GENOTYPE BY ENVIRONMENT INTERACTION AND YIELD STABILITY OF MAIZE HYBRIDS EVALUATED IN ETHIOPIA

BY

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DECLARATION

I, the undersigned, hereby declare that this thesis, prepared for the degree of *Magister Scientiae Agriculturae*, which was submitted by me to the University of the Free State, is my original work and has not been submitted previously to any other University/Faculty. All sources of materials and financial assistances used for the study have been duly acknowledged. I furthermore cede copyright of the thesis in favour of the University of the Free State.

Signed on the 31th of July 2009 at the University of the Free State, Bloemfontein, South Africa.

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ABBREVIATIONS

AMMI	Additive Main effects and Multiplicative Interaction
ANOVA	Analysis of variance
ASV	AMMI Stability Value
BLUP	Best Linear Unbiased Predictors
CIMMYT	Centro Internacional de Mejoramiento de Maiz y Trigo (International Maize and Wheat Improvement Center)
cm	Centimetre
CSA	Central Statistical Agency
CV	Coefficient of Variation
DF	Degrees of Freedom
ESE	Ethiopian Seed Enterprise
FAO	Food and Agriculture Organization
G x E	Genotype x Environment
ha	Hectare
IAR	Institute of Agricultural Research
IPCA	Interaction Principal Component Analysis
JLR	Joint Linear Regression
km	Kilometre
LR	Linear Regression
LSD	Least Significant Difference
m	Meter
MET	Multi-environment Trials
mm	Milimeter
ML	Maximum Likelihood

MS	Mean Square
NCSS	Number Cruncher Statistical System
NPSA	Non-parametric Stability Analysis
PCA	Principal Component Analysis
REML	Restricted Maximum Likelihood
SAS	Statistical Analysis System
SS	Sum of Squares
t	tons
UN	United Nations
UPGMA	Unweighted Pair Group Method with Arithmetic average

CHAPTER 1

GENERAL INTRODUCTION

Maize (*Zea mays* L.) is one of the oldest food grains. It belongs to the grass family Poaceae (Gramineae), tribe Maydeae and is the only cultivated species in this genus. It is the most productive food plant with a multiplication ratio of 1:600 or more per plant bases under optimum conditions (Aldrich *et al*., 1975). It is grown from sea level to over 3000 meters above sea level (Singh, 1987; Dowswell *et al.*, 1996).

Maize grain today is recognized worldwide as a strategic food and feed crop that provides an enormous amount of protein and energy for humans and livestock. Data from the United Nations (UN) Food and Agriculture Organization (FAO) showed that for 2006 world maize production was 144 million ha while that for wheat was 216 million and for rice it was 154 million ha. In terms of production, however, maize exceeds wheat and rice. World maize production for 2006 was 695 million mt, while that of wheat was 606 and rice was 635 million mt (FAOSTAT, 2008). Although 70% of the world maize area was in developing countries, only 49% of the world's maize was produced there (FAOSTAT, 2008). It is estimated that by the year 2020, demand for maize in developing countries will surpass the demand for both wheat and rice. From 1995 to 2020, global and sub-Saharan Africa consumption was projected to increase by 50% and by 93% respectively (CIMMYT, 2001). Its advantages in the ethanol industry also keep maize in high demand.

In Ethiopia cereals account for about 80% of the annual crop production and maize is the first in total production and yield per unit area and second in area coverage among all the cereals. Total area covered by maize during the 2006/07 growing season was 1.7 million ha and the national average yield was about 2.2 t ha^{-1} (CSA, 2007).

Maize improvement in Ethiopia started half a century ago (Benti, 1988). During the late 1960s and early 1970s, several promising hybrids and composite varieties of East African origin were introduced and evaluated at different locations. These resulted in the recommendation of several maize varieties for the maize growing regions of the country (Benti, 1988; Benti *et al*., 1997). Through time, most of these varieties have been replaced by locally developed and better adapted varieties (Mosisa *et al.*, 1994). However, the changing environmental conditions affect the performance of maize genotypes which requires a breeding programme that

needs to take into account the consequences of environment and genotype interaction in the selection and release of improved varieties.

Crop breeders have been striving to develop genotypes with superior grain yield, quality and other desirable characteristics over a wide range of different environmental conditions. Genotype x environment (G x E) interaction is one of the main complications in the selection of broad adaptation in most breeding programmes. The phenotype of an organism is determined by the combined effect of the environment and the genotype which interact with one another. Numerous studies have shown that a proper understanding of the environmental and genetic factors causing the interaction as well as an assessment of their importance in the relevant G x E system could have a large impact on plant breeding (Magari and Kang, 1993; Basford and Cooper, 1998). G x E interaction occurs universally when genotypes are evaluated in several different environments (Becker and Léon, 1988; Magari, 1989; Kang, 1990). Magari and Kang (1993) found that the contribution of different environmental factors, to the yield stability of maize in yield trials, had a significant impact on the heterogeneity of the results.

When environmental differences are large like in Ethiopia, it may be expected that the interaction of G x E will also be higher. As a result, one cultivar may have the highest yield in some environments while a second cultivar may excel in others. Hence, it is important to know the magnitude of the interactions in the selection of genotypes across several environments besides calculating the average performance of the genotypes under evaluation (Fehr, 1991; Gauch and Zobel, 1997).

The effect of G x E becomes more apparent by conducting multi-location and multi-years trials, that have three main objectives: a) to accurately estimate and predict yield based on limited experimental data; b) to determine yield stability and the pattern of response of genotypes across environments; and c) to provide reliable guidance for selecting the best genotypes or agronomic treatments for planting in future years at new sites (Crossa, 1990).

A number of parametric statistical procedures have been developed over the years to analyze G x E interaction and especially yield stability over environments. The effects of genotype and environments are statistically non-additive, which means that differences between genotypes depend on the environment. For data sets with more than two genotypes and more than two environments, the G x E interactions are commonly calculated by analysis of variance (ANOVA), leading to an estimated variance component for G x E interactions. Performance tests over a series of environments give information on G x E interactions at population level, but

from a practical point view, it is important to measure the stability of the performance of individual genotypes (Eberhart and Russell, 1966).

Ethiopia is known for its diverse/heterogeneous agro-ecology ranging from 100 m below sea level in the Danakil depression to 4620 m above sea level at Mount Ras Dashen that contributes further to the problem of selecting stable maize varieties for wider adaptation. To reduce the effect of G x E interaction, crop improvement programmes usually run performance trials across a wide range of environments to ensure that the selected genotypes have a high and stable performance across several environments.

Various studies have been conducted to analyze the effect of G x E interaction on the Ethiopian maize varieties. However, the changing environmental conditions of Ethiopia, the expansion of maize to new agro-ecologies coupled with inadequate maize varieties available for the different environments necessitate a rigorous and continuous study of G x E interaction for a dynamic crop improvement programme. Hence, the objectives of this study were:

1. To evaluate the adaptability of 17 maize genotypes under the maize growing environments of Ethiopia, and to identify the best performing ones for future uses.

2. To utilize various statistical procedures for analyzing G x E interaction and yield stability of Ethiopian Maize hybrids across nine environments.

3. To indicate breeding strategies for releasing genotypes with adaptation to target environments in Ethiopia.

CHAPTER 2

LITERATURE REVIEW

2.1 Origin of maize and its uses

Maize (*Zea mays* L.) is belongs to the grass family Poaceae (Gramineae), tribe Maydeae. While maize comes in five phenotypes (sweet, pop, floury, dent, and flint) all its forms derive from a single ancestor domesticated in central Mexico around 7000 years ago (McCann, 2005). It was the principal food plant of the Indians when Columbus arrived, and it is still the most important cereal food crop in Mexico, Central America and many countries in South America and Africa. Two locations have been suggested as possible centres of origin of maize, namely the highlands of Peru, Ecuador and Bolivia, and the region of Southern Mexico and Central America. Many types of maize have been found in both areas (Poehlman, 1987).

Though the exact date and circumstances of *Zea mays'* first cultivation is a mystery, by 1500 A.D. the Aztec and Mayan civilization had long called the descendants of that plant "maize," literally " that which sustains life," and claimed that the crop was flesh and blood. In the modern economies of the U.S., East Asia, and Europe, however, it is the important/legible industrial row material: agribusiness uses its starch and cellulose for fuel, fodder, paints, plastic, and penicillin (McCann, 2005).

Maize is grown on global scale on 144 million ha and has an annual production of about 700 million mt (FAOSTAT, 2008). In the tropics, maize is grown in 66 countries and is of major economic significance in 61 of those countries (Palliwal, 2000). Maize is one of the most productive species of food plants. Its multiplication ratio on per plant basis is 1:600 to 1000 (Aldrich *et al*., 1975).

Maize has the highest potential for carbohydrate production per unit area and is an important cereal in many developing and developed countries of the world. In developing countries maize is generally used as food, while in the developed world it is used widely as a major source of carbohydrate in animal feed and as industrial raw materials for wet and dry milling (Palliwal, 2000). Apart from a strong demand for starches and sweeteners, there has been exponential growth in maize-based ethanol production, fuelled by rapid increases in world energy and petrol prices (FAO Food Outlook, 2006).

After its introduction to Africa around 15th century, maize has become the continent's most important crop. African countries rank first in the world with the highest percentage of

maize consumed in the national diet (Fig.2.1). Zambia has the world's highest percentage of maize consumption in the national diet (56% of total calories) (McCann, 2005). In South Africa, maize comprises 60% of all land planted with cereals and 40% of total calories consumed (McCann, 2005). Moreover the top three African countries on the list surpass even Guatemala and Mexico, maize's homeland. In East Africa as a whole, maize accounts for 30% of all calories. Ethiopia, one of the world's centres of genetic diversity of crop germplasm, now produces more maize than any other crop (McCann, 2005).

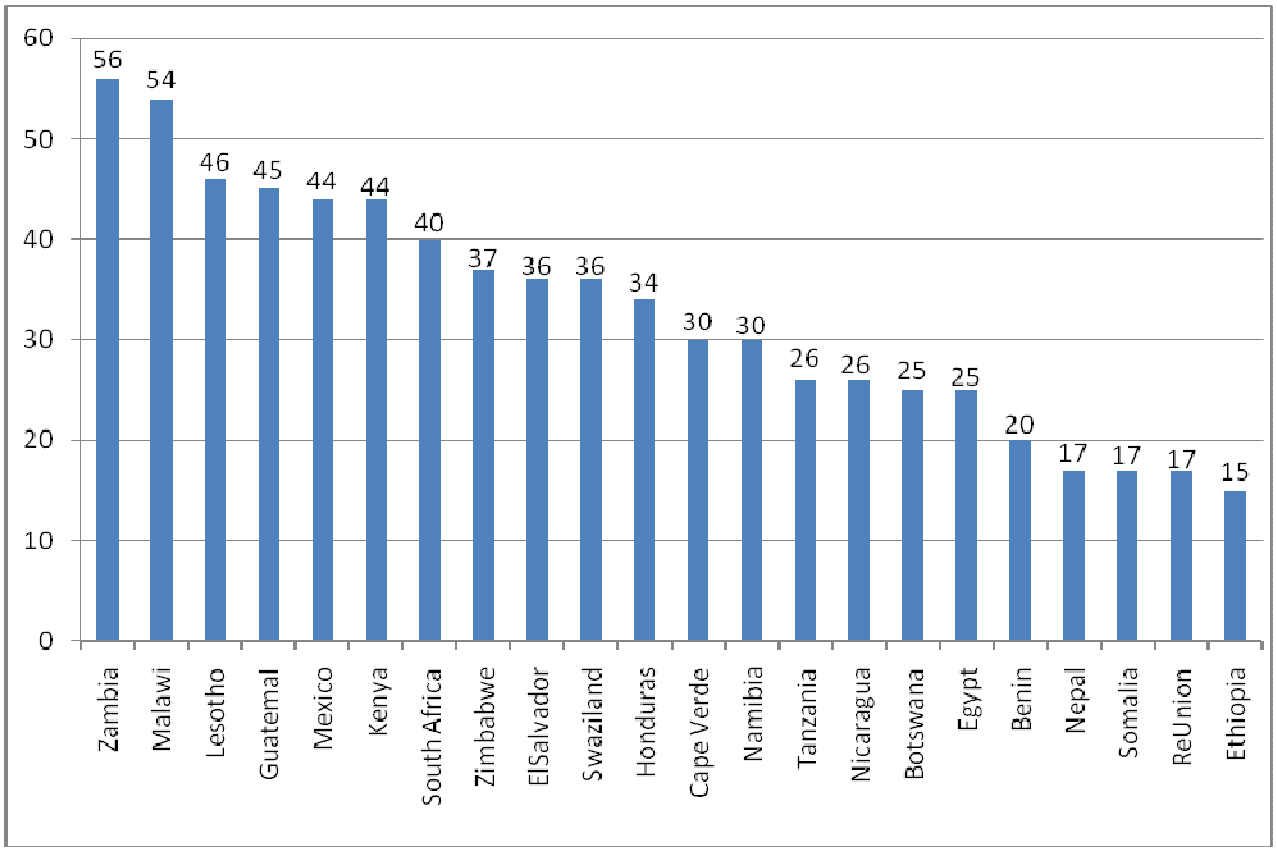

Figure 2.1 Maize calorie consumption as percentage of total diet (McCann, 2005)

2.2 Maize production in Ethiopia

Maize is believed to have reached Ethiopia in the 16th or 17th centuries (Haffanagel, 1961). Since its introduction it has gained importance as a food and feed crop. As Ethiopia is a diverse or heterogeneous country in terms of altitude, temperature, rain fall and soil types, maize can grow in extensive areas ranging from sea level up to 2800 m above sea level (IAR, 1980). It is grown on light soils and wide ranges of temperature and rain fall, which indicates its potential for wider adaptation.

Currently, maize is the second most important crop exceeded only by teff [*Eragrostis tef* (Zucc) Trotter] in terms of production area. However, it is the first in total production and yield per unit area among all the cereals which accounts for about 80% of the annual crop production in Ethiopia. It is cultivated on about 1.7 million ha, accounting for about 20% of the land allocated for all cereals (CSA, 2007).

Maize is the major staple food for millions of people living in the maize producing regions of the country. It is one of the cereals that provide most of the calorie requirements in the traditional Ethiopian diet. It is prepared and used as unleavened bread, as roasted and boiled green ears, parched mature grain porridge and in local drinks (Kebede *et al*., 1993). Between 2003 and 2006 a rapid expansion of maize production was noticed mainly because of the growing demand for consumption and also by the increased supply of maize based technologies that helped greatly with the increment of the productivity of maize per unit area (Table 2.1).

Table 2.1 Trend of area of production and productivity for the three major cereal crops in Ethiopia (CSA, 2007)

Year	Teff		Maize		Wheat	
	Area (million ha)	Productivity (t ha^{-1})	Area (million ha)	Productivity (t ha^{-1})	Area (million ha)	Productivity (t ha^{-1})
2003/04	2.13	0.95	1.39	1.72	1.40	1.56
2004/05	2.25	0.97	1.53	2.19	1.46	1.5
2005/06	2.40	1.01	1.69	2.29	1.47	1.67

2.3 Genotype x environment interaction

Successful cultivars must have good yield and other essential agronomic characters. Besides, their performance should be reliable over a wide range of environmental conditions. The basic cause of differences in stability between genotypes is a wide occurrence of genotype x environment interactions (G x E). It is therefore the interplay between genetic and non-genetic effects on development (Comstock and Moll, 1963). G x E interaction causes fluctuations of yield across environments. In other words, G x E is a differential genotypic expression across environments (Basford and Cooper, 1998).

The phenotype of an individual is determined by the effects of its genotype and the environment surrounding it. The effects of genotype and environment on phenotype may not be always independent. The phenotypic response to change in environment is not the same for all genotypes, the consequences of variation in phenotype depend upon the environment. Very often breeders encounter situations where the relative rankings of varieties change from location to location and/or from year to year.

G x E interaction is of major consequence to breeders in the process of developing improved varieties. When varieties are grown at several locations for testing their performance, their relative rankings usually do not remain the same. This causes difficulty in demonstrating significant superiority of any variety. G x E interaction is present whether varieties are pure lines, single crosses, double crosses, top-crosses, S_1 lines or any other material with which the breeder is working (Dabholkar, 1999).

An understanding of environmental and genotypic causes of G x E interaction is important at all stages of plant breeding, including ideotype design, parent selection based on traits, and selection based on yield (Jackson *et al.*, 1998; Yan and Hunt, 1998). Understanding of the causes of G x E interaction can be used to establish breeding objectives, to identify ideal test conditions, and to formulate recommendations for areas of optimal cultivar adaptation. It can also help to reduce the cost of extensive genotype evaluation by eliminating unnecessary testing sites and by fine tuning the breeding programmes. The presence of a large G x E interaction may necessitate establishment of additional testing sites, thus increasing the cost of developing commercially important varieties (Kang, 1996).

2.3.1 Genes and environment

Organisms are determined neither by their genes nor by their environment; they are the consequence of the interaction of genes and environment (Suzuki *et al*., 1981). Genotype describes the complete set of genes inherited by an individual that is important for the expression of a trait under investigation. Phenotype describes all aspects of the individual's morphology, physiology and ecological relationships. The genotype is essentially a fixed character of the organism; it remains constant throughout life and is unchanged by environmental effects. The phenotype changes continually and the direction of that change is a function of the sequence of environments that the individual experiences (Suzuki *et al*., 1981).

The sum total of the effects of physical, chemical and biological factors of an individual other than its genotype is known as the environment. The individuals or populations of plants do not live in a vacuum but are surrounded and influenced by these factors. Comstock and Moll (1963) classified environments into two categories, (i) Macro-environment i.e. the environment which is associated with a given location or area at a particular period of time. (ii) Micro-environment i.e. the environment of a single organism as opposed to that of another organism growing at the same time and in almost the same place. It includes physical and chemical attributes of soil, climatic variables, solar radiation, insect pests and disease. The macro-environments reflect a collection of micro-environments which are more alike within each macro-environment with the result that macro-environments substantially differ from each other.

The terms 'predictable and unpredictable environments' were coined by Allard and Bradshaw (1964) to define and classify environments. The predictable environment includes the regular and more or less permanent features of the environment such as climate as determined by its longitude and latitude, soil type, rainfall and day length. It also includes what are called controllable variables (Perkins and Jinks, 1971) e.g. the level of fertilizer applied, sowing date and sowing density, amount of irrigation and others that can be artificially created. The unpredictable or uncontrollable environments, on the other hand, include weather fluctuations such as differences between seasons in terms of amount and distribution of rainfall and the prevailing temperature during the crop growth. The absence or low level of interaction will be useful for uncontrollable variables, whereas for the controllable variables a high level of interaction in the favourable direction is desirable to obtain maximal performance (Chahal and Gosal, 2002).

2.3.2 Classification of genotype x environment interaction

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

$$A1\text{-}B1 \neq A2\text{-}B2 \text{ or } A1\text{-}B1\text{-}(A2\text{-}B2) \neq 0$$

where, A1 is the performance of genotype A in environment 1, A2 is the performance of genotype A in environment 2, B1 is the performance of genotype B in environment 1, B2 is the performance of genotype B in environment 2.

When two genotypes A and B are grown in two different environments E_1 and E_2, six types of interactions, some of which are crossovers and others non-crossovers, are possible (Allard and Bradshow, 1964). The two varieties may show similar behaviour i.e. parallel lines when grown in two environments (Fig. 2.2a) which indicates independence in the performance of genotype and environment. The presence of G x E interaction leads to non-parallel response curves of varieties without intersecting each other (Fig. 2.2b) or with interaction (Fig. 2.2c). The existence of non-intersecting but non-parallel lines suggests the relative ranking of varieties remains same, though their absolute differences vary with the environment. The G x E interaction is considered as crossover or qualitative if it leads to change in relative ranking of genotypes in different environments. The non-crossover or quantitative G x E interaction, on the other hand results in differential change of mean but not of ranking of different genotypes.

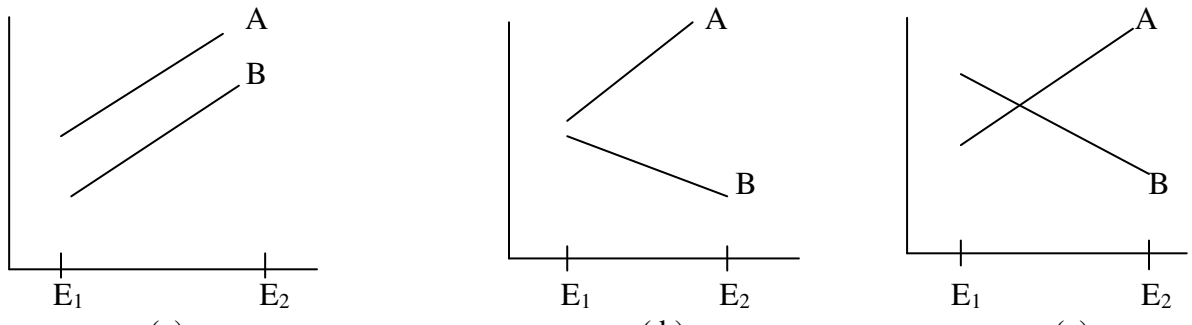

Figure 2.2 Different types of G x E interactions shown by two varieties grown in two environments

Crossover interactions are of interest in plant breeding because these affect the genotypes to be selected in a given environment. Such interactions also suggest that genotypes are specifically adapted to environments. The non-crossover interaction, on the other hand, influences the nature and magnitude of components of genetic variances and other related parameters like heritability and genetic advance.

Changes in relative ranking appear to be the inevitable consequence of growing a set of plant genotypes in even a few locations and seasons. This is especially true in tropical regions, where not only environmental fluctuations are greater, but crops also lack the protection conferred by purchased inputs. Thus, for plant breeders large G x E interaction impedes progress from selection and has important implications for testing and cultivar release (Smithson and Grisely, 1992). According to Ramagosa and Fox (1993), G x E interaction reduces association between phenotypic values, and may cause promising selections from one environment to perform poorly in another, forcing plant breeders to examine genotypic adaptation. Its measurement is also important to determine an optimum breeding strategy for releasing genotypes with adaptation to target environments.

Performance tests over a series of environments give information on G x E interaction at population level, but from a practical point of view, it is important to measure the stability of the performance of an individual genotype (Eberhart and Russell, 1966). The effects of genotypes and environments are statistically non-additive, which means that differences between genotypes depend on the environment. For data sets with more than two genotypes and more than two environments, the G x E interaction is commonly calculated by analyses of variance (ANOVA) techniques, leading to an estimated variance component for G x E interactions. G x E interaction occurs in both short term (less than five years testing at a location) and long term (several years at various locations) crop performance testing. Usually researchers ignore G x E interaction encountered, especially in short term trials, and base genotype selection solely on mean performance across environments. Only recently it was found that it could be useful to incorporate G x E interaction into genotype selection in short term trials (Kang and Pham, 1991; Kang, 1993; Magari and Kang, 1993).

2.3.3 Significance of genotype x environment interaction

What breeders can do to overcome the problem of G x E interaction depends upon the relative importance of variance components. Moreover, breeding programmes aimed to develop stable genotypes also depend upon whether a breeder is dealing with predictable or unpredictable environmental variation. Whenever dealing with predictable environmental variation, the first step that should be taken is to identify the differences. There is no difficulty when differences are recognizable, for example, differences in the seasons such as varieties to be developed for the rainy season or post-rainy season. Breeders can develop varieties suitable for both these seasons because environmental variation is defined.

For variety trials, which are tested in the same locations (L) and genotypes (G) and over years (Y), G x E analysis of variance may be partitioned into components due to G x L, G x Y and G x L x Y. Significance of mean square for G x L generally suggests that the region for which genotypes are being bred comprises of a number of special environments. In such circumstances the geographic region could be subdivided into sub regions which are relatively homogeneous. Varieties should be bred which are specifically adapted to these ecotypes. Implication of G x Y interaction is very different from G x L interaction. This is so because year-to-year fluctuations cannot be predicted in advance and breeders can hardly aim their programmes to develop varieties suited to particular years (Dabholkar, 1999).

In some situations, environmental variation is predictable but can also be corrected. For example, saline soils can be corrected by certain agronomic practices or by addition of some amendments. This is easier and quicker than evolving varieties suitable for such situations. However, breeding of varieties suitable for saline or acidic soils is low cost input and also a relatively permanent solution to the problem.

It is relatively easier to develop varieties specifically adapted to predictable environmental situations than to breed for unpredictable environmental variations. The aim of the breeding programme should, therefore be to develop genotypes that can withstand unpredictable transient environmental fluctuations. In other words, breed widely adapted genotypes (Dabholkar, 1999).

According to Allard and Bradshaw (1964) “a variety which can adjust its genotypic or phenotypic state in response to transient fluctuations in environment in such a way that it gives high and stable economic returns for place and year, is termed as well buffered”. Plant breeders generally agree that the new variety must show a high degree of stability in performance.

The context of G x E interaction in crop production systems and how they are encountered in mutli-environmental trials are shown in Table 2.2, as summarized by DeLacy *et al. (*1996). It also shows the objectives of selection in breeding programmes and how G x E interaction influences the selection strategies and the response to selection. Accordingly, phenotypic performance of genotypes in combination with different environments can be analyzed to qualify the amount of variation attributable to the effects of the environment, genotype, and G x E interactions. DeLacy *et al.* (1996) recommended the use of restricted maximum likelihood (REML) analysis of variance and prediction of genotype performance by the use of the best linear unbiased predictors (BLUPs) to investigate patterns of adaptation of genotypes across environments.

The existence of G x E interactions complicates the identification of superior genotypes for a range of environments. G x E interactions can be an outcome of genotype rank changes from one environment to another, a difference in scale among environments, or a combination of these phenomena. According to Becker and Léon (1998), cultivar rank changes are of greater importance than scale change interactions in cultivar trials conducted over a series of environments. Hence, G x E interaction is critical only if it involves significant crossover interactions (significant reversal in genotypic rank across environments) (Becker and Léon, 1988).

The statistical analysis of G x E is important in applied statistics as well as for the analysis of experiments in pant breeding and crop production (Kang, 1996). Different statistical methods such as variance components, regression models, multivariate analysis and cluster techniques have been proposed for the estimation and partitioning of G x E interactions (Freeman, 1973; Hill, 1975; Cox, 1984; Skroppa, 1984; Freeman, 1985, 1990; Westcott, 1986; Crossa, 1990). In many practical situations, the researcher is not interested in knowledge of the numerical amount of G x E interaction *per se*, but interested in the existence (or non-existence) of different rankings of genotypes. This concept of G x E interaction is closely related to the concept of selection in plant breeding. The breeder is mainly interested in the ranking of genotypes in different environments and in the changing of these rankings (Kang, 1996).

Breeders are interested in questions such as whether the best genotype in one environment is also the best in the other, which means that the relative characterizations and comparisons of the genotypes (orderings) are often more important than absolute characterizations and comparisons.

Table 2. 2 Consideration for the analysis and understanding of the form of G x E interaction in terms of their application to selection in plant breeding (DeLacy *et al.*, 1996)

Form of G x E	Applications in plant breeding			
	Model assumptions	Analysis Method	Objectives of analysis	Selection strategy
Non repeatable	Environments: random Genotypes: random	Analysis of variance REML Best linear unbiased predictors (BLUP)of genotype performance	1. Estimate components of variance to determine the relative sizes of sources of variation and estimate heritability. 2. Characterise the form of G x E by examining them for both G and E for: a. heterogeneity + lack of correlation partition (this enables calculation of the pooled genetic correlation) b. Rank change + no rank change partition c. The impact of rank change on the composition of the select group at a defined selection intensity	Selection for broad adaptation. Decisions on sample size (i.e. how many test environments, replicates and genotypes to use?)
Mixture of non repeatable and repeatable	Environments: a mixture of random and fixed Genotype: random	Indirect selection pattern analysis	3.Relationships among environments measured in terms of indirect response to selection 4. Grouping, ordination and partitioning (size and shape) of G x E interactions for individual Environment.	Selection for broad and specific adaptation to types of environments
Mixture of non repeatable and repeatable	Environments: a mixture of random and mixed Genotypes: a mixture of random and fixed	Pattern analysis	5. Grouping, ordination and partitioning of G x E interactions for environments and genotypes 6. Investigation of causes of differences in patterns of adaptation.	Selection for specific adaptation and stability
Repeatable,	Environments: fixed, Genotypes: fixed	Pattern analysis Biological model	7.Interpretation of causes of G x E interactions	Decisions on breeding and selection strategies

2.4 The concept of stability

The term "stability of genotypes" is central to all types of analyses of G x E interactions especially with reference to plant breeding. Stability has been described in many different ways over the years and there have also been different concepts of stability (Lin *et al.,* 1986). Researchers use the terms adaptation, phenotypic stability and yield stability in different ways (Becker and Léon, 1988). Stability in common usage connotes consistency in performance that would mean minimum variation among environments for a particular genotype (Chahal and Gosal, 2002).

The stability with which a plant breeder is concerned implies stability in those aspects of phenotype which are important economically, such as grain yield and quality. Such stability may depend upon holding some aspects of morphology and physiology in a steady state but allowing others to vary. In this way, the desirable varieties will show low G x E interaction for agriculturally important characters, especially grain yield, but not necessarily for other characteristics. Two basic concepts of phenotypic stability are distinguished: i) the biological concept, and ii) the dynamic concept. The biological concept of stability refers to the constant performance of a genotype over a wide range of environments. This idea of stability is in agreement with the concept of homeostasis widely used in genetics. According to Becker and Léon (1988) in static stability a genotype posses unchanged performance regardless of variation of the environments, thus implying that its variance among environments is zero. This type is seldom a desired feature of crop cultivars, since no response to improved growing conditions would be expected. On the other hand dynamic stability, also termed as agronomical concept of stability, implies that a stable genotype should always give high yield expected at the level of productivity of the respective environments, i.e., a variety with G x E interaction as small as possible (Becker, 1981; Dabholkar, 1999). With quantitative traits, the majority of genotypes often react similarly to favourable or unfavourable environmental conditions. Becker and Léon (1988) stated that all stability procedures based on quantifying G x E interaction effects belong to the dynamic stability concept. This includes the procedures for partitioning the G x E interactions of Wricke's (1962) ecovalence and Shukla's (1972) stability of variance, procedures using the regression approach such as proposed by Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Perkins and Jinks (1968), as well as non-parametric stability statistics.

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

1. Specific genotypic adaptation: it is close to adaptation of the corresponding genotypes to a limited environment.
2. General genotypic adaptation: is the capacity of a genotype to produce a range of phenotypes adapted to a variety of environments.
3. Specific population adaptation: is analogous to (1) and is the aspect of specific adaptation of heterogeneous population that is attributable to interaction between components rather than to the adaptations of components themselves.
4. General population adaptation: is analogous to general genotypic adaptation and is the capacity of a heterogeneous population to adapt to a variety of environments.

The aim of a breeding programme is to identify genotypes which are widely adapted. Ramagosa and Fox (1993) concluded that if a genotype maintains high yield over a wide range of environments, it is referred to as having general or wider adaptation. On the other hand, if this is true only for a limited range of environments, that genotype has specific or narrow adaptation.

Further to the stability concept by Becker and Léon (1988), Lin *et al.* (1986) categorized stability in to three types:

I. If the among-environment variance of a genotype is small, the genotype is considered to be stable. This concept is useful for quality traits, disease resistance or for stress characters. According to this concept a genotype performs the same in different environments or under different environmental conditions. This stability is static or can be seen as a biological concept of stability (Becker and Léon, 1988). Genotype variances across environments (Si^2) and the coefficient of variability (CV_i) are used as parameters to describe this type of stability (Francis and Kannenburg, 1978).

II. A genotype is considered to be stable if its response to environments is parallel to the mean response of all genotypes in the trial. According to Becker and Léon (1988) this concept is called the dynamic or agronomic concept of stability. In this

case, a stable genotype has no deviations from the general response to environments and creates a possible way of predicting the response of a genotype to a certain environment. Parameters used to describe this type of stability are regression coefficients (b_i) (Finlay and Wilkinson, 1963) and Shukla's (1972) stability variance (σ^2_i).

III. A genotype is considered to be stable if the residual mean square from the regression model on an environmental index is small. The environmental index is the mean yield of all the genotypes in each location minus the grand mean of all the genotypes in all locations. The method of Eberhart and Russell (1966) and Tai (1971) can be used for estimating type III stability.

2.5 Statistical methods to measure G x E interaction

The statistical analysis of G x E interaction is important in applied statistics as well as for the analysis of experiments in plant breeding and crop production (Kang, 1996). Different statistical methods have been proposed for the estimation and partitioning of G x E interactions and can be broadly categorized into four groups: the analysis of components of variance, stability analysis, multivariate methods and qualitative methods. The analysis of G x E interaction is closely linked with the quantitative estimation of phenotypic stability of genotypes over environments (Kang, 1996). When significant G x E interactions are present, the effects of genotypes and environments are statistically non-additive, which means that the differences between genotypes depend on the environment. Existing G x E interactions may, but will not necessarily, lead to different rank orders of genotypes in different environments.

The statistics, which can be used to identify stable genotypes, are classified into parametric and non-parametric. Parametric (empirical and statistical one) is more common and involves relating observed genotypic responses, in terms of yield, to a sample of environmental conditions. It is useful when the data are continuous. Non-parametric (analytical clustering) approach defines environments and phenotypes in terms of biotic and abiotic factors and is useful when the data are discontinuous. Non-parametric data analysis has the potential to reduce complex data into intuitive measures of stability. In practice, however, most breeding programmes incorporate some elements of both approaches (Becker and Léon, 1988; Ramagosa and Fox, 1993).

Lin *et al*. (1986) described nine parametric stability statistics: (1) the variance of a genotype across environments (S_i^2); (2) coefficient of variability (CV_i); (3) Plaisted and Peterson's (1959) mean variance component of pairwise G x E interaction ($\bar{\theta}_i$); (4) Plaisted's (1960) variance component for G x E interaction ($\theta_{(i)}$); (5) Wricke's (1962) ecovalence (W_i) ; (6) Shukla's (1972) stability variance (σ^2_i); (7) Finlay and Wilkinson's (1963) regression coefficient (b_i); (9) Eberhart and Russell's (1966) deviation parameters (S^2_{di}).

According to Becker and Léon (1988) the parametric approach gives only the individual aspects of the stability but cannot provide an overall picture of the response. The basic reason for this apparent difficulty is that a genotype's response to environment is multivariate yet the multivariate approach tries to transform it into a univariate problem, via a stability index. To avoid this problem, a different line of thought has emerged, namely to cluster genotypes according to their response structure ;i.e., non-parametric method (Becker and Léon, 1988).

Although the parametric approach to stability is relatively simple, it does not provide information for the resolution of any conflicting type I and type II inferences. Under these circumstances, quantitative mathematical characterization should be considered as well as qualitative descriptions of genotypes, as like or unlike genotypes ; i.e., to adopt a non-parametric clustering procedure (Lin *et al*., 1986) .

Numerous methods have been used in the search for an understanding of the cause of G x E interactions (Van Eeuwijk *et al*., 1996). These methods can be categorized into two major categories. The first category involves factorial regression analysis of the G x E matrix (i.e. the yield matrix after the environment and genotype main effects are removed) against environmental factors, genotypic traits, or combination thereof (Baril *et al*., 1995). The second category involves the correlation or regression analysis, which relates the genotypic and environmental scores, derived from principal component analysis of the G x E interaction matrix to genotypic and environmental covariates.

Frensham *et al*. (1998) and Vargas *et al*. (1998) used methods that belong to the first category. Frensham *et al.* (1998), when analyzing 10 years of oat (*Avena sativa* L.*)* evaluation data in Australia, incorporated several genotypic covariates into a mixed model. They indicated that plant type (plant height, kernel type) by environment interaction explained 50% of the observed G x E interaction. Vargas *et al.* (1998) used a partial least squares regression procedure in studying the causes of G x E interaction in wheat multi-environment trial (MET) data sets.

Their procedures involved partial regression of the G x E interaction matrix against some latent variables derived from principal component analysis of various explanatory traits or environmental variables. The partial regression procedure was introduced to avoid the problem of explanatory variables.

The second category is associated with the use of additive main effects and multiplicative interaction model (AMMI) in MET data analysis, which partitions the G x E interaction matrix into individual genotypic and environmental scores.

2.5.1 Conventional analysis of variance

In a conventional cultivar evaluation trial in which the yield of G genotypes is measured in E environments over R replicates, the classic model to analyze the total yield variation contained in GER observations is the analysis of variance (Fisher, 1918; 1925). After replicate effects are removed when combining the data, the G x E observations are partitioned into two sources: a) additive main effects for genotype and b) the non-additive effect due to G x E interaction. The analysis of variance of the combined data expresses to the observed (Y_{ij}) mean yield of the i^{th} genotype at the j^{th} environments as:

$$Y_{ij} = \mu + G_i + E_j + GE_{ij} + e_{ij}$$

where μ is the general mean, G_i , E_j and GE_{ij} represent the effects of the genotype, environment and G x E interaction respectively, and e_{ij} is the average random error associated with r^{th} plot that receives the i^{th} genotype in the j^{th} environment. The non-additive interaction (GE_{ij}) as defined in the above equation implies that an expected value (Y_{ij}) depends not only on the level of G and E separately, but also on the particular combination of levels and G and E (Crossa, 1990)

The most important limitation in this analysis is that error variance over environments should be homogeneous to test for genotype differences. If error variances are heterogeneous, this analysis is open for criticism as the F-test of the G x E interaction mean squares against the pooled error variances is biased towards significant results.

The principal deficiency of the combined analysis of variance in multi-location yield trials is that it does not explore the underlying structure within the observed non-additive G x E

interaction. Analysis of variance fails to determine the pattern of response of the genotypes and environments, in other words the valuable information contained in (G-1)(E-1) degrees of freedom is practically lost if no further analysis is performed (Crossa,1990).

The important advantage of the analysis of variance is that the variance component related to the different sources of variation, including genotype and G x E interaction can be estimated. It is important in multi location trials since G x E interaction is one of the main reasons for errors in determining yield performance of genotypes. The size of this interaction is required to i) obtain efficient estimates of the genotypic effects and ii) determine optimum resource allocations (number of plots and locations to be included in future trials). In breeding programmes, variance component methodology is used to measure genetic variability, to estimate the heritability and to predict the gain of the trait under selection. However, the nature and causes of the G x E interaction cannot be established with variance components (Crossa, 1990).

2.5.2 Parametric approach

Stability analysis provides a general summary of the response patterns of genotypes to environmental change. The main type of stability analysis, namely joint linear regression (JLR), was first proposed by Yates and Cochran (1938) and then widely used and described by many authors (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Perkins and Jinks, 1968; Shukla, 1972; Becker and Léon, 1988; Baker, 1988; Crossa, 1990). Linear regression models combine additive and multiplicative components and thus analyze main effects and their interaction (Zobel *et al*., 1988). Joint regression analysis provides a method of testing a genotype for characteristic linear response to changes in environments. This process is done by regressing genotypic means on environmental index.

2.5.2.1 Regression coefficient (b_i) and deviation mean square (S^2_{di})

According to Ramagosa and Fox (1993) simple linear regression provides a conceptual model for genotypic stability and is the most widely used statistical technique in plant breeding. This model is also called the Finlay and Wilkinson (1963) approach. The regression of each

genotype's mean yield against the mean yields of an environment is determined and the stability range is determined by the main effects multiplied by the regression coefficients of genotypes. The G x E interaction is divided into two segments i) a component due to linear regression (b_i) of the i^{th} genotype on the environment mean and ii) a deviation (d_{ij}) :

$$GE_{ij} = b_i E_j + d_{ij}$$

therefore

$$Y_{ij} = \mu + G_i + E_j + (b_i E_j + d_{ij}) + e_{ij}$$

The marginal means of the environments is used as independent variables in the regression analysis and the interaction is restricted to a multiplicative form. The G x E from analysis of variance is portioned between heterogeneity of regression and deviations from regressions (Becker and Léon, 1988). Different authors used different b_i values to define genotype stability. Finlay and Wilkinson (1963) defined a genotype with $b_i = 0$ as stable (static concept) and Eberhart and Russell (1966) defined a genotype with $b_i = 1$ as stable (dynamic concept). Becker and Léon (1988) suggested that ecovalence rather be used, since it combines b_i and S^2_{di} as a stability parameter. Many scientists consider b_i as a response parameter and S^2_{di} as a stability parameter, since additional information on the average response of a genotype to favourable environments is given by b_i, this is schematically presented in Figure 2.3.

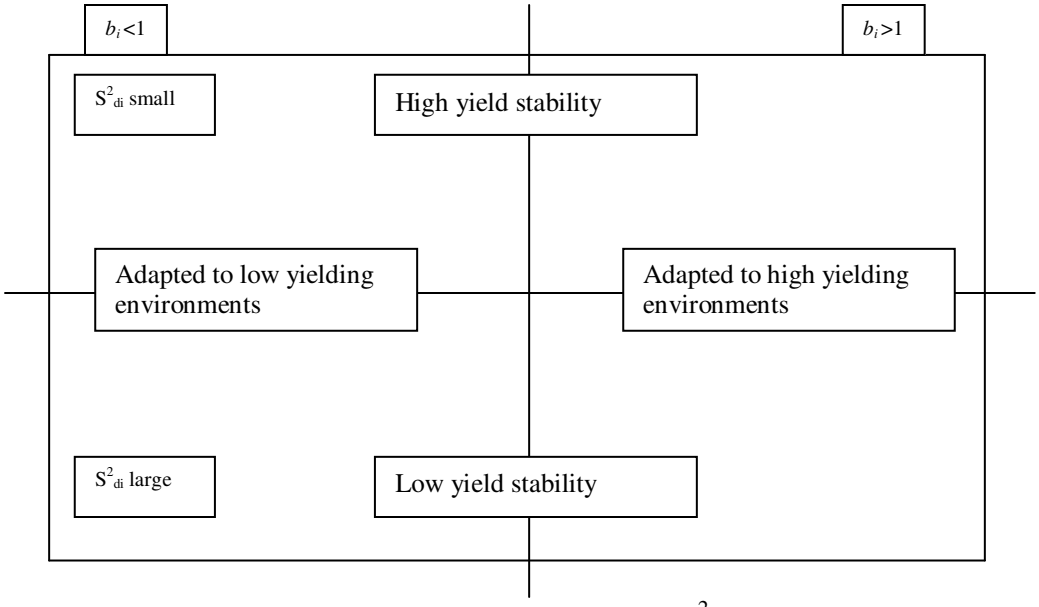

Figure 2.3 Interpretation of the parameters b_i and S^2_{di} of the regression approach (Becker and Léon, 1988)

Finlay and Wilkinson (1963) determined the regression coefficient by regressing the mean of all genotypes on the environmental mean, and plotting the obtained genotype regression coefficients against the genotype mean yields. Figure 2.4 illustrates the genotype pattern obtained when genotype regression coefficients are plotted against genotype mean yields. Regression coefficients approximating 1.0 indicate average stability. When this is associated with high mean yield, varieties have good general adaptability. When associated with low mean yield, genotypes are poorly adapted to all environments. Regression values above 1.0, describe genotypes with increasing sensitivity to environmental change (below average stability) and greater specificity of adaptability to high yielding environments. Regression coefficients below 1.0 provide a measure of greater resistance to environmental change (above average stability) and, therefore, increasing specificity of adaptability to low yielding environments.

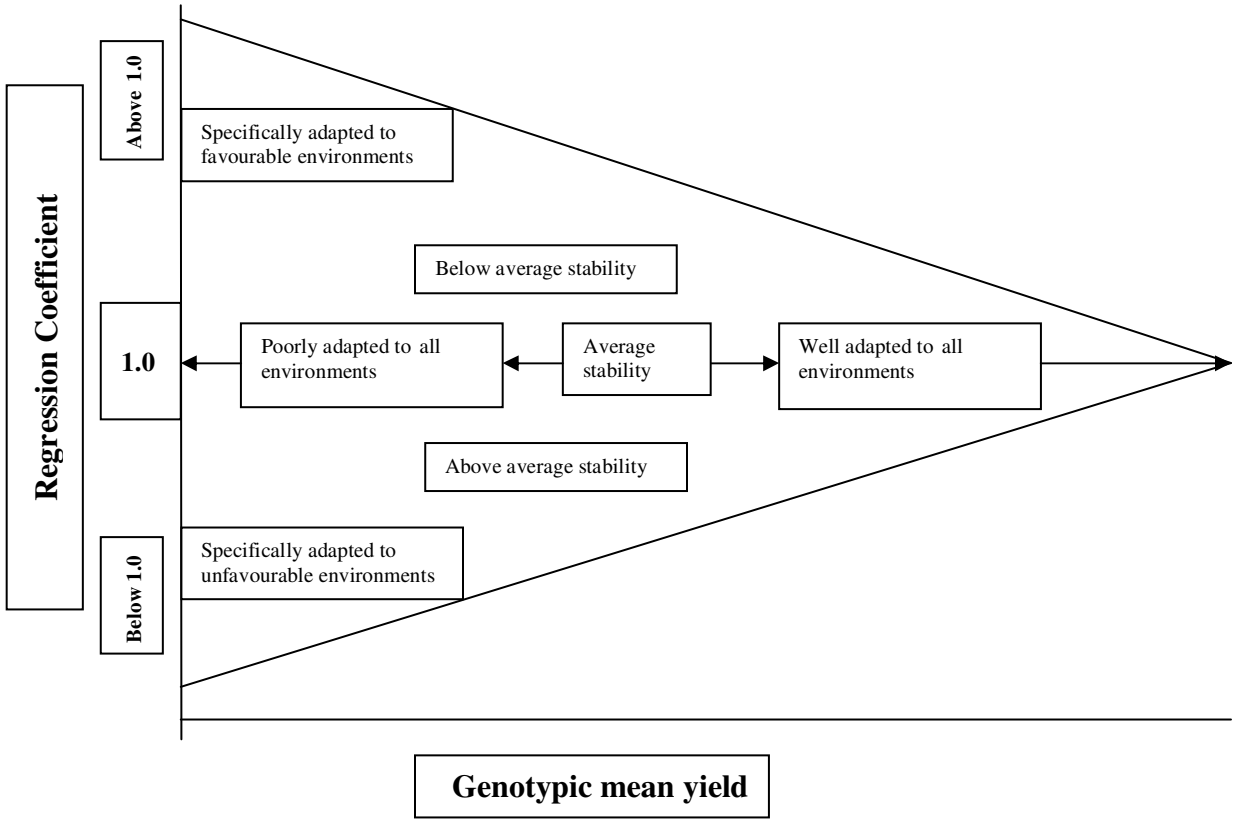

Figure 2.4 A generalized interpretation of the genotypic pattern obtained when, genotypic regression coefficients are plotted against genotypic mean, adapted from Finlay and Wilkinson (1963)

The deviation sums of squares are the sums of variance due to deviation from regression divided by (S-2), and subtracting pooled error mean square, where S stands for the number of locations for each variety (Eberhart and Russell, 1966). Therefore, varieties which have a less predictable response for a given set of environments, have a probability of F value to zero and will deviate significantly from linearity.

$$S^2_{di} = \frac{1}{S-2}\left[E_j(X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X}...)^2 - (b_i - 1)^2 E_j(\bar{X}_j - \bar{X}...)^2\right]$$

Although many authors and breeders used the regression approach, simultaneous studies emphasized the limitations, biologically and statistically (Freeman and Perkins, 1971; Westcott, 1986). There are statistical limitations: firstly the genotypes mean and marginal means of the environments are not independent from one another. Regressing one set of variables on another that is not independent violates one of the assumptions of regression analysis. This problem may be overcome by a large number of genotypes used (Freeman and Perkins, 1971). Secondly, errors associated with the slopes of the genotypes are not statistically independent, because the sum of squares for deviation, with (G-1) (E-1) df, can not be subdivided orthogonally among the G genotypes (Crossa, 1990) and thirdly, this method assumes a linear relationship between interaction and environmental means, which is not always the case and results may be misleading (Westcott, 1986).

Biologically the limitation seems to be in the case where only a few low or high yielding sites are included in the analysis and the genotype's position in the range is mostly determined by its performance in a few extreme environments which in turn generates misleading results (Westcott, 1986). Regression analysis should be used with caution when the data set includes results from only a few extremely high or low yielding locations (Crossa, 1990).

2.5.2.2 Ecovalence (*Wi*)

Wricke (1962) proposed using the contribution of each genotype to the G x E interaction sum of squares as a stability measure and defined this concept or statistics as ecovalence (W_i). Ecovalence is simple to calculate and is expressed as:

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

where, Y_{ij} is the mean performance of genotype *i* in the j^{th} environment and $Y_{i.}$ and $Y_{.j}$ are the genotype and environment mean deviations respectively, and $\bar{Y}$ .. is the overall mean. For this reason, genotypes with a low W_i value have smaller deviations from the overall mean across environments and are thus more stable. According to Becker and Léon (1988) ecovalence measures the contribution of a genotype to the G x E interaction; a genotype with zero ecovalence is regarded as stable. According to the meaning of the ecovalence, this stable genotype possesses a high ecovalence (low values of W_i = high ecovalence).

Becker and Léon (1988) illustrated ecovalence by using a numerical example of plot yields of genotypes *i* in various environments against the respective mean of environments (Fig. 2.5).

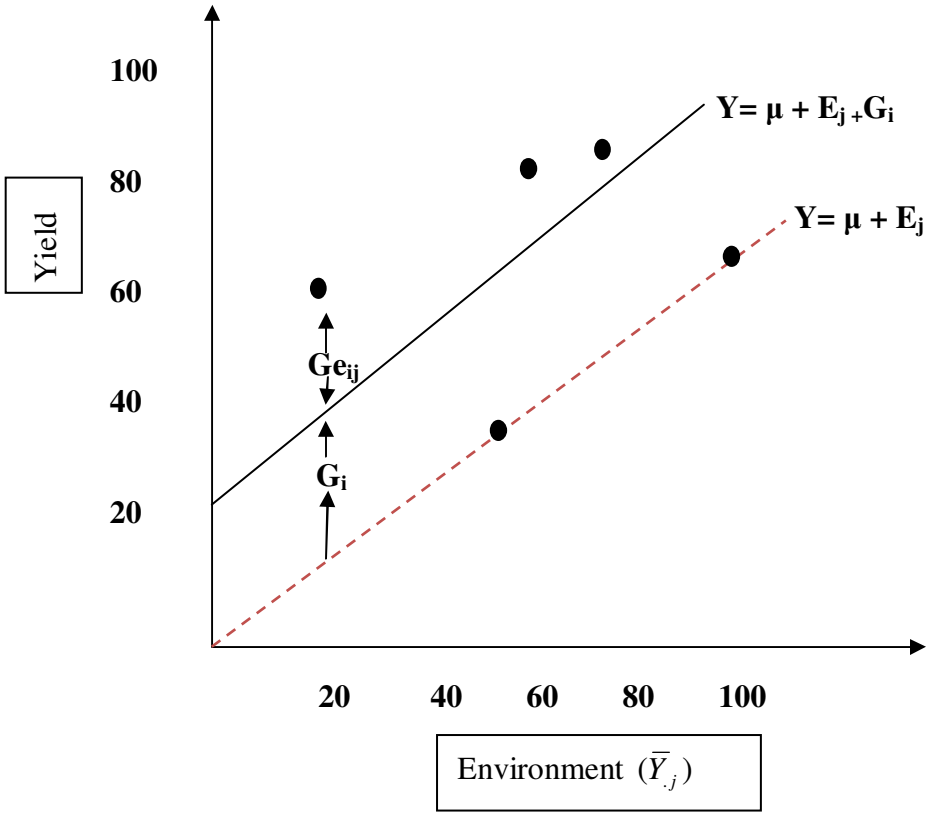

Figure 2.5 Graphical representation of G x E interactions: the stability statistics ecovalence (W_i) is the sum of squares of deviations from the upper straight line (Becker and Léon,1988)

The lower straight line estimates the average yield of all genotypes simply using information about the general mean (μ) and the environmental effects (E_j), while the upper line takes into account the genotype effect (G_i) and therefore estimates the yield of genotypes *i*.

Deviations of yield from the upper straight line are the G x E interaction effects of genotype i and are summed and squared across environments and constitutes ecovalence.

2.5.2.3 Coefficient of determination (r_i^2)

Pinthus (1973) as cited by Becker (1981) proposed to use the coefficient of determination (r_i^2) instead of deviation mean squares to estimate stability of genotypes, because r_i^2 is strongly related to S^2_{di}.

$$r_i^2 = 1 - \frac{S^2_{di}}{S^2_{xi}}$$

both r_i^2 and b_i has the advantage of being dependent of units of measurement.

2.5.2.4 Shukla's stability variance parameter (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 (GE_{ij+} e_{ij}) matrix in a two way classification. The stability statistic is termed "stability variance" (σ^2) and is estimated as follows:

$$\sigma_i^2 = \frac{1}{(G-1)(G-2)(E-1)}\left[G(G-1)\sum_j (Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}..)^2 - \sum_i \sum_j (Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}..)^2 \right]$$

where Y_{ij} is the mean yield of the i^{th} genotype in the j^{th} environment, $\bar{Y}_{.j}$ is the mean of all genotypes in j^{th} environments and $\bar{Y}..$ is the mean of all genotypes in all environments. A genotype is called stable if its stability variance (σ^2) is equal to the environmental variance σ_e^2 which means that $\sigma_i^2 = 0$. A relatively large value of (σ_i^2) will thus indicate greater instability of genotype *i.* As the stability variance is the difference between two sums of squares, it can be negative, but negative estimates of variance are not uncommon in variance component problems. Negative estimates of (σ_i^2) may be taken as equal to zero as usual (Shukla, 1972). Homogeneity of estimates can be tested using Shukla's (1972) approximate test (Lin *et al.*, 1986). The stability variance is a linear combination of the ecovalence, and therefore both W_i and (σ_i^2) are equivalent for ranking purposes (Wricke and Weber, 1980).

2.5.2.5 Cultivar performance measure

Lin and Binns (1988) defined the superiority measure (P_i) of the i^{th} genotype as the mean square of distance between the i^{th} genotype and the genotype with the maximum response as:

$$P_i = \frac{\left[n(Y_{i.} - M..)^2 + (Y_{ij} - Y_i + M_{j.} + M..)^2\right]}{2n}$$

where Y_{ij} is the average response of the i^{th} genotype in the j^{th} environment, $Y_{i.}$ is the mean deviation of genotype *i*, M_j is the genotype with maximum response among all the genotypes in the j^{th} locations, and n is the number of locations. The smaller the value of P_i, the less is the distance to the genotype with maximum yield and the better the genotype. A pair wise G x E interaction mean square between the maximum and each genotype is also calculated and it is similar to the method used by Plaisted and Peterson (1959), except that a) the stability statistics are based on both the average genotypic effects and G x E interaction effects and b) each genotype is compared only with the one maximum response at each environment (Crossa, 1990).

2.5.3 Cross over interactions and non-parametric techniques for stability analysis

Lin *et al.* (1986) explained this approach as the grouping of genotypes according to their similarity of response to a range of environments. These interactions may (not necessarily), result in different rank orders of genotypes in different environments (see, Figure 2.1). Crossover or qualitative interactions are more important in agricultural production than non-crossover or quantitative interactions (Baker, 1988; Crossa, 1990).

If the breeder is only interested in the existence of rank order differences over different environments, the non-parametric statistics for G x E interactions based on ranks provide a useful alternative to parametric statistics approaches currently used, which are based on absolute data. In these cases, the relative characteristics and comparisons of the genotypes are more important than absolute characterization and comparisons. Further advantages are that non-parametric stability statistics are expected to be less sensitive to errors of measurement than parametric estimates and the addition or deletion of one or a few observations is not like to cause great variation in the estimate as would be the case for parametric stability statistics (Nassar and

Huehn, 1987). Huehn (1990) also included the following advantages of non-parametric statistics over the parametric ones: reduction or avoidance of the bias caused by outliers, no assumptions are needed about the distribution of the phenotypic values and for many applications (e.g. selection in plant breeding and testing programme) the rank orders of the genotypes are the most essential information.

However, as suggested by Huehn (1990), for an efficient use of stability estimation techniques in practical applications, knowledge on the following aspects is essential: relations between different statistical measures of phenotypic stability (parametric and non-parametric); consistency of relationships among stability parameters; and repeatability of stability parameters.

According to Ramagosa and Fox (1990), analysis of ranks (stratified ranking) evaluates the proportion of sites where any genotype ranks in the top, middle or bottom third of the entries. A genotype found in the top third of the entries across sites can be considered relatively well adapted. A genotype *'i'* is stable over environments if its ranks are the same over environments. These measures of stability define it in the sense of homeostasis or ability of genotype to stabilize itself in different environments (Huehn, 1990).The similarity of two rankings in any two environments can be estimated by Spearman's rank correlation coefficient. Any two environments in which ranking of tested genotypes remains the same can be used for selection purposes, even if their overall yield levels are substantially different.

Huehn (1990) has concluded the following from his investigations on non-parametric measures of stability:

- Corrected or transformed data should be used to perform analysis of phenotypic stability, if one wants to estimate the phenotypic stability independent from yield level effects.
- For quantitative estimation of phenotypic stability the non-parametric measure (mean rank difference) is preferable, as it is easy to calculate and interpret.
- If one is interested in a simultaneous consideration of both stability and yield the non-parametric stability parameter (sum of deviations) can be applied, measuring stability in units of yield by using the original non-corrected yield data.

2.5.4 Multivariate analysis techniques

Multivariate techniques are widely applied in stability analysis to provide further information on real multivariate response of genotypes to environments. According to Becker and Léon (1988) multivariate analysis has three main purposes: 1) to eliminate noise from the data pattern, 2) to summarize the data, 3) to reveal the structure in the data. Through multivariate analysis, genotypes with similar responses can be clustered, hypothesized, and later tested, and their data can be easily summarized and analysed (Crossa, 1990; Gauch, 1982a; Hohls, 1995).

Multivariate analyses are appropriate for analysing two-way matrices of G genotypes and E environments. According to Crossa (1990) the response of any genotype in E environments may be conceived as a pattern in E-dimensional space, with the coordinate of an individual axis being the yield or other metric of the genotype in one environment. Crossa (1990) has also distinguished two groups of multivariate techniques used to elucidate the internal structure of G x E interactions:

1. Ordination techniques, such as principal component analysis, principal coordinate analysis and factor analysis, assume that the data are continuous. These techniques attempt to represent G x E relationships as faithfully as possible in a low dimensional space. A graphical output displays similar genotypes or environments close to each other and dissimilar items farther apart. Ordination is effective for showing relationships and reducing noise (Gauch, 1982b).
2. Classification techniques such as cluster analysis and discriminant analysis, seek discontinuities in the data. These methods involve grouping similar entities in clusters and effective for summarizing redundancy in the data (Crossa, 1990).

Williams (1976) recommended pattern analysis for describing G x E interactions, defining it as the joint use of classification and ordination methods. This method groups genotypes and environments according to either their similarity (ordination method) or dissimilarity (classification methods). Similar measures such as Pearson's coefficient, which are larger for genotypes that are more similar for a set of environments and dissimilarity measures such as Euclidean distance, which are larger the more the genotypes are different (DeLacy *et al.,* 1996). The output from cluster analysis is displayed as a dendrogram or hierarchical tree. Multivariate methods usually present most of the total variation in a few dimensions, in a dendrogram or

scattergram. However, the pattern analysis methods have been criticized on the grounds of their inability to distinguish between real pattern and background noise. The various multivariate techniques of stability analysis are briefly described in the following sub sections.

2.5.4.1 Principal component analysis (PCA)

Crossa (1990) and Purchase (1997) found PCA to be a frequently used multivariate method. This method aims to transform the data from one set of coordinate axis to another, which preserves, as much as possible, the original configuration of the set of points and concentrates most of the data structure in the first principal component axis. Principal component analysis assumes that the original variables define a Euclidean space in which similarity between items is measured as Euclidean distance. This analysis can effectively reduce the structure of a two-way G x E data matrix of G (genotypes) points in E (environments) dimension in a subspace of fewer dimensions. The matrix can also be conceptualized as E points in G dimensions.

The principal component analysis was found to be efficient in describing G x E interactions. Cruz (1992) showed that the principal component analysis was more efficient than the regression model when he analysed a set of maize data. Principal component analysis combined with cluster analysis was effective in forming sub groups among 29 populations of faba bean (*Vicia faba* L.), which differed in mean performance of and response across environments (Polignano *et al*., 1989).

Ordination techniques such as principal component analysis may have some limitations, e.g., in reducing dimensionality of multivariate data distortion may occur. If the percentage of variance accounted for by the first principal components axis is small, individuals that are really far apart may be represented by points that are close together. Various limitations for this technique have been noted (Zobel *et al*., 1988; Crossa, 1990).

However, principal component analysis has an obvious advantage as compared to the linear regression methods. The regression analysis uses only one statistic, the regression coefficient, to describe the pattern of response of a genotype across environments, and most of the information is wasted in accounting for deviations. Principal component analysis overcomes this difficulty by providing the scores on the principal component axes to describe the response pattern of genotypes (Crossa, 1990). These scores allow depicting G x E interactions into two dimensions (biplot) and identifying the factor responsible for the interaction.

2.5.4.2 Principal coordinate analysis

Principal coordinate analysis is a generalization to the PCA in which any measure of similarity between individuals can be used. Its objectives and limitations are similar to those of PCA. Crossa (1990) highlighted some of the advantages:

i. it is trustworthy when used for data that include extremely low or high yielding sites;

ii. it does not depend on the set of genotypes included in the analysis;

iii. and it is simple to identify stable varieties from the sequence of graphic displays.

2.5.4.3 Factor analysis

Factor analysis is also related to PCA. The variables of the factor analysis are similar to the components of the latter. In this procedure, a large number of variables are reduced to a small number of main factors. Variation is explained in terms of general factors common to all variables and in terms of factors unique to each variable (Crossa, 1990).

2.5.4.4 Cluster analysis

Cluster analysis is a numerical classification technique that defines groups or clusters of individuals. Two types of classification can be distinguished. The first is non-hierarchical classification, which assigns each item into a class. The second type is hierarchical classification, which groups individuals into clusters and arranges these into a hierarchy for the purpose of studying relationships in the data (Crossa, 1990).

In the process of 'clustering', all genotypes are assessed for similarity of response and grouped together on the basis of proximity to each other such that clubbing any other genotype in a group, leads to relatively higher sum of squares within the groups. So starting from individual values of genotypes or environments, the subgroups are made which further are continued to be successively grouped until all variation is covered in one large group. The whole structure from the individual values to final groups is represented like branches of a tree in a dendrogram that depicts composition of groups and degree of dissimilarity among groups both for genotypes as well as environments. The genotypes or environments in each group or cluster are expected to have a similar contribution towards G x E interaction as compared to the constituents of the other group at each level of clustering (Ramagosa and Fox, 1993).

2.5.4.5 Additive main effects and multiplicative interaction method (AMMI)

According to Zobel *et al*. (1988), considering the three traditional models, analysis of variance (ANOVA) fails to detect a significant interaction component, principal component analysis (PCA) fails to identify and separate the significant genotype and environment main effects, and linear regression models accounts for only a small portion of the interaction sum of squares. But AMMI analysis reveals a highly significant interaction component that has a clear agronomic meaning and it has no specific design requirements, except for a two-way data structure.

The AMMI method is used for three main purposes. The first is model diagnoses, AMMI is more appropriate in the initial statistical analysis of yield trials, because it provides an analytical tool of diagnosing other models as sub cases when these are better for particular data sets (Gauch, 1988). Secondly, AMMI clarifies the G x E interaction and it summarizes patterns and relationships of genotypes and environments (Zobel *et al*., 1988; Crossa *et al*., 1990). The third use is to improve the accuracy of yield estimates. Gains have been obtained in the accuracy of yield estimates that are equivalent to increasing the number of replicates by a factor of two to five (Zobel *et al*., 1988; Crossa, 1990). Such gains may be used to reduce testing cost by reducing the number of replications, to include more treatments in the experiments or to improve efficiency in selecting the best genotypes.

The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the G x E interaction. It has proven useful for understanding complex G x E interactions. The results can be graphed in a useful biplot that shows both main and interaction effects for both genotypes and environments. AMMI combines analysis of variance (ANOVA) into a single model with additive and multiplicative parameters. The model equation is:

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij}$$

where Y_{ij} is the yield of the i^{th} genotype in the j^{th} environment; μ is the grand mean; G_i and E_i are the genotype and environment deviations from the grand mean, respectively; λ_k is the eigenvalue of the PCA analysis axis k; α_{ik} and γ_{jk} are the genotype and environment principal component scores for axis k; n is the number of principal components retained in the model and e_{ij} is the error term.

In the initial analysis of variance, the total variation is partitioned into three sources, namely genotypes, environment and G x E interactions. In this regard, a review of Purchase (1997) revealed that, in most yield trials, the proportion of sum of squares due to differences among sites ranged from 80 to 90% and the variation due to G x E interactions is often larger than that of the genotypes. Hence AMMI model can produce biplot graphs, which display the variability of genotypes and G x E interactions.

Regarding agricultural problems from G x E interaction, there exists two basic options, one aimed at the genotypes and the other at the environments (Ceccarelli, 1989; Simmonds, 1991; Zavala-Garcia *et al*., 1992). One option is to seek a high yielding, widely adapted genotype that wins throughout the growing region of interest. The other option, particularly relevant when the first fails, is to sub divide the growing region into several relatively homogeneous macro-environments (with little interaction within each macro-environment) and then breed and recommend varieties for each. As explained earlier, AMMI can help with both of these options.

The advantages of the AMMI model or its variants are that, they use overall fitting, impose no restrictions on the multiplicative terms and result in least square fit (Freeman, 1990). Within limits, any model may be expected to fit the data from which it was derived. However, the AMMI model has a good chance of being able to predict for new sites and new years, thus contributing a real advance (Gauch, 1988).

The principal components analysis of AMMI partitions G x E interactions into several orthogonal axes, the interaction principal component analyses (IPCA). Gauch and Zobel (1996) showed that AMMI 1 with IPCA 1 and AMMI 2 with IPCA 1 and IPCA 2 are usually selected and the graphical representation of axes, either as IPCA 1 or IPCA 2 against main effects or IPCA 1 against IPCA 2 is generally informative. When AMMI 3 and higher models are presented for agricultural data, the third and higher IPCA axes are dominated by noise and have no predictive value (Van Eeuwijk, 1995).

Since AMMI has the biplot feature, genotypes and environments are plotted on the same diagram, facilitating inference about specific interactions of individual genotypes and environments by using the sign and magnitude of PCA 1 values. Any genotype with a PCA 1 value close to zero shows general adaptation to the tested environment. A large genotypic PCA 1 scores reflects more specific adaptation to environments with PCA 1 scores of the same sign. AMMI is proved to provide a more adequate biological explanation of G x E than the regression

model and it has been found useful when applied to across years analyses with a higher element of unpredictability (Crossa *et al*., 1990; Yau, 1995; Gauch and Zobel, 1996; Annicchiarico, 1997).

The combination of analysis of variance and principal components analysis in the AMMI model, along with prediction assessment, is a valuable approach for understanding G x E interaction and obtaining better yield estimates. The interaction is explained in the form of a biplot display where, PCA scores are plotted against each other and it provides visual inspection and interpretation of the G x E interaction components. Integrating biplot display and genotypic stability statistics enable genotypes to be grouped based on similarity of performance across diverse environments (Tsige, 2002).

Like every other model, AMMI has its weaknesses. The nature of the residuals after fitting the additive main effects inevitably produces the appearance of multiplicative effects. Consequently the sum of square for fitting the multiplicative term, which may be read directly from the latent root proportions of explained variation, will tend to be much larger than the expected value. Therefore, it is not possible to recommend a single model to be used at all times, because these models depending on the type of data and research purposes can be complimentary rather than being competitive. Although strategies may differ in overall appropriateness, different methods usually lead to the same conclusions for a given data set. For example, Baril *et al.* (1995) compared factorial regression and AMMI score-based analysis for a potato (*Solanum tuberosum* L.) data set and came to the same conclusion, that the interaction between maturity and cold or drought stress explained the G x E interaction for yield. Using the method of Van Eeuwijk (1996), the partial least square regression method and the factorial regression method (Vargas *et al*., 1998) arrived at similar conclusions. Thus, it appears that it is the quality of data, rather than the method of analysis, that is more limiting to the understanding of G x E interaction.

2.6 Optimum allocation of resources

Plant breeders test large numbers of family lines, inbreds, hybrids and/or clones before discarding most and releasing a few as varieties. Genotypes that perform well across a wide range of environmental conditions are most useful to growers and seed companies, because such genotypes have greater probability of performing well in future years and in diverse production areas. Therefore, breeding trials are usually conducted over years, seasons (or planting dates), and locations to provide a number of test environments, and with replications (William and Todd, 1989). This practice is costly and time-consuming, so that the question naturally arises `How can resources be optimally allocated over years, seasons, locations, and replications to provide as much information as possible, as cost-effectively as possible?'

Miller *et al.* (1962) used the theoretical variance of the mean to evaluate the relationship between the number of testing environments used and the precision with which the evaluation of the variety could be made. The theoretical variance of a genotype (g) mean ($V_{\bar{x}}$) from replicated trials over locations and years can be expressed in general as:

$$V_{\bar{x}} = \frac{\sigma_e^2}{rly} + \frac{\sigma_{gly}^2}{ly} + \frac{\sigma_{gl}^2}{l} + \frac{\sigma_{gy}^2}{y}$$

where the numerators are the variance components and r, l and y are the number of replications, locations and years respectively in which the varieties are to be tested. The numerators can be substituted by the variance components estimated from the analysis of variance. The variance of a mean can then be predicted for any combination or combinations of r, l and y. The smaller the variance of the mean with the different combinations of r, l and y, the more precise the estimates of variety performance would be.

In general, the efficiency of yield trials for selecting superior genotypes is affected strongly by experimental designs, including the choice of the number of replications, locations and years. Increasing the number of locations or replications may be expensive, and adding years can seriously delay a breeding program. Therefore, knowing the best application of resources in the yield trial is important to offset the allocation of meager resources of research which is the case in Ethiopia and to get precise information from a breeding program.

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CHAPTER 3

ASSESSMENT OF GENOTYPE X ENVIRONMENT INTERACTION AND GRAIN YIELD EVALUATION OF ETHIOPIAN MAIZE HYBRIDS

3.1 Abstract

Maize (Zea mays L.) is one of the leading economic crops of the world. Beside its uses as food and feed, maize is a priority and strategic crop to respond to the world's quest for alternative energy sources. In Ethiopia it ranks first in total production and yield per unit area and it is the staple crop for millions of people. The national average grain yield is about 2.2 t ha^{-1} which is far less than the global average. In addition to the lack of maize genotypes with wide adaptation, the diverse environmental conditions of Ethiopia makes the selection and release of stable maize genotypes a challenging breeding activity, mainly due to genotype x environment interaction (GxE). This is the phenomenon that different genotypes respond differently to variations in environment. Seventeen experimental maize genotypes were used to examine the magnitude and nature of G x E interaction for grain yield and hence to select the best genotypes for the maize growing environments of Ethiopia. The genotypes were evaluated in a multi-location yield trial conducted across three years (2004-2006) and three locations. The combined data were analyzed and the variance components for G x E interaction were found to be highly significant, including the variation among the genotypes (G). The location (L) and Location x Year (L x Y) interaction were the largest components of variance for grain yield, which indicates that the variation among the testing sites and the presence of year-to-year fluctuation of the environment was high. Furthermore the significant level of G x L indicates that some genotypes can be released for specific environments based on their favourable interaction. According to the mean grain yield value based on the analysis of variance results, maize genotype PR1 (mean yield =7.05 t ha^{-1}) was found to be the highest yielder, followed by PR13 (6.73 t ha^{-1}) and the check hybrid BH540 (6.49 t ha^{-1}).These results show the potential of the experimental genotypes for large scale production. This study further emphasized the importance of stability analysis based on various parameters to extract more information on the G x E interaction and grain yield stability of Ethiopian maize hybrids.

Key Words: Maize; grain-yield; genotype x environment interaction

3.2 Introduction

Maize is an important food crop in Ethiopia. Currently it ranks first in total production and yield per unit area among the cereals (CSA, 2007). The production of maize in Ethiopia is in an increasing trend (Table 2.1), which shows that maize will probably become Ethiopia's most important crop in area coverage by surpassing tef (*Eragrostis tef* T.), the current most widely cultivated staple crop.

Ethiopia is known for its heterogeneous agro-ecology; as a result the performance of maize genotypes differs within and across environments. When environmental differences are large like in Ethiopia, it may be expected that the interaction of genotype x environment will also be higher. This interaction may result in one cultivar having the highest yield in some environments while a second cultivar excels in others. Hence it is important to know the magnitude of the interactions in the selection of genotypes across several environments besides calculating the average performance of the genotypes under evaluation (Fehr, 1991; Gauch and Zobel, 1997).

Genotype x environment (G x E) interaction is one of the main complications in the selection of varieties with broad adaptation in most breeding programs. Numerous studies have shown that a proper understanding of the environmental and genetic factors causing the interaction as well as an assessment of their importance could have a large impact on the development of superior germplasm (Magari and Kang, 1993; Basford and Cooper, 1998). G x E interaction occurs universally when genotypes are evaluated in several different environments (Becker and Léon, 1988; Magari, 1989; Kang, 1990). Magari and Kang (1993) found that the contribution of different environmental factors, to the yield stability of maize in yield trials, had a significant impact on the heterogeneity of the results.

The main purpose of evaluating genotypes across environments is to estimate or predict genotype performance in future years, based on past performance data, and to develop or recommend superior ones. In almost all multi-location trials, there exists interaction and noise (Purchase, 1997). If there were no interactions, one variety would have been good enough for all environments and variety trials would have been conducted only at one location to provide universal results. If there was no noise, results would be exact and there would be no need for replications. But since the reality is quite different, two options are available to deal with these problems. The first one targets the genotypes while the second aims at the environment. The first

option is to search for high yielding and widely adapted cultivars that are successful across the growing environment of interest. The second alternative is to sub-divide the target regions into several relatively homogeneous macro-environments, then to develop and recommend suitable genotypes for specific regions.

Evaluation of maize genotypes across the different environments of Ethiopia is a general practice within the national maize research system. However, no information is documented on the estimation of G x E interaction on these experimental maize hybrids listed in the following section. Hence, to analyze G x E interaction a multi-location yield trial of maize was conducted in Ethiopia during 2004-2006. The purpose of this study was to evaluate 17 experimental maize hybrids across three locations and over three years, and to select the superior ones for commercial production. This chapter focuses on the magnitude and nature of G x E interaction based on analysis of variance techniques as a primary tool to differentiate genotypes according to their grain yield performance.

3.3 Materials and methods

3.3.1 Materials

Seventeen experimental maize hybrids, including a locally released standard check, were evaluated over a period of three years (2004 to 2006) across three locations (nine environments) (Table 3.1).

Table 3.1 Description of the maize genotypes tested over three years across three locations

Entry no	Entry code	Entry no	Entry code
1	GA3	10	AS7
2	AS13	11	AS10
3	PR1	12	PR2
4	PR7	13	JZ12
5	SE4	14	PR13
6	SE21	15	AS9
7	SE22	16	PR3
8	BH540 (check)	17	JA25
9	GA15		

These maize hybrids were selected based on their relative yield performance among the different experimental hybrids developed by the Ethiopia Seed Enterprise (ESE) maize breeding program. The check hybrid was a released variety from the national maize project and adapted to the mid altitude maize growing areas of Ethiopia. All the hybrids are categorized under the medium maturity group (between 140-145 days) and their broad adaptation zone is mid-altitude sub-humid which includes areas with an elevation range of 1000-2000 m above sea level and an annual rainfall between 1000-1200 mm.

3.3.2 Methods

3.3.2.1 Description of the experimental sites

The trial sites were located in the mid-altitude sub-humid maize producing mega-environments of Ethiopia (Table 3.2).

Table 3.2 Description of the test locations used in the study

Location	Latitude	Longitude	Altitude(m)	Annual rain fall (mm)	Plant population (plants ha^{-1})
Awassa	7^0 08'N	$38^0$48'E	1700	1110	53,333
Bako	$9^0$06'N	$37^0$09'E	1650	1245	44,444
Upper Bir	$10^0$58'N	$37^0$17'E	1750	1200	53,333

Awassa is located 275 km south of the capital Addis Ababa and it is within the Great Rift Valley region and the soil type is Andosol. Bako is 250 km west of Addis Ababa and Upper Bir is 493 km North West of the capital and the soil type for these sites is similar and categorized under Nitosol. All the locations are among the principal maize testing sites in Ethiopia and believed to represent the maize belt regions of the country.

3.3.2.2 Experimental design and data measurement

The genotypes were planted in a randomized complete block design with four replications at each location except at Awassa in 2006 which had three replications. Plots consisted of two rows, 5.1m in length; the whole rows were harvested for analysis. The spacing between rows was 75cm, while spacing between plants was 25cm the exception was at Bako where the between plant spacing was 30cm. The plots were over sown with two seeds per hill and later thinned to the desired plant densities of 53 333 at Awassa and Upper Bir and 44 444 at Bako. The experiments received 100 kg ha^{-1} P_2O_5 at planting and 100 kg ha^{-1} N in two splits (at planting and shortly before flowering). The trials were conducted under rain-fed condition and other management practices were done according to the recommendations of the specific areas.

Grain yield (t ha^{-1}) was the major character measured for the analysis. Grain weight from all the ears of each experimental plot was measured and used to calculate grain yield.

3.3.2.3 Statistical analysis

Analysis of variance for grain yield for each environment was conducted with the PROC ANOVA procedure in SAS (2003). The effects of the genotypes, locations and years as well as their first and second order interaction were determined from the ANOVA analysis. Genotypes were assumed to be fixed, and year and location effects as random. The ANOVA method for estimating variance components consists of equating mean squares to their expectations and solving the resulting set of simultaneous equations as shown in Table 3.3 and is based on the model developed by Comstock and Moll (1963) for the determination of interaction variance components.

Table 3.3 Form of variance analysis and mean square expectations for G x E interaction

Source	DF	MS	Expected mean square
Years (Y)	(Y-1)		
Locations (L)	(L-1)		
Y x L	(Y-1) (L-1)		
Reps in loc and Years	LY(R-1)		
Genotypes (G)	(G-1)	MS5	$\sigma^2 + r\sigma^2_{gly} + rl\sigma^2_{gy} + ry\sigma^2_{gl} + rly\sigma^2_g$
G x L	(G-1) (L-1)	MS4	$\sigma^2 + r\sigma^2_{gly} + ry\sigma^2_{gl}$
G x Y	(G-1) (Y-1)	MS3	$\sigma^2 + r\sigma^2_{gly} + rl\sigma^2_{gy}$
G x L x Y	(G-1)(L-1)(Y-1)	MS2	$\sigma^2 + r\sigma^2_{gly}$
Error	LY(G-1)(R-1)	MS1	σ^2

where Y, L, G and R are the number of years, locations, genotypes and replications respectively. The σ^2 and σ^2_g are components of variance of error and genotypes respectively.

The following statistical analyses were performed to test the significance level of grain yield of the genotypes, locations and their interactions:

- Separate trial analysis for each location and year- This was done for the nine separate trials planted across the three locations for the years 2004-2006.
- The combined analyses of the trials (across years and locations) were done in order to determine differences between genotypes across locations and years, and also to determine whether there was a significant difference among locations and different years.

3.4 Results and discussions

Trial season 2004

From the 2004 trial season the variations among entries were found to be highly significant ($P \leq 0.01$) at Awassa and significant ($P \leq 0.05$) at Bako and Upper Bir. During the season entries explained the largest amount of variation (48.55%) followed by other factors indicated under error (40.69%) at Upper Bir, while blocks contributed least to the variation (Table 3.4).

Among the experimental hybrids AS10, PR1 and GA15 had the highest yields at Awassa, Bako and Upper Bir respectively. Experimental hybrid PR1 was ranked first as it had the highest average yield (6.94 t ha^{-1}) across all the three locations followed by PR2 (6.31 t ha^{-1}) and GA15 (6.23 t ha^{-1}), the check variety BH540 (5.78 t ha^{-1}) ranked seventh from the over all average analysis (Table 3.5). Generally the genotypes performed well at Awassa followed by Bako and Upper Bir (Table 3.5).

Table 3.4 Mean squares from analysis of variance and percentage of variance components for grain yield of 17 maize genotypes tested across three locations in Ethiopia, during 2004

Source	DF	Locations					
		Awassa		Bako		Upper Bir	
		MS	%SS	MS	%SS	MS	%SS
BLOCK	2	1.59	3.14	3.43	9.16	3.24	10.76
ENTRY	16	3.97**	62.87	2.18*	46.53	1.82*	48.55
ERROR	32	1.07	33.99	1.04	48.35	0.76	40.69
TOTAL	50		100		100		100
CV %		15.38		16.87		20.84	

*$P \leq 0.05$, ** $P \leq 0.01$

Table 3.5 Grain yield performance (t ha^{-1}) of 17 genotypes of maize tested across three locations in Ethiopia, during 2004

No	Entry code	Locations				
		Awassa	Bako	Upper Bir	Mean	Rank
1	AS10	8.53	5.17	3.90	5.87	6
2	PR1	8.44	7.93	4.44	6.94	1
3	SE4	8.22	5.58	2.75	5.52	11
4	PR2	8.09	6.84	4.00	6.31	2
5	AS13	7.42	6.33	3.20	5.65	10
6	GA15	7.24	5.96	5.50	6.23	3
7	PR3	7.24	6.55	4.50	6.10	4
8	PR7	6.75	5.52	4.75	5.67	9
9	SE21	6.53	5.53	3.90	5.32	13
10	SE22	6.48	5.50	5.20	5.73	8
11	BH540	6.40	6.36	4.57	5.78	7
12	PR13	6.13	7.78	4.28	6.04	5
13	GA3	5.73	5.49	4.20	5.14	14
14	JA25	5.55	5.02	4.04	4.87	16
15	AS7	5.42	6.31	2.95	4.89	15
16	AS9	5.15	5.52	5.38	5.35	12
17	JZ12	5.06	5.36	3.80	4.74	17
Mean		6.73	6.04	4.20	5.66	
$LSD_{0.05}$		1.72	1.69	1.45	1.62	
CV %		15.38	16.87	20.84	17.70	

Trial season 2005

Highly significant differences (P< 0.01) were found among the genotypes across all the locations during the year. The percentage sum of squares were high for the genotypes under the three locations compared to the other sources of variation (block and error) which can be an indication that genotypes contributed significantly to the variation (Table 3.6).

During the season, the check hybrid BH540 showed good performance and ranked first with an average yield of 6.86 t ha^{-1} followed by PR13 (6.84 t ha^{-1}) and AS10 (6.73 t ha^{-1}). Among the specific sites experimental hybrids SE4 (7.24 t ha^{-1}), BH540 (8.87 t/ha) and AS7 (6.35 t ha^{-1}) were the top yielders at Awassa, Bako and Upper Bir respectively (Table 3.7). From the results of this trial, genotypes performance was inconsistent across the locations as well as across the two years. This variation in rank shows the existence of G x E interaction, that necessitates a closer evaluation of the genotypes according to their interaction with the environment. For mean yield, genotypes performed well at Bako (7.14 t ha^{-1}) followed by nearly similar performance at Awassa and Upper Bir.

Table 3.6 Mean squares from analysis of variance and percentage of variance components for grain yield of 17 maize genotypes tested across three locations in Ethiopia, during 2005

Source	DF	Locations					
		Awassa		Bako		Upper Bir	
		MS	%SS	MS	%SS	MS	%SS
BLOCK	3	0.91	1.90	2.53	6.00	0.98	3.75
ENTRY	16	5.75**	64.15	4.99**	63.00	3.02**	61.83
ERROR	48	1.01	33.95	0.82	31.00	0.56	34.42
TOTAL	67		100		100		100
CV %		19.58		12.67		14.60	

** P ≤ 0.01

Table 3.7 Grain yield performance (t ha^{-1}) of 17 genotypes of maize tested across three locations in Ethiopia, during 2005

No	Entry code	Locations				
		Awassa	Bako	Upper Bir	Mean	Rank
1	AS10	5.25	8.59	6.34	6.73	3
2	PR1	6.01	7.82	5.43	6.42	5
3	SE4	7.24	7.75	4.76	6.58	4
4	PR2	6.77	6.49	5.37	6.21	6
5	AS13	4.60	7.75	5.12	5.82	8
6	GA15	2.88	8.32	5.06	5.42	12
7	PR3	5.22	5.84	6.12	5.73	10
8	PR7	4.00	7.90	5.02	5.64	11
9	SE21	4.84	6.14	5.12	5.37	13
10	SE22	4.67	6.96	4.05	5.23	14
11	BH540	6.50	8.87	5.22	6.86	1
12	PR13	6.08	8.09	6.34	6.84	2
13	GA3	2.91	6.95	3.56	4.47	17
14	JA25	4.57	6.64	3.77	4.99	15
15	AS7	5.14	6.22	6.35	5.90	7
16	AS9	5.41	6.50	5.32	5.74	9
17	JZ12	5.31	4.61	4.23	4.72	16
Mean		5.14	7.14	5.13	5.80	
$LSD_{0.05}$		1.43	1.29	1.06	1.26	
CV %		19.57	12.67	14.06	15.43	

Trial season 2006

The differences among the genotypes were highly significant (P≤ 0.01) at Awassa and Bako and it was significant (P≤ 0.05) at Upper Bir. From the values of the percent sum of squares the contributions of genotypes were high both at Awassa and Bako, while it was low at Upper Bir which can be an indication that the trial was affected by environmental factors among others (Table 3.8).

Experimental hybrids PR1, PR13 and SE4 were the top three hybrids according to the average grain yield of 8.05 t ha^{-1}, 7.42 t ha^{-1} and 7.09 t ha^{-1} respectively. Among the specific sites PR1 (10.80 t ha^{-1}), PR13 (7.93 t ha^{-1}) and PR1 (5.63 t ha^{-1}) ranked first at Awassa, Bako and Upper Bir respectively. The general performance of genotypes were high at Awassa (8.18 t ha^{-1}) followed by Bako (6.29 t ha^{-1}).The performance of the genotypes were relatively low (4.54 t ha^{-1}) at Upper Bir compared to the previous seasons (Table 3.9), the reason can be attributed to the unfavourable environmental conditions that prevailed during the season. The summary of the different variance components is presented under Table 3.10.

Table 3.8 Mean squares from analysis of variance and percentage of variance components for grain yield of 17 maize genotypes tested across three locations in Ethiopia, during 2006

Source	DF[Ŧ]	Locations					
		Awassa		Bako		Upper Bir	
		MS	%SS	MS	%SS	MS	%SS
BLOCK	3	0.92	1.90	2.05	6.80	6.23	15.55
ENTRY	16	9.24**	64.15	4.11**	72.46	2.52*	33.50
ERROR	48	1.18	33.95	0.39	20.74	1.28	50.95
TOTAL	67		100		100		100
CV %		13.29		9.94		24.9	

*P ≤ 0.05, ** P ≤ 0.01

[Ŧ] DF values for Awassa are 2, 16, 32, 50 for block, entry, error and total respectively

Table 3.9 Grain yield performance (t ha^{-1}) of 17 genotypes of maize tested across three locations in Ethiopia, during 2006

No	Entry code	Locations			Mean	Rank
		Awassa	Bako	Upper Bir		
1	AS10	7.11	6.47	5.20	6.26	11
2	PR1	10.80	7.72	5.63	8.05	1
3	SE4	9.82	7.23	4.23	7.09	3
4	PR2	9.69	6.53	3.77	6.66	8
5	AS13	4.22	4.60	3.40	4.07	16
6	GA15	9.96	6.54	4.03	6.84	6
7	PR3	9.07	6.30	5.50	6.96	5
8	PR7	5.87	4.31	3.47	4.55	15
9	SE21	7.33	5.67	4.87	5.96	12
10	SE22	7.78	6.32	4.70	6.27	10
11	BH540	9.47	6.95	4.80	7.07	4
12	PR13	8.84	7.93	5.50	7.42	2
13	GA3	8.22	6.72	5.12	6.69	7
14	JA25	8.89	6.36	3.83	6.36	9
15	AS7	9.24	6.06	5.23	6.84	6
16	AS9	6.58	6.55	4.53	5.89	13
17	JZ12	6.13	4.64	3.27	4.68	14
Mean		8.18	6.29	4.54	6.33	
$LSD_{0.05}$		1.81	0.89	1.61	1.44	
CV %		13.28	9.95	24.90	16.04	

Table 3.10 Summary of variance components for grain yield of 17 maize genotypes tested across three locations in Ethiopia from 2004 - 2006

Locations	Sources	2004	2005	2006	Mean
Awassa	Block	3.14	1.90	1.90	2.31
	Entry	62.87	64.15	64.15	63.72
	Error	33.99	33.95	33.95	33.96
	Total	100	100	100	100.00
	LSD	1.72	1.43	1.81	1.65
	CV %	15.38	19.58	13.29	16.08
Bako	Block	9.16	6.00	6.80	6.54
	Entry	46.53	63.00	72.46	60.10
	Error	48.35	31.00	20.74	33.36
	Total	100	100	100	100.00
	LSD	1.69	1.29	0.89	1.34
	CV %	16.87	12.63	9.94	13.60
Upper Bir	Block	10.76	3.75	15.55	10.02
	Entry	48.55	61.83	33.50	47.96
	Error	40.69	34.42	50.95	42.02
	Total	100	100	100	100.00
	LSD	1.45	1.06	1.61	1.37
	CV %	20.84	14.60	24.90	20.11

Combined analysis of variance across locations and years

The combined analysis of variance across locations and years showed highly significant differences among locations (L) and genotypes (G) and their interaction (G x L). The high mean square values for locations across the three years indicated that the performance was affected significantly by variations among locations (Table 3.11). Table 3.12 shows the results of the combined analyses of variance, that shows locations contributed the major share (24.51%) of variability followed by location by year interaction (18.02%).

Table 3.13 shows the ranking of the genotypes across the three years, and accordingly PR1, PR13 and BH540 were the top three hybrids that performed well across the three years based on the average grain yield of 7.05 t ha^{-1}, 6.73 t ha^{-1} and 6.49 t ha^{-1} respectively. From the table it can be concluded that year 2006 was the good year for grain yield as compared to the previous seasons.

Table 3.11 Mean squares of the combined analyses of variance for grain yield of 17 maize genotypes tested across three locations in Ethiopia, 2004-2006

Years	Sources	DF	MS
2004	Location	2	87.72**
	Block in location	6	2.75*
	Genotype	16	3.01**
	Genotype by Loc (GxL)	32	2.48**
	Residual	96	0.96
	CV %	17.31	
2005	Location	2	91.05**
	Block in location	9	1.47
	Genotype	16	6.35**
	Genotype by Loc (GxL)	32	3.70**
	Residual	144	0.79
	CV %	15.38	
2006	Location	2	193.93**
	Block in location	8	3.34**
	Genotype	16	11.09**
	Genotype by Loc (GxL)	32	2.39**
	Residual	128	0.92
	CV %	15.56	

* P≤0.05, ** P ≤0.01

Table 3.12 Mean squares of the combined analyses of variance and percentage of the variance components for grain yield of 17 maize genotypes tested across nine environments of Ethiopia, 2004-2006

Years	Sources	DF	MS	% SS
2004-2006	Location (L)	2	214.83**	24.51
	Block in (Loc x year)	23	2.46**	3.22
	Year (Y)	2	12.11**	1.38
	Genotype (G)	16	12.93**	11.81
	Genotype x Year (GxY)	32	3.76**	6.87
	Genotype x Loc (GxL)	32	3.41**	6.23
	Location x year	4	78.93**	18.02
	Genotype x year x Location (GxYxL)	64	2.58**	9.43
	Residual	368	0.88**	18.53
	Total	543		
	CV % = 16%			

** P≤ 0.01

Table 3.13 Mean grain yield (t ha^{-1}) and the rank of 17 genotypes of maize tested across three locations in Ethiopia, 2004-2006

No	Entry code	2004	Rank	2005	Rank	2006	Rank	Mean	Rank
1	AS10	5.86	6	6.73	3	6.26	10	6.28	6
2	PR1	6.94	1	6.42	5	8.05	1	7.14	1
3	SE4	5.52	11	6.58	4	7.09	3	6.40	4
4	PR2	6.31	2	6.21	6	6.66	9	6.39	5
5	AS13	5.65	10	5.82	8	4.07	17	5.18	16
6	GA15	6.23	3	5.42	12	6.84	8	6.16	8
7	PR3	6.10	4	5.73	10	6.96	5	6.26	7
8	PR7	5.67	9	5.64	11	4.55	16	5.29	15
9	SE21	5.32	13	5.37	13	5.96	13	5.55	12
10	SE22	5.73	8	5.23	14	6.27	12	5.74	10
11	BH540	5.78	7	6.86	1	7.07	4	6.57	3
12	PR13	6.06	5	6.84	2	7.42	2	6.77	2
13	GA3	5.14	14	4.47	17	6.69	7	5.43	13
14	JA25	4.87	16	4.99	15	6.36	11	5.41	14
15	AS7	4.89	15	5.90	7	6.84	6	5.88	9
16	AS9	5.35	12	5.74	9	5.89	14	5.66	11
17	JZ12	4.74	17	4.72	16	4.68	15	4.71	17
Mean		5.66		5.80		6.33		5.93	
$LSD_{0.05}$		0.92		0.73		0.85		0.84	
CV %		17.31		15.38		15.56		16.08	

To summarize, from the trials, genotypes contributed significantly to the existing variation except at Bako, 2004 and Upper Bir, 2006 where variation due to other factors contributed more (Table 3.4, Table 3.8). From the results of the combined analysis of variance, differences among the testing locations were high as indicated in its percentage contribution to variation (Table 3.12). Furthermore, the highly significant values for the interaction between location and year indicated that inconsistent environmental conditions prevailed across locations and across years. All these contributed to the existence of G x E interaction, where genotypes showed fluctuations in their response to different environments. In addition, the significant interactions showed the existence of unstable genotypes.

Among the experimental hybrids PR1 (7.14 t ha^{-1}), PR13 (6.77 t ha^{-1}) and the check hybrid BH540 (6.57 t ha^{-1}) were the top yielders based on the average grain yield across the three years and the three locations. Hence, hybrids PR1 and PR13 can be considered as candidate varieties for commercial production. Among the specific locations, no variety showed a consistent yield advantage. This is also an indication for the existence of G x E interaction due to year to year fluctuation as well as variation among the testing locations.

Because of the interactions between genotypes and environments, yield of genotypes tested across locations and across years vary and it is a problem for breeders to identify varieties that consistently give high yields in locations with diverse environmental conditions. Kang and Gorman (1989) reported that G x E interactions significantly reduced correlations between phenotypic and genotypic values. In other words, G x E interactions of multi-location trials tend to confound varietal selection and make varietal recommendation difficult, which indicates a need for analyzing stability of genotypes across environments. Pham and Kang (1988) indicated that since G x E interactions minimize the usefulness of genotypes, it is thus imperative that yield levels, adaptation and stability are taken into account in multi-location trials. Furthermore, Crossa (1990) elaborated that only qualitative or crossover interactions are relevant in agriculture, and appropriate statistical analyses are required for quantifying them.

The results of this research confirmed that the main problem in selecting superior varieties in Ethiopia is associated with the unpredictable environmental conditions. The year-to-year fluctuation and variability among locations were important contributors for the G x E interactions. Hence, it is important to look for stable genotypes by using appropriate stability analysis techniques that will help to get more information on the G x E interaction as well as to

assess the adaptation regions of the genotypes according to their favourable interaction. This topic will be addressed in depth in the following chapter. However, the findings of these trials are in accordance with other workers (Wende, 2003; Mosisa and Habtamu, 2008; Solomon *et al*., 2008) who reported that rainfall and other environmental factors are important in selecting maize genotypes in Ethiopian conditions.

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CHAPTER 4

G x E INTERACTION AND GRAIN YIELD STABILITY OF ETHIOPIAN MAIZE HYBRIDS BASED ON VARIOUS STABILITY PARAMETERS

4.1 Abstract

Genotypes x environment interactions indicate the inconsistency of relative performance of genotypes over environments. Assessment of the stability of a genotype to different environments is useful for recommending cultivars for known conditions of cultivation. Genotype x environment interaction and stability was evaluated in terms of grain yield in 17 experimental maize (Zea mays L.) hybrids including a standard check planted at three different locations over three years in the maize growing regions of Ethiopia. Observation of the pattern of grouping of the genotypes and the environments based on grain yield response and comparing the various stability parameters were included among the objectives of this study. The level of association among six parametric and non-parametric stability measures was assessed using Spearman's rank correlation. Highly significant correlation (P≤0.01) was obtained among Eberhart and Russell's deviation from regression (S^2_{di})*, Wricke's ecovalence (Wi), Shukla's* (σ_i^2) *stability variance and AMMI Stability Value (ASV). Mean yield and Lin and Binns's cultivar superiority performance (Pi) showed high correspondence but they showed no correlation with the rest of the parameters. The non-parametric measure of Nassar and Hühn's absolute rank difference S(1) and variance of ranks S(2) was significantly correlated* ($P \leq 0.05$) *with ASV, however it did not correlate with the rest of the parametric measures. Hybrids PR1, PR13 and BH540 were found to be more stable and responsive to favourable environments while SE21 and SE22 showed their stability in the low yielding environments. The analysis of variance for the AMMI model indicated highly significant differences between genotypes and environments as main effects and the interaction effect of G x E was also highly significant. The first two interaction principal component axes (IPCA) of the AMMI model together accounted between 34% and 56% of the total G x E interaction sum of squares for grain yield. The AMMI biplot depicted the genotypes on the bases of their adaptation patterns. Hierarchical clustering using unweighted pair group method with arithmetic average (UPGMA) grouped the genotypes into five and the environments into three clusters.*

Key Words: Maize, grain-yield, stability parameters, cluster

4.2 Introduction

Cultivar performance is a function of the genotype and the nature of the production environment (Cooper and Byth, 1996). Environmental factors have a greater effect on quantitative than qualitative traits, as a result of which performance tests of potential cultivars are conducted in multiple years and locations (Bernardo, 2002). In addition to genotype and environment main effects, performance of cultivars is also determined by the G x E interactions, which is a differential response of cultivars to environmental changes (Hallauer and Miranda, 1988; Crossa *et al*., 1990; Vargas *et al*., 1999). Various causes have been implicated as a source of G x E interactions in African maize growing environments; for example, factors related to temperature, season rainfall, season length, within-season drought, sub-soil pH and socio-economic factors that result in sub-optimal input application (Banzinger *et al*., 2006). The relative magnitude of G x E provides information concerning the likely area of adaptation of a given genotype. It is also useful in determining efficient methods of using time and resources in a breeding program (Ceccarelli, 1989; Kang, 1998).

Large G x E interaction is expected when genotypes are grown under a wide range of environments and outside their normal zone of adaptation (Beck *et al*., 1991). The extent of performance testing depends on the magnitude of G x E, which occurs when genotypes differ in their relative performance across environments (Bernardo, 2002). Yield trials frequently have both significant main effects and a significant G x E interaction (Zobel *et al*., 1988). The existence of G x E interaction necessitates that breeders evaluate genotypes in more than one environment to obtain repeatable rankings of genotypes (Hallauer and Miranda, 1988). However, G x E becomes of practical significance only when cross over interactions occur (Baker, 1988; Crossa and Cornelius, 1997). Crossover interactions occur in evaluation trials when ranks of cultivars change across environments (Russell *et al*., 2003).

In varying environments, genotypes that provide high average yields with minimum G x E interaction have been gaining importance over increased yields (Ceccarelli, 1989; Gauch and Zobel, 1997; Kang, 1998). The definition of a stable cultivar varies with the type of stability analysis used, but generally breeders want cultivars with high mean yield that respond to improved environments (Hallauer and Miranda, 1988).

The G x E interaction expressed as the linear regression coefficient of the genotype on the site mean was first proposed by Yates and Cochran (1938). This was later used by Finlay and Wilkinson (1963) and modified by Eberhart and Russell (1966), who incorporated the deviation from regression as stability parameter. According to the joint regression model, a stable variety is one with a high mean yield, regression coefficient equals to one (b_i=1) and deviation from regression equals to zero (S^2_{di}=0) (Eberhart and Russell, 1966). In most cases, S^2_{di} is considered as stability parameter rather than b_i (Eberhart and Russell, 1966; Becker and Léon, 1988).

Wricke (1962) proposed using the contribution of each genotype to the G x E interaction sum of squares as a stability measure and defined this concept or statistics as ecovalence (W_i). Genotypes with a low W_i value have smaller deviations from the overall mean across environments and are thus more stable. According to Becker and Léon (1988) ecovalence measures the contribution of a genotype to the G x E interaction; a genotype with zero ecovalence is regarded as stable.

Shukla (1972) defined the stability variance of genotype *i* as its variance across environments after the main effects of environmental means have been removed. A genotype is called stable if its stability variance (σ^2) is equal to the environmental variance σ_e^2 which means that $\sigma_i^2 = 0$. A relatively large value of (σ_i^2) will thus indicate greater instability of genotype *i*. As the stability variance is the difference between two sum of squares, it can be negative, but negative estimates of variance are not uncommon in variance component problems. Negative estimates of (σ_i^2) may be taken as equal to zero (Shukla, 1972). Homogeneity of estimates can be tested using Shukla's (1972) approximate test (Lin *et al*., 1986). The stability variance is a linear combination of the ecovalence, and therefore both W_i and σ_i^2 are equivalent for ranking purposes (Wricke and Weber, 1980). However, Kang and Miller (1984) suggested Shukla's method as more effective than Wricke's when the presence of covariates is considered. Shukla's (S_i^2) is an extension of the model to calculate (σ_i^2) and takes into account the covariate z_j (environmental index). If some genotypes show low stability in the basis of σ_i^2 and are judged as stable after taking the covariate into account, it may be inferred that the instability was introduced by the linear effect of the covariate (Shukla, 1972).

The conventional method of partitioning total variation into components due to genotype, environment, and G x E conveys little information on the individual patterns of response (Zobel *et al*., 1988). To optimize growers' yields, despite G x E interactions that cause no one genotype to win every where and always, the growing region must be subdivided to relatively homogenous mega-environments and appropriate genotypes must be targeted for each of these mega-environments (Gauch and Zobel, 1997). The additive main effects and multiplicative interaction (AMMI) model meets these criteria effectively (Zobel *et al*., 1988; Crossa *et al*., 1990; Gauch and Zobel, 1997). The usual analysis of variance (ANOVA) fails to detect a significant interaction component, principal component analysis (PCA) fails to identify and separate the significant genotype and environment main effects, and linear regression (LR) accounts for only a small portion of the interaction sum of squares (Zobel *et al*., 1988). Since ANOVA, PCA, and LR are sub-cases of the more complete AMMI model (Zobel *et al*., 1988), AMMI offers a more appropriate first model of choice when main effects and interaction are both important (Zobel *et al*., 1988; Crossa *et al*., 1990; Gauch and Zobel, 1997). AMMI increases the precision of yield estimation and selection of higher yielding genotypes than treatment means (Crossa *et al*., 1990). AMMI has no specific experimental design requirements, except for a two way data structure (Zobel *et al*., 1988).

The estimation of G x E interaction and yield stability analysis of Ethiopian maize has been addressed by other workers (Wende, 2003; Gezahegn *et al.*, 2008; Mosisa and Habtamu, 2008; Solomon *et al.*, 2008). However, no information is available on the G x E interaction and stability in grain yield performance of these hybrids that are newly developed by the Ethiopian seed enterprise. Hence, the objectives of this study were, (1) to analyze G x E interaction and stability of the Ethiopian maize hybrids for grain yield across the target environments, (2) to observe the pattern of grouping of the genotypes and the environments based on grain yield response of the hybrids and (3) to compare the different methods that are applicable for grain yield stability analysis.

4.3 Materials and methods

4.3.1 Materials

Seventeen experimental maize hybrids including a locally released standard check were evaluated over a period of three years (2004 to 2006) across three locations (nine environments). The details of the genotypes are given in the materials and methods section of Chapter 3.

4.3.2 Methods

4.3.2.1 Experimental design and data measurement

The details of these are also presented under section 3.3.2.2. of Chapter 3.

4.3.2.2 Statistical analysis

The statistical analyses were conducted using the following statistical software: Agrobase Generation II (Agronomix, 2008), SAS (SAS Institute Inc., 2003) and NCSS 2004 (Hintze, 2001).

The following analyses of the stability models were performed using Agrobase Generation II (Agronomix, 2008):

- Lin and Binns cultivar superiority measure (P_i), (Lin and Binns, 1988).
- Joint linear regression model (b_i and S^2_{di}) (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966).
- Wricke's ecovalence (W_i), (Wricke, 1962).
- Shukla's stability variance (σ^2) (Shukla, 1972).
- Nassar and Hühn's non-parametric measure of stability (Nassar and Hühn, 1987).
- The AMMI stability value (ASV) as proposed by Purchase (1997).

The AMMI model, which combines the standard analysis of variance with principal component analysis (Zobel *et al*., 1988), was used to investigate the agronomic nature of G x E interaction. The AMMI model first fits additive effects for the main effects of genotypes and environments, using the additive analysis of variance procedure. Subsequently the program fits multiplicative effects for G x E by principal component analysis (Zobel *et al*., 1988; Gauch and Zobel, 1996, 1997). Biplots (Biplot, 2007) were used to illustrate the relationships among genotypes, environments and between genotypes and environments.

The AMMI model does not make provision for a specific stability measure to be determined, such a measure is essential in order to rank genotypes in terms of stability, the following measure was proposed by Purchase (1997):

$$\text{AMMI Stabilty Value (ASV)} = \sqrt{[\frac{IPCA1SumofSquares}{IPCA2SumofSquares}(IPCA1score)]^2 + [IPCA2score]^2}$$

In effect the ASV is the distance from zero in a two dimensional scattergram of IPCA1 (Interaction Principal Component Analysis axis 1) score against IPCA2 scores. Since the IPCA1 score contributes more G x E sum of squares, it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 total G x E sum of squares.

To statistically compare the six stability analysis procedures used in this study, Spearman's coefficient of rank correlation (r_s) was employed (Steel and Torrie, 1980). All the genotypes evaluated were respectively assigned stability values according to the procedure and definitions used, and were then ranked in order to determine Spearman's rank correlation coefficient between the different procedures. Assume n genotypes are arranged in the same following order to two stability parameters X_i indicates the ranking order (or ranking number) of the i^{th} genotype for the first parameter, Y_i, indicates the ranking number of the i^{th} genotype of the second parameter, then $d_i = X_i - Y_i$ (i= 1,2,...n) and Spearman's rank correlation coefficient (r_s) can be described as:

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

Ranking numbers are whole numbers and when two or more equal ranking numbers occur, the average of the ranking numbers that they otherwise would have received, are ascribed to each genotype. The correlation of the parameters and its significance level was determined by using the software package Agrobase Generation II (Agronomix, 2008).

Cluster analysis of genotypes and environments based on AMMI adjusted means was performed using the NCSS 2004 Software (Hintze, 2001). For the purpose of classification, cluster analysis with the unweighted pair group method with arithmetic average (UPGMA) clustering method has been applied and Euclidean distance matrix was computed (Hintze, 2001).

4.4 Results and discussions

4.4.1 Lin and Binns cultivar superiority measure (P_i)

As a stability statistic the cultivar superiority measure (P_i) of Lin and Binns (1988) is estimated by the square of differences between a genotype's and the maximum genotype mean at location, summed and divided by twice the number of locations. The genotypes with the lowest (P_i) values are considered the most stable. Table 4.1 presents the cultivar performance measure (P_i) for grain yield of the 17 hybrids tested at three locations per year for three years, 2004-2006.

Table 4.1 Lin and Binns's cultivar superiority measure and mean yield (t ha^{-1}) of 17 maize genotypes tested at nine environments in Ethiopia, 2004-2006

No	Entry code	Cultivar Superiority Measure	Rank	Mean Yield	Rank
1	PR1	0.248	1	7.05	1
2	PR13	0.719	2	6.73	2
3	BH540	0.729	3	6.49	3
4	PR2	0.931	4	6.30	5
5	SE4	1.12	5	6.32	4
6	PR3	1.275	6	6.20	7
7	AS10	1.673	7	6.26	6
8	GA15	1.754	8	6.07	8
9	AS7	1.987	9	5.81	9
10	SE22	2.108	10	5.70	10
11	SE21	2.46	11	5.50	12
12	JA25	2.625	12	5.35	14
13	AS9	2.647	13	5.64	11
14	GA3	2.986	14	5.39	13
15	PR7	3.592	15	5.25	15
16	AS13	4.338	16	5.18	16
17	JZ12	4.734	17	4.63	17

From this analysis, the most stable hybrid ranked first for P_i and for mean yield was PR1 followed by PR13 and BH540 ranked second and third. The ranks of the P_i and mean yields are nearly similar and indicate that the Pi measure is more an indication of performance rather than stability. Similar results and conclusion were reached by other workers about the ability of P_i to classify genotypes based on their stability (Tsige, 2002; Alberts, 2004). However, the most unstable hybrids according to this measure were JZ12, AS13 and PR7.

4.4.2 Joint linear regression model

According to the joint linear regression model which was developed by Finlay and Wilkinson (1963) and modified by Eberhart and Russell (1966), a stable variety is one with a high mean yield, regression coefficient equals to one (b_i=1) and deviation from regression equals to zero (S^2_{di}=0) (Eberhart and Russell, 1966). A genotype with b_i value less than 1.0 has above average stability and is especially adaptable to low-performing environments. A genotype with b_i value greater than 1.0 has below average stability and is especially adaptable to high performing environments and a genotype with b_i value equal to 1.0 has average stability and is well or poorly adaptable to all environments depending on high or low mean performance (Finlay and Wilkinson, 1963). A cultivar with b_i = 1 and S^2_{di} = 0 may be defined as stable. However, in most cases, S^2_{di} is considered as stability parameter rather than b_i which is more about responsiveness of genotypes (Eberhart and Russell, 1966; Becker and Léon, 1988).

The analysis of variance for the regression model is presented in Table 4.2. The sum of squares due to environments and genotype x environment are partitioned into environments (linear), genotype x environment (linear) and the pooled deviations from the regression model.

Table 4.2 Analysis of variance for stability analysis according to the joint regression model (Eberhart and Russell, 1966)

Sources	DF	SS	MS	F-value	Pr>F
Total	458	402.90			
Genotypes	16	58.70	3.67	4.80	0.0000
Env. + in Gen. x Env.	136	344.19	2.53		
Env. In linear	1	229.53			
Gen. x Env.(linear)	16	23.61	1.48	1.93	0.0239
Pooled deviation	119	91.05	0.76		
Residual	306	101.23	0.33		
Grand Mean= 5.933			R-Squared= 0.7355		

From the table, the value for the Gen x Env (linear) sum of squares was not as a large portion of the G x E interaction when compared with the environment E (linear) sum of squares and the residual. The table shows the variation among the genotypes and for G x E interaction were significant. It means that genotypes exhibited different performance in different locations / environments which is due to their different genetic make up or the variation due to the environments or both.

According to the joint regression model, the most stable hybrid with highest mean yield and lowest S^2_{di} value (0.000) was PR1 and its regression coefficient (b_i) is 1.4390, which can be an indication of its responsiveness to favorable environments (Table 4.3). According to the model, the second most stable hybrid was SE22 with b_i = 0.8464, S^2_{di} = -0.004 and mean yield 5.7 t ha^{-1}. Although the mean yield value of SE22 is less than that of the other hybrids, the performance of the hybrid under unfavorable environments can be predicted. The most unstable/unpredictable hybrid was AS13 with the highest S^2_{di} value of 1.89 and b_i=0.6740 with the mean yield of 5.18 t ha^{-1} which ranked 16^{th}. If the mean yield, b_i and S^2_{di} values are considered together, then the second and third most stable hybrids would be PR13 and BH540. PR13 had a mean yield of 6.73 t ha^{-1} ranked second, b_i=0.9806 which is close to unity and S^2_{di} =0.284 ranked ninth. BH540 (the check hybrid) had a mean yield of 6.49 t ha^{-1}, b_i =1.2016 and S^2_{di}=0.094 ranked sixth (Table 4.3).

Although the regression model is widely used, some difficulties can be realized from the results of the above analysis, particularly in identifying high-yielding and stable genotypes. One of the problems can be associated with reconciling the parameters of the models, which makes it difficult to decide or recommend high yielding and stable genotypes for future production. It is a general breeders' interest to develop genotypes with high mean yield and which can withstand both predictable and unpredictable environmental variations.

Table 4.3 Mean yield (t ha^{-1}) and stability parameters of 17 maize genotypes tested in nine environments of Ethiopia, 2004-2006

No	Entry code	SS	F-Ratio	Pr. > F	b_i	S^2_{di}	Rank	Mean yield	Rank
1	AS10	8.118	3.5054	0.001	0.9480	0.829	14	6.26	6
2	PR1	2.313	0.9988	0.432	1.4390	0.000	1	7.05	1
3	SE4	7.019	3.0311	0.004	1.5536	0.672	11	6.32	4
4	PR2	5.588	2.4132	0.020	1.2832	0.468	10	6.30	5
5	AS13	15.549	6.7143	0.000	0.6740	1.890	17	5.18	16
6	GA15	8.644	3.7326	0.001	1.4590	0.904	16	6.07	8
7	PR3	3.770	1.6278	0.127	0.8671	0.208	7	6.20	7
8	PR7	8.229	3.5533	0.001	0.7426	0.845	15	5.25	15
9	SE21	0.586	0.2530	0.971	0.7587	-0.247	8	5.50	12
10	SE22	2.286	0.9869	0.441	0.8464	-0.004	2	5.70	10
11	BH540	2.954	1.2843	0.258	1.2016	0.094	6	6.49	3
12	PR13	4.303	1.8582	0.076	0.9806	0.284	9	6.73	2
13	GA3	7.069	3.0526	0.004	1.0957	0.679	12	5.39	13
14	JA25	2.872	1.2401	0.280	1.2047	0.079	5	5.35	14
15	AS7	7.269	3.1387	0.003	1.0281	0.708	13	5.81	9
16	AS9	1.900	0.8203	0.571	0.4071	-0.059	4	5.64	11
17	JZ12	2.564	1.1070	0.358	0.5108	0.035	3	4.63	17

4.4.3 Wricke's ecovalence analysis (W_i)

Wricke (1962) proposed using the contribution of each genotype to the G x E interaction sum of squares as a stability measure and defined this concept or statistics as ecovalence (W_i). Genotypes with a low W_i value have smaller deviations from the overall mean across environments and are thus more stable. According to Becker and Léon (1988) ecovalence measures the contribution of a genotype to the G x E interaction; a genotype with zero ecovalence is regarded as stable.

Wricke's ecovalence was calculated for each of the 17 maize hybrids evaluated at three locations for three years (2004-2006) in the maize belt regions of Ethiopia (Table 4.4).

Table 4.4 Wricke's ecovalance value, overall mean (t ha^{-1}) and their ranks for 17 maize genotypes tested in nine environments of Ethiopia, 2004-2006

No	Entry Code	Ecovalence	Rank	Mean Yield	Rank
1	SE21	1.372	1	5.50	12
2	SE22	2.604	2	5.70	10
3	JA25	3.437	3	5.35	14
4	BH540	3.523	4	6.49	3
5	PR3	4.008	5	6.20	7
6	PR13	4.308	6	6.73	2
7	PR1	4.945	7	7.05	1
8	JZ12	5.795	8	4.63	17
9	AS9	6.646	9	5.64	11
10	PR2	6.671	10	6.30	5
11	GA3	7.193	11	5.39	13
12	AS7	7.279	12	5.81	9
13	AS10	8.154	13	6.26	6
14	PR7	9.123	14	5.25	15
15	SE4	11.158	15	6.32	4
16	GA15	11.488	16	6.07	8
17	AS13	16.984	17	5.18	16

According to the Wricke (1962) method, the most stable hybrids were SE21, SE22 and JA25. These hybrids were not the highest in rank for the mean yield, being 12^{th}, 10^{th} and 14^{th}. Similarly, the most unstable hybrids were AS13, GA15 and SE4.

4.4.4 Shukla's stability variance (σ^2 and S_i^2)

Shukla (1972) developed a modified version of the ecovalence in order to give unbiased estimate of the G x E variance for every genotype using the stability variance (σ_i^2). A genotype is called stable if its stability variance (σ^2) is equal to the environmental variance (σ_e^2) which means that $\sigma_i^2 = 0$. A relatively large value of σ_i^2 will thus indicate greater instability of genotype *i.* Shukla (1972) also proposed a criteria for testing the significance of the stability variance of each genotype and extended the model to allow the removal of the linear effects due to covariates.

According to this stability parameter the most stable hybrids were SE21, SE22 and JA25. Similarly, the most unstable hybrids were AS13, GA15 and SE4 (Table 4.5). From the results of this analysis it can be seen that the stability estimates by Wricke (1962) and Shukla (1972) are identical. However, Shukla's (1972) model differs in the ranking of the genotypes from Wricke (1962) when covariates (locations means) were considered (Table 4.6).

Table 4.5 Shukla's stability variance, overall mean yield (t ha^{-1}) and their ranks for 17 maize genotypes tested in nine environments of Ethiopia, 2004-2006

No	Entry code	Stability Variance (σ_i^2)	Rank	Mean Yield	Rank
1	SE21	0.404	1	5.50	12
2	SE22	0.928	2	5.70	10
3	JA25	1.282	3	5.35	14
4	BH540	1.318	4	6.49	3
5	PR3	1.524	5	6.20	7
6	PR13	1.652	6	6.73	2
7	PR1	1.91	7	7.05	1
8	JZ12	2.284	8	4.63	17
9	AS9	2.645	9	5.64	11
10	PR2	2.656	10	6.30	5
11	GA3	2.878	11	5.39	13
12	AS7	2.914	12	5.81	9
13	AS10	3.286	13	6.26	6
14	PR7	3.698	14	5.25	15
15	SE4	4.565	15	6.32	4
16	GA15	4.703	16	6.07	8
17	AS13	7.039	17	5.18	16

Shukla's stability variance (S_i^2) was calculated based on the following formula:

$$S_i^2 = \frac{t}{(s-2)(t-2)}\left[S_i - \sum_j \frac{S_i}{t(t-1)}\right]$$ where $S_i = \sum_{j=1}^{s}(Y_{ij} - \bar{Y}_{j.} - \hat{b}_i z_i)^2$, $\hat{b}_i$ is the estimated regression coefficient for the i[th] genotype, the covariate z_i (the environmental index) is the deviation of the j[th] environment from the overall mean, t is the number of genotypes, and s is the number of environments. Both estimates of the stability variance were done by Agrobase Generation II (Agronomix, 2008) computer program. The results of the analysis are presented in Table 4.6.

Table 4.6 Shukla's stability variance with locations means as covariate, overall mean yield (t ha^{-1}) and their ranks for 17 maize genotypes tested in nine environments of Ethiopia

No	Entry code	Stability variance (S_i^2)	Rank	Mean yield	Rank
1	SE21	0.122	1	5.50	12
2	AS9	0.760	2	5.64	11
3	SE22	0.948	3	5.70	10
4	PR1	0.961	4	7.05	1
5	JZ12	1.083	5	4.63	17
6	JA25	1.232	6	5.35	14
7	BH540	1.282	7	6.49	3
8	PR3	1.668	8	6.20	7
9	PR13	1.928	9	6.73	2
10	PR2	2.552	10	6.30	5
11	SE4	3.247	11	6.32	4
12	GA3	3.271	12	5.39	13
13	AS7	3.368	13	5.81	9
14	AS10	3.780	14	6.26	6
15	PR7	3.834	15	5.25	15
16	GA15	4.036	16	6.07	8
17	AS13	7.390	17	5.18	16

The ranking pattern of the genotypes was changed after the covariates were taken into consideration (Table 4.6). AS9 and PR1, which were not among the most stable hybrids, became top ranking for stability when the covariates were taken into account. PR1 was also the top

yielder according to the mean yield. The most unstable hybrid identified by both methods was AS13.

4.4.5 Nassar and Hühn's non-parametric measure of yield stability

Non-parametric measures for phenotypic stability based on ranks provide a useful alternative to parametric measures which are based on absolute data. Some advantages of the non-parametric stability statistics compared to parametric measures are: reduction or even avoidance of the bias caused by outliers, no assumptions are needed about the distribution of the phenotypic values and stability parameters based on ranks are easy to use and interpret and compared with parametric measures, are less sensitive to errors of measurement (Huehn, 1990a). Several non-parametric methods are based on the ranks of genotypes in each environment and use the idea of homeostasis as a measure of stability. Genotypes with similar rankings across environments are classified as stable. The statistical properties and significance for measures of non-parametric stability analysis (NPSA) were given by Nassar and Hühn (1987).

Two rank stability measures from Nassar and Hühn (1987) were expressed as S1 and S2. The S1 statistic measures the mean absolute rank difference of a genotype over environments. For a genotype with maximum stability, S1 = 0 and it estimates all possible pair wise rank differences across locations for each genotype. S2 gives the variance among the ranks over environments. For variance of ranks (S2), smaller estimates indicate relative stability and zero variance is an indication of maximum stability (Huehn, 1990a). The parameters S1 and S2 are measurements of the stability alone and they are strongly intercorrelated with each other even in the case of using the uncorrelated yield data (Huehn, 1990b). Approximate tests of significance Z1 and Z2 were developed based on the chi-squared distribution for these two non-parametric measures (Nassar and Hühn, 1987). For S1, genotypes may be tested as significantly less stable or more stable than the average stability/instability. For several reasons, S1 against S2 parameter is preferred, because S1 is very easy to compute and allows a clear and relevant interpretation (mean absolute rank difference between the environments). Furthermore, an efficient test of significance is available (Huehn, 1990a).

Table 4.7 presents the non-parametric stability measure for grain yield of 17 maize hybrids evaluated under nine environments in Ethiopia.

Table 4.7 Mean absolute rank difference (S1) and variance of ranks (S2) for grain yield of 17 maize hybrids tested over three years and three locations in Ethiopia

No	Entry code	S(1)	Rank	Z(1)	S(2)	Rank	Z(2)	Mean yield (t ha^{-1})	Rank
1	AS9	0.826	1	21.908**	0.46	1	8.312**	5.64	11
2	JZ12	1.042	2	19.983**	0.676	2	8.16**	4.63	17
3	SE21	1.215	3	18.512**	0.929	3	7.984**	5.50	12
4	SE22	1.47	4	16.443**	1.329	4	7.71**	5.70	10
5	PR3	1.497	5	16.233**	1.547	5	7.562**	6.20	7
6	PR7	1.661	6	14.973**	1.742	6	7.432**	5.25	15
7	PR13	1.744	7	14.357**	1.921	7	7.312**	6.73	2
8	AS10	1.76	8	14.239**	2.25	8	7.096**	6.26	6
9	AS7	1.882	9	13.357**	2.393	9	7.003**	5.81	9
10	AS13	1.918	10	13.102**	2.409	10	6.992**	5.18	16
11	JA25	1.948	11	12.896**	2.496	11	6.936**	5.35	14
12	BH540	1.953	12	12.861**	2.497	12	6.936**	6.73	3
13	GA3	2.056	13	12.152**	2.587	13	6.878**	5.39	13
14	PR2	2.178	14	11.343**	3.091	14	6.558*	6.30	5
15	PR1	2.271	15	10.74**	3.364	15	6.388*	7.05	1
16	GA15	2.588	16	8.817**	4.154	16	5.908*	6.07	8
17	SE4	2.659	17	8.412**	4.401	17	5.762*	6.32	4

Overall Chi-square for stability = 240.33, 17 df. Individual Z(1) distributed as single df Chi-squares. Overall Chi-square for stability = 120.93, 17 df. Individual Z(2) distributed as single df Chi-squares.

According to this procedure the most stable hybrid was AS9 which was not the case with the other stability parameters. Hybrids with high mean yield were found to be less stable in this stability measure.The two overall chi-square calculated stabilities (Z1= 240.33 and Z2= 120.93) were far greater than the tabulated chi-square values ($\chi^2_{0.01,}17 = 33.4$) which can be an indication for the existence of significant differences in stability among the 17 hybrids.

4.4.6 The AMMI stability value (ASV)

The ASV as described by Purchase (1997) was calculated for each hybrid. Hybrids with lower ASV values are considered more stable than hybrids with higher ASV.

Table 4.8 AMMI stability value (ASV) and ranking with the IPCA 1 and 2 scores for the 17 maize hybrids evaluated in Ethiopia from 2004-2006

No	Entry code	Mean Yield	Rank	IPCA1	IPCA2	ASV	RANK
1	SE21	5.50	12	-0.1606	0.1168	0.279	2
2	SE22	5.70	10	0.5886	-0.3079	0.479	5
3	JA25	5.35	14	0.0435	-0.4745	0.977	9
4	BH540	6.49	3	0.267	0.0253	0.421	3
5	PR3	6.20	7	0.2678	0.1734	0.456	4
6	PR13	6.73	2	0.1444	0.1126	0.254	1
7	PR1	7.05	1	0.6625	0.1122	1.050	10
8	JZ12	4.63	17	0.2331	0.5245	0.640	7
9	AS9	5.64	11	0.3825	-0.1551	0.622	6
10	PR2	6.30	5	0.4392	0.7915	1.051	11
11	GA3	5.39	13	0.3565	-0.9851	1.134	12
12	AS7	5.81	9	0.5371	0.3422	0.913	8
13	AS10	6.26	6	-0.7565	0.0889	1.195	13
14	PR7	5.25	15	-1.0685	-0.3747	1.724	16
15	SE4	6.32	4	0.581	0.8962	1.281	14
16	GA15	6.07	8	0.3271	-1.2346	1.338	15
17	AS13	5.18	16	-1.5265	0.3484	2.430	17

According to the ASV ranking the most stable hybrids were PR13, SE21 and BH540. PR13 and BH540 were the second and third highest yielder based on the mean yield value (Table 4.8). However, PR1 which was the highest for mean yield, ranked tenth for the ASV. The most unstable hybrids according to the ASV were AS13, PR7 and GA15 and this result is similar with most of the stability procedures.

4.4.7 Comparison of the stability measures

The overall ranking and values of the 17 maize hybrids for stability is presented in Table 4.9. According to Wricke's (1962) ecovalence, Shukla's (1972) stability variance, Nassar and Hühn's (1987) absolute rank difference and variance of ranks and the AMMI stability value the most stable hybrids were SE21 and SE22. The parameter of Eberhart and Russell's (1966) deviation from regression, Wricke's (1962) ecovalence, Shukla's (1972) stability variance and the AMMI stability value all ranked AS13 as the most unstable hybrid. Mean yield, Lin and Binns's (1988) cultivar superiority performance and Eberhart and Russell's (1966) deviation from regression ranked PR1 as stable hybrid while PR13 the second highest yielder for mean yield, ranked as most stable hybrid for ASV (Table 4.9).

Spearman's coefficient of rank correlation (Steel and Torie, 1980) was then determined for each of the possible pair wise comparisons of the ranks of the different stability statistics (Table 4.10). Mean yield and P_i were found to be highly correlated ($P < 0.001$) in the ranking of the hybrids ($r = 0.98^{**}$). However, both were generally quite poorly correlated with the rest of the parameters. In addition, Mean yield and P_i were negatively correlated ($r = -0.46$ and $r = -0.47$) with the Nassar and Hühn's (1987) absolute rank difference and variance of ranks.

The highly significant rank correlation of mean yield with P_i indicates that selection for yield would change yield stability by increasing P_i leading to development of genotypes that are specially adapted to environments with optimal growing conditions. The Lin and Binns's procedure defines stability as the deviations of a specific genotype's performance from the performance of the best cultivar. In other words, a stable cultivar is the one that performs in tandem with the environment. A genotype with an inherent high yield would be classified as stable if its yield over locations is similar to that of the top performer, over the respective locations. Thus, the Lin and Binns's procedure appears to be more of a genotype performance measure, rather than a stability measure over sites. Negative rank correlation was observed between mean yield and Pi with S(1) and S(2). This negative rank correlation suggests that the genotypes that were highly responsive to high yielding environments were less responsive to low yielding environments, and vice versa (Jalaluddin and Harrison, 1993).

Eberhart and Russell's (1966) deviation from regression (S^2_{di}) procedure showed highly significant correlation ($P < 0.01$) with the parameter of Wricke (W_i) ($r=0.78^{**}$) , Shukla

(σ_i^2) (r=0.78**), Shukla (S_i^2)(r = 0.91**) and ASV (r = 0.65**), but was quite poorly correlated with mean yield (r = 0.16), Lin and Binns's (1988) cultivar superiority performance (P_i) (r = 0.18) and Nassar and Hühn's (1987) absolute rank difference and variance of ranks (S(1) and S(2), r = 0.33 and r = 0.33 respectively).

The Wricke's procedure of stability statistic showed the highest significant positive correlation (P < 0.01) with Shukla (no covariates, r =1.00**) and ASV (r = 0.86**). The perfect correlation between Wricke's and Shukla indicates that the two procedures are equivalent for ranking purposes. Shukla's stability variance is a linear combination of the ecovalence and therefore, both W_i and σ_i^2 are equivalent for ranking (Wricke and Weber, 1980). The perfect correlation among Wricke and Shukla (with no covariate) is consistent with other workers who reported similar results (Purchase, 1997; Tsige, 2002; Alberts, 2004). The consistency of high rank correlations, particularly among these two parameters, indicates that the parameters yield similar rank orders in a given set of genotypes. However, the covariates in the analysis of Shukla did not show a perfect correlation with Wricke, although there exists a highly significant correlation (r = 0.85**).

The non-parametric measures S(1) and S(2) did not correlate (P > 0.05) with most of the parametric measures except for ASV, where they showed significant positive correlation (P < 0.05). S(1) and S(2) were non-significantly negatively correlated with mean yield and P_i. S(1) and S(2) were highly correlated (r =1.00**) indicating that the stability estimates of the S(2) did not add important information to that obtained by the S(1). The stability parameters S(1), S(2) and ASV were positively and significantly correlated (P < 0.05), indicating that the three measures can classify the genotypes according to their stability under different environmental conditions. This suggests that non-parametric stability measurements seem to be useful alternatives to parametric measurements (Yue *et al.*, 1997), although they do not supply information about genotype adaptability.

Purchase's AMMI stability value (ASV) was highly significantly (P < 0.01) correlated with W_i, σ_i^2 and S^2_{di}. This is also consistent with the finding in the wheat study of Purchase *et al.* (2000). ASV was also positively significantly (P < 0.05) correlated with the non-parametric stability measures of Nassar and Hühn's (1987) (Table 4.10).

Table 4.9 Mean yield (t ha^{-1}), various stability measurements and ranking orders of 17 maize hybrids evaluated in the major maize growing regions of Ethiopia for three years (2004-2006)

No	Entry code	Mean yield	Rank	P_i	Rank	S^2_{di}	Rank	W_i	Rank	σ_i^2	Rank	S_i^2	Rank	S(1)	Rank	S(2)	Rank	ASV	Rank
1	AS10	6.26	6	1.67	7	0.829	14	8.154	13	3.29	13	3.780	14	1.760	8	2.250	8	1.200	13
2	PR1	7.05	1	0.25	1	0.000	1	4.945	7	1.91	7	0.960	4	2.270	15	3.360	15	1.050	10
3	SE4	6.32	4	1.12	5	0.672	11	11.16	15	4.57	15	3.250	11	2.660	17	4.400	17	1.289	14
4	PR2	6.3	5	0.93	4	0.468	10	6.671	10	2.66	10	2.550	10	2.180	14	3.090	14	1.050	11
5	AS13	5.18	16	4.34	16	1.890	17	16.98	17	7.04	17	7.390	17	1.920	10	2.410	10	2.430	17
6	GA15	6.07	8	1.75	8	0.904	16	11.49	16	4.70	16	4.040	16	2.590	16	4.150	16	1.340	15
7	PR3	6.2	7	1.28	6	0.208	7	4.008	5	1.52	5	1.670	8	1.500	5	1.550	5	0.460	4
8	PR7	5.25	15	3.59	15	0.845	15	9.123	14	3.70	14	3.830	15	1.660	6	1.740	6	1.720	16
9	SE21	5.5	12	2.46	11	-0.250	8	1.372	1	0.40	1	0.120	1	1.220	3	0.930	3	0.280	2
10	SE22	5.7	10	2.11	10	-0.004	2	2.604	2	0.93	2	0.950	3	1.470	4	1.330	4	0.480	5
11	BH540	6.49	3	0.73	3	0.094	6	3.523	4	1.32	4	1.280	7	1.950	12	2.500	12	0.420	3
12	PR13	6.73	2	0.72	2	0.284	9	4.308	6	1.65	6	1.930	9	1.740	7	1.920	7	0.250	1
13	GA3	5.39	13	2.99	14	0.679	12	7.193	11	2.88	11	3.270	12	2.060	13	2.590	13	1.130	12
14	JA25	5.35	14	2.63	12	0.079	5	3.437	3	1.28	3	1.230	6	1.950	11	2.500	11	0.980	9
15	AS7	5.81	9	1.99	9	0.708	13	7.279	12	2.91	12	3.370	13	1.880	9	2.390	9	0.910	8
16	AS9	5.64	11	2.65	13	-0.060	4	6.646	9	2.65	9	0.760	2	0.830	1	0.460	1	0.620	6
17	JZ12	4.63	17	4.73	17	0.035	3	5.795	8	2.28	8	1.080	5	1.040	2	0.680	2	0.640	7

Note: $P_{i=}$ Linn and Binns's (1988) cultivar superiority performance; S^2_{di}= Eberhart and Russell's (1966) deviation from regression parameter; W_i = Wricke's(1962) ecovalence; σ_i^2 = Shukla's (1972) stability variance with no covariates; S_i^2 Shukla's (1972) stability variance with covariates; S(1) and S(2) Nassar and Hühn's (1987) absolute rank difference and variance of ranks; ASV = AMMI stability value.

Table 4.10 Rank correlation between stability parameters for 17 maize hybrids evaluated in Ethiopia (2004-2006)

	Mean Yield	P_i	S^2_{di}	W_i	σ_i^2	S_i^2	S(1)	S(2)	ASV
Mean Yield									
P_i	0.983**								
S^2_{di}	0.162	0.186							
W_i	0.115	0.201	0.784**						
σ_i^2	0.115	0.201	0.784**	1.000**					
S_i^2	0.076	0.101	0.914**	0.848**	0.848**				
S(1)	-0.461	-0.471	0.326	0.421	0.421	0.468			
S(2)	-0.461	-0.471	0.326	0.421	0.421	0.468	1.000**		
ASV	0.260	0.299	0.654**	0.858**	0.858**	0.750**	0.517*	0.517*	

* P ≤ 0.05, ** P ≤ 0.01

Note: $P_{i=}$ Linn and Binns's (1988) cultivar superiority performance; S^2_{di}= Eberhart and Russell's (1966) deviation from regression parameter; W_i = Wricke's(1962) ecovalence; σ_i^2 = Shukla's (1972) stability variance with no covariates; S_i^2 Shukla's (1972) stability variance with covariates; S(1) and S(2) Nassar and Hühn's (1987) absolute rank difference and variance of ranks; ASV = AMMI stability value.

4.4.8 Additive Main Effects and Multiplicative Interaction (AMMI) model / Multivariate analysis technique

Multivariate techniques are widely applied in stability analysis to provide further information on real multivariate response of genotypes to environments. Among the multivariate analysis techniques, the AMMI model is the powerful method in assessing G x E interaction and stability/adaptation of genotypes from multi-environment trials. AMMI is essentially effective where the assumption of linearity of responses of genotype to a change in environment is not fulfilled, which is important in stability analysis. The results can be graphed in a useful biplot that shows both main and interaction effects for both genotypes and environments (Gauch and Zobel, 1996).

The AMMI analyses and the IPCA1 versus mean yield biplot were performed using Agrobase Generation II (Agronomix, 2008). Biplots of the first two principal components were constructed using Biplot v1.1 (Biplot, 2007) and used to illustrate the relationships among genotypes, environments, and between genotypes and environments. Environments and genotypes are shown as vectors and points on the biplot. Genotypes and environments that are close together tend to be similar. The angle between two vectors indicates the degree of association or correlation. Small angles indicate similarity, 90^0 angles indicate orthogonality and no association, and angles > 90^0 indicate a negative correlation. The orthogonal projections of genotypes on environment vectors indicate the relative performance of genotypes in a given environment; that is the greater the projection of the genotype in the positive direction, the better the performance of that genotype in that environment.

The combined analyses of variance (ANOVA) of the 17 maize hybrids evaluated over three years and across three locations according to the AMMI model are presented in Table 4.11. The ANOVA indicated highly significant differences ($P < 0.01$) for environments, genotypes and genotypes x environment interaction. The IPCA are ordered according to decreasing importance. The F-test was highly significant ($P < 0.01$) for the first three IPCA axes and significant ($P < 0.05$) for the fourth and fifth IPCA.

Table 4.11 Analysis of variance (ANOVA) based on the AMMI model for grain yield (t ha^{-1}) for the three years (2004-2006)

Sources	df	SS	MS	Total variation explained (%)	G x E explained (%)	Cumulative (%)
Total	458	1512.38				
Environments	8	688.60	86.08**	45.53		
Reps within Env.	18	43.79	2.43			
Genotype	16	176.11	11.01**	11.65		
Genotype x Env.	128	343.98	2.68**	22.74		
IPCA1	23	118.12	5.14**		34.34	34.34
IPCA2	21	74.99	3.57**		21.80	56.14
IPCA3	19	59.94	3.15**		17.43	73.57
IPCA4	17	29.50	1.74*		8.58	82.14
IPCA5	15	26.44	1.76*		7.69	89.83
Residual	288	259.91	0.90			

*P < 0.05, ** P < 0.01; IPCA= Interaction principal component axis

Grand mean = 5.933 R-squared=0.8281 C.V. =16.01%

The total variation explained (%) , ranged from 11.65% for genotypes, 45.53% for environments and 22.74% for G x E. The high percentage of the environment is an indication that the major factor that influence yield performance of maize in Ethiopia is the environment. The variation due to G x E is nearly double the variation due to genotypes as main effect. Out of the total eight IPCA, the first five IPCA axes explained 89.83% of the G x E interaction. The first IPCA captured 34.34% of the total interaction sum of squares in 18% of the interaction degrees of freedom. The second IPCA also explained 21.80% of the interaction sum of squares in 16 % of the interaction degrees of freedom (Table 4.11).

Table 4.12 and Table 4.13 present the AMMI analysis data with the IPCA1 and IPCA2 scores for the hybrids and the environments. The tables also show the names and graph ID of the hybrids and the environments. In Figure 4.1 the IPCA1 scores for both the hybrids (lower case) and the environments (upper case) were plotted against the mean yield for the hybrids and the environments respectively.

Table 4.12 IPCA1, IPCA2 scores and graph ID for the 17 maize hybrids sorted on mean yield and evaluated in nine environments

No	Entry code	Graph ID	Mean Yield	IPCA1	IPCA2
1	SE21	f	5.50	-0.1606	0.1168
2	SE22	g	5.70	0.5886	-0.3079
3	JA25	q	5.35	0.0435	-0.4745
4	BH540	h	6.49	0.267	0.0253
5	PR3	p	6.20	0.2678	0.1734
6	PR13	n	6.73	0.1444	0.1126
7	PR1	c	7.05	0.6625	0.1122
8	JZ12	m	4.63	0.2331	0.5245
9	AS9	o	5.64	0.3825	-0.1551
10	PR2	l	6.30	0.4392	0.7915
11	GA3	a	5.39	0.3565	-0.9851
12	AS7	j	5.81	0.5371	0.3422
13	AS10	k	6.26	-0.7565	0.0889
14	PR7	d	5.25	-1.0685	-0.3747
15	SE4	e	6.32	0.581	0.8962
16	GA15	i	6.07	0.3271	-1.2346
17	AS13	b	5.18	-1.5265	0.3484

Table 4.13 The IPCA1, IPCA2 scores and the graph ID for the nine environments, sorted on environmental mean yield

No	Environment	Env. code	Graph ID	Env. mean	IPCA1	IPCA2
1	Awassa 2004	AW04	I	6.73	-0.5866	0.3681
2	Bako 2004	BK04	G	6.04	-0.1399	0.2048
3	Upper Bir 2004	UB04	A	4.20	-0.5303	-1.1433
4	Awassa 2005	AW05	F	5.14	-0.0284	1.6374
5	Bako 2005	BK05	E	7.14	-0.7650	-0.6973
6	Upper Bir 2005	UB05	C	5.13	-0.6407	0.3888
7	Awassa 2006	AW06	H	8.18	2.0616	-0.2212
8	Bako 2006	BK06	D	6.29	0.6189	-0.2266
9	Upper Bir 2006	UB06	B	4.54	0.0104	-0.3105

By plotting both the hybrids and the environments on the same graph, the associations between the hybrids and the environments can be seen clearly. The IPCA scores of a genotype in the AMMI analysis are an indication of the stability of a genotype over environments. The

greater the IPCA scores, either positive or negative, as it is a relative value, the more specifically adapted a genotype is to certain environments. The more IPCA scores approximate to zero, the more stable the genotype to over all environments sampled.

From the biplot, environments are distributed from lower yielding environments in quadrants I (top left) and IV (bottom left) to the high yielding environments in quadrants II (top right) and III (bottom right) (Fig.4.1). The high yielding environments classified according to the AMMI 1 model are AW06 (H), BK06 (D), AW04 (I), and BK05 (E). The lower yielding environments are UB04 (A), BK04 (G) and UB05(C). Therefore, Upper Bir is generally categorized under low yielding maize environment as compared to the two relatively categorized under high yielding environments (Awassa and Bako). It is further noted that Awassa 2006 (H) was the most favourable season and Upper 2004 (A) was less favourable among the nine environments, this situation is clearly indicated in Fig.4.1 (that plots genotypes/environments that do not have similar means) where the two environmental variations are plotted far apart from the mean.

The genotypes categorized under favourable environments with above-average means are PR1(c), SE4 (e), PR2 (l), PR3 (p), BH540 (h) and PR13 (n) among them PR13 is found to be more stable. Genotypes grouped under low yielding environments are shown at the lower left quadrant of the biplot. Generally AS13 (b) is the most unstable genotype identified by the AMMI model (Fig. 4.1), which is also consistent with most of the stability parameters used in this study. Genotypes that are close to each other tend to have similar performance and those that are close to environment indicates their better adaptation to that particular environment. Hence hybrid SE4(e) was better adapted to Bako environment and hybrids PR13 and BH540 showed similar performance as they are close to each other.

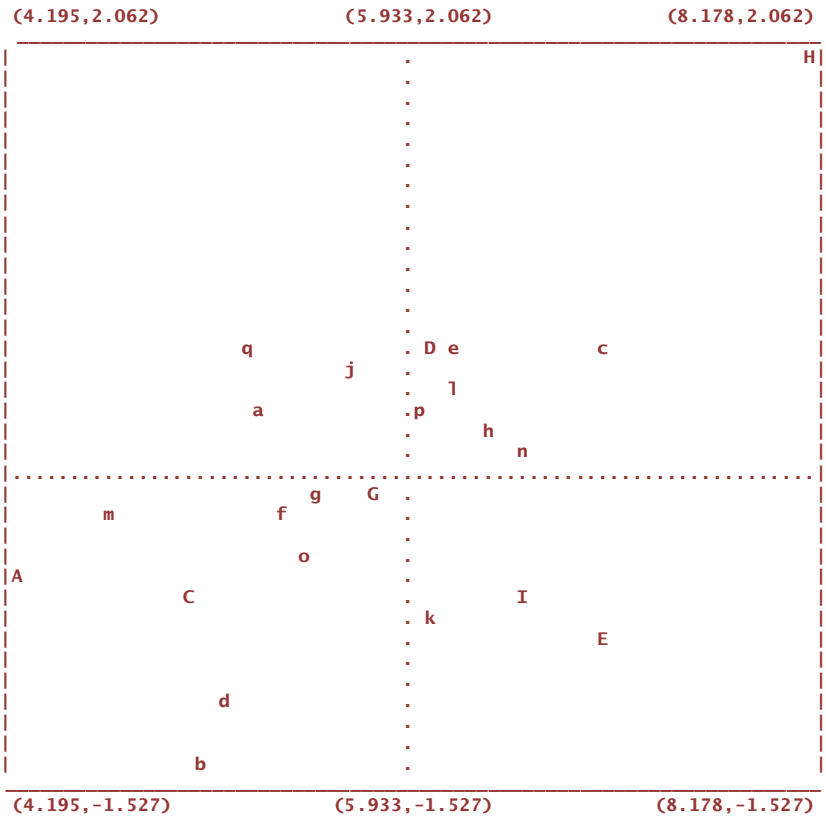

Figure 4.1 AMMI 1 biplot for grain yield of maize hybrids showing means of genotypes (lower case letters) and environments (upper case letters) plotted against their IPCA1 scores (genotypes/environments in place of others with similar means are not shown)

The five IPCA axes can be taken as adequate dimensions for the data; however, only the first two IPCA axes were plotted against one another to help investigate the G x E interactions pattern of each genotype. The AMMI 2 biplot generated using the first two principal component scores showed a clear association between genotypes and environments (Fig. 4.2 and 4.3). The biplot showed that AW06 was the most discriminating environment for the genotypes as indicated by the longest distance between its marker and the origin and gave information on the performance of the hybrids. However, due to its high IPCA score, genotype variability at this environment may not exactly reflect the average genotypes performance across environments. For the environments closer relationships was observed between AW04 and UB05. Bako (BK04) is identified as stable environment as its IPCA2 score and vector is near to the source (zero).

Environments UB06 and AW05 projected in the opposite direction and UB06 has a shorter vector than AW05 (Fig. 4.2).

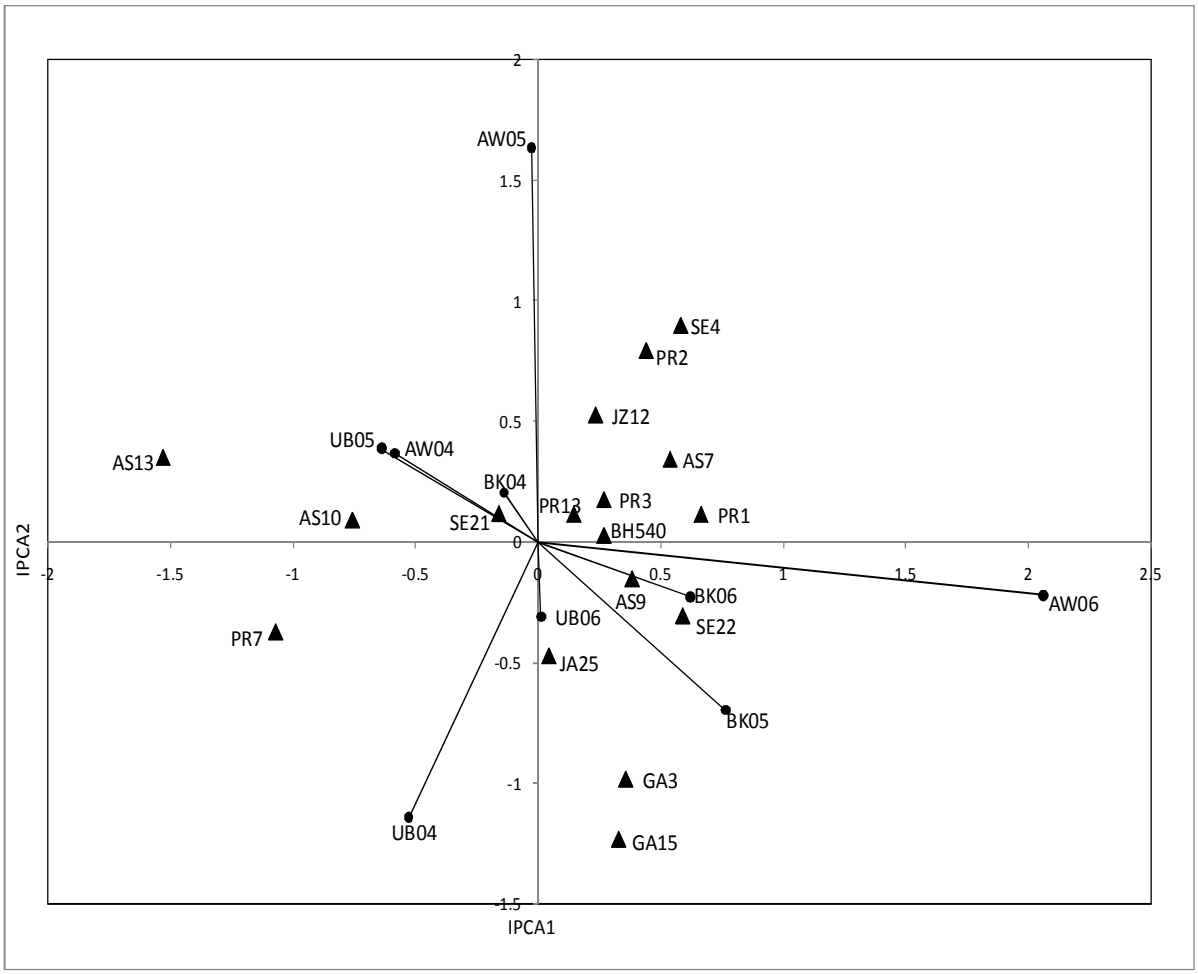

Figure 4.2 AMMI 2 biplot for grain yield of maize hybrids showing the plotting of IPCA1 and IPCA2 of genotypes (▲) and environments (●) with vectors. The angle and the projection of the vectors indicate the association among the environments

The AMMI 2 biplot also indicated the relationship among the maize hybrids. AS13 was different from the other hybrids as it is located far apart from the other hybrids in the biplot. It is also the unstable hybrid. Hybrids GA15 and GA3, SE22 and AS9, SE4 and PR2, PR3 and PR13 showed a similar performance for grain yield. Hybrids PR13, SE21, PR3 and BH540 were

positioned closer to the origin of the biplot which indicates their stability in performance across environments, while the direction of SE21 shows the hybrid's stability in the low yielding environment. Hybrid PR7 was more adapted to low yielding environment and hybrids AS9 and SE22 were more close to BK06. Generally hybrids with a smaller vector angle in between and have similar projection, designate their proximity in the grain yield performance. Those genotypes that are clustered close to the centre tend to be stable, and those plotted far apart are unstable in performance (Fig 4.3).

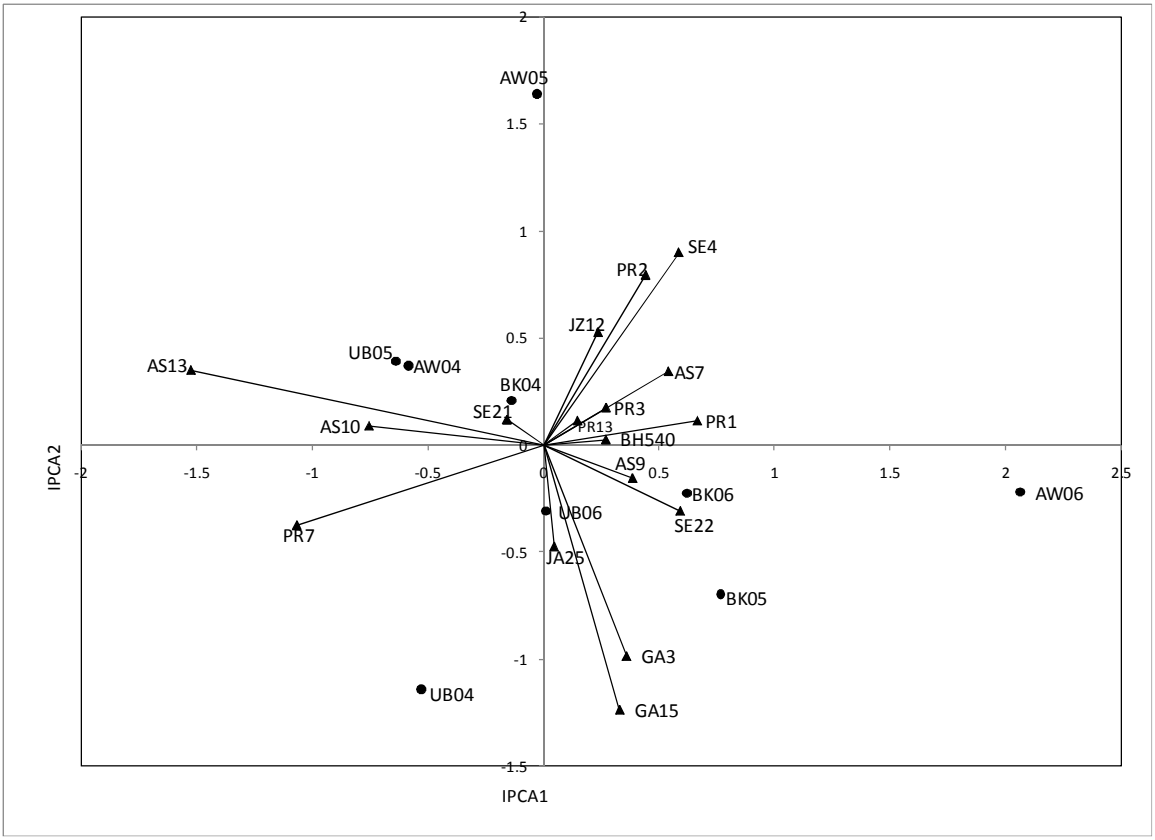

Figure 4.3 AMMI 2 biplot for grain yield of maize hybrids showing the plotting of IPCA1 and IPCA2 of genotypes (▲) and environments (●) with vectors. The angle and the projection of the vectors indicate the association among the genotypes

4.4.9 Cluster analysis of genotypes and environments

Cluster analysis is the most widely used technique for classifying environments or genotypes into homogeneous groups. It operates on a matrix of dissimilarity (or similarity) indexes for all possible pairs of genotypes or pairs of environments, depending on which is being clustered (Ghaderri *et al*., 1980).

Cluster analysis was performed to study the patterns of groupings of genotypes and environments. The dendrograms (Fig. 4.4 and 4.5) were generated from UPGMA clustering method of genotypes and environments based on Euclidean distances using AMMI adjusted mean yields of genotypes and environments respectively. Clustering of genotypes at a cut-off value of 1.0 produced five clusters (Fig 4.4). Cluster one consisted of four hybrids (AS10, PR3, SE21 and AS7). Cluster two consisted of five hybrids (PR1, PR13, BH540, SE4, PR2), the three genotypes in this group PR1, PR13 and BH540 were categorized as high yielder and clearly indicated in the biplot by the close association of the vectors (Fig 4.3). The third cluster also consisted of five hybrids (GA15, SE22, JA25, GA3 and AS9) and all the hybrids were grouped under the same category in the AMMI2 biplot. The fourth group holds two hybrids and both are shown projected in a similar direction in the AMMI 2 biplot. The last group identified is one with JZ12. The hybrid was the lowest yielder among the 17 maize hybrids that were evaluated under the nine environments.

Cluster analysis of environments at cut-off point 1.0 produced three clusters two of the clusters consist four environments each and the third cluster consist only one environment. UB04, UB05, UB06 and AW05 consists of the first group, among them AW05 and UB05 shows 100% similarity for the environments. The second clustering consisted BK04, BK06, BK05 and AW04. The third cluster identified AW06 as a separate group (Fig.4.5). This is also consistent with the results of the AMMI 2 biplot (Fig.4.2).

To summarize, the stability parameters ranked the hybrids differently. However, some parameters are identical in ranking without adding additional information. Parameters like Wricke's ecovalence and Shukla's stability variance were almost similar for ranking purposes. The correlation of the ASV with other parameters makes it a preferable choice to analyze yield stability. The information from the AMMI model was important to release genotypes to target environments based on their responsiveness.

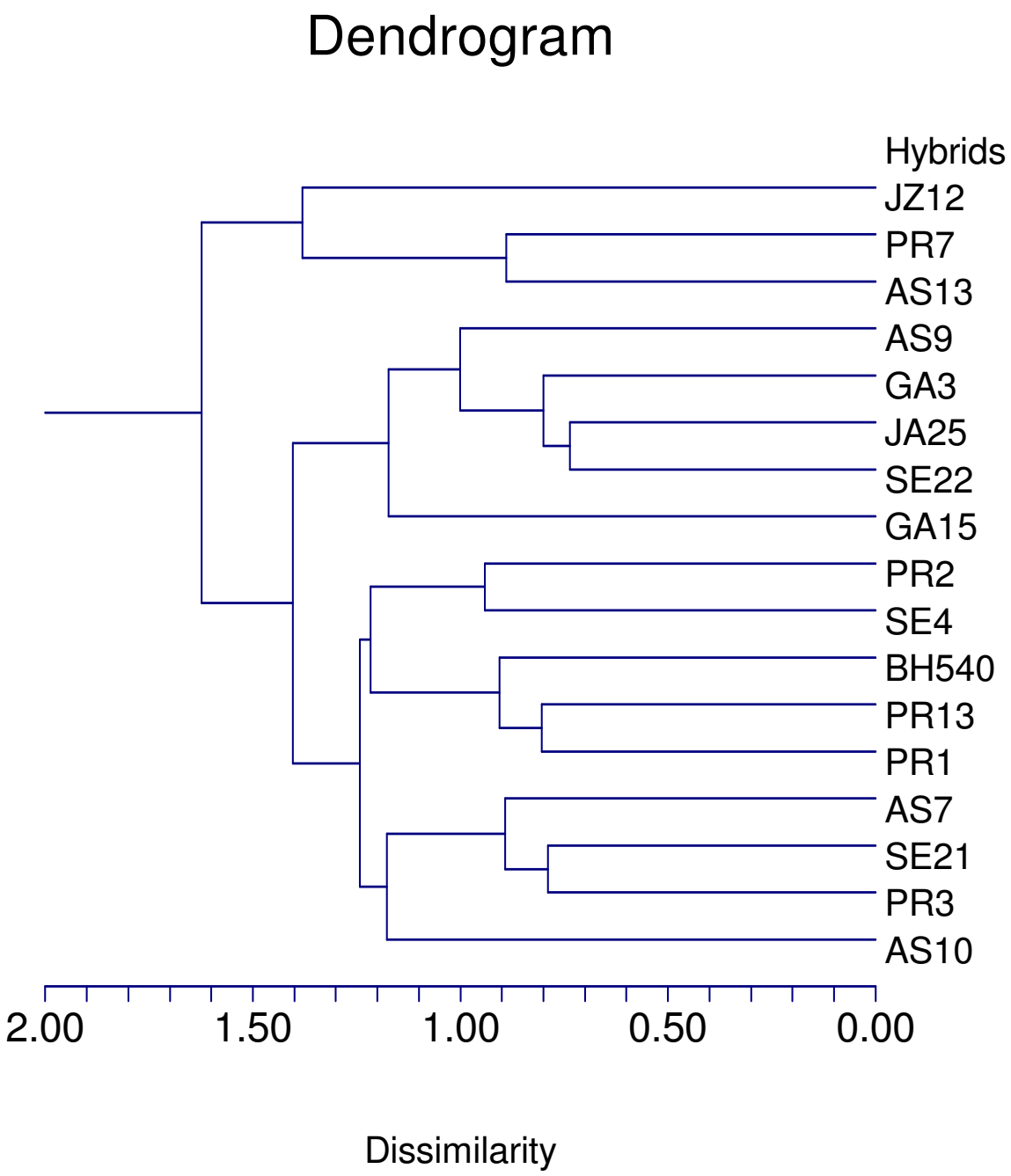

Figure 4.4 Dendrogram depicting the clustering of 17 Ethiopian maize hybrids using AMMI adjusted means of nine environment

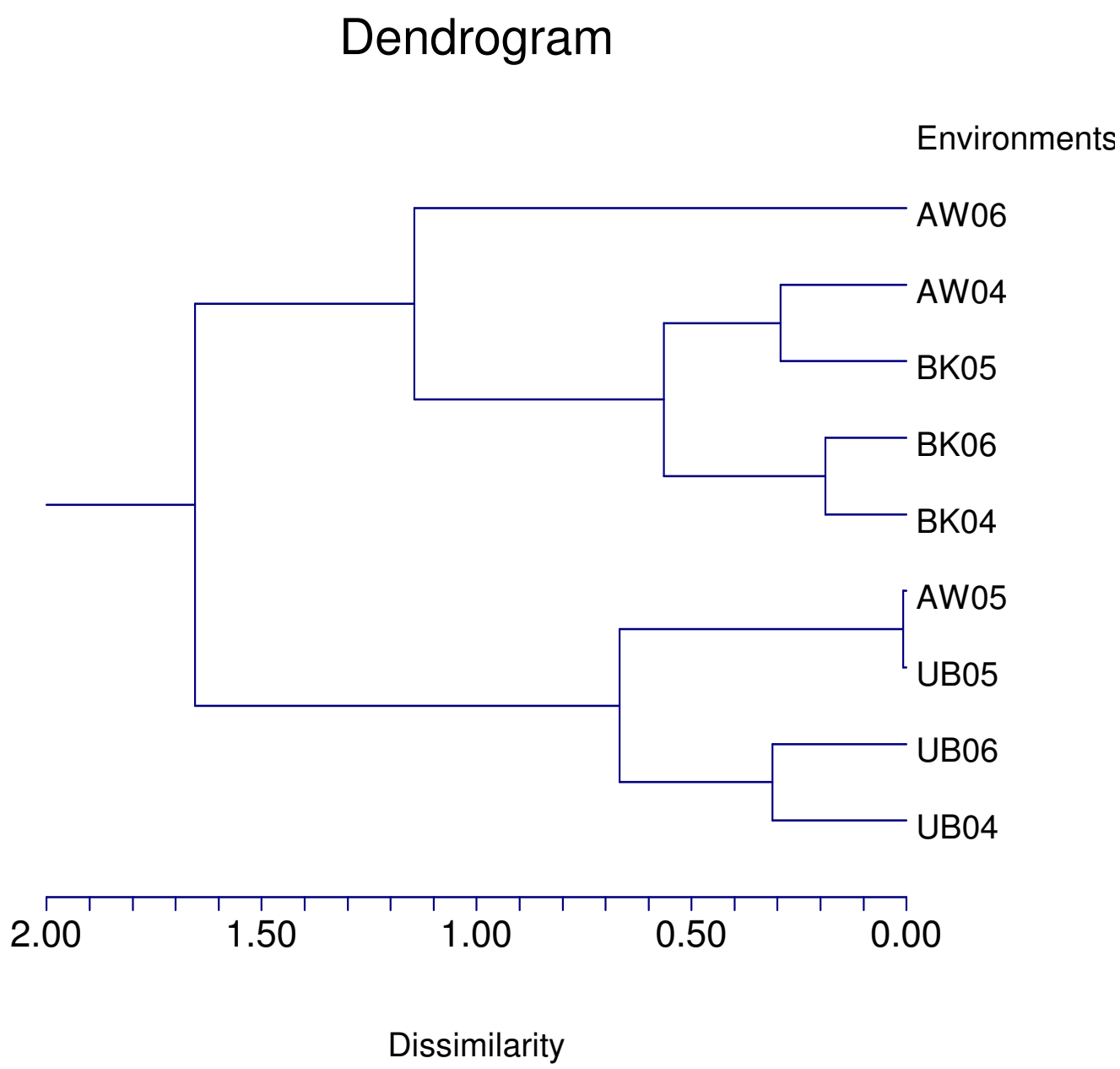

Figure 4.5 Dendrogram depicting the clustering of nine environments using AMMI adjusted means of 17 Ethiopian maize hybrids

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CHAPTER 5

OPTIMUM ALLOCATION OF REPLICATIONS, LOCATIONS AND YEARS AND ITS APPLICATION TO MAIZE YIELD TRIALS IN ETHIOPIA

5.1 Abstract

The efficiency of yield trials for selecting superior genotypes is affected strongly by experimental designs, including the choice of the number of replications, locations and years. Increasing the number of locations or replications may be expensive, and adding years can seriously delay a breeding programme. Therefore, knowing the best application of resources in a yield trial is important to offset the allocation of meager resources of research which is the case in Ethiopia. Getting precise information from the experiments is also important. To examine the optimum number of locations, replications and years required in the final and releasing stage of maize yield trials and to develop guidance to breeders and agronomist who are planning maize yield trials in Ethiopia, a replicated maize yield trial was conducted for three years in three locations within the mid altitude sub-humid mega environments of Ethiopia. Variance component analyses were conducted to get estimates of a genotypic mean and values of LSD percentage were also used for comparison of different combinations of replications, locations and years. Various combinations of the three factors were analyzed to achieve experimental precision. The results indicated that allocation of two or three replications, three to five locations for three to four testing years will give adequate information for the yield estimates of a maize trial, will help to minimize trial costs and provide more precise data for variety release in Ethiopian conditions. The research also proved that locations-years tradeoff is more effective than locations/years-replications tradeoff in getting statistically efficient data from a maize yield trial.

Key Words: Maize, optimum resource allocation, variance components

5.2 Introduction

The optimal breeding strategy for highly variable change of target environments involves the careful characterization of the target area so that the selection criteria and selection environments can be identified (Bramel-Cox, 1996). This will allow for the best allocation of maximum gain in varietal performance.

It is generally agreed that data from only one location, year, or season is insufficient if interaction of genotype with the environment is known or suspected. Therefore, researchers commonly test genotype x environment interactions to decide whether data need be collected over more than one location, year, or season (Miller *et al*., 1959; Jones *et al*., 1960). A few researchers have explored the matter of whether one should use more years and/or locations, or more replications. The usual approach has been to see which allocation of sampling effort would minimize the variance of a genotype mean. This has been done for crops including cereals (Sprague and Federer, 1951; Rasmusson and Lambert, 1961; Kaltsikes, 1970; Patterson *et al*., 1977; Mycroft, 1983), peanuts (Shorter and Norman, 1983), potato (Sekioka and Lauer, 1970) and sugarcane (Milligan, 1994; Brown and Glaz, 2001). In general, these studies have concluded that adding more locations and/or years will be more advantageous than adding replications. Gauch and Zobel (1996) described the effect of experimental design and the analysis to be applied to the data in reducing the number of replications and achieving statistical efficiency.

The optimum number of locations, years and replications required for multi-environment trials can be determined by manipulating these factors to minimize the variance of the genotype means (Crossa, 1990; Basford and Cooper, 1998). The genotype mean is a function of the components of variance for genotype x location (G x L), genotype x years (G x Y), genotype x location x year interaction (G x L x Y) and error. By comparing the designs/combinations, the one with the smaller variance of a genotype mean is preferred as an optimal application of resources.

Miller *et al*. (1962) used the theoretical variance of the mean to evaluate the relationship between the number of testing environments used and the precision with which the evaluation of the variety could be made. The theoretical variance of a genotype (g) mean ($V_{\bar{x}}$) from replicated trials over locations and years can be expressed in general as:

$$V_{\bar{x}} = \frac{\sigma_e^2}{rly} + \frac{\sigma_{gly}^2}{ly} + \frac{\sigma_{gl}^2}{l} + \frac{\sigma_{gy}^2}{y} \quad \text{...(1)}$$

where the numerators are the variance components and r, l and y are the number of replications, locations and years respectively in which the varieties are to be tested. The numerators can be substituted by the variance components estimated from the analysis of variance. The variance of a mean can then be predicted for any combination or combinations of r, l and y. The smaller the variance of the mean with the different combinations of r, l and y, the more precise the estimates of variety performance would be.

The numerators in the terms of equation 1 are variance components associated with G x E interactions, plus the error variance component from the replication. $V_{\bar{x}}$, is thus a weighted sum of the variance components, the weights being reciprocals of r, l and y, and their products. An individual term to be summed in equation 1 will be more or less important according to (i) the relative size of its particular variance component (numerator), and (ii) the weight (divisor) for that component. Prevailing environmental conditions and their effects on the genotypes used determine the values of the variance components, but the experimenter has control over the divisors through choosing r, l and y. That is central to any discussion of allocation of resources over years, locations, and replications (William and Todd, 1989).

In general, the efficiency of yield trials for selecting superior genotypes is affected strongly by experimental designs, including the choice of the number of replications, locations and years. Increasing the number of locations or replications may be expensive, and adding years can seriously delay a breeding programme. Therefore, it is imperative to know the best application of resources in the yield trials for the wise utilization of scarce resources of research and to get precise information. Hence, the objectives of this research were to examine the optimum number of locations, replications and years required in the final and releasing stage of maize yield trials and to develop guidance to breeders and agronomist who are planning maize yield trials in Ethiopia.

5.3 Materials and methods

5.3.1 Materials

Test environments and genotypes: Seventeen experimental medium maturity (135-145 days) hybrid maize (*Zea mays*) genotypes were planted in nine environments, as combinations of three years (2004, 2005 and 2006) by three locations in three replications (the details of the genotypes are given in the materials and methods section of Chapter 3). The locations used were: Ethiopian Seed Enterprise Awassa-Shallo basic seed farm located 271 km south east of Addis Ababa, Bako National Maize Research Center located 250 km west of Addis Ababa and Upper Bir private farm which is located around 400 km north west of Addis Ababa. All three locations are situated in the mid-altitude sub-humid maize growing mega environments of Ethiopia. Fertilizer application, weed, disease, and insect control at these three locations were done in accordance with the recommended cultural practices for the specific sites.

5.3.2 Methods

Planting and data collection: genotypes were planted in plots consisted of two rows of 5.1m long and 0.75m wide. Each plot was planted with 40 seeds, and thinned to 20 plants at the 3-4 leaves stage. Each year planting was done in the main cropping season following the recommendations for each specific site. The trials at Awassa were planted around mid April and trials at Bako and Upper Bir were planted around mid May. A randomized complete bock design with three replications was used at all environments. Grain yield (t ha^{-1}) was the major character measured in this trial.

Statistical analysis: the variance components in equation 1 are unknown parameters to be estimated from the available data. When estimates are used in place of the parameters in equation 1, the estimated variance of a genotype mean is obtained. Type I estimates of the variance components is used from the results of PROC ANOVA procedure of SAS (2003). Type I estimators are often called analysis of variance (ANOVA) estimators, being obtained by equating observed and expected mean squares from an analysis of variance and solving the resulting equations. They are unbiased and, provided the data are balanced (having equal numbers of observations in corresponding subclasses), have some appealing properties: they are easy to compute, and have minimum variance among all unbiased estimators that are quadratic functions

of the observations. Under normality, they have minimum variance among all unbiased estimators. Type I estimators, like all unbiased estimators, must permit negative estimates of the (non-negative) variance components. Should negative estimates arise in practice, they should be used in equation 1, not set to zero as they sometimes are when one is interested only in reporting estimates of the individual variance components. Type I estimates of variance components lose their appealing properties when they must be obtained from unbalanced data. Especially when using very unbalanced data, one should consider using instead maximum likelihood (ML) or restricted maximum likelihood (REML) estimators (William and Todd, 1989).

The ANOVA for estimation of the genotypic and non-genetic variance and the formula for determination of variance components are presented in Tables 5.1 and 5.2.

Table 5.1 ANOVA for estimation of the genotypic and non-genetic variance for several environments (l-locations, y-years)

Source	Df	m.s	E(m.s)
genotypes	f_1=g-1	m_1	$\sigma^2 + r\sigma^2_{gly} + rl\sigma^2_{gy} + ry\sigma^2_{gl} + rly\sigma^2_g$
Locations	f_2= l-1	m_2	-
Years	f_3= y-1	m_3	-
g x l	$f_4=f_1f_2$	m_4	$\sigma^2 + r\sigma^2_{gly} + ry\sigma^2_{gl}$
g x y	$f_5=f_2f_3$	m_5	$\sigma^2 + r\sigma^2_{gly} + rl\sigma^2_{gy}$
l x y	$f_6=f_2f_3$	m_6	-
g x l x y	$f_7=f_1f_2f_3$	m_7	$\sigma^2 + r\sigma^2_{gly}$
Blocks	f_8=(r-1)ly	m_8	-
Error	f_9=(r-1)(g-1)ly	m_9	σ^2

Table 5.2 Determination of variance components

Variance components	Method of determination
Genotypes	$\frac{m_1 - m_4 - m_5 + m_7}{rly}$
Genotypes x location	$\frac{m_4 - m_7}{ry}$
Genotype x year	$\frac{m_5 - m_7}{rl}$
Genotype x location x year	$\frac{m_7 - m_9}{r}$
Error	m_9

Once the variance components in equation 1 have been estimated, the estimates and various combinations of y, l, and r can be substituted into that equation to study the behavior of the estimated variance of a genotype mean as a function of y, l, and r that is, of the allocation of resources to years, locations, and replication. The lower the genotype variance, the more precise the estimate of the mean and the assumption is that the variance components estimates employed are reasonable estimates for the future trial being designed.

The least significant difference (LSD) can be used as a measure of precision where the smaller the LSD, the higher the precision. The values of the genotypic variance ($V_{\bar{x}}$) can be used to determine the different LSD for the various combinations of l, y and r. This LSD can then be expressed as a percentage of the grand mean for standardization and comparison purposes (Pillay, 2000). The LSD percentage can be calculated using the following formula:

$$\text{LSD\%} = \frac{(t - value)(\sqrt{2V_{\bar{x}}})(100)}{GrandMean} \qquad \text{.................................. (2)}$$

5.4 Results and discussions

Table 5.3 presents the values of the variance component estimates that were obtained from the three years maize trial in Ethiopia. These estimates were used in equation 1, along with various combinations of values of locations, years and replications that will help to describe the allocation of resources based on minimizing the variance of a genotype mean.

Table 5.3 Estimates of variance components for error and the interaction of genotype and environmental effects (genotype, years and locations) in maize trials conducted in Ethiopia

Variance components	Values
σ^2_{gl}	0.05
σ^2_{gy}	0.13
σ^2_{gly}	0.49
σ^2_{e}	0.97
Over all mean (t ha^{-1})	5.90
Critical t-value	1.97

The combination of the number of locations, years and replications that results in the lowest $V_{\bar{x}}$ will be the best combination to use, which are assumed to be reasonable yield estimates for future trials. The effectiveness of these three different factors on increasing precision was also considered to explore which factor is more effective in reducing the $V_{\bar{x}}$.

Table 5.4 displays the estimated variances of a genotype mean for 20 alternative allocations of locations and five various replications while keeping the number of years fixed to one. From the table it can be seen that the increase in locations and replications have the ability to increase the precision of trial means. However, the increase in precision gained by increasing the number of locations is by far more effective than the gain from increasing the number of replications. This implies that allocation of more locations is preferable to an increase in the number of replications to get increased precision in a maize testing programme. By increasing the number of locations from one to two a precision of about 45% was gained while increasing the number of replication from two to three only contributed about 15% increase in precision. Furthermore, the increase of replications from two to six could not yield a precision that is

equivalent to an increase in locations from one to two (Table 5.4). Hence, it is recommended that in a maize trial a maximum number of replications of three can be considered as an optimum allocation. The results of the estimated variances of a genotype mean is also presented in a three dimensional graph in Figure 5.1 to show the trend.

Table 5.4 Comparisons of estimated variances of a genotype mean in a maize trials for alternative allocations of replications and locations while keeping the years fixed

Number of	Number of replications				
locations	Rep 2	Rep 3	Rep 4	Rep 5	Rep 6
1	1.1550	0.9930	0.9120	0.8640	0.8320
2	0.6420	0.5620	0.5210	0.4970	0.4810
3	0.4720	0.4180	0.3910	0.3750	0.3640
4	0.3860	0.3460	0.3260	0.3140	0.3050
5	0.3350	0.3030	0.2860	0.2770	0.2700
6	0.3000	0.2740	0.2600	0.2520	0.2470
7	0.2760	0.2530	0.2420	0.2350	0.2300
8	0.2580	0.2380	0.2290	0.2220	0.2180
9	0.2440	0.2260	0.2170	0.2110	0.2080
10	0.2330	0.2160	0.2080	0.2030	0.2000
11	0.2230	0.2080	0.2010	0.1970	0.1940
12	0.2150	0.2020	0.1950	0.1910	0.1880
13	0.2090	0.1960	0.1900	0.1860	0.1840
14	0.2030	0.1920	0.1860	0.1820	0.1800
15	0.1980	0.1870	0.1820	0.1790	0.1770
16	0.1940	0.1840	0.1790	0.1760	0.1740
17	0.1900	0.1810	0.1760	0.1730	0.1710
18	0.1850	0.1780	0.1730	0.1710	0.1690
19	0.1840	0.1750	0.1710	0.1690	0.1670
20	0.1810	0.1730	0.1690	0.1670	0.1650

From Table 5.4 and the graph (Fig. 5.1), it can be seen that the rate of gain in precision declines as the number of locations increases which is similar to the classic economic concept of the law of diminishing returns.

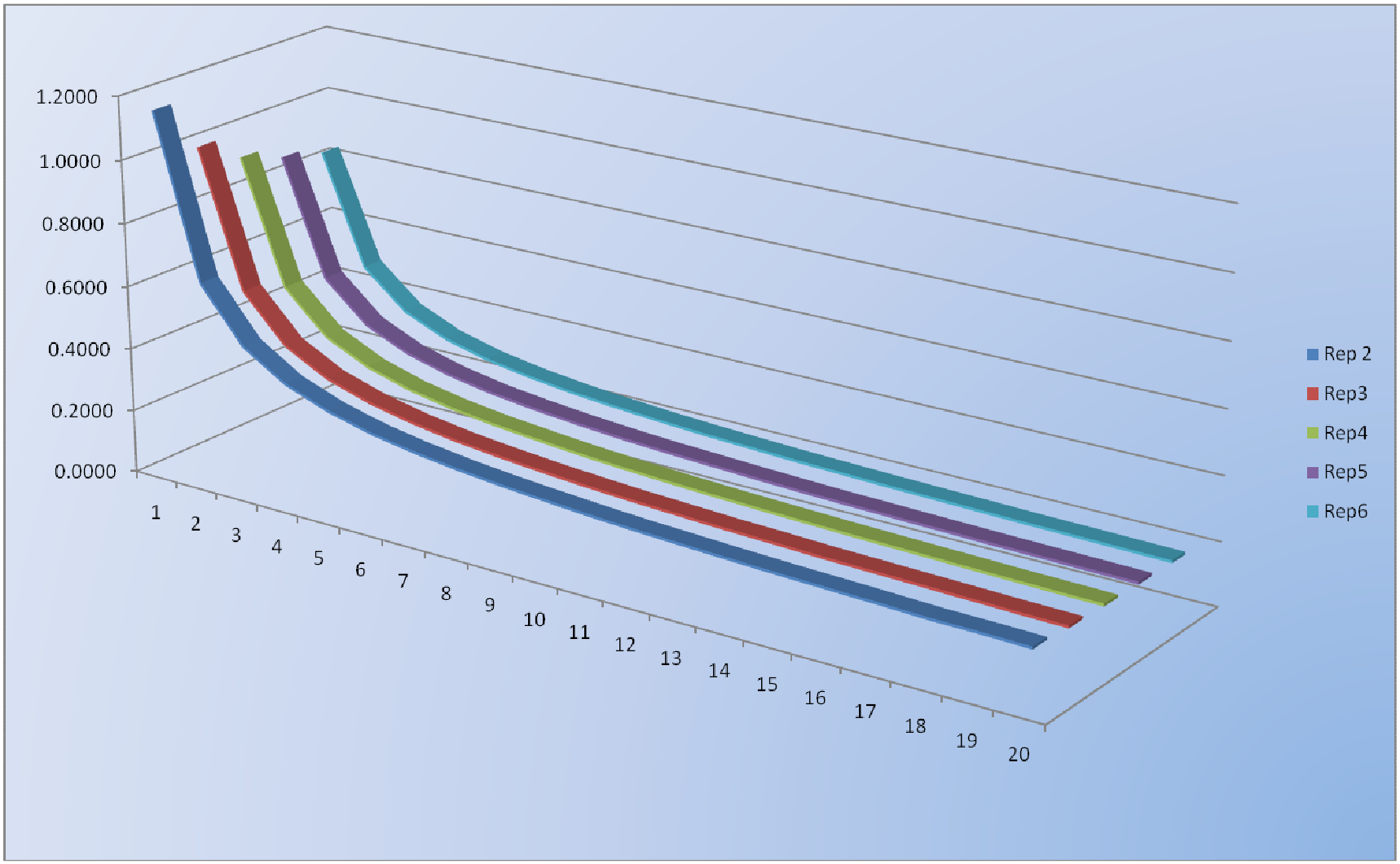

Figure 5.1 Three dimensional graph depicting the allocation of different locations (horizontal axis) and replications on the estimated variances of a genotype mean (vertical axis)

Based on the calculation of the Least Significant Difference (LSD %), increasing the number of locations from one to two resulted in a 13% gain in precision. A further addition of one location resulted in a 5.4% gain in precision, after the allocation of six locations the rate of precision dropped to below 1% (Table 5.5). Hence, considering the costs involved in a maize testing programme the optimum number of locations to be assigned is recommended to be between three and five and not to exceed six locations, as this yields smaller and smaller increases in precision (Fig.5.2).

Similarly, an increase in the number of years in a maize testing programme also contributed substantially to the gain in precision. This indicates that the number of years is equally important as the number of locations in the yield evaluation of maize in Ethiopia where a year-to-year fluctuation of the environment is common. From Table 5.5 it can be seen that an increase of one year resulted in a 14% gain in precision by reducing the LSD% and a further addition also resulted in 6% precision gain. However, the rate of gain in precision tended to decrease as the number of years increased. After year five the gain in precision is less than 1% which indicates that the optimum years for a maize testing programme are three or maximum of four years.

To conclude, in Ethiopian conditions yield evaluation of maize can best be conducted with a combination of 2-3 replications, 3-5 locations for about 3-4 years, which will help to get the best estimate of future yields by increasing precision and reducing experimental errors. However, researchers can manipulate the combination of these factors based on the availability of resources and time. For instance, instead of conducting a trial for three years and three locations, a similar precision would be achieved by conducting a trial for two years at five locations with two replications (Table 5.5) or four locations, two years with three replications (Table 5.6 and Fig. 5.3). Tables 5.5 - 5.9 are presented to make such comparisons. These tables give the value of LSD% for yield based on the various combinations of years and locations with different alternatives of replications. This experiment proved that locations-years tradeoff is more effective than locations/years-replications tradeoff in getting efficient data in a maize testing programme. However, it is important to consider additional factors such as design of the experiment, the analysis to be applied to the data, the number of genotypes included in an experiment and the objective of the trial whether it is for early selection or for final release of a variety.

Table 5.5 Comparison of Least Significant Difference (LSD %) values for the various combinations of locations and years with two replications

Number of	Number of years									
locations	1	2	3	4	5	6	7	8	9	10
1	50.75	36.65	30.54	26.97	24.58	22.85	21.53	20.48	19.63	18.92
2	37.84	27.28	22.69	20.00	18.20	16.89	15.89	15.09	14.45	13.91
3	32.44	23.33	19.37	17.05	15.49	14.36	13.49	12.81	12.24	11.77
4	29.34	21.08	17.48	15.37	13.95	12.91	12.12	11.49	10.98	10.55
5	27.33	19.61	16.24	14.26	12.93	11.96	11.22	10.62	10.14	9.73
6	25.86	18.57	15.36	13.48	12.21	11.28	10.57	10.01	9.54	9.15
7	24.81	17.78	14.70	12.89	11.66	10.77	10.08	9.54	9.09	8.72
8	23.98	17.17	14.18	12.42	11.24	10.37	9.70	9.17	8.74	8.37
9	23.33	16.68	13.77	12.05	10.89	10.05	9.40	8.88	8.45	8.10
10	22.79	16.27	13.43	11.75	10.61	9.78	9.14	8.63	8.22	7.87
11	22.30	15.93	13.14	11.49	10.37	9.56	8.93	8.43	8.02	7.67
12	21.90	15.65	12.90	11.27	10.17	9.37	8.75	8.26	7.85	7.51
13	21.59	15.40	12.69	11.08	10.00	9.21	8.60	8.11	7.70	7.37
14	21.28	15.18	12.50	10.92	9.85	9.06	8.46	7.98	7.58	7.24
15	21.01	14.99	12.34	10.78	9.72	8.94	8.34	7.86	7.47	7.14
16	20.80	14.83	12.20	10.65	9.60	8.83	8.23	7.76	7.37	7.04
17	20.58	14.68	12.08	10.54	9.49	8.73	8.14	7.67	7.28	6.95
18	20.31	14.54	11.96	10.43	9.40	8.64	8.05	7.58	7.20	6.87
19	20.26	14.42	11.86	10.34	9.31	8.56	7.98	7.51	7.13	6.80
20	20.09	14.31	11.77	10.26	9.24	8.49	7.91	7.44	7.06	6.74

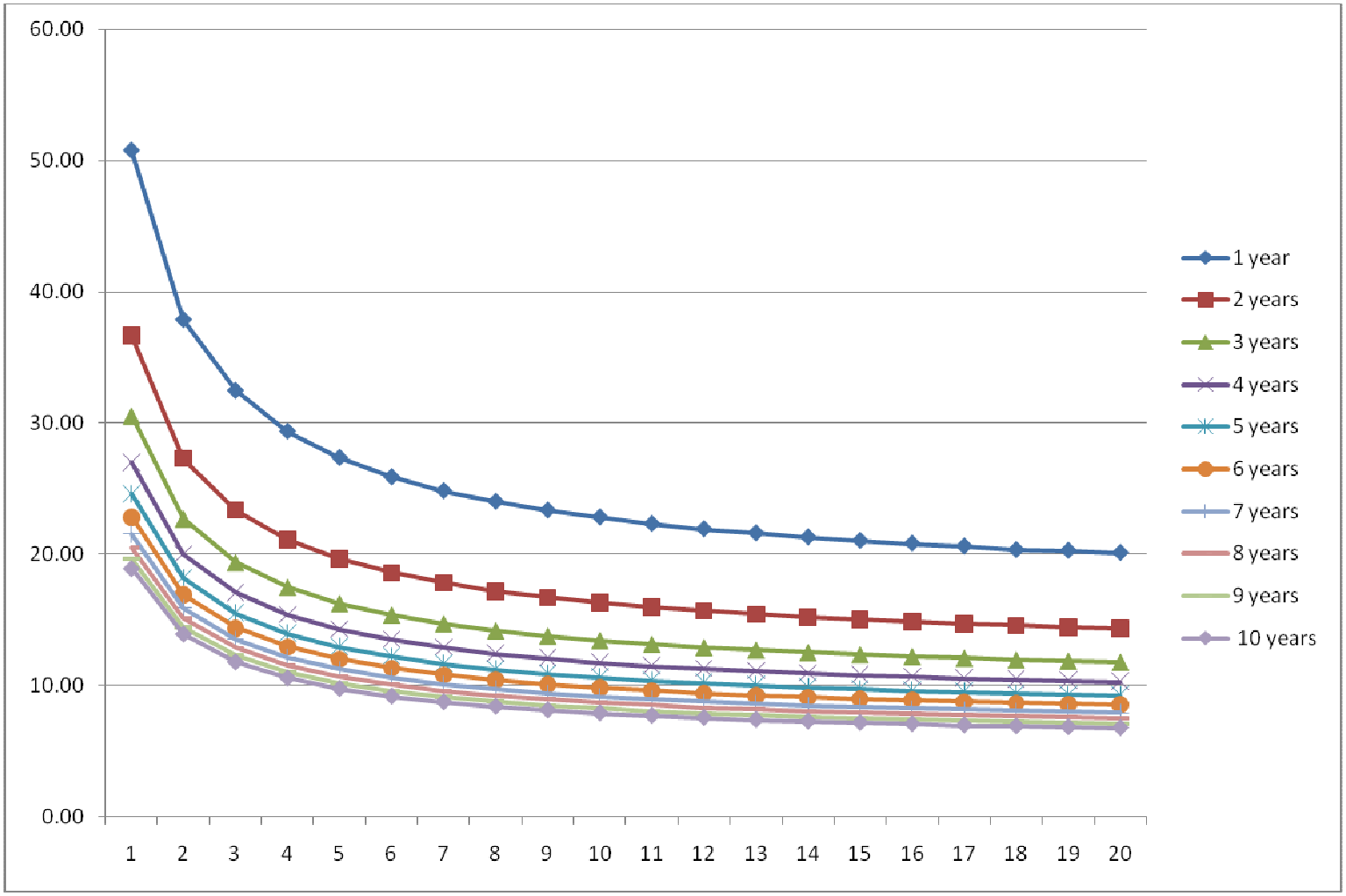

Figure 5.2 Graph showing the trend of allocation of different locations (X-axis) and years on the LSD% (Y-axis) of a maize trial with two replications

Table 5.6 Comparison of Least Significant Difference (LSD %) values for the various combinations of locations and years with three replications

Number of	Number of years									
Locations	1	2	3	4	5	6	7	8	9	10
1	47.05	34.11	28.51	25.25	23.07	21.50	20.30	19.35	18.58	17.94
2	35.40	22.01	21.32	18.84	17.18	15.97	15.06	14.33	13.74	13.24
3	30.53	19.99	18.31	16.15	14.70	13.65	12.84	12.20	11.68	11.25
4	27.78	18.67	16.60	14.62	13.29	12.32	11.58	10.99	10.51	10.11
5	25.99	17.74	15.49	13.62	12.36	11.45	10.75	10.19	9.74	9.36
6	24.72	17.04	14.70	12.91	11.70	10.83	10.16	9.62	9.19	8.82
7	23.75	16.50	14.10	12.38	11.21	10.36	9.71	9.19	8.77	8.42
8	23.04	16.06	13.64	11.96	10.83	10.00	9.37	8.86	8.45	8.10
9	22.45	15.71	13.27	11.63	10.52	9.71	9.09	8.59	8.18	7.84
10	21.95	15.41	12.97	11.36	10.27	9.47	8.86	8.37	7.97	7.63
11	21.54	15.16	12.72	11.13	10.05	9.27	8.67	8.18	7.79	7.46
12	21.22	14.94	12.50	10.93	9.87	9.10	8.50	8.03	7.63	7.31
13	20.91	14.75	12.32	10.77	9.72	8.95	8.36	7.89	7.50	7.18
14	20.69	14.59	12.16	10.62	9.58	8.82	8.24	7.77	7.39	7.06
15	20.42	14.44	12.01	10.49	9.47	8.71	8.13	7.67	7.29	6.96
16	20.26	14.31	11.89	10.38	9.36	8.61	8.04	7.57	7.20	6.88
17	20.09	14.20	11.78	10.28	9.27	8.52	7.95	7.49	7.11	6.80
18	19.92	14.09	11.68	10.19	9.18	8.44	7.87	7.42	7.04	6.73
19	19.75	14.09	11.59	10.11	9.11	8.37	7.80	7.35	6.98	6.66
20	19.64	13.99	11.51	10.04	9.04	8.31	7.74	7.29	6.92	6.61

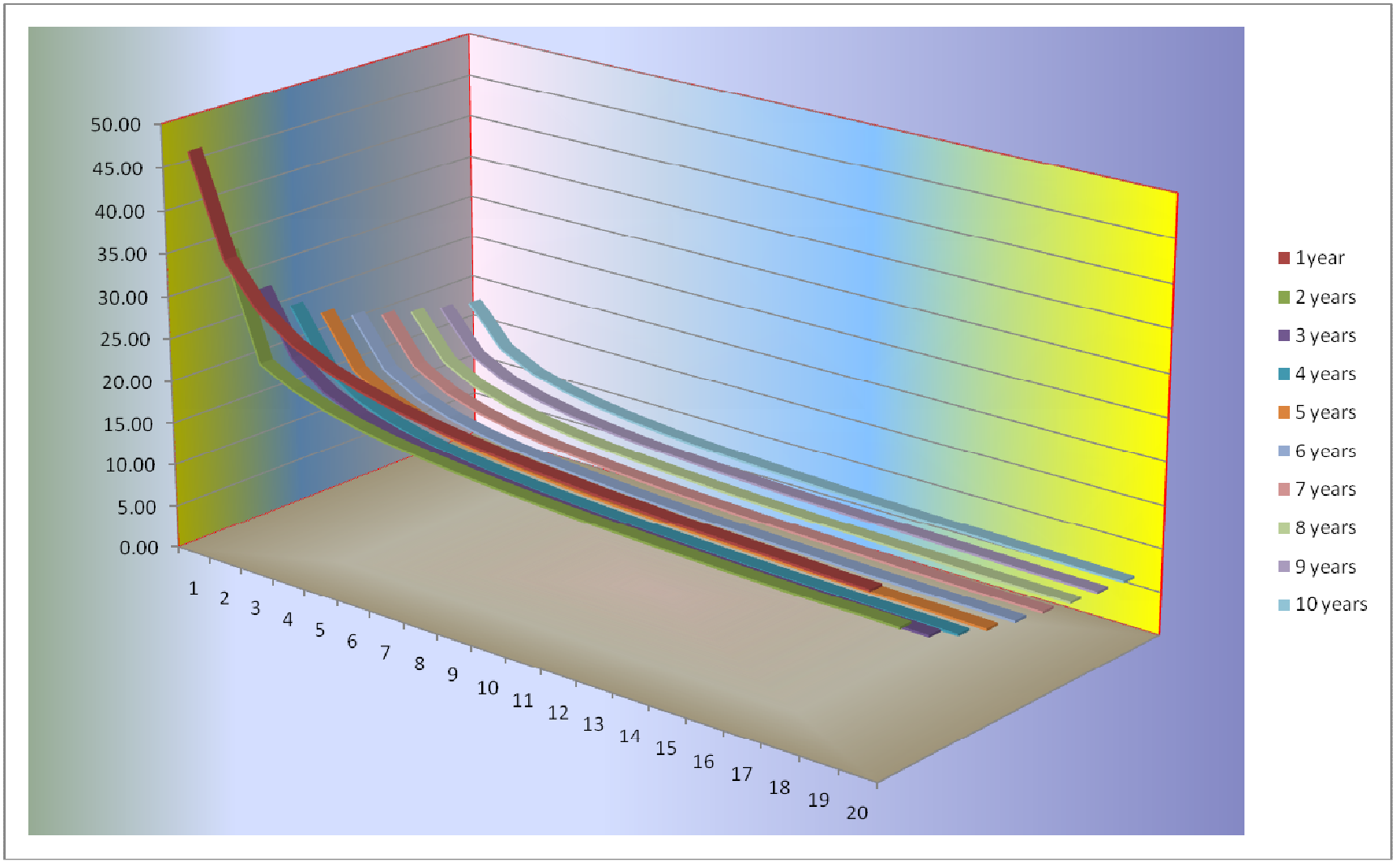

Figure 5.3 A three dimensional graph showing the trend of allocation of different locations (horizontal axis) and years on the LSD% (vertical axis) of a maize trial with three replications

Table 5.7 Comparison of Least Significant Difference (LSD %) values for the various combinations of locations and years with four replications

Number of	Number of years									
Locations	1	2	3	4	5	6	7	8	9	10
1	45.09	32.76	27.43	24.34	22.27	20.79	19.65	18.76	18.03	17.43
2	34.08	24.68	20.61	18.23	16.64	15.50	14.62	13.93	13.37	12.90
3	29.53	21.31	17.76	15.68	14.28	13.27	12.50	11.89	11.40	10.98
4	26.96	19.42	16.14	14.23	12.94	12.01	11.30	10.73	10.27	9.88
5	25.25	18.18	15.09	13.28	12.07	11.18	10.51	9.97	9.53	9.16
6	24.08	17.31	14.35	12.61	11.45	10.60	9.94	9.43	9.00	8.65
7	23.23	16.66	13.80	12.11	10.98	10.16	9.52	9.02	8.61	8.26
8	22.60	16.15	13.36	11.72	10.62	9.81	9.19	8.70	8.30	7.96
9	22.00	15.75	13.02	11.41	10.33	9.54	8.93	8.44	8.05	7.72
10	21.54	15.42	12.74	11.16	10.09	9.31	8.71	8.23	7.84	7.51
11	21.17	15.14	12.50	10.94	9.89	9.12	8.53	8.06	7.67	7.35
12	20.85	14.91	12.30	10.76	9.72	8.96	8.38	7.91	7.52	7.20
13	20.58	14.71	12.13	10.60	9.57	8.82	8.24	7.78	7.40	7.08
14	20.37	14.53	11.98	10.47	9.45	8.70	8.13	7.67	7.29	6.97
15	20.14	14.38	11.85	10.35	9.34	8.60	8.02	7.57	7.19	6.88
16	19.98	14.25	11.73	10.24	9.24	8.50	7.93	7.48	7.11	6.79
17	19.81	14.13	11.63	10.15	9.15	8.42	7.85	7.40	7.03	6.72
18	19.64	14.02	11.54	10.07	9.07	8.34	7.78	7.33	6.96	6.65
19	19.53	13.92	11.45	9.99	9.00	8.28	7.72	7.27	6.90	6.59
20	19.41	13.83	11.38	9.92	8.94	8.22	7.66	7.21	6.85	6.54

Table 5.8 Comparison of Least Significant Difference (LSD %) values for the various combinations of locations and years with five replications

Number of	Number of years									
Locations	1	2	3	4	5	6	7	8	9	10
1	43.89	31.92	26.77	23.77	21.78	20.35	19.26	18.39	17.70	17.12
2	33.29	24.12	20.16	17.86	16.32	15.20	14.36	13.69	13.14	12.69
3	28.92	20.89	17.41	15.39	14.03	13.05	12.30	11.70	11.22	10.82
4	26.46	19.06	15.86	13.99	12.73	11.82	11.12	10.57	10.12	9.75
5	24.85	17.88	14.85	13.08	11.89	11.02	10.36	9.83	9.40	9.04
6	23.70	17.05	14.14	12.43	11.29	10.45	9.81	9.31	8.89	8.54
7	22.89	16.43	13.61	11.95	10.84	10.03	9.41	8.91	8.51	8.17
8	22.25	15.94	13.19	11.58	10.49	9.70	9.09	8.60	8.21	7.87
9	21.69	15.56	12.86	11.28	10.21	9.43	8.83	8.35	7.96	7.64
10	21.28	15.24	12.59	11.03	9.98	9.21	8.62	8.15	7.77	7.44
11	20.96	14.98	12.37	10.83	9.79	9.03	8.45	7.98	7.60	7.28
12	20.64	14.76	12.18	10.66	9.63	8.88	8.30	7.84	7.46	7.14
13	20.37	14.57	12.01	10.51	9.49	8.74	8.17	7.71	7.34	7.02
14	20.14	14.40	11.87	10.38	9.37	8.63	8.06	7.60	7.23	6.92
15	19.98	14.26	11.75	10.26	9.26	8.53	7.96	7.51	7.14	6.83
16	19.81	14.13	11.63	10.16	9.17	8.53	7.87	7.42	7.05	6.74
17	19.64	14.01	11.54	10.07	9.08	8.36	7.80	7.35	6.98	6.67
18	19.53	13.91	11.45	9.99	9.01	8.28	7.73	7.28	6.91	6.61
19	19.41	13.82	11.37	9.92	8.94	8.22	7.66	7.22	6.86	6.55
20	19.30	13.73	11.30	9.85	8.88	8.16	7.61	7.17	6.80	6.50

Table 5.9 Comparison of Least Significant Difference (LSD %) values for the various combinations of locations and years with six replications

Number of	Number of years									
Locations	1	2	3	4	5	6	7	8	9	10
1	43.07	31.35	26.31	23.39	21.45	20.05	18.99	18.15	17.47	16.91
2	32.75	23.75	19.86	17.60	16.09	15.00	14.18	13.52	12.99	12.55
3	28.49	20.60	17.18	15.19	13.86	12.89	12.16	11.57	11.10	10.70
4	26.08	18.83	15.67	13.83	12.59	11.69	11.01	10.46	10.02	9.65
5	24.54	17.68	14.69	12.94	11.76	10.91	10.26	9.74	9.32	8.96
6	23.47	16.87	14.00	12.31	11.18	10.36	9.73	9.22	8.81	8.47
7	22.65	16.27	13.48	11.84	10.74	9.94	9.33	8.84	8.44	8.10
8	22.05	15.80	13.08	11.48	10.40	9.62	9.02	8.54	8.14	7.82
9	21.54	15.43	12.76	11.19	10.13	9.36	8.77	8.29	7.91	7.58
10	21.12	15.12	12.50	10.95	9.91	9.15	8.56	8.10	7.71	7.39
11	20.80	14.87	12.28	10.75	9.72	8.97	8.39	7.93	7.55	7.23
12	20.47	14.66	12.09	10.58	9.56	8.82	8.25	7.79	7.41	7.10
13	20.26	14.47	11.94	10.44	9.43	8.69	8.12	7.67	7.29	6.98
14	20.03	14.31	11.80	10.31	9.31	8.58	8.01	7.56	7.19	6.88
15	19.87	14.17	11.68	10.20	9.21	8.48	7.92	7.47	7.10	6.79
16	19.70	14.05	11.57	10.11	9.12	8.39	7.83	7.39	7.02	6.71
17	19.53	13.94	11.47	10.02	9.03	8.31	7.76	7.31	6.95	6.64
18	19.41	13.84	11.39	9.94	8.96	8.24	7.69	7.25	6.88	6.58
19	19.30	13.75	11.31	9.87	8.90	8.18	7.63	7.19	6.82	6.52
20	19.18	13.67	11.24	9.81	8.84	8.12	7.57	7.13	6.77	6.47

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CHAPTER 6

CONCLUSIONS AND RECOMMENDATIONS

Maize is one of the most important cereal crops of Ethiopia. Its rapid expansion trend enabled maize to be a strategic priority crop in new agro ecologies where its cultivation was unknown in the past.

Apart from the introduction of maize into new environmental niches, the existing heterogeneous agro-ecology of Ethiopia emphasizes the importance of a robust and efficient variety testing scheme to identify stable and widely adapted varieties.

The selection process of good performing and stable genotypes is mainly complicated by the phenomenon of genotype by environment (G x E) interaction. G x E interaction is a differential genotypic expression across environments or generally the inconsistency of relative performance of genotypes over environments. The large occurrence of G x E interactions causes the relative rankings of genotypes to change from location to location and/or from year to year. Hence, it is imperative to have a proper understanding of the effects of G x E interactions on variety evaluation, which will help to apply appropriate analytical methods and wise application of resources. It was with this aim that this research was conducted in the different maize growing regions of Ethiopia for three consecutive years.

From this study it was found that the G x E interaction recorded during the trial periods was highly significant. Although, the genotype variability was highly significant within and across the testing years, the major contributors to the interactions were found to be locations and their interactions with years. This indicates that the unpredictable environmental conditions is the major player in selecting superior and well adapted maize varieties in Ethiopian conditions. Hence, this study reinforced the concept of variety release for specific adaptation based on their favourable interactions with the test environments.

Among the 17 experimental hybrids that were tested in the nine environments, two experimental hybrids PR1 (7.14 t ha^{-1}) and PR13 (6.77 t ha^{-1}) out yielded the check hybrid BH540 (6.57 t ha^{-1}) and seven experimental hybrids performed similarly with the commercially released check. Therefore, it is recommended that further trials should be carried out to examine for any additional superior trait(s) among the experimental hybrids that will favour them for commercial release.

From the results of the grain yield stability study, the top yielding varieties (PR1, PR13 and BH540) showed better stability and more responsiveness in the favourable environments as compared to the rest of the experimental hybrids. SE21 and SE22 were also highly stable hybrids in low yielding environments which indicated their predictable performance in less favourable areas. The experimental hybrid AS13 was found to be the most unstable hybrid categorized by all stability parameters applied in this study.

The different stability measurements (parametric and non-parametric) used in this study demonstrated association and dissociation among them in ranking of the genotypes based on stability. Eberhart and Russell's deviation from regression (S^2_{di}) procedure showed highly significant correlation ($P < 0.01$) with the parameter of Wricke (W_i) ($r = 0.78^{**}$) , Shukla (σ_i^2) ($r = 0.78^{**}$), Shukla (S_i^2)($r = 0.91^{**}$) and ASV ($r = 0.65^{**}$), but it was quite poorly correlated with mean yield, Lin and Binns's (1988) cultivar superiority performance (P_i) and Nassar and Hühn's (1987) absolute rank difference and variance of ranks(S(1) and S(2)). Wricke's procedure of stability statistic indicated the highest significant positive correlation ($P < 0.01$) with Shukla (no covariates, $r = 1.00^{**}$) and ASV ($r = 0.86^{**}$). The perfect correlation between Wricke's and Shukla indicates that the two procedures are equivalent for ranking purposes. However, considering the covariates in the analysis of Shukla did not show a perfect correlation with Wricke, although there exists a highly significant correlation ($r = 0.85^{**}$). So it is important to include Shukla's stability variance (with the assumption of covariates) to get more information and difference in ranking with that of Wricke's ecovalence. Furthermore, the non-parametric measures S(1) and S(2) were found to be highly correlated ($r = 1.00^{**}$) among each other indicating that the stability estimates of the S(2) did not add important information to that obtained by the S(1). However, the significant correlation with parametric measures like ASV allows the use of non-parametric measures in the analysis of grain yield stability.

From this study the multivariate analysis (AMMI) procedure is recommended to identify genotypes according to their adaptation environment. The categorization of genotypes according to their response to the different environments has an agronomic advantage for breeders and farmers. With AMMI it is also possible to target the different production environments by developing genotypes for specific adaptation.

The study of GxE interactions always involves the issues of resources allocation. Almost all breeding programs are based on effective evaluation and selection of the best genotypes through statistically efficient methods that will precisely estimate true future performance. Increasing the number of testing sites and replications will give more precise information but it is highly resource demanding and the increase in the number of years/seasons may seriously delay experimental results. So it is very important to compromise this situation for countries like Ethiopia, where research budgets are very limited and the demand for improved technology is a priority agenda.

This study tried to recommend the best combinations of locations, replications and years for the maize variety testing programme in Ethiopia. The recommendations are aimed to balance the best utilization of meagre resources as well as the acquisition of precise information from maize trials. Hence, for the final stage evaluation of maize in the mid altitude sub humid mega environments the allocation of two or three replications, three to five locations and three to four evaluation years are assumed to be optimum to select best performing genotypes with statistically efficient data. However, the study also suggested alternative combinations that can be manipulated by breeders/researchers according to the availability of resources and time.

In general, results from this study give valuable information for researchers who are interested to examine the effect of G x E interactions on the performance of maize genotypes in the Ethiopian condition. The stability analysis and correlation study among parametric and non-parametric measures used in this research will give direction on the wise application of these parameters. In addition, the study will help as a reference for the optimum allocation of resources in maize variety testing programmes to develop statistical strategies for decreasing experimental errors and improving genotypes selections. The study also provides researchers with additional hypothesis to conduct further trials that will help to enhance research outputs.

CHAPTER 7

SUMMARY

The objectives of the study were to evaluate the adaptability of 17 experimental maize genotypes under the maize growing environments of Ethiopia, to select the best hybrids for commercial production, to utilize various statistical procedures for analyzing G x E interactions and yield stability of Ethiopian maize hybrids across nine environments and to indicate breeding strategies for releasing genotypes with adaptation to target environment.

Seventeen experimental maize hybrids, including a locally released standard check, were evaluated for grain yield in a mid altitude areas of Ethiopia, for a period of three years (2004 to 2006) across three locations. The genotypes were planted in a completely randomized block design. G x E interactions and variance components were calculated using factorial analyses. Stability parameters were calculated using various parametric and non-parametric methods. While, a cluster analysis was done to classify the different genotypes and environments. The computer programmes, Agrobase Generation II (Agronomix, 2008), SAS (SAS Institute Inc., 2003) and NCSS 2004 (Hintze, 2001) were utilized to perform the different analyses.

The mean squares for G x E interaction were found to be highly significant for yield including the variation among the genotypes (G). The Location (L) and Location x Year (L x Y) interactions have the largest components of variance for grain yield, which is an indication of the variation among testing sites and year to year fluctuation of the weather. The experimental maize hybrid PR1 (mean yield =7.14 t ha^{-1}) was found to be the highest yielder followed by PR13 (6.77 t ha^{-1}) .This result shows the potential of the experimental genotypes to be released for commercial production.

Highly significant correlations ($P<0.01$) was obtained among Eberhart and Russell's deviation from regression (S^2_{di}), Wricke's ecovalence (Wi), Shukla's (σ_i^2) stability variance and AMMI Stability Value(ASV). Mean yield and Lin and Binns's cultivar superiority performance (Pi) showed high correlations but they showed no correlations with the rest of the stability parameters. The non-parametric measure of Nassar and Hühn's absolute rank difference S(1) and variance of ranks S(2) was significantly correlated ($P \leq 0.05$) with ASV, however they did not correlate with the rest of the parametric measures.

Based on the different stability parameters, hybrids PR1, PR13 and BH540 were found to be more stable and responsive to favourable environments while SE21 and SE22 hybrids showed their stability in the low yielding environments. Since, ASV showed higher correlations with both parametric and non-parametric measures, and the mean yield, it is recommended to use ASV as a stability parameter in identifying stable genotypes from multi-environment trials.

The analysis of variance for the AMMI model indicated highly significant differences between genotypes and environments as main effects and the interaction effect of G x E was also highly significant. The first two interaction principal component axes (IPCA) of the AMMI model together accounted between 34% and 56% of the total G x E interaction sum of squares for grain yield. The AMMI biplot categorized the genotypes PR1, SE4, PR2, PR3, BH540 and PR13 as well adapted to favourable environments with above average yield.

Hierarchical clustering using unweighted pair group method with arithmetic average (UPGMA) grouped the genotypes into five and the environments into three clusters.

The results from the study of optimum allocation of resources indicated that allocation of two or three replications, three to five locations for three to four testing years will give adequate information for yield estimates, help to minimize trial costs and provide more precise data for variety release decisions in Ethiopian condition. The research also proved that locations-years tradeoffs are more effective than locations/years-replications tradeoffs in getting statistically efficient data from a maize yield trial.

CHAPTER 8

Opsomming

Die doel van die studie was om die aanpasbaarheid van 17 eksperimentele mieliegenotipes in veskillende omgewings in Ethiopië te evalueer, die beste basters vir kommersiële produksie te selekteer, verskillende statistiese procedures vir die ontlending van G x E interaksies oor nege omgewings te vergelyk en teelstrategië vir die vrystelling van aangepaste genotipes te bepaal.

Sewentien experimentele mieliebasters insluitende ‘n standaard cultivar is in die mid-hooglande van Ethiopië vir ‘n periode van drie jaar (2004 tot 2006) oor drie lokaliteite vir graanopbrengs geevalueer. Die genotipes is in ‘n gerandomiseede blokontwerp aangeplant. G x E interaksie en variansiekomponente is m.b.v. ‘n faktoriaalontlending bereken. Stabilititeitsparameters is m.b.v. verskillend parametriese en nie-parametriese metodes bereken,terwyl ‘n trosontlending uitgevoer is om die omgewings te klassifiseer. Die rekenaarprogramme, Agrobase Generation II (Agronomix, 2008), SAS (SAS Institute Inc., 2003) en NCSS 2004 (Hintze,2001) is gebruik om die verskillende ontledings uit te voer.

Die gemiddelde kwadrate vir G x E interaksie was betekenisvol vir opbrengs asook die variasie tussen genotipes(G). Die lokaliteit (L) en Lokaliteit x Jaar (L x J) interaksie het die grootste varinsiekomponente vir graanopbrengs. Dit is ‘n aanduiding van die groot verskille tussen toetslokaliteite wat die gevolg is van jaar tot jaar fluktuasies in reënval. Die eksperimentele mieliebaster PR1 (gemiddelde opbrengs= 7.14 t ha $^{-1}$) het die hoogste opbrengs gehad, gevolg deur PR13 (6.77 t ha $^{-1}$). Die resultate toon die potensiaal van die basters vir moontlike vrystelling en kommersiële produksie.

Hoogsbetekenivalle korrelasies ($P < 0.01$) is tussen Eberhart en Russell se afwyking van die regressie (S^2_{di}), Wricke se Ecovalence (W_i), Shukla (σ_i^2) se stabiliteitsvariansie en AMMI se stabiliteitswaarde (ASV) gevind. Die gemiddelde opbrengs en Lin en Binn se cultivar superieur prestasie het ‘n groot mate van ooreenstemming getoon maar geen korrelasie getoon met die res van die stabiliteitsparameters. Die nie-parametriese meting van Nassar en Hühn se absolute rangverskille S(1) en rangvariansies S(2) was betekenisvol ($P \leq 0.05$) met ASV gekorreleer, alhoewel dit nie betekenisvol met die res van die parametriese metodes gekorreleer was.

Die verskillende stabiliteitsparameters toon dat die basters PR1, PR13, en BH540 die stabielste is in meer gunstige omgewings terwyl die basters SE21 en SE22 die stabielste is in

omgewings waar lae opbrengste geld. Aangesien ASV hoë korrelasies toon met beide parametriese en nie-parametriese metings en die gemiddelde opbrengs, word aanbeveel dat ASV as ‘n stabiliteitsparameter gebruik word om stabiele genotipes in multi-omgewings te identifiseer.

Die variansie-ontleding vir die AMMI model toon hoogsbetekenisvolle verskille tussen genotipes en omgewings as hoofeffkte asook betekenisvolle G x E interaksie effekte. Die eerste twee interaksie hoofkompenente (IPCA) van die AMMI model het onderskeidelik tussen 34% en 56% van die totale G x E interaksie som van kwadrate vir graanopbrengs verklaar.Die AMMI biplot het die genotipes PR1, SE4, PR2,PR3,BH540 en PR13 as goed aangepas in meer gunstige omgewings geklassifiseer.

Die hieragale tros-ontleding gebaseer op die ongeweegde paar groeperingsmetode (UPGMA) het die genotipes in vyf en die omgewings in drie groepe geklassifiseer.

Die resultate van die studie oor die optimum allokasie van lokaliteit en jare, toon dat twee tot drie herhalings, drie tot vyf lokaliteite en drie tot vier jaar van toetsing voldoende inligting verskaf vir die akkurate bepaling van opbrengs. Laasgenoemde inligting sal daartoe bydrae om proefkoste te minimiseer en meer akkurate data vir vrystellingsbesluite in Etiopiese toestande te verskaf. Die navorsing toon verder dat ‘n vermeerdering in lokaliteite en jare ‘n groter bydrae lewer tot die akkuraatheid van data in vergelyking met ‘n toename in herhalings.