) (β_i and $\sigma^2{}_{d_i}$) Coefficient of Variation (CV) of Francis and Kannenberg (1978), cultivar superiority measure (P_i) of Lin and Binns (1988), Shukla's (1972) stability variance ($\sigma^2{}_i$), Wrick's (1962) ecovalence (W_i) and AMMI stability value (ASV) of Purchase (1997) were used for estimating stability of the genotypes. Spearman's rank correlation between the different stability parameters was also computed. Stability analysis was conducted using means of genotypes at each environment. All statistical computations were performed using SAS software package using the program developed by Hussien *et al*., (2000).

i) Eberhart and Russell's joint linear regression analysis is described as:

$$Y_{ij} = \mu + \beta_i I_j + \delta_{ij} \qquad (i = 1, 2, \ldots, v \text{ and } j = 1, 2, \ldots, n)$$

Where,

Y_{ij} = mean of i^{th} genotype in j^{th} environment,

μ = mean of all the genotypes over all the environments,

β_i = the regression coefficient of the i^{th} variety on the environmental index,

I_j = the environmental index,

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

v = number of genotypes and

n = number of environments

The two stability parameters used in this model and their computation are discussed as follows:

1) Regression coefficient (β_i): is the regression of the performance of each genotype under different environments and is estimated as:

$$\beta_i = \frac{\sum_j Y_{ij} I_j}{\sum_j I^2{}_j}$$

Where,

$\sum_j Y_{ij} I_j$ = the sum of products and

$\sum_j I_j^2$ = the sum of squares.

2) Mean square deviation ($\sigma^2{}_{d_i}$) from linear regression is estimated as:

$$\sigma^2{}_{d_i} = \left[\frac{\sum_j \hat{\delta}^2{}_{ij}}{n-2}\right] - \frac{S^2{}_e}{r}$$

Where,

$$\sum_j \hat{\delta}^2_{ij} = \left[\sum_j Y^2_{ij} - \frac{Y^2{}_{i.}}{v}\right] - \left[\frac{\left(\sum_j Y_{ij}\ I_j\right)^2}{\sum_j I^2{}_j}\right],$$

S_e^2 = estimate of mean square of error from the combined analysis and

r = the number of replications within environment.

ii) Lin and Binns' (1988) cultivar superiority measure (P_i) was obtained as:

$$P_i = \frac{\sum (Y_{ij} - M_j)^2}{2n}$$

Where,

Y_{ij} = mean of i^{th} genotype in j^{th} environment,

P_i = superiority index of the i^{th} cultivar,

M_j = maximum response obtained among all the cultivars in the j^{th} environment, and

n = number of environments

This expression was further partitioned into:

$$P_i = \frac{[n(\overline{Y_{i.}} - \overline{M})^2 + \sum_{j}^{n}(Y_{ij} - Y_{i.} - M_j + \overline{M})^2]}{2n}$$

Where,

$$\overline{M} = \frac{\sum_{j}^{n} M_j}{n},$$

$\overline{M}$ = mean of the maximum response in the s environments.

$\overline{Y_{i.}}$ = the genotype and environment mean deviations, respectively, and

According to Lin and Binn (1988), the first part of the P_i expression quantifies the genetic deviation and the second quantifies the GEI.

iii) Shukla (1972) stability variance is estimated as follows:

$$\sigma^2_i = \frac{1}{(v-1)(v-2)(n-1)}[v\,(v\text{-}1)\sum_{j=1}^{n}(Y_{ij} - \overline{Y_{i.}} - \overline{Y_{.j}} + \overline{Y..})^2 - \sum_{i=1}^{v}\sum_{j=1}^{n}(Y_{ij} - \overline{Y_{i.}} - \overline{Y_{.j}} + \overline{Y_{..}})^2]$$

Where,

Y_{ij} = mean of i^{th} genotype in j^{th} environment,

$\overline{Y_{i.}}$ and $\overline{Y_{.j}}$ = the genotype and environment mean deviations, respectively, and

$\overline{Y_{..}}$ = the overall mean

v = number of genotypes and

n = number of environments

iv) Wrick's (1962) ecovalence (W_i) or stability of the i^{th} genotype is its interaction with the environments, squared and summed across environments and expressed as:

$$W_i = \sum_j (Y_{ij} - \overline{Y_{i.}} - \overline{Y_{.j}} + \overline{Y..})^2$$

Where,

Y_{ij} = mean of i^{th} genotype in j^{th} environment,

$\overline{Y_{i.}}$ and $\overline{Y_{.j}}$ = the genotype and environment mean deviations, respectively, and

$\overline{Y_{..}}$ = the overall mean

v) AMMI model as described by Zobel *et al.* (1988) is estimated as:

$$Y_{ij} = \mu + \alpha_i + I_j + \sum_{n=1}^{N} \lambda_n \xi_{in} \eta_{jn} + \theta_{ij}$$

Where,

μ = grand mean,

α_i = genotypic effect,

I_j = environmental effect (index),

λ_n = the eigenvalue of the IPCA axis, n,

ξ_{in} and η_{jn} = genotype and environment IPCA scores for the IPCA axis, and

θ_{ij} = residual.

As stated by Alberts (2004), since AMMI model does not make provision for a quantitative stability measure, AMMI stability value (ASV) measure of Purchase (1997) is essential in order to quantify and rank genotypes according to their yield stability.

The ASV can be estimated using the following formula:

$$ASV = \sqrt{\left[\frac{IPCA1\ sum\ of\ squares\ (IPCA1\ score)}{IPCA2\ sum\ of\ squares}\right]^2 + (IPCA2\ score)^2}$$

ASV is the distance from zero in a two dimensional scattergram of IPCA1 scores against IPCA2 scores. Since the contribution of IPCA1 score to GEI sum of squares is outsized, it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relatively greater contribution of IPCA1 and IPCA2 to total GEI sum of squares. Accordingly the distance from zero is determined by using the Pythagoras theorem (Alberts, 2004).

vi) SREG model: to generate a GGE biplot, the GEI two-way table of yield was first environment standardized; the environment-standardized table was then decomposed into principal components (PC) via singular value decomposition (SVD). The first two PC (PC1 and PC2) were used to generate a GGE biplot, whereas the rest were regarded as residuals (Yan et al., 2000a) as follows:

$$\frac{(Y_{ij} - \beta_j)}{s_j} = \lambda_1 \xi_{i1} \eta_{1j} + \lambda_2 \xi_{i2} \eta_{2j} + \varepsilon_{ij}$$

Where,

Y_{ij} = mean of ith genotype in jth environment,

β_j = mean yield in jth environment,

s_j = standard deviation in environment j,

λ_1 and λ_2 = singular values of PC1 and PC2, respectively,

ξ_{i1} and ξ_{i2} = eigenvectors of genotype i for PC1 and PC2, respectively,

η_{1j} and η_{2j} = eigenvectors of environment j for PC1 and PC2, respectively, and

εij = the residual associated with genotype i and environment j.

To generate a GGE biplot, the first equation was reorganized as follows:

$$\frac{\left(Y_{ij} - \beta_j\right)}{s_j} = g_{i1}e_{1j} + g_{i2}e_{2j} + \varepsilon_{ij}$$

By assigning $g_{il} = \xi_{il}$ *and* $e_{lj} = \lambda_l \eta_{lj}$

Where,

$l = 1, 2.$

g_{il} = PC scores for genotype i, and

e_{lj} = PC scores for environment j

4.5.3 Comparison of stability measures

The Spearman's coefficient of rank correlation (r_s) as determined by Steel and Torrie (1980) is used to examine the degree of correlation between the above stability analyses (Alberts, 2004). By considering t genotypes arranged in the same following order to two stability parameters, X_i indicates the ranking order (or number) of the i^{th} genotype for the first parameter, Y_i, indicates the ranking order of the i^{th} genotype of the second parameter, then $d_i = X_i - Y_i$ (i = 1, 2, 3 … t) and Spearman's rank correlation coefficient (r_s) can be described as:

$$r_s = \frac{6\sum d_i^2}{t(t^2 - 1)}$$

The significance of r_s was tested by means of Student's *t* test

Where,

$t = \frac{r_s\sqrt{t-2}}{\sqrt{1-r_s^2}}$, with t-2 degrees of freedom.

5. RESULTS AND DISCUSSION

5.1 Description of the Experiment Condition

The initial design of the experiment was to plant the genotypes both under striga free and striga infested field conditions at each of the six locations (Pawe, Manbuk, Shewa Robit, Ataye, Alupe and Kibos), however at Ataye, due to excessive rainfall the free field was completely devastated by water logging and no data was obtained (Figure 4). The experiment was therefore carried out using 25 maize genotypes at six striga infested and five striga free environments during the 2006/07 cropping season. The six locations vary in their mean annual rainfall, temperature, altitude and soil type. The cropping seasons vary from early June to mid November for Pawe and Manbuk, from early July to late November for Shewa Robit and Ataye, from early September to late March for Alupe and from late September to early March for Kibos.

At Pawe and Manbuk both striga free field experiments were in good condition. In the striga infested field experiment of both locations termite problem and high lodging were observed due to striga damage, heavy rain and windy condition. The lodging problem was also observed in most of the other environments. At Alupe and Kibos during the cropping season there was lower than the expected average rainfall and at the same time the high storm that occurred during early stage of the crop growth affected the stand.

The experiment at Shewa Robit exhibited a different trend as compared to all other trials. In the striga infested field there was very limited emergence of striga plants per plot and the checks gave comparable yield with the IR maize genotypes (Appendix 4 and 5). Moreover, the average grain yield of the striga infested field was better than the average yield of the striga free field (Appendix 3 and 4). The lower level of striga emergence may be due to the shortage of rain and as a result the striga seeds may have entered a dormancy period. The better performance of striga infested field over the striga free field

could be attributed to higher root and stalk lodging in the striga free field and we also speculate soil fertility difference between the fields. Therefore, we could not consider the striga infested experiment at Shewa Robit as truly infested condition. In addition, since planting was done late and the rainfall was interrupted during the grain filling stage of the crop at Shewa Robit, the genotypes grew very well vegetatively but it was difficult to observe grain yield difference (Figure 3). Due to the above mentioned reasons at Shewa Robit and Ataye, contrasting striga free and infested conditions could be possible only at four locations; Pawe, Manbuk, Alupe and Kibos.

5.2 Analysis of Variance

The relative efficiencies of simple lattice over randomized complete block design (RCBD) were calculated from the analysis of variance. Similarly, the coefficient of variation (CV) values were also estimated for both designs at individual environments. Comparison of values as presented in Appendix 2 indicated that in most of the environments the relative efficiencies of simple lattice were very low over RCBD; further the CV values were also comparable for both designs. Hence, further analyses were done using RCBD. In this section we mainly focus on grain yield (Q/ha) although analysis of other traits will also be reported briefly. For ANOVA of individual environments all the 25 maize genotypes were used, whereas for the combined ANOVA only the standard check was included since the local checks used differ from location to location.

5.2.1 ANOVA of individual environments

ANOVA of grain yield for individual environments revealed non-significant differences among the genotypes evaluated for most of the environments except for striga free and striga infested fields at Alupe and Kibos (Table 2). Under the Ethiopian environments, although the difference between the highest yielding and the lowest yielding genotypes ranged from 15.91 Q/ha for Ataye striga infested to 37.67 Q/ha for Manbuk striga free environments (Appendix 3 and 4), this large difference could not be declared statistically significant due to the large error value (Table 2). CV of the experiments ranged between

13.34 for Alupe striga free to 60.01 for Shewa Robit striga free fields. The mean CV of striga infested experiments (32.8%) was higher than the CV of striga free experiments

Figure 2. Pawe striga infested field

Figure 3. Shewa Robit striga infested field

Figure 4. Ataye striga free field damaged by water logging

Figure 5. Manbuk striga infested field

Figure 6. Ataye striga infested field

(27.5%). If the atypical striga free experiment at Shewa Robit with very high CV (60%) is not considered, mean CV of striga free experiments will be 19.4%, which is much lower than the CV of the striga infested experiments (Table 2).

From the ANOVA results of the contrast between the 23 IR maize genotypes and the two checks (Table 2), highly significant difference was observed for all Kenyan environments, except for Kibos striga infested field; to the contrary non-significant difference was observed for Ethiopian locations except for Shewa Robit striga infested field. Also the ANOVA results of percent reduction in grain yield between striga free and infested fields at Alupe and Kibos showed non-significant yield reduction among the genotypes tested but significant difference was observed when yield reduction between the IR maize genotypes and the checks were considered and yield reduction was lower in the IR genotypes. Similar to the above result, no significant yield reduction was observed for the Ethiopian locations both among genotypes and between the IR maize genotypes and the checks (Table 3).

Superiority of the IR maize genotypes was expressed in all the striga infested and some striga free environments. Under the striga infested environments, 11 to 23 IR maize genotypes outperform the best check; WH-403. In addition, 4 to 13 IR maize genotypes outperform the best check; Gibe Composite-1 in some striga free environments. However, under Alupe and Kibos striga free field experiments, the standard check, WH-403 was the top yielder with 55.11 Q/ha and 38.87 Q/ha, respectively with highly significant differences among the maize genotypes evaluated (Appendix 3 and 4). This variety is a released and adapted variety with better performance under the agro-ecological conditions of Western Kenya. In general, the above observations shed light on the superiority of most of the IR maize genotypes under striga infested conditions and to a lesser extent under striga free conditions.

The reduction in yield at Pawe, Manbuk, Alupe and Kibos and the overall mean yield reduction of each genotype due to striga infestation, i.e. the difference between average yield under striga free and striga infested conditions, are presented in Table 4. For trials

Table 2. ANOVA of yield (Q/ha) and contrast of IR maize genotypes vs checks for individual environments

Source	df	Mean squares										
		PAF	PAI	MAF	MAI	SRF	SRI	ATI	ALF	ALI	KBF	KBI
Total	48											
Reps	1	427.38	2445.55***	10.20	1533.44***	112.50	123.72	4.80	34.72	2.73	39.35	26.32
Genotype	24	89.47	56.98	118.93	54.35	68.36	151.14	28.05	124.80***	41.62**	63.02***	17.04*
Error	23	134.74	44.44	68.75	59.40	62.55	81.67	47.31	13.41	16.62	13.31	8.67
IR vs checks	1	112.23	21.57	216.96	183.40	63.64	432.48*	2.10	812.52***	126.44**	412.73***	20.71
CV		24.13	31.76	20.32	27.34	60.01	35.55	46.63	13.34	25.21	19.84	30.56
R-square		0.45	0.79	0.63	0.66	0.55	0.65	0.37	0.90	0.71	0.83	0.68

Abbrevtions: *PAF, PAI, MAF, MAI, SRF, SRI, ATI, ALF, ALI, KBF and KBI; Striga free and infested fields of Pawe, Manbuk, Shewa Robit, Ataye, Alupe and Kibos.*

Table 3. AVOVA for percent reduction in yield in striga infested fields as compared to striga free fields

Contrast	df	Mean squares			
		Pawe	Manbuk	Alupe	Kibos
Genotypes	24	0.06	0.04	0.05	0.08
IR vs Checks	1	0.03	0.01	0.46***	0.36**

, **, * Significant at P< 0.05, 0.01, and 0.001 level, respectively.*

where successful striga infestation was achieved, yield was reduced on average from 8.62 to 26.87 Q/ha. The highest reduction of 26.87 Q/ha was recorded at Pawe by 54.88% yield reduction whereas the lowest reduction in terms of absolute measure (Q/ha) was recorded at Kibos with 8.62 Q/ha, which was the second in percent yield reduction (43.64%) following Pawe (Table 4)

A closer look at the yield reduction of each environment elucidated that at Pawe the yield reduction ranges from 11.72 Q/ha for ECA-18 (5) to 41.31 Q/ha for ECA-E-IR (19), which corresponds to 30.55% to 85.00% reductions, respectively. At Manbuk the yield reduction (Q/ha) ranges from 0 (ECA-131 (10)) to 30.61 (INTA/CML390/373 (21)) and percent reduction ranges from 0 (ECA-131 (10)) to 57.86% (ECA-216 (18)). In similar fashion, Alupe also showed 3.88 (Z97SYNGLS (A) (6)) to 43.53 (WH-403 (24)) yield reduction (Q/ha) and 18.54% (ECA-17 (4)) to 79.00% (WH-403 (24)) yield reduction. The highest range in percent yield reduction was observed at Kibos; 0.60% for ECA-20 (3) to 75.54% for WH-403 (24), which corresponds to 0 to 29.36 Q/ha yield reduction, respectively (Table 4).

Apart from the above observations, the highest percent reduction due to striga infestation was observed on the standard check, WH-403 at Alupe (79.00%) and Kibos (75.54%). The highest average yield reduction of 29.61 Q/ha and average percent reduction of 65.00% was observed on the standard check, WH-403. The average percent reduction in yield for all the IR maize genotypes was 40.40% whereas it was 65.00% for the standard check. On top of this, if the mean yield of the striga free and infested fields over the four locations was considered, the mean of the standard check was the lowest (12.67 Q/ha) under striga infested condition and highest (42.29 Q/ha) under striga free condition. Under striga free fields, the standard check had a yield advantage of only 3.37% over the best IR genotype (INTA/CML390/373 (21)), while under striga infested fields the highest yielding IR maize genotype (CML445/390/373 (20) had a yield advantage of 86.50% over the standard check. The same trend was observed under striga infested fields at individual locations in that the highest yielding genotypes were among the IR genotypes. These observations can be taken as substantiation for better performance of the IR maize genotypes under striga infestation than the standard check (Table 4 and Figure 7).

Table 4. Reduction in yield due to striga infestation at Pawe, Manbuk, Alupe and Kibos

Entry No.	Pawe Red	Man Red	Alupe Red	Kibos Red	Pawe Per	Man Per	Alupe Per	Kibos Per	AV Red	AV Per	Free Yield	Inf Yield
1	39.56	14.16	4.26	8.63	67.84	35.71	19.34	40.71	16.65	40.90	35.30	18.65
2	23.03	21.03	6.00	2.86	50.11	37.89	23.08	19.87	13.23	32.74	35.47	22.23
3	13.61	18.20	10.23	0.07	31.09	39.71	40.61	0.59	10.53	28.00	31.57	21.05
4	20.03	19.27	4.08	8.05	40.90	47.18	18.55	43.40	12.86	37.51	32.59	19.73
5	11.72	11.81	19.81	7.15	30.55	30.17	54.37	39.13	12.62	38.55	33.05	20.43
6	18.28	11.05	3.88	1.94	41.74	30.92	18.95	17.64	8.79	27.31	27.75	18.97
7	21.21	16.58	11.24	14.28	46.06	38.78	39.51	71.59	15.83	48.98	34.30	18.47
8	17.76	0.78	8.81	12.10	42.54	2.15	51.82	60.69	9.86	39.30	28.71	18.85
9	14.03	17.59	14.82	10.21	36.55	42.68	46.92	49.00	14.16	43.79	33.00	18.84
10	40.31	-0.02	13.91	5.41	69.26	-0.06	51.63	33.52	14.90	38.59	33.77	18.86
11	26.04	3.08	10.80	8.75	55.30	8.30	40.73	50.17	12.17	38.62	32.04	19.87
12	33.18	12.43	9.47	18.36	54.21	32.28	33.94	70.14	18.36	47.64	38.44	20.09
13	22.68	8.93	4.55	8.97	57.47	24.69	24.36	58.45	11.28	41.24	27.41	16.13
14	25.37	8.24	14.36	6.17	58.57	18.30	45.43	36.02	13.54	39.58	34.27	20.74
15	29.28	4.34	12.88	9.59	56.47	13.07	51.29	55.85	14.02	44.17	31.83	17.81
16	28.20	20.9	9.03	7.63	59.06	44.37	42.14	66.04	16.44	52.90	31.96	15.52
17	14.49	9.97	7.81	8.87	37.76	26.01	36.65	51.34	10.29	37.94	28.83	18.54
18	33.42	28.55	8.55	4.29	73.69	57.86	36.87	31.74	18.70	50.04	32.84	14.14
19	41.31	8.65	7.25	5.60	85.01	22.38	34.39	39.55	15.70	45.33	30.62	14.92
20	28.24	13.27	8.24	12.14	56.35	29.23	20.84	56.75	15.47	40.79	39.10	23.63
21	38.33	30.61	8.30	1.60	72.05	50.82	26.73	8.39	19.71	39.50	40.90	21.19
22	38.55	5.21	9.83	6.09	65.48	12.56	33.13	33.12	14.92	36.07	37.11	22.19
23	28.10	6.34	13.13	8.77	56.50	20.36	42.58	38.15	14.08	39.40	33.67	19.59
24	38.18	7.38	43.53	29.36	72.58	32.72	79.00	75.54	29.61	64.96	42.28	12.67
Average	**26.87**	**12.43**	**11.03**	**8.62**	**54.88**	**29.10**	**38.04**	**43.64**	**14.74**	**41.41**	**33.62**	**18.88**

Abbrevtions: ***Pawe Red, Man Red, Alupe Red, Kibos Red and AVRed****; Pawe, Manbuk, Alupe and Kibos yield reduction (Q/ha) and average yield reduction.*

Pawe Per, Man Per, Alupe Per, Kibos Per and AVPer*; Pawe, Manbuk, Alupe and Kibos percent yield reduction and average percent yield reduction.*

Free Yield and Inf Yield*; average yield of striga free and infested fields at the four locations*

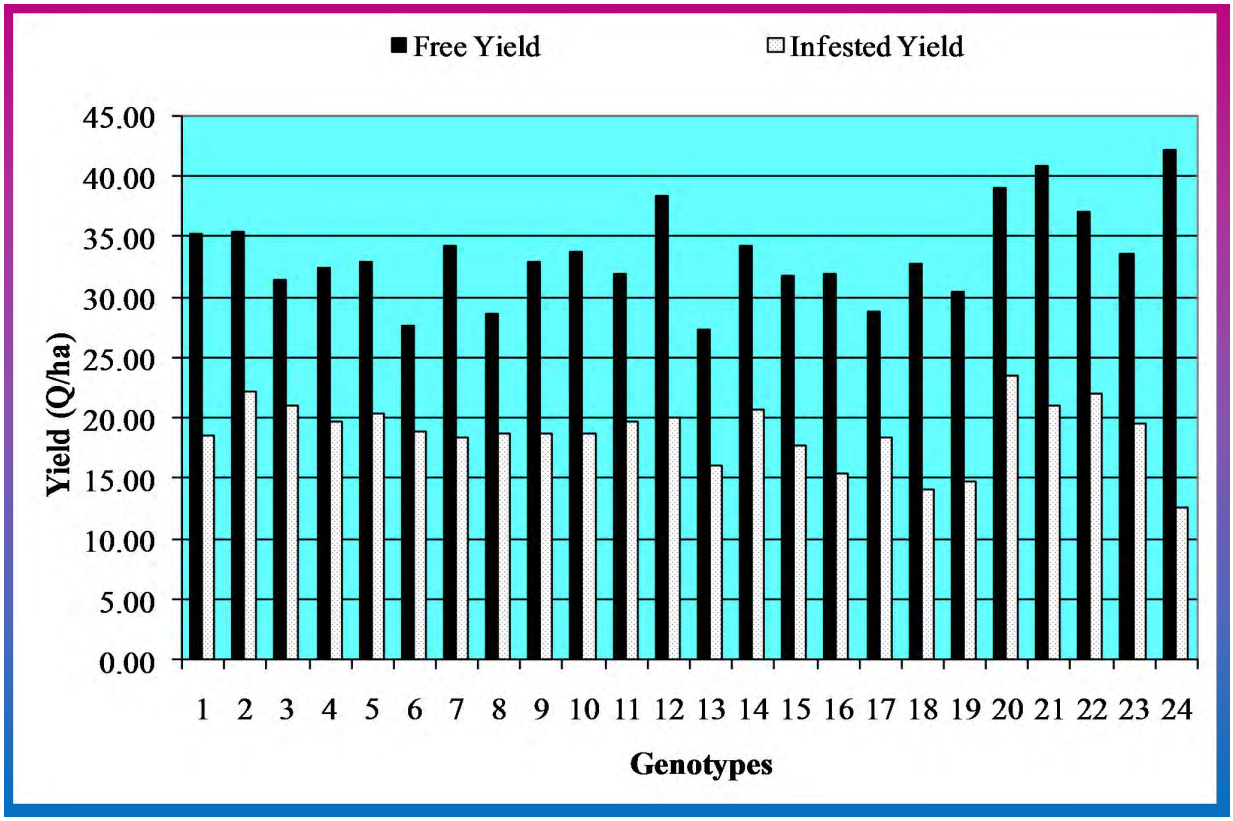


Figure 7. Yield (Q/ha) of the 24 maize genotypes under striga free and infested fields (Mean of Pawe, Manbuk, Alupe and Kibos)

Taking striga count into account, highly significant ($P \leq 0.001$) difference among the genotypes at Alupe and Kibos and significant ($P \leq 0.05$) difference at Shewa Robit was observed. Striga infestation was relatively high at Pawe, Manbuk, Ataye, Alupe and Kibos, with location means of 69, 37, 43, 30 and 36 emerged striga plants per plot, respectively at about 12 weeks after planting. Average striga count was lowest in Shewa Robit (1.08 emerged striga plants per plot). Except for Manbuk striga infested field, similar trend was observed in all other striga infested fields in that, the standard and the local checks hold the largest number of striga count as compared to the 23 IR maize genotypes. At Manbuk 11 IR maize genotypes had more number of striga plants per plot than the standard check, WH-403 and 19 IR maize genotypes had more number of striga plants per plot than the local check, Gibe Composite-1. The reason for such discrepancy is not known and needs further investigation (Appendix 5).

The highest striga records were 400, 244 and 154 emerged striga plants per plot at Alupe, Pawe and Kibos, respectively on the standard check and 156, 108 and 107 emerged striga plants per plot at Pawe, Kibos and Alupe, respectively on the local checks of the respective areas, while the highest number of striga plants under the IR maize genotypes under striga infested fields at Ataye, Kibos and Pawe were 80, 99 and 127, respectively (Appendix 5). These results can be taken as one testimony for the new herbicide seed coating technology on maize (IR maize) to reduce striga attack under striga infested field conditions.

5.2.2 Combined ANOVA

Combined ANOVA of grain yield of the 24 genotypes in eleven environments revealed highly significant differences among the environments (P≤0.001) and genotypes (P≤0.01) and highly significant Genotype x Environment Interaction (GEI) (P≤0.001) (Table 5). Partitioning of the sum of squares of the components for grain yield indicated that 64.35% was due to environments, 2.24% due to genotypes, 16.68% due to GEI and 12.33% due to error (Table 5). Epinat-Le Signor *et al*. (2001) in GEI study in early maize hybrids also reported that about 80% of the total variance was explained by environmental differences, about 11% by GEI differences, 6% by variety differences and 3% by experimental error.

Table 5. Combined ANOVA of grain yield (Q/ha)

Sources	Df	Sum of square	Mean square	% SS Explained
Total	524	101378.72		
Environment (E)	10	65232.50	6523.25***	64.35
Reps (Env.)	11	4468.36	406.21***	4.41
Genotype (G)	23	2270.40	98.71 **	2.24
Genotype x Environment	230	16906.18	73.51***	16.68
Error	250	12501.28	50.01	12.33

*** and *** represent significant at p ≤ 0.01 and 0.001level, respectively.*

The relative magnitude of the SS due to environments, genotypes and GEI components for yield was greatly different. The variation due to environment was larger than that due to GEI and also the relative magnitude of GEI in this study exceeded that of the genotypes, which is a common scenario in yield trials (Gauch and Zobel, 1996). This variability was mainly due to the infestation of striga and the distribution of rainfall, which differed greatly across the environments. Adugna and Labuschagne (2003) on phenotypic stability of linseed also reported very high fluctuations in the growing environments of Ethiopia.

The highly significant mean square of the environment indicated that the environments were different in yield potential, with large differences among environmental means causing most of the variation in yield, signifying the big influence of environment on yield performance of maize genotypes. From the environmental mean yield, under striga free field condition Pawe was the most conducive environment for realizing the yield potential of the genotypes with mean yield of 48.09 Q/ha followed by Manbuk with mean yield of 40.79 Q/ha while Shewa Robit was the poorest yielding environment with mean yield of 13.18 Q/ha (Appendix 3). Similarly under striga infested field condition, Manbuk was the most favorable environment with mean yield of 28.20 Q/ha being the third in striga infestation followed by Pawe with mean yield of 21.00 Q/ha being the first in striga infestation while Kibos was the poorest yielding environment with mean yield of 9.63 Q/ha (Appendix 4 and 5).

The significant difference among the genotypes also revealed the presence of genetic variability in the maize genotypes included in this study. Mean yields of the genotypes varied from 19.34 Q/ha to 28.45 Q/ha. The performances of genotypes were not consistent across all the environments; as a result, no single genotype was consistently superior nor performed least from the rest of the genotypes across all the environments. The presence of significant GEI showed the inconsistency in performance of maize genotypes across environments. A similar result was recorded by different authors on different crops. Gelana *et al*. (2001), Mosisa *et al*. (2001) and Pixley and Bjarnason (2002) on maize, Haussmann *et al*. (2001) on sorghum and Akcura *et al*. (2005) on durum wheat

reported highly significant GEI on yield of the respective crops across testing environments.

Taking the combined ANOVA of yield and other traits (Appendix 6a and 6b) into account, significant difference was observed among genotypes for days to anthesis, days to silking, ear height, plant aspect, ear aspect and number of ears harvested. In both Ethiopian and Kenyan environments, there was highly significant difference between striga free and infested fields for yield and some yield related traits (Appendix 6). From this result, it can be depicted that the impact of striga on the host is very significant and highly damaging. In striga infested environments reduction in grain yield, plant height, ear height and number of ears harvested and increase in stalk and root lodging were observed. These observations agree with the observations reported by Kim (1991).

Based on mean yield over all the 11 environments, among the maize genotypes evaluated INTA/CML 390/373 (21) was the top yielder with average mean yield of 28.45 Q/ha followed by ECA-144 (12) and CML78/390/202 (22), which gave 27.48 and 27.17 Q/ha, respectively. ECA-203 (13) was the least performing genotype (19.34 Q/ha) (Table 6). Nine IR maize genotypes; CML445/390/373 (20), INTA/CML390/373 (21), CML78/390/202 (22), ECA-144 (12), ECA-206 (14), ZM521 (1), ZM421 (2), ECA-20 (3) and ECA-18 (5) outsmart both the local and the standard checks in most of the striga infested fields and in some striga free fields (Appendix 3 and 4).

Gelana *et al*. (2001) stated that highly significant yield differences between genotypes and environments and highly significant interaction of genotypes with environments indicated the need to develop cultivars that are adapted to specific environmental conditions and the need to identify cultivars that are exceptional in their stability across environments. The above results, therefore, suffice the basic condition for further analysis of GEI and warranted consideration of different stability parameters.

5.3 Stability Analyses

As already described in section 5.2.2 of this paper, highly significant differences existed among environments, genotypes and GEI for yield on the maize genotypes evaluated. The highly significant GEI obtained paves the way to further analyze the prevailing GEI under various stability models (Singh and Chaudhary, 2001). The reliability of a cultivar's performance across environments is an important consideration in plant breeding. Some cultivars are adapted to a broad range of environmental conditions, while others are more limited in their potential distribution. There are cultivars that perform similarly regardless of the productive potential of the environment, and others whose performance is directly related to the productivity potential of the environment (Fehr, 1992). This clearly indicates the importance of stability analysis.

According to Ghaderi *et al*. (1980) standard ANOVA procedure is useful for estimating the magnitude of GEI but fails to provide information on the contribution of individual genotypes to GEI. To alleviate the problem, a number of statistical procedures have been developed. Accordingly, in this paper, the following stability parameters were used to shade more light on the statistically significant GEI.

5.3.1 Francis and Kannenberg's (1978) coefficient of variation (CV)

The method of Francis and Kannenberg's (1978) uses grain yield and CV of each genotype over all environments to identify stable genotypes. Alberts (2004) elucidated that a stable genotype is the one that gives high yield and consistently low CV. The CV of each genotype can be plotted against the mean yield in a yield-CV plane, which can be partitioned into four quadrants as shown in Figure 9. Genotypes on the right corner of quadrant IV are the most stable, having above average yield and below average CV while genotypes on the top left corner of quadrant II are unstable, having below average yield and above average CV.

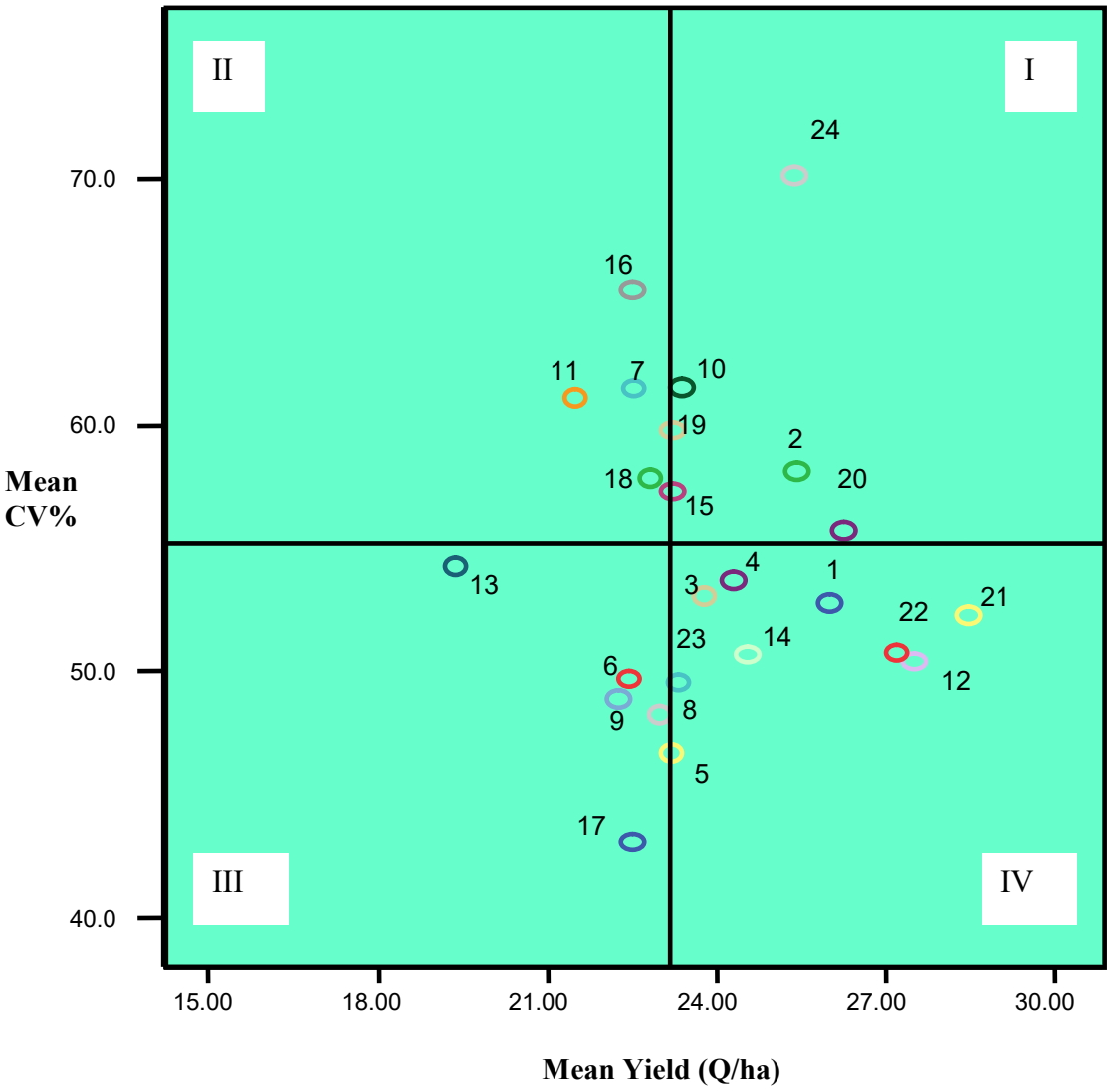


Figure 8. Distribution of the 24 genotypes in the yield-CV plane

Taking this into account ECA- 144 (12), CML78/390/202 (22), INTA/CML390/373 (21), ZM521 (1) and CML445/390/373 (20) fall into the high yield and low CV group and can be considered the most stable whereas the late maturing IR maize OPV's; ECA-209 (16), ECA-140 (11) and Z97SYNGLS (B) (7) were unstable having high CV and relatively low yield. Although the average yield of the standard check, WH-403 (24), is better than the yield of many IR genotypes it is the most unstable having the highest CV (70%) (Figure 8).

5.3.2 Lin and Binns's (1988) cultivar performance measure (P_i)

The cultivar general superiority (P_i) is the distance mean square between the cultivar's response and the maximum response at each location. The smaller this mean square the more superior yield the cultivar has. According to this stability parameter genotypes with lowest cultivar performance measure (P_i) values are considered the most stable. The three way cross IR maize genotypes INTA/CML390/373 (21), CML78/390/202 (22) and CML445/390/373 (20) and the late maturing OPV ECA-144 (12) were the most stable. The late maturing IR maize OPV's; ECA-203 (13), ECA-140 (11), ECA-102 (8) and Z97SYNGLS (A) (6) were genotypes with the lowest rank both in P_i value and mean yield. The standard check, WH-403, is better than many IR genotypes in stability according to this parameter (Table 6).

5.3.3 Wricke's (1962) ecovalence (W_i)

Genotypes with low ecovalence, *i.e.*, small contribution of the genotype to the GEI sum of squares, have smaller fluctuations across environments and therefore are stable (Wricke, 1962). Hence the late maturing IR maize OPV's; ECA-203 (13), Z97SYNGLS (B) (7), ECA-210 (17), ECA-20 (3) and ECA-208 (15), were the most stable but all these genotypes were not the best in mean yield, ranking 24th, 18th, 19th, 10th and 13th, respectively (Table 6). The most unstable genotypes according to the ecovalence method were the standard check, WH403 (24), INTA/CML390/373 (21), CML445/390/373 (20), ECA-E-IR (19) and ECA-102 (8) and these genotypes were ranked 7th, 1st, 4th, 13rd and 16th, respectively for mean yield (Table 6).

Table 6. Cultivar performance measure (P_i), Shukla's stability variance (σ^2_i) and Wricke's ecovalence (W_i) values of the 24 maize genotypes

Entry No	Code	P_i	Rank	W_i	Rank	σ^2_i	Rank	Mean Yield	Rank
1	ZM521	109.67	6	308.49	17	31.96	17	25.99	5
2	ZM421	108.93	5	307.46	16	31.85	16	25.41	6
3	ECA-20	135.16	11	192.64	4	19.32	4	23.76	10
4	ECA-17	130.89	8	286.50	13	29.56	13	24.28	9
5	ECA-18	132.49	9	306.30	15	31.72	15	23.18	15
6	Z97SYNGLS (A)	162.72	21	207.54	6	20.95	6	22.43	21
7	Z97SYNGLS (B)	133.29	10	165.05	2	16.31	2	22.51	18
8	ECA-102	167.06	22	338.61	20	35.25	20	22.97	16
9	ECA-125	145.59	17	314.50	19	32.62	19	22.25	22
10	ECA-131	145.14	16	250.19	11	25.60	11	23.36	11
11	ECA-140	167.28	23	245.32	9	25.07	9	21.48	23
12	ECA-144	85.22	2	240.65	8	24.56	8	27.48	2
13	ECA-203	208.20	24	142.48	1	13.85	1	19.34	24
14	ECA-206	122.35	7	281.89	12	29.06	12	24.53	8
15	ECA-208	143.03	14	198.28	5	19.94	5	23.20	13
16	ECA-209	153.56	18	250.11	10	25.59	10	22.49	19
17	ECA-210	156.00	19	172.70	3	17.15	3	22.49	19
18	ECA-216	144.68	15	291.24	14	30.08	14	22.80	17
19	ECA-E-IR	156.30	20	501.60*	21	53.03*	21	23.20	13
20	CML445/390/373	93.17	4	523.49*	22	55.42**	22	26.24	4
21	INTA/CML390/373	80.96	1	535.00**	23	56.67**	23	28.45	1
22	CML78/390/202	89.99	3	209.47	7	21.16	7	27.17	3
23	CML78/373/202	141.27	13	312.35	18	32.38	18	23.30	12
24	WH-403	140.12	12	1985.9***	24	214.95***	24	25.37	7

, **, * Significantly unstable at $p \leq 0.05$, 0.01 and 0.001 level, respectively.*

5.3.4 Shukla's (1972) stability variance (σ^2)

Based on this procedure a genotype is said to be stable when its contribution to GEI is small. The most stable genotypes as indicated by this stability parameter were the late maturing IR maize OPV's; ECA-203 (13), Z97SYNGLS (B) (7), ECA-210 (17), ECA-20 (3) and ECA-208 (15), but all these genotypes were not the best in mean yield, ranking 24th, 18th, 19th, 10th and 13th, respectively (Table 6). The genotypes with poor stability according this procedure were the standard check, WH403 (24), INTA/CML390/373 (21), CML445/390/373 (20), ECA-E-IR (19) and ECA-102 (8), which ranked 7th, 1st, 4th, 13th and 16th, respectively for mean yield (Table 6). Genotypes, ECA-144 (12) and CML78/390/202 (22) ranked second and third for mean yield and ranked 8th and 7th for stability variance, respectively, showing intermediate stability.

5.3.5 Eberhart and Russell's (1966) joint linear regression analysis

The Eberhart and Russell (1966) procedure involves the use of joint linear regression where the yield of each genotype is regressed on the environmental mean yield. The analysis of variance for the regression model is presented in Table 7. In this model the total SS is partitioned into SS of genotypes, SS of environment + GEI and SS of error. The SS of environments + GEI is further partitioned into SS due to environments (linear), GEI (linear) and pooled deviation.

Table 7. Results of joint linear regressions analysis

Source	DF	SS	MS
Total	524	42913.48	
Genotypes	23	1107.81	48.165
E+ in GEI	240	41805.90	174.19
E (linear)	1	33238.12	33238.12***
GEI (linear)	23	525.37	22.84
Pooled deviation	216	8042.40	37.23***
Error	250	6310.37	25.24

Grand mean = 23.91 R-squared = 0.81 C.V. = 33.54%
**** represent significance at p ≤ 0.001 level.*

The GEI (linear) SS was not a large portion of the GEI when compared with E (linear) and the deviation SS. The E (linear) and deviation MS are highly significant indicating the large difference between the environments. Both genotypes and GEI (linear) were non-significant. This means that the GEI of a genotype has no relationship with mean yields of the environments or it has non-linear relationship. This may be attributed to the fact that the GEI (linear) explains only about 6 % of the total GEI. Alberts (2004) also reported non- significant GEI (linear) in 23 maize hybrids tested over three years at 42 locations, where the GEI (linear) contributed only about 7 % to the total GEI.

Finlay and Wilkinson (1963) showed that regression coefficients approximating to 1.0 indicate average stability, but must always be coupled and interpreted with the genotype mean yield to make a decision on adaptability. The IR maize OPV's; ECA-20 (3), ECA-17 (4), ECA-206 (14) and ECA-E-IR (19) had regression coefficients close to 1.0 with average mean yield and stability (Figure 9). INTA/CML390/373 (21), ECA- 144 (12), CML78/390/202 (22), CML445/390/373 (20), ZM521 (1) and ZM421 (2) had regression coefficients above 1.0; these are genotypes with increasing sensitivity to environmental changes, showing below average stability but with above average mean yield and specifically adapted to high yielding environments. The late maturing IR maize OPV's; namely, ECA-125 (9), ECA-210 (17), ECA-102 (8) and ECA-18 (5) had regression coefficients below 1.0; these genotypes display greater resistance to environmental changes, having above average stability but below average mean yield and are more specifically adapted to lower yielding environments. ECA-203 (13) was not adapted to any of the environments, and is low yielding. The other genotypes in the center of the triangle were of average stability according to this procedure (Figure 9).

Finlay and Wilkinson (1963) and Perkins and Jinks (1968) found that linear response is positively associated with mean performance. Eberhart and Russel (1966) and Paroda and Hayes (1971), however, emphasized that both linear (β_i) and non-linear ($\sigma^2{}_{d_i}$) components of GEI should be considered in judging the stability of a particular genotype and the two are independent from each other. In the Eberhart and Russel (1966) model the genotype's performance is generally expressed in terms of three parameters: mean yield ($\hat{Y}$), regression coefficient (β_i) and the deviation from the regression ($\sigma^2{}_{d_i}$).

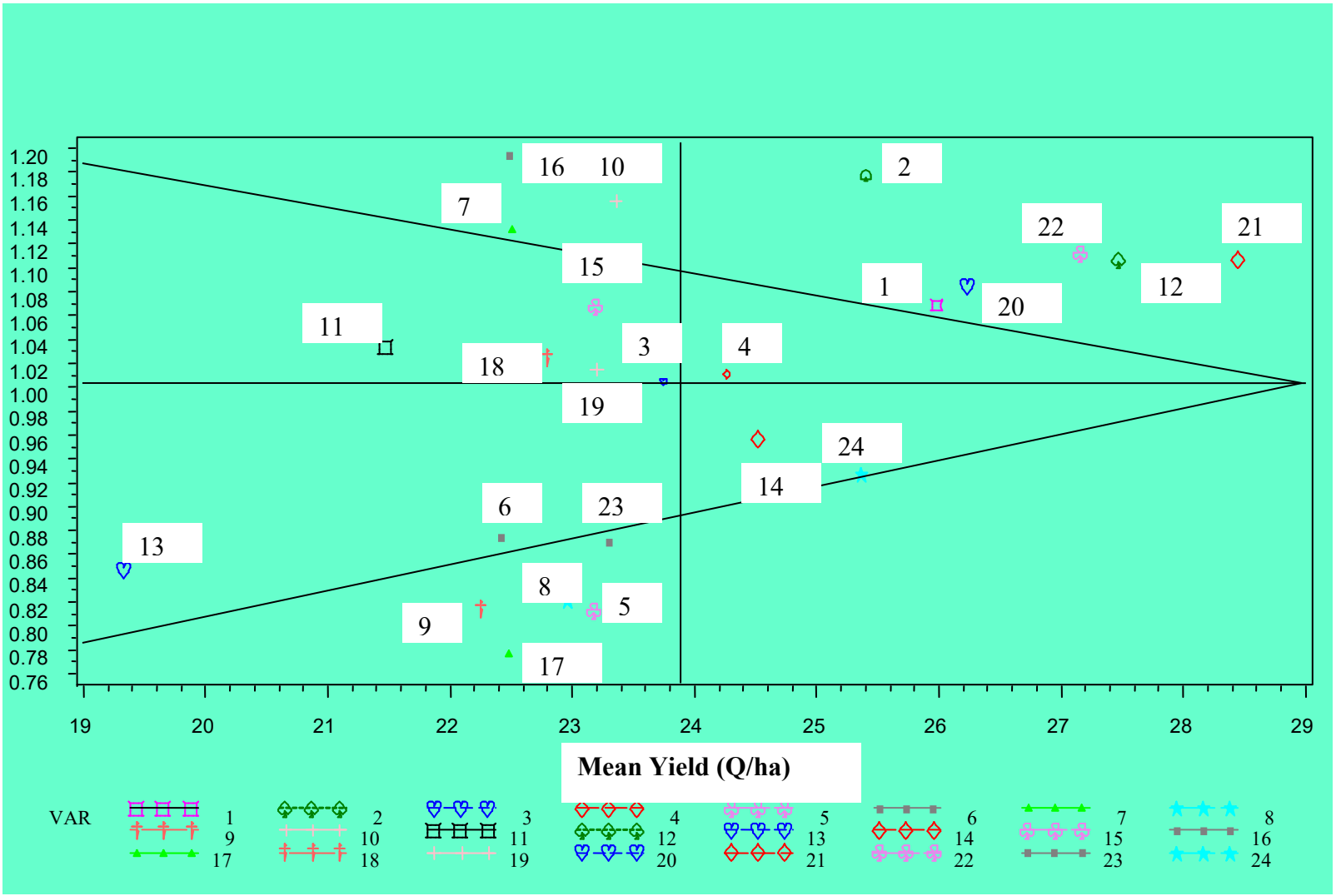


Figure 9. Genotype regression coefficients plotted against genotype mean yield

According to this model a stable genotype should have a high mean yield, regression coefficient equal to unity (β_i = 1) and deviation from regression as small as possible ($\sigma^2{}_{d_i}$ = 0). It is however specifically the deviation from the regression ($\sigma^2{}_{d_i}$) which is used as a measure of a genotype's stability across environments (Adugna and Labuschagne, 2002; Alberts, 2004; Ali *et al.*, 2006). These authors indicated that regression coefficient (β_i) reflects the general response, or adaptation of a genotype in various environments, rather than indicating stability, whereas $\sigma^2{}_{d_i}$ actually measures the yield stability.

Even when the total SS due to GEI (linear) is statistically non-significant Eberhart and Russel recommend looking the values for each genotype. Regression coefficient, deviations from regression and mean yield of the 24 maize genotypes tested across eleven environments are presented in Table 8. None of the regression coefficients of the genotypes, except for ECA-210 (17), were significantly different from unity (β_i =1) suggesting that all the genotypes with the exception of ECA-210 (17) have average response across the environments. Taking the three parameters into account, CML78/390/202 (22) can be considered as the most stable across all environments with a high mean yield 27.17 Q/ha (ranked third), β_i = 1.1123 (close to 1) and $\sigma^2{}_{d_i}$ = 21.335 (ranked 6th), followed by ECA-144 (12); ranked second by mean yield (27.48 Q/ha), β_i = 1.1065 (close to 1) and $\sigma^2{}_{d_i}$ = 24.994 (ranked 10th). The top-yielding genotype, INTA/CML390/373 (21), though identified with b_i values close to unity (β_i = 1.1066), had $\sigma^2{}_{d_i}$ values that deviate significantly from 0 and is considered unstable (Table 8).

From the standpoint of taking $\sigma^2{}_{d_i}$ as the actual measure of yield stability, the most stable genotypes with the lowest $\sigma^2{}_{d_i}$ values not significantly deviating from zero were ECA-210 (17) which ranked first, ECA-203 (13) ranked second and Z97SYNGLS (B) (7) which ranked third, but all are low yielders. The most unstable genotypes with the highest $\sigma^2{}_{d_i}$ values significantly deviating from zero were WH403 (24), INTA/CML390/373 (21), CML445/390/373 (20) and ECA-E-IR (19). All other genotypes showed non-

significant deviation from regression ($\sigma^2_{d_i}$ = 0) and could be considered as stable genotypes, though most of them were low yielders (Table 8).

Table 8. Regression coefficients and deviations from regression of the 24 maize genotypes

Entry No	Code	β_i	Rank	$\sigma^2_{d_i}$	Rank	Mean Yield	Rank
1	ZM521	1.0690	8	33.544	20	25.99	5
2	ZM421	1.1780	19	29.285	13	25.41	6
3	ECA-20	1.0048	1	21.401	7	23.76	10
4	ECA-17	1.0109	2	31.815	16	24.28	9
5	ECA-18	0.8135	22	28.683	12	23.18	15
6	Z97SYNGLS (A)	0.8746	14	20.642	4	22.43	21
7	Z97SYNGLS (B)	1.1333	16	15.604	3	22.51	18
8	ECA-102	0.8220	19	32.747	19	22.97	16
9	ECA-125	0.8149	21	29.673	14	22.25	22
10	ECA-131	1.1564	18	24.034	9	23.36	11
11	ECA-140	1.0344	5	27.076	11	21.48	23
12	ECA-144	1.1065	11	24.994	10	27.48	2
13	ECA-203	0.8467	17	12.214	2	19.34	24
14	ECA-206	0.9572	6	31.039	15	24.53	8
15	ECA-208	1.0678	7	21.325	5	23.20	13
16	ECA-209	1.1942	24	21.986	8	22.49	19
17	ECA-210	0.7770*	23	11.534	1	22.49	19
18	ECA-216	1.0241	4	32.271	18	22.80	17
19	ECA-E-IR	1.0150	3	55.699*	21	23.20	13
20	CML445/390/373	1.0843	10	57.073*	22	26.24	4
21	INTA/CML390/373	1.1066	11	57.697*	23	28.45	1
22	CML78/390/202	1.1123	13	21.335	6	27.17	3
23	CML78/373/202	0.8700	5	32.099	17	23.30	12
24	WH-403	0.9268	9	219.830***	24	25.37	7

** and *** indicate significant differences of values from $\sigma^2_{d_i}$ = 0 and β_i =1 at p ≤ 0.05 and 0.001 level, respectively (i.e, $\sigma^2_{d_i}$ is different from zero and b_i different from one).*

5.3.6 Additive main effects and multiplicative interaction (AMMI) analysis

In the AMMI analysis the GEI component of variation was partitioned into 11 possible interaction principal component axes (IPCA), equal to the number of environments. The first principal component axis (IPCA 1) of the interaction alone captured 32.55% of the interaction SS in 13.91% of the interaction degrees of freedom. Furthermore, the second interaction principal component axis (IPCA 2) explained a further 25.44% of the interaction SS in 13.00% of the interaction degrees of freedom (Table 9). F tests used to measure significance of these components recommended inclusion of the first two interaction principal component axes in the model with 62 degrees of freedom and the IPCA 1 and IPCA 2 cumulatively explained 58% of the total GEI SS as compared to only 6% explained by linear regression. The remaining 42% of GEI (IPCA3 – IPCA11) is considered as noise, which is not interpretable and therefore was pooled with the residual.

Hence, AMMI with only two interaction principal component axes was the best predictive model, which is in agreement with results obtained by Zobel *et al.* (1988), Adugna and Labuschagne (2002) and Annicciarico (2002). Other authors also found out that the most accurate model for AMMI can be obtained by using the first two IPCA axes (Gauch and Zobel, 1996; Yan *et al.*, 2000). However, Sivapalan *et al.* (2000) recommended a predictive AMMI model with the first four IPCAs.

Table 9. Results of AMMI analysis of grain yield (Q/ha)

Source	DF	SS	MS	% SS Explained
Genotype x Environment	230	8567.77	37.25***	
IPCA 1	32	2788.74	87.15***	32.55
IPCA 2	30	2179.73	72.65***	25.44
Residual	418	9909.67	23.71	

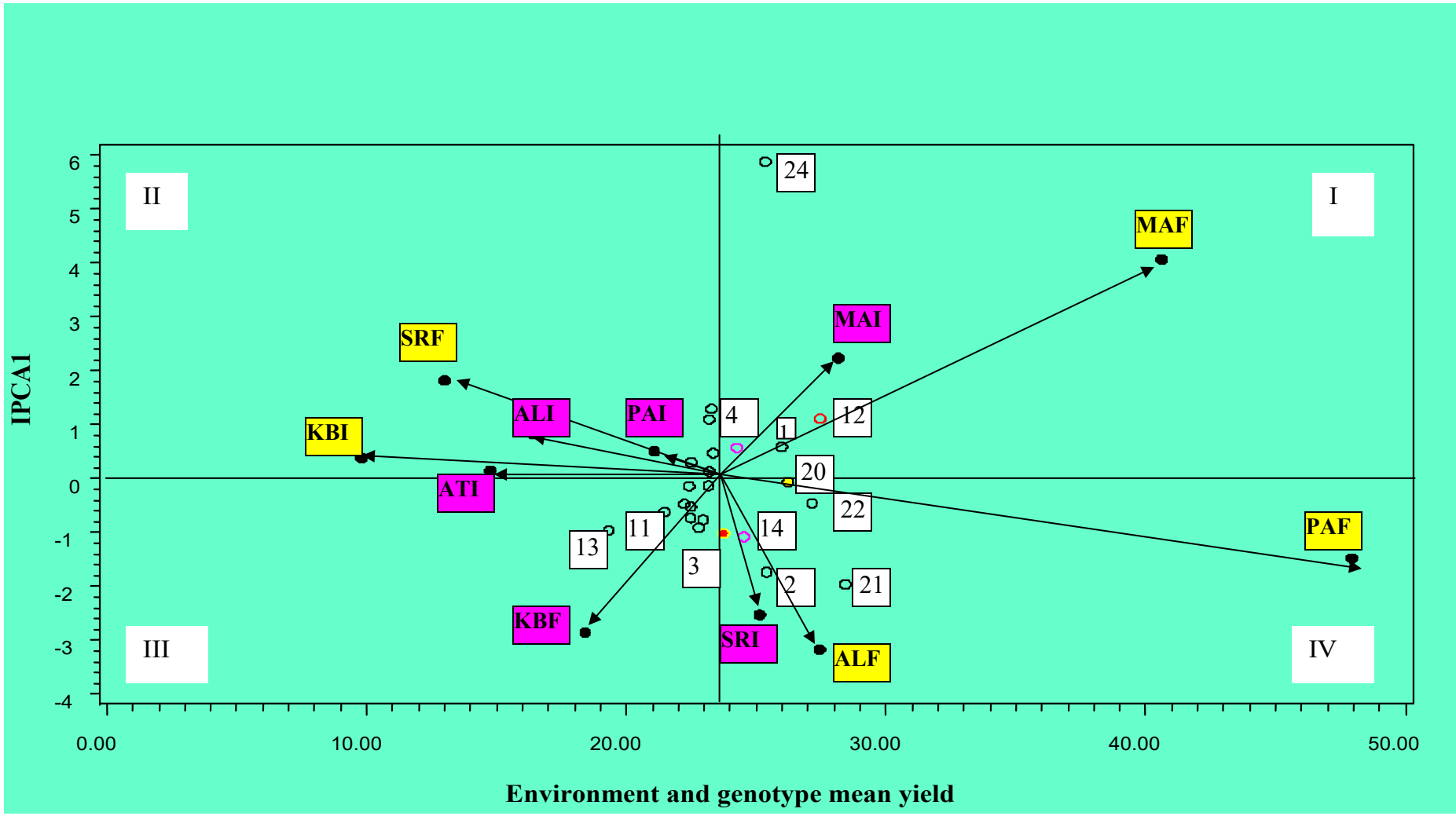
Grand mean = 23.91; R-squared = 0.88; C.V. = 29.58 %

**** represents significance at P≤ 0.001 level.*

The IPCA scores of the genotypes in the AMMI analysis were reported as indication of the stability of a genotype across environments (Gauch and Zobel, 1996; Purchase, 1997; Alberts, 2004). The greater the IPCA scores, negative or positive, (as these are relative values), the more specifically adapted is a genotype to certain environments. Genotypes with IPCA 1 score near zero had little interaction across environments; hence they are the most stable genotypes across the testing environments (Yau, 1995; Purchase, 1997).

Both environments and genotypes showed variability in both main effects and interaction (IPCA 1) for mean yield, variability of the environments being more manifested (Figure 10). When looking at the environments it is clear that there is high variation in the different environments sampled. They are spread from the lower yielding environments in quadrants II and III to the high yielding environments in quadrants I and IV. The high yielding environments are Pawe and Manbuk striga free fields where maximum mean yields of 47.96 and 40.62 Q/ha, respectively were recorded. Environments Manbuk and Shewa Robit striga infested and Alupe striga free fields are average environments for the performance of the genotypes where relatively better mean yields of 28.19, 25.16 and 27.46 Q/ha, respectively were obtained. Kibos striga infested field was the least yielding site where lowest mean yield (9.81 Q/ha) was recorded. Environments with high positive EIPCA1 value are Manbuk free, Manbuk infested and Shewa Robit free and those with high negative EIPCA1 value are Pawe free, Shewa Robit infested, Alupe free and Kibos infested while others have little interaction (Table 11 and Figure 10).

The genotypes have considerably less variation around the mean yield (23.91 Q/ha) and the center of the first IPCA than the environments. According to the IPCA 1 scores, the three-way cross CML445/390/373 (20) was the most stable genotype. In contrast, the standard check, WH-403 (24) was highly unstable followed by INTA/CML390/373 (21) and ZM421 (2) (Figure 10 and Table 10).



Abbrevtions: *PAF, PAI, MAF, MAI, SRF, SRI, ATI, ALF, ALI, KBF &KBI; Striga free and infested fields of Pawe, Manbuk, Shewa Robit, Ataye, Alupe & Kibos.*

Figure 10. AMMI biplot of main effects and IPCA1 for mean yield

Table 10. GIPCA1 and GIPCA2 scores and ASV of the 24 genotypes

Entry No	Code	Mean Yield	GIPCA Score 1	GIPCA Score 2	ASV	Rank
1	ZM521	25.99	0.5925	-2.1043	2.24	20
2	ZM421	25.41	-1.7318	-0.0847	2.22	19
3	ECA-20	23.76	-1.0149	-0.2407	1.32	5
4	ECA-17	24.28	0.5787	-1.3412	1.53	9
5	ECA-18	23.18	-0.1281	2.1054	2.11	17
6	Z97SYNGLS (A)	22.43	-0.1347	-1.4235	1.43	8
7	Z97SYNGLS (B)	22.51	0.3044	0.4193	0.57	1
8	ECA-102	22.97	-0.7604	-1.0272	1.42	7
9	ECA-125	22.25	-0.4640	1.9356	2.03	15
10	ECA-131	23.36	0.4788	0.1195	0.62	3
11	ECA-140	21.48	-0.6148	1.6871	1.86	14
12	ECA-144	27.48	1.1151	-0.8858	1.68	12
13	ECA-203	19.34	-0.9559	0.7065	1.41	6
14	ECA-206	24.53	-1.0765	1.5460	2.07	16
15	ECA-208	23.20	1.1027	-1.2127	1.86	13
16	ECA-209	22.49	-0.5168	-1.4349	1.58	11
17	ECA-210	22.49	-0.7302	-0.4821	1.05	4
18	ECA-216	22.80	-0.9070	-1.0488	1.56	10
19	ECA-E-IR	23.20	0.1350	-2.6174	2.62	22
20	CML445/390/373	26.24	-0.0596	2.7868	2.80	23
21	INTA/CML390/373	28.45	-1.9540	0.5497	2.56	21
22	CML78/390/202	27.17	-0.4474	-0.1788	0.60	2
23	CML78/373/202	23.30	1.3000	1.3720	2.16	18
24	WH-403	25.37	5.8891	0.8540	7.58	24

N.B. Ranks are given by ASV

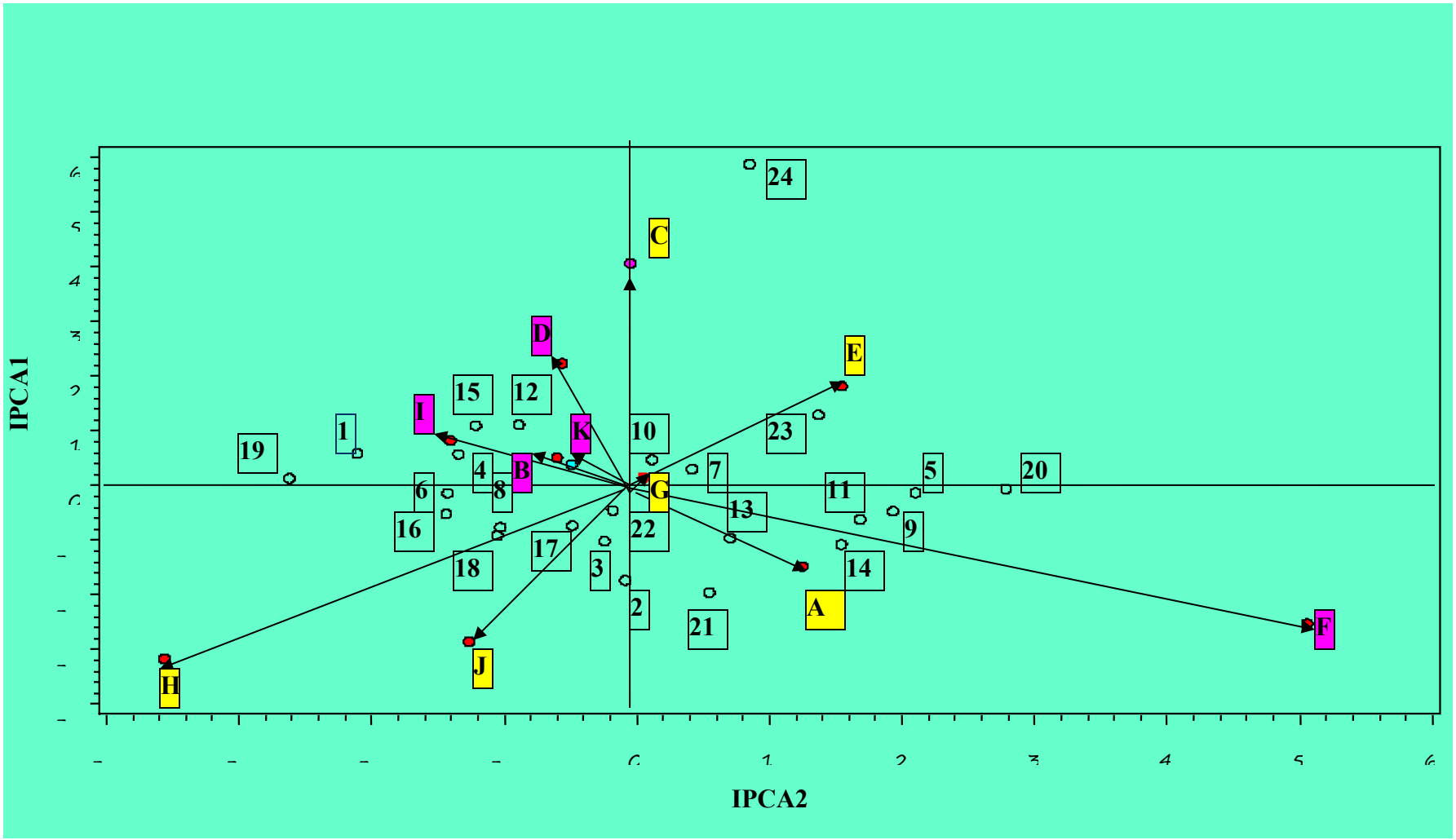
Table 11. EIPCA1 and EIPCA2 scores of the eleven environments

Environments	Mean yield	EIPCA Score 1	EIPCA Score 2
Pawe Free	47.96	-1.475	1.252
Pawe Infested	21.09	0.514	-0.599
Manbuk Free	40.62	4.074	-0.044
Manbuk Infested	28.19	2.242	-0.560
Shewa Robit Free	13.02	1.825	1.548
Shewa Robit Infested	25.16	-2.525	5.058
Ataye Infested	14.78	0.151	0.054
Alupe Free	27.46	-3.170	-3.560
Alupe Infested	16.43	0.828	-1.401
Kibos Free	18.43	-2.853	-1.263
Kibos Infested	9.81	0.390	-0.490

Since IPCA2 scores also explain 25.44% of the GEI, the IPCA1 scores were plotted against IPCA2 scores to further explore adaptation and for a clearer view of interaction among the genotypes and environments (Figure 11). This IPCA discriminate the genotypes more than IPCA1. When plotted on the IPCA1 and IPCA2 scores, the standard check, WH-403 (24) is unstable with CML78/373/202 (23) and ECA-208 (15) unstable but to a lesser extent. CML78/390/202 (22), ECA-131 (10), Z97SYNGLS (B) (7) and ECA-210 (17) are the stable genotypes (Table 10and Figure 11).

5.3.7 AMMI stability value (ASV)

Considering the AMMI stability value ranking, Z97SYNGLS (B) (7), CML78/390/202 (22), ECA-131 (10), ECA-210 (17) and ECA-20 (3) were found to be the most stable genotypes. Among which only CML78/390/202 (22) had relatively comparable stability (2^{nd}) and mean yield (3^{rd}) and the rest are low yielder not exceeding even the overall mean yield. According to this ranking the unstable genotypes were WH403 (24), CML445/390/373 (20), ECA-E-IR (19), INTA/CML390/373 (21) and ZM521 (1). Out of these genotypes INTA/CML390/373 (21), CML445/390/373 (20) and ZM521 (1) had relatively better mean yield performance (1^{st}, 4^{th} and 5^{th}, respectively) (Table 10).



Abbrevtions: *A, B, C, D, E, F, G, H, I, J & K; Striga free and infested fields of Pawe, Manbuk, Shewa Robit, Ataye, Alupe & Kibos.*

Figure 11. Plot of the first two interaction principal component axes of 24 genotypes and eleven environments

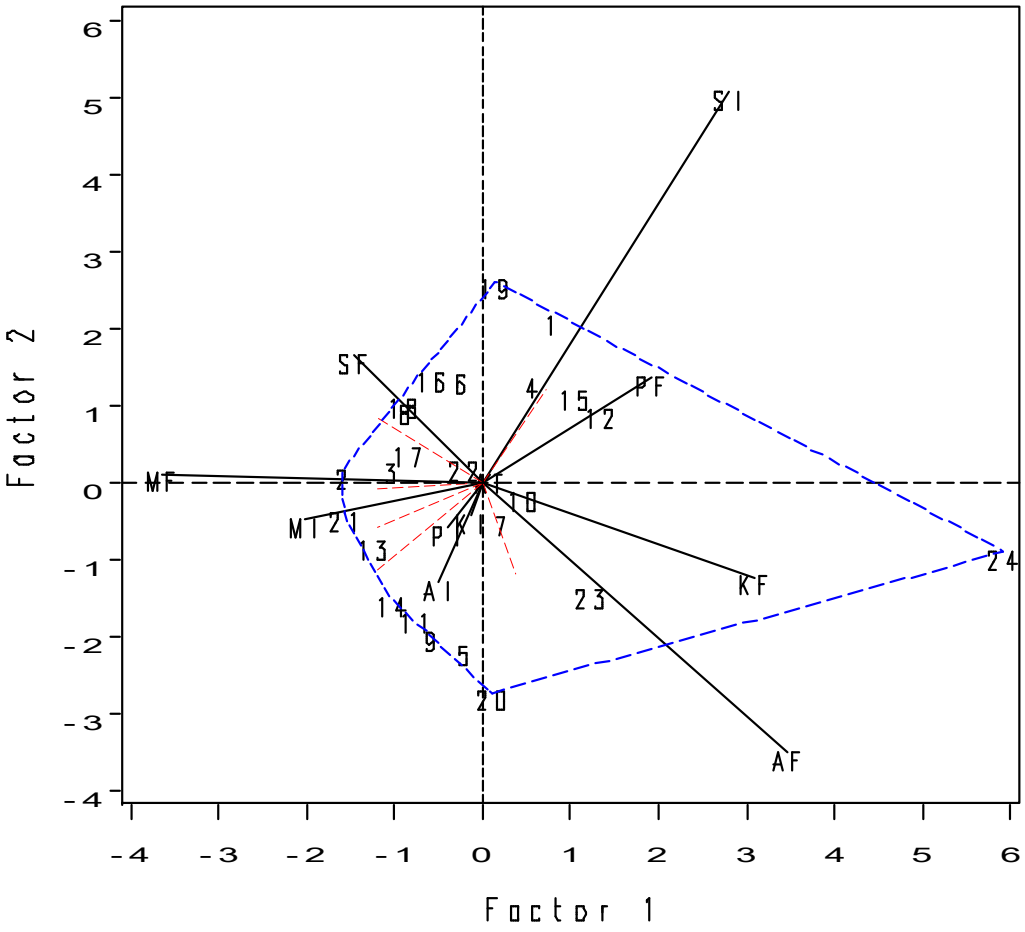
In general, the three way cross IR maize, CML78/390/202 (22) was found to be the most stable genotype based on Francis and Kannenberg's (1978) coefficient of variability (CV), Lin and Binns's (1988) cultivar performance measure (P_i), Eberhart and Russell's (1966) deviation from regression (S^2_{di}) and regression coefficient (b_i) and Purchase's (1997) AMMI Stability Value. The late maturing OPV IR maize, ECA-144 (12) was the second most stable genotype based on the above-mentioned parameters except for Purchase's (1997) AMMI Stability Value. Therefore the above two IR maize genotypes can be used for wide adaptation.

5.3.8 Specific adaptation of genotypes using site regression (SREG) model

In the AMMI model, only the GEI term is absorbed, whereas in the SREG model, the main effects of genotypes (G) plus the GEI, which are the two sources of variation of SREG model, are absorbed and can be presented in a GGE graph (Figure 12). The biplot from SREG model shows that ideal genotypes should have large primary effects (high mean yield) and near zero secondary effects (more stable) and the ideal sites should have large primary effects (high power to discriminate genotypes) and small secondary effects (Yan *et al.,* 2000).

According to the GGE biplot of SREG model, the most extreme genotypes at the vertices, (ECA-E-IR (19), ZM421 (2), INTA/CML390/373 (21), CML445/390/373 (20) and WH-403 (24)) are the most responsive and are the winner genotypes in the sites included in that sector (Figure 12). The above genotypes form a five-sided polygon and four sectors. The IR genotype ECA-E-IR (19) was specifically adapted to Shewa Robit striga infested environment showing better performance (39.44 Q/ha) at the respective sites. The standard check, WH-403 (24) is a winner genotype at Alupe and Kibos striga free environments with mean yield of 55.11 and 38.87 Q/ha, respectively (Figure 12 and Appendix 3). The three-way cross CML445/390/373 (20) was specifically adapted to Alupe striga infested environment with 31.29 Q/ha. ZM421 (2) and INTA/CML 390/ 373 (21) are winner genotypes at Manbuk striga free environment with 55.50 and 60.23 Q/ha, respectively. INTA/CML 390/ 373 (21) is also specifically adapted to Shewa Robit striga free and Kibos striga infested environments.

Among the testing sites, Shewa Robit striga infested and Alupe and Manbuk striga free environments that are found at longer distance from the center of the GGE graph had high power of discriminating the genotypes with mean grain yield of the genotypes ranging from 10.63 to 39.44 Q/ha, 17.00 to 55.11 Q/ha and 22.56 to 60.23 Q/ha, respectively (Figure 12 and Appendix 3 and 4). On the other hand, sites near the center of the GGE graph, namely, Kibos, Ataye and Pawe striga infested environments, had less power of discriminating the performance of the genotypes.



Abbrevtions: *PF, PI, MF, MI, SF, SI, ATI, AF, AI, KF and KI; Striga free and infested fields of Pawe, Manbuk, Shewa Robit, Ataye, Alupe and Kibos.*

Figure 12. GGE graph in SREG model

5.4 Comparison of Stability Parameters

Values and ranking orders for stability of the 24 maize genotypes according to the different stability parameters are indicated in Table 13. Spearman's coefficient of rank correlation (Steel and Torrie, 1980) was determined for each of the possible pair wise comparisons of the different stability parameters and mean grain yield (Table 12). It has to be noted that we have given a rank of 1 for the most stable genotype and a rank of 1 for the highest yielding genotype. Computer programs do not rank the genotypes as in Table 13 below, rather they give rank of 1 for the genotype with the highest value, be it yield or stability parameter, therefore Spearman's coefficient of rank correlation was done based on such ranking procedure.

Spearman's coefficient of rank correlation between mean yield and Eberhart and Russells' (1966) regression coefficient (β_i), Shukla's stability (1972) variance (σ^2_i), Wricke's (1962) ecovalence (W_i) and Eberhart and Russells' (1966) deviation from regression ($\sigma^2_{d_i}$) was positive and significant, but there was non-significant positive correlation between mean yield and Francis and Kannenberg's (1978) coefficient of variation (CV) and Purchase's (1997) AMMI stability value (ASV). However, mean yield was negatively and significantly correlated with Lin and Binns's (1988) cultivar performance measure (P_i). The higher the mean yield of a genotype the higher the regression coefficient (β_i), stability variance (σ^2_i), ecovalence (W_i) and deviation from regression ($\sigma^2_{d_i}$, indicating high yielding genotype tend to be unstable.

The non-significant correlation of coefficient of variation (CV) with mean yield and most of the stability parameters except regression coefficient (β_i) may implicate that this procedure may measure stability of genotypes in a different way. This method measures static phenotypic stability, *i.e.*, the variance of a genotype across environments, and a genotype is stable if the variance of the genotype across environment is small (Lin and Binns, 1991; Hill *et al.,* 1998). The significant positive correlation between coefficient of variation (CV) and regression coefficient (β_i) requires further investigation.

Highly significant and positive Spearman's coefficient of rank correlation was observed among the following; stability variance (σ^2_i), ecovalence (W_i), deviation from regression ($\sigma^2_{d_i}$) and ASV. This finding is in conformity with the findings of Purchase *et al*. (2000) in South African wheat and Alberts (2004) in 23 South African maize hybrids. The result indicated that these procedures evaluate stability of a genotype in a similar way. Among these parameters since ASV explains both main effects and interaction effects and provides agronomically meaningful insights into the data structure, it is better if used as stability measure for reliable selections of stable genotypes. The methods of Shukla and Wricke had perfect correspondence (r = 1.00***), indicating that these two procedures are equivalent for ranking purposes. This observation was in correspondence with previous findings in maize and other crops by Becker and Léon (1988), Purchase *et al*. (2000), Annicchiarico (2002) and Alberts (2004). Therefore one of the two measures can be used for stability evaluation.

The Spearman's rank correlation between cultivar performance measure (P_i) and regression coefficient (β_i) was negative and significant. This estimate indicates that more responsive genotypes tended to have lower P_i values and hence are high yielders. Similar results were obtained in barley (*Hordeum vulgare*) (Lin and Binns, 1988) and cotton (*Gossypium hirsutum*) (Farias *et al*., 1997). These two procedures; cultivar performance measure and regression coefficient showed negative rank correlation coefficients with the other stability parameters, which is in harmony with the findings of Alberts (2004).

In addition, first ranked genotypes by P_i measure are the best performing genotypes in their mean yield, *i.e.*, ranks of the P_i measure and mean yield were in agreement (Table 6), and indicated that this procedure appears more an indication of yield performance and not really an indication of stability. Scapim *et al*. (2000) and Alberts (2004) also pointed out the same observation. This suggests that the parameter shall be considered only in measuring dimensions of yield but could not adequately detect stability and, hence, its efficiency in selecting stable genotypes is limited when used alone.

Table 12. Spearman's coefficient of rank correlation among stability parameters

	Yield	β_i	CV	P_i	σ^2_i	W_i	$\sigma^2_{d_i}$	ASV
Yield	*	0.450*	0.019	-0.882***	0.414*	0.414*	0.492**	0.383
β_i		*	0.639***	-0.449*	-0.042	-0.042	-0.004	-0.018
CV			*	0.078	0.011	0.011	0.088	0.093
P_i				*	-0.242	-0.242	-0.305	-0.292
σ^2_i					*	1.000***	0.946***	0.788***
W_i						*	0.946***	0.788***
$\sigma^2_{d_i}$							*	0.777***
ASV								*

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

Abbreviations: *CV = Francis and Kannenberg's (1978) coefficient of variation; σ^2_i = Shukla's (1972) stability variance; W_i = Wricke's (1962) ecovalence; P_i = Lin and Binns's (1988) cultivar performance measure; $\sigma^2_{d_i}$ = Eberhart and Russells' (1966) deviation from regression; β_i = Eberhart and Russells' (1966) regression coefficient and ASV = Purchase's (1997) AMMI Stability Value.*

Table 13. Ranking of the 24 maize genotypes by mean grain yield and stability parameters.

Entry No	Code	Mean yield	R_1	CV	R_2	σ^2_i	R_3	W_i	R_4	P_i	R_5	$\sigma^2_{d_i}$	R_6	β_i	R_7	ASV	R_8
1	ZM521	25.99	5	52.82	11	31.96	17	308.49	17	109.67	6	33.544	20	1.069	8	2.24	20
2	ZM421	25.41	6	58.18	18	31.85	16	307.46	16	108.93	5	29.285	13	1.178	19	2.22	19
3	ECA-20	23.76	10	53.09	12	19.32	4	192.64	4	135.16	11	21.401	7	1.005	1	1.32	5
4	ECA-17	24.28	9	53.74	13	29.56	13	286.50	13	130.89	8	31.815	16	1.011	2	1.53	9
5	ECA-18	23.18	15	46.75	2	31.72	15	306.30	15	132.49	9	28.683	12	0.814	22	2.11	17
6	Z97SYNGLS (A)	22.43	21	49.75	6	20.95	6	207.54	6	162.72	21	20.642	4	0.875	14	1.43	8
7	Z97SYNGLS (B)	22.51	18	61.53	21	16.31	2	165.05	2	133.29	10	15.604	3	1.133	16	0.57	1
8	ECA-102	22.97	16	48.30	3	35.25	20	338.61	20	167.06	22	32.747	19	0.822	19	1.42	7
9	ECA-125	22.25	22	48.95	4	32.62	19	314.50	19	145.59	17	29.673	14	0.815	21	2.03	15
10	ECA-131	23.36	11	61.56	22	25.60	11	250.19	11	145.14	16	24.034	9	1.156	18	0.62	3
11	ECA-140	21.48	23	61.15	20	25.07	9	245.32	9	167.28	23	27.076	11	1.034	5	1.86	14
12	ECA-144	27.48	2	50.44	7	24.56	8	240.65	8	85.22	2	24.994	10	1.107	11	1.68	12
13	ECA-203	19.34	24	54.30	14	13.85	1	142.48	1	208.20	24	12.214	2	0.847	17	1.41	6
14	ECA-206	24.53	8	50.72	8	29.06	12	281.89	12	122.35	7	31.039	15	0.957	6	2.07	16
15	ECA-208	23.20	13	57.35	16	19.94	5	198.28	5	143.03	14	21.325	5	1.068	7	1.86	13
16	ECA-209	22.49	19	65.54	23	25.59	10	250.11	10	153.56	18	21.986	8	1.194	24	1.58	11
17	ECA-210	22.49	19	43.11	1	17.15	3	172.70	3	156.00	19	11.534	1	0.777	23	1.05	4
18	ECA-216	22.80	17	57.89	17	30.08	14	291.24	14	144.68	15	32.271	18	1.024	4	1.56	10
19	ECA-E-IR	23.20	13	59.84	19	53.03	21	501.60	21	156.30	20	55.699*	21	1.015	3	2.62	22
20	CML445/390/373	26.24	4	55.76	15	55.42	22	523.49	22	93.17	4	57.073*	22	1.084	10	2.80	23
21	INTA/CML390/373	28.45	1	52.31	10	56.67	24	535.00	23	80.96	1	57.697*	23	1.107	11	2.56	21
22	CML78/390/202	27.17	3	50.81	9	21.16	7	209.47	7	89.99	3	21.335	6	1.112	13	0.60	2
23	CML78/373/202	23.30	12	49.62	5	32.38	18	312.35	18	141.27	13	32.099	17	0.870	5	2.16	18
24	WH-403	25.37	7	70.16	24	214.95	24	1985.9	24	140.12	12	219.830**	24	0.927	9	7.58	24

, **, * represent significance at $P \leq 0.05$, 0.01 and 0.001 level, respectively.*
N.B. The ranks are given based on the stability of the genotypes according to the stability parameters.

Abbreviations: *CV = Francis and Kannenberg's (1978) coefficient of variation; σ^2_i = Shukla's (1972) stability variance; W_i = Wricke's (1962) ecovalence; P_i = Lin and Binns's (1988) cultivar performance measure; $\sigma^2_{d_i}$ = Eberhart and Russells' (1966) deviation from regression; β_i =*

Eberhart and Russells' (1966) regression coefficient; ASV = Purchase's (1997) AMMI Stability Value and R_1- R_8= Rank by yield and 7 stability parameters.

6. CONCLUSIONS AND RECOMMENDATIONS

Imidazolinone (imazapyr) is a systemic herbicide which has the capacity to destroy germinating striga seeds attempting to parasitise maize plants and giving almost season-long striga control when used as a seed coating. The herbicide also kills any germinating seeds of maize genotypes which are not resistant against its action. Genotypes possessing genes resistant to the herbicide are known as imidazolinone (imazapyr) resistant (IR) maize genotypes. In this study 23 IR maize genotypes along with standard and local checks were tested at eleven environments (6 striga infested and 5 striga free) in Ethiopia and Kenya during 2006/07 cropping season. The objectives of the experiment were evaluating the IR maize genotypes for grain yield and adaptability under striga infestation and striga free field conditions, determining the magnitude of GEI of IR maize genotypes for grain yield, determining stability of yield performance among the IR maize genotypes and identifying the stable genotype(s) and those with specific adaptation. Studying the correlation among various stability parameters was another objective of this study.

ANOVA of grain yield for individual environments revealed non-significant differences among the genotypes evaluated for most of the environments except for striga free and striga infested environments at Alupe and Kibos. Under the Ethiopian environments, although the difference between the highest yielding and the lowest yielding genotypes ranged from 15.91 Q/ha for Ataye striga infested environment to 37.67 Q/ha for Manbuk striga free environment, this large differences could not be declared statistically significant due to the large errors. There was also significant difference between striga counts at Alupe, Kibos and Shewa Robit. Except for Manbuk striga infested field, similar trend was observed in all other striga infested fields in that, the standard and the local checks hold the largest number of striga count as compared to the 23 IR maize genotypes. The mean yield of all the IR maize genotypes was better than that of the standard check, WH-403. This result can be taken as one testimony for the new herbicide seed coating technology on maize (IR maize) to reduce striga attack under striga infested field conditions.

At four locations, namely, Pawe, Manbuk, Alupe and Kibos, where successful striga infestation was achieved, yield was reduced on average from 8.62 at Kibos to 26.87 Q/ha at Pawe. The highest percent reduction due to striga infestation was observed on the standard check, WH-403 at Alupe (79.00%) and Kibos (75.54%). The average percent reduction in yield for all the IR maize genotypes was 40.40% whereas it was 65.00% for the standard check. If the mean yield of the striga free and infested fields over the four locations was considered, the mean of the standard check was the lowest (12.67 Q/ha) under striga infested condition and highest (42.29 Q/ha) under striga free condition. Under striga free fields, the standard check had a yield advantage of only 8.2% over the best IR genotype (INTA/CML390/373 (21)) while under striga infested fields the highest yielding IR maize genotype (CML445/390/373 (20) had a yield advantage of 85.8%.

Combined ANOVA of grain yield of the 24 genotypes in eleven environments revealed highly significant differences among the environments, genotypes and GEI, indicating differential response of the genotypes across the 11 environments. Partitioning of the sum of squares of the components for grain yield indicated that 64.28% of the GEI SS was due to environments, 2.24% due to genotypes, 16.65% due to GEI and 12.32% due error. Among the traits studied significant difference was observed among genotypes for days to anthesis, days to silking, ear height, plant aspect, ear aspect and number of ears harvested. A single degree of contrast to compare performance under striga free and striga infested condition was highly significant for these traits. From this result it can be seen that the impact of striga on the host is very significant and highly damaging. In striga infested environments reduction in grain yield, plant height, ear height and number of ears harvested and increase in stalk and root lodging were observed. This implies that striga is an important limiting factor for maize production.

In AMMI analysis the first principal component axis (IPCA 1) of the interaction captured 32.55% of the interaction SS and the second IPCA explained 25.44% of the interaction SS and cumulatively the two IPCAs explained 58% of the total GEI as compared to only 6% explained by linear regression. The remaining 42% of GEI was considered as noise, which is not interpretable and therefore was pooled with the residual. The high yielding

environments are Pawe and Manbuk striga free fields where maximum mean yields (47.96 and 40.62 Q/ha, respectively) were recorded while Kibos striga infested field was the least yielding site where lowest mean yield (9.81 Q/ha) was recorded. According to the IPCA 1 scores, the three-way cross CML445/390/373 (20) was the most stable genotype followed by ECA-18 (5), Z97SYNGLS (A) (6), ECA-E-IR (19), Z97SYNGLS (B) (7) and CML78/390/202 (22). In contrast, the standard check, WH-403 was highly unstable followed by INTA/CML390/373 (21) and ZM421 (2).

In general, the three way cross IR maize, CML78/390/202 (22) was found to be the most stable genotype based on coefficient of variability (CV), cultivar performance measure (P_i), deviation from regression ($\sigma^2{}_{d_i}$) and ASV and with acceptable average stability based on the regression coefficient (β_i),) ecovalence and stability variance. The late maturing OPV IR maize, ECA-144 (12) was the second most stable genotype based on the above-mentioned parameters except for ASV. They are among the top yielding genotypes both under striga infestation and striga free conditions. Therefore the above two IR maize genotypes can be used for wide adaptation.

The IR genotype ECA-E-IR (19) was specifically adapted to Shewa Robit striga free and infested environments showing better performance at this location. The standard check, WH-403 (24) was a winner genotype at Alupe and Kibos striga free environments and to a lesser extent at Pawe striga free environment. The three-way cross CML445/390/373 (20) was specifically adapted to Alupe striga infested environment with 31.29 Q/ha. ZM421 (2) and INTA/CML 390/ 373 (21) are winner genotypes at Manbuk striga free environment.

Spearman's coefficient of rank correlation between mean yield and regression coefficient (β_i), stability variance (σ^2_i), ecovalence (W_i) and deviation from regression ($\sigma^2{}_{d_i}$) was positive and significant, but there was non-significant correlation between mean yield and coefficient of variation (CV) and ASV. However, mean yield was negatively and significantly correlated with cultivar performance measure (P_i).

Among the stability parameters used since ASV explains the highest proportion of the interaction effects and provides agronomically meaningful insights in to the data structure, it is better if it is used as stability measure for reliable selections of stable genotypes. The methods of Shukla and Wricke had perfect positive correlation, indicating that these two procedures are equivalent for ranking purposes. Therefore, one of the two measures can be used for genotypes' stability evaluation.

The lack of correlation between coefficient of variation (CV) and many of the stability parameters indicated that coefficient of variation (CV) measures a specific aspect of stability, i.e. static phenotypic stability. The cultivar performance measure (P_i) and regression coefficient (β_i) showed negative rank correlation coefficients with each other and other stability parameters. In addition, first ranked genotypes by cultivar performance measure (P_i) are the best performing genotypes in their mean yield, i.e., ranks of the cultivar performance measure (P_i) and mean yield were in agreement and indicated that cultivar performance measure (P_i) appears more an indication of yield performance than an indication of stability. This suggests that the parameter shall be considered only in measuring dimensions of yield but could not adequately detect stability and, hence, its efficiency in selecting stable genotypes is limited when used alone.

Based on the results of this investigation, the following recommendations can be forwarded:

- The three-way cross IR maize hybrid, CML78/390/202 (22) and the late maturing IR maize OPV, ECA-144 (12) had higher grain yields and were the most stable genotypes and therefore, they are recommended for the study areas.

- The following genotypes have good specific adaptation: ECA-E-IR (19) was specifically adapted to Shewa Robit, the standard check, WH-403 (24) to Alupe and Kibos striga free environments, the three-way cross CML445/390/373 (20) to Alupe striga infested environment and ZM421 (2) and INTA/CML 390/ 373 (21) to Manbuk striga free environment.

- Since the environments differ in their climatic and edaphic conditions, higher rates of the herbicide may be necessary to achieve full season control using late maturing maize genotypes or where the season is longer, therefore the rate of application of the imazapyr herbicide should be determined for the study areas, especially for Ethiopian conditions.

- Since there is no any single control option, which can solve the problem of striga, the IR technology should combine other proven striga suppressive technologies that can reduce striga biomass and seed banks in the soil.

- ASV can be used as stability measure for reliable selections of stable genotypes replacing other stability parameters such as stability variance (σ^2_i), ecovalence (W_i) and deviation from regression ($\sigma^2_{d_i}$), but concurrent use of more than one stability statistics is recommended to more predict the stability of the genotypes. The regression coefficient (β_i) can be used to measure responsiveness of genotypes to different environment.

- In order to give more sound and reliable recommendation this experiment should be repeated at least for one year.

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8. APPENDICES

Appendix 1. Rainfall of test locations for the year 2006/07

Months	Pawe	Shewa Robit	Months	Alupe	Kibos
	Rainfall (mm)	Rainfall (mm)		Rainfall (mm)	Rainfall (mm)
Jan. 2006	9.2	27.6	July 2006	166.7	52.8
Feb. 2006	11.2	28.1	Aug. 2006	84.7	93.3
Mar. 2006	0.0	52.7	Sep. 2006	278.3	46.1
Apr. 2006	18.6	200.7	Oct. 2006	210.2	253.8
May 2006	152.7	22.4	Nov. 2006	212.3	326.5
June 2006	216.6	48.6	Dec. 2006	231.9	423.2
July 2006	401.9	200.3	Jan. 2007	115.8	NA
Aug. 2006	706.2	340.5	Feb. 2007	85.1	NA
Sep. 2006	263.1	97.8	Mar. 2007	85.6	NA
Oct. 2006	192.3	19.4	Apr. 2007	168.2	NA
Nov. 2006	5.9	0.0	May 2007	201.1	NA
Dec. 2006	0.0	100.8	June 2007	89.7	NA

Source: Meteorological Stations of the respective sites

Appendix 2. Relative efficiency of simple lattice over RCBD

Environments	RE (%) over RCBD	CV (%) RCBD	CV (%) Lattice
Pawe free	1.011	23.74	22.98
Pawe infested	2.412	33.00	18.72
Manbuk free	1.043	20.33	18.93
Manbuk infested	1.297	27.34	21.82
Shewa Robit free	1.340	59.64	46.67
Shewa Robit infested	1.147	35.55	30.70
Ataye infested	1.748	46.64	31.41
Alupe free	1.236	13.34	10.97
Alupe infested	1.000	25.21	28.54
Kibos free	1.351	19.84	15.45
Kibos infested	1.000	30.56	30.91

Appendix 3. Mean yield (Q/ha) of the 25 maize genotypes tested under striga free field conditions

Entry No	Code	Environments									
		Pawe Free	Rank	Manbuk Free	Rank	SR Free	Rank	Alupe Free	Rank	Kibos Free	Rank
1	ZM521	58.32	3	39.66	13	20.23	3	22.02	18	21.21	5
2	ZM421	45.96	16	55.50	2	12.14	14	26.01	14	14.40	20
3	ECA-20	43.78	19	45.84	5	12.49	12	25.20	15	11.49	24
4	ECA-17	48.99	11	40.85	12	7.26	21	21.99	19	18.55	10
5	ECA-18	38.36	25	39.14	14	12.99	11	36.44	3	18.26	12
6	Z97SYNGLS (A)	43.80	18	35.75	21	13.87	10	20.45	23	11.02	25
7	Z97SYNGLS (B)	46.06	15	42.75	9	5.04	24	28.45	9	19.95	7
8	ECA-102	41.75	21	36.18	19	19.35	4	17.00	25	19.93	8
9	ECA-125	38.38	23	41.20	11	15.62	9	31.60	5	20.84	6
10	ECA-131	58.20	4	33.78	22	8.19	18	26.95	12	16.14	18
11	ECA-140	47.09	14	37.11	18	8.52	17	26.52	13	17.44	13
12	ECA-144	61.20	1	38.50	16	17.94	8	27.90	10	26.17	2
13	ECA-203	39.47	22	36.16	20	10.83	16	18.68	24	15.35	19
14	ECA-206	43.31	20	45.03	7	11.98	15	31.62	4	17.13	17
15	ECA-208	51.86	8	33.19	23	7.89	19	25.11	16	17.17	16
16	ECA-209	47.76	13	47.10	4	7.47	20	21.43	20	11.55	23
17	ECA-210	38.38	24	38.35	17	19.27	5	21.31	21	17.27	15
18	ECA-216	45.35	17	49.34	3	17.96	7	23.18	17	13.52	22
19	ECA-E-IR	48.60	12	38.66	15	19.15	6	21.08	22	14.16	21
20	CML445/390/373	50.11	9	45.39	6	5.52	23	39.53	2	21.38	4
21	INTA/CML390/373	53.20	6	60.23	1	25.02	1	31.04	6	19.12	9
22	CML78/390/202	58.88	2	41.51	10	23.76	2	29.66	8	18.39	11
23	CML78/373/202	49.73	10	31.14	24	3.99	25	30.83	7	22.99	3
24	WH-403	52.61	7	22.56	25	6.06	22	55.11	1	38.87	1
25	LOCAL CHECK	53.37	5	44.90	8	12.38	13	27.13	11	17.40	14
	Mean Yield	*48.09*		*40.79*		*13.18*		*27.45*		*18.39*	
	CV (%)	*24.13*		*20.32*		*60.01*		*13.34*		*19.84*	
	LSD	*24.50*^{NS}		*17.11*^{NS}		*16.68*^{NS}		*7.56*** *		*7.53****	

**** represent significance at p ≤ 0.001level, NS = non-significant.*

Appendix 4. Mean yield (Q/ha) of the 25 maize genotypes tested under striga infested field conditions

Entry No	Code	Environments											
		Pawe Infested	Rank	Manbuk Infested	Rank	SR Infested	Rank	Ataye Infested	Rank	Alupe Infested	Rank	Kibos Infested	Rank
1	ZM521	18.75	17	25.50	19	36.75	3	13.14	19	17.76	7	12.57	3
2	ZM421	22.93	10	34.47	4	26.93	11	9.65	22	20.00	3	11.54	5
3	ECA-20	30.17	1	27.64	13	26.08	12	12.30	21	14.95	15	11.42	6
4	ECA-17	28.95	2	21.57	23	35.90	4	14.57	12	17.91	6	10.50	11
5	ECA-18	26.64	4	27.33	14	15.13	21	13.00	20	16.63	12	11.11	7
6	Z97SYNGLS (A)	25.52	5	24.70	21	32.36	6	13.60	17	16.57	13	9.08	15
7	Z97SYNGLS (B)	24.85	6	26.17	17	25.42	14	6.11	25	17.21	10	5.67	23
8	ECA-102	23.99	8	35.40	3	25.86	13	17.14	8	8.19	25	7.84	19
9	ECA-125	24.35	7	23.62	22	12.50	24	9.31	24	16.77	11	10.63	10
10	ECA-131	17.89	19	33.80	6	21.34	17	16.90	9	13.03	20	10.73	9
11	ECA-140	21.05	14	34.03	5	10.63	25	14.89	11	15.72	14	8.69	16
12	ECA-144	28.02	3	26.07	18	31.68	9	18.51	4	18.43	5	7.82	20
13	ECA-203	16.78	20	27.23	15	12.84	23	9.49	23	14.12	17	6.38	22
14	ECA-206	17.95	18	36.80	1	15.84	20	22.02	1	17.25	9	10.96	8
15	ECA-208	22.57	11	28.85	10	33.80	5	15.01	10	12.23	22	7.58	21
16	ECA-209	19.55	16	26.20	16	24.85	15	17.91	5	12.39	21	3.92	25
17	ECA-210	23.90	9	28.37	11	34.24	7	13.77	16	13.50	19	8.41	18
18	ECA-216	11.93	24	20.80	24	27.32	10	17.61	6	14.63	16	9.23	14
19	ECA-E-IR	7.30	25	30.00	8	39.44	1	14.48	13	13.82	18	8.56	17
20	CML445/390/373	21.87	12	32.12	7	15.03	22	17.20	7	31.29	1	9.25	13
21	INTA/CML390/373	14.87	22	29.62	9	19.84	18	19.82	3	22.74	2	17.51	1
22	CML78/390/202	20.33	15	36.29	2	24.36	16	13.51	18	19.84	4	12.30	4
23	CML78/373/202	21.63	13	24.80	20	18.65	19	20.65	2	17.70	8	14.22	2
24	WH-403	14.42	23	15.17	25	39.05	2	14.14	14	11.57	23	9.51	12
25	LOCAL CHECK	15.31	21	28.22	12	31.73	8	13.97	15	9.98	24	5.39	24
	Mean Yield	*21.00*		*28.20*		*25.41*		*14.75*		*16.17*		*9.63*	
	CV (%)	*31.76*		*27.34*		*35.55*		*46.63*		*25.21*		*30.56*	
	LSD	*14.06* ^{NS}		*15.91* ^{NS}		*19.72* ^{NS}		*14.26* ^{NS}		*8.42***		*6.08**	

** and ** represent significance at p ≤ 0.05 and 0.01 level of significance, respectively , NS = non-significant.*

Appendix 5. Striga count (per plot) under the 25 maize genotypes tested under striga infested field condition

Entry No	Code	Environments											
		Pawe Infested	Rank	Manbuk Infested	Rank	SR Infested	Rank	Ataye Infested	Rank	Alupe Infested	Rank	Kibos Infested	Rank
1	ZM521	53.00	17	42.50	7	0.00		44.00	10	17.00	7	23.50	13
2	ZM421	64.50	11	32.50	14	0.00		19.00	23	15.00	10	12.50	23
3	ECA-20	67.00	8	40.50	8	0.50	11	40.00	14	22.00	5	32.50	8
4	ECA-17	67.00	8	64.50	2	0.00		40.00	14	9.00	13	63.00	4
5	ECA-18	109.00	4	34.50	13	1.00	8	45.00	9	3.00	21	30.50	10
6	Z97SYNGLS (A)	79.50	6	59.50	3	2.00	3	53.00	7	5.00	18	29.00	11
7	Z97SYNGLS (B)	61.00	14	48.50	6	0.50	11	16.50	24	9.00	13	23.50	12
8	ECA-102	63.50	13	29.00	18	0.00		31.00	18	1.00	23	32.00	9
9	ECA-125	54.50	16	29.50	16	0.50	11	32.50	17	10.00	12	15.00	19
10	ECA-131	38.50	23	21.50	23	1.00	8	53.00	7	6.50	16	35.50	7
11	ECA-140	41.50	22	14.50	24	0.00		12.00	25	3.50	20	10.50	24
12	ECA-144	65.50	10	53.50	4	1.50	5	41.00	13	0.00		15.50	17
13	ECA-203	40.00	21	48.50	5	0.00		26.50	20	16.50	8	43.00	6
14	ECA-206	127.00	3	37.50	10	0.00		71.00	3	8.50	15	15.50	17
15	ECA-208	46.00	18	14.50	25	0.00		26.00	21	2.00	22	22.00	14
16	ECA-209	30.50	24	32.00	15	1.00	8	56.50	6	5.00	18	14.50	20
17	ECA-210	24.50	25	28.50	19	0.00		20.50	22	15.50	9	13.00	22
18	ECA-216	46.00	18	29.00	17	1.50	5	60.00	5	0.00		18.00	15
19	ECA-E-IR	45.50	20	36.00	11	1.50	5	42.00	12	11.50	11	8.50	25
20	CML445/390/373	91.00	5	68.50	1	0.50	11	31.00	18	29.00	3	14.50	21
21	INTA/CML390/373	59.00	15	28.00	21	0.50	11	34.50	16	5.50	17	99.00	3
22	CML78/390/202	64.00	12	40.50	9	2.00	3	80.00	2	27.00	4	47.50	5
23	CML78/373/202	75.00	7	27.00	22	0.00		42.50	11	17.50	6	17.50	16
24	WH-403	244.00	1	35.50	12	4.50	2	85.00	1	400.00	1	153.50	1
25	LOCAL CHECK	155.50	2	28.50	20	8.50	1	61.50	4	107.00	2	107.50	2
	Mean Striga count	*69.00*		*36.98*		*1.08*		*42.56*		*29.84*		*35.88*	
	CV (%)	*58.58*		*51.88*		*158.00*		*54.87*		*190.2*		*60.03*	
	LSD	*85.28* ^{NS}		*39.60* ^{NS}		*3.52* *		*48.20* ^{NS}		*117.1* ***		*44.46* ***	

** and *** represent significance at $p \leq 0.05$ and 0.001level, respectively, NS-non-significant.*

Appendix 6. Combined ANOVA of yield and other traits of the 24 genotypes

Source	Df	Mean squares			
		Yield	Plant aspect	Ear aspect	No of Ears harvested per plot
Env	10	6523.25***	15.20***	5.03***	1280.61***
Reps (Env)	11	406.21***	5.25***	3.10***	44.85
Genotype	23	98.71**	1.18**	1.14*	62.44***
GEI	230	73.50***	0.73	0.72	40.91**
IR Vs Checks	1	107.60	1.05	0.10	194.40*
Free Vs Infested (Ethiopia)	1	8649.57**	2.11	0.22	65.07
Free Vs Infested (Kenya)	1	5015.79***	54.08***	2.31**	1320.98***
CV (%)		*29.58*	*32.00*	*33.31*	*21.43*
Mean		*23.91*	*2.54*	*2.44*	*24.24*
R-square		*0.88*	*0.71*	*0.63*	*0.78*

Appendix 6. Continued…

Source	Df	Mean squares						
		Days to anthesis	Days to silking	Days to maturity	Plant height	Ear height	Stalk lodging	Root lodging
Env	8(3)	904.53***	640.63***	756.80***	22776.41***	9769.37***	186.71***	217.80***
Rep (Env)	9(4)	3.62	29.31***	11.00**	2125.26***	390.11**	13.70*	18.22**
Genotype	23	22.97***	27.76***	3.60	364.20	280.41**	9.67	10.30
GEI	184(69)	4.48***	6.68*	4.01**	266.83	136.47	5.31	7.22
IR Vs Checks	1	75.03***	32.36*	3.26	90.74	193.10	1.36	8.43
Free Vs Inf.(Ethio)	1				40792.86**	11816.23**	287.58**	50.51*
Free Vs Inf. (Keny)	1				13572.25**	8281.00**	40.96	0.00
CV (%)		*2.30*	*3.27*	*1.25*	*9.68*	*13.87*	*94.66*	*91.20*
Mean		*61.41*	*65.68*	*126.90*	*176.52*	*81.89*	*2.84*	*3.07*
R-square		*0.95*	*0.89*	*0.92*	*0.82*	*0.81*	*0.67*	*0.69*

, ** and * represent significance at p ≤ 0.05, 0.01 and 0.001level, respectively.*
Numbers in the parenthesis are df for plant height, ear height, stalk lodging and root lodging, which were measured from four locations.
N.B. *For plant aspect, ear aspect and number of ears harvested per plant data was taken from 11 environments; for days to anthesis, days to silking and days to maturity data was taken from 9 environments; for plant height, ear height, stalk lodging and root lodging data was taken from 4 environments.*

Appendix 7. Protocol for harvesting of striga seed and Sand-striga inoculums preparation

Harvesting of striga seeds and preparation of sand-striga inoculum protocol used for striga related researches in CIMMYT/Kenya.

Harvesting of striga seed

1. Harvest striga plants with mature capsules from a maize or sorghum field, cut the stem of mature striga plants with a knife.
2. Sun dry the materials for 10-14 days and keep on turning them to achieve uniform drying.
3. Keep the materials in a cool dry place, after drying, to avoid rotting and contamination from bacteria and fungi.
4. Thresh the materials gently on a clean polythene sheet using a wooden stick to attain about 90% and above of the seeds from the striga capsules.
5. After threshing all of striga, material is screened on the sheeting by passing it through sieves of 250, 180 and 90-micron openings, respectively. Most of striga seed is collected on the 90-micron sieve.
    - The 250µm sieve is placed on top of 180µm sieve to remove bigger particles but striga seeds and other small particles will pass through on to the 180µm sieve which only allows the striga seeds and other small particles which are of similar or smaller size of striga seeds.
    - This will pass onto the 90µm sieve and only very fine particles will pass through. Most striga seeds will be trapped here.
    - This will give about 50-80% striga seeds.

Sand-striga inoculum preparation

1. Mix thoroughly 5 kg of sieved sand with 10gm of striga seeds.
2. At planting, apply one tablespoonful or two teaspoonfuls per planting hole (hill).
3. This gives approximately 15 gram of the inoculum per hill. This is estimated to give about 2,500 viable striga seeds per hill.