ADDIS ABABA UNIVERSITY
GRADUATE STUDIES PROGRAM
DEPARTMENT OF STATISTICS

COMPARISON OF PARAMETRIC AND NON-PARAMETRIC METHODS TO DESCRIBE GENOTYPE BY ENVIRONMENT INTERACTION AND GRAIN YIELD STABILITY OF BREAD WHEAT

By

Sisay Awoke

A THESIS SUBMITTED TO THE SCHOOL OF GRADUATE STUDIES OF ADDIS ABABA UNIVERSITY
IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTERS OF SCIENCE

October 31, 2013

ADDIS ABABA UNIVERSITY
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October 31, 2013

DECLARATION

I, the undersigned, declare that the thesis is my original work, has not been presented for a degree in any university and that all sources of material used for the thesis have been duly acknowledged.

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Date	October 31, 2013

This thesis has been submitted for examination with my approval as a University advisor.

Name	M. K. Sharma (Professor)
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Date	October 31, 2013

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ABSTRACT

The nature and magnitude of the genotype by environment (G×E) interactions is important to identify superior and stable genotypes under the target environments. 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. Therefore, the objective of this study was to analyze genotype by environment interaction and stability of 20 Ethiopian wheat genotypes in 8 environments. The experiment was conducted during 2007/08 growing seasons in a randomized complete block design with four replications. Parametric and nonparametric statistical methods were used to test the significance of genotype by environment (G×E) interaction and to identify stable genotypes in 8 environments. Combined ANOVA and nonparametric tests (Kubinger and Hildebrand) of genotype × environment interaction indicated the presence of significant interactions, as well as significant differences between genotypes and environments. However no cross-over and non-crossover interactions were detected by the de Kroon/van der Laan and Bredenkamp procedure respectively. According to the parametric methods, genotype G11, G10, G5 and G12 were stable and genotypes G16, G3, G20 & G1 were unstable. According to the nonparametric methods, genotype G11, G10, G5, G18 & G12 were stable and genotypes G3, G16, G19, G1 and G20

were unstable. The result shows that both the parametric and nonparametric methods gave a relatively same result. This implied that the nonparametric stability measurements are useful alternatives to parametric measurements. According to the biplot, Adet was generally categorized under high yielding wheat environment as compared to the three relatively categorized under low yielding environments (Holeta, Kulumsa and Sinana). Mean yield performance across environments was significantly positively correlated with RS and TOP measures ($P<0.05$ and $P<0.01$ respectively) and there were significant negative correlations between mean yield and $s_i^{(3)}$, $s_i^{(6)}$, $NP_i^{(2)}$, $NP_i^{(3)}$. This study recommends genotypes G19, G1 and G15 as superior genotypes in favorable environments.

ACKNOWLEDGEMENT

First and foremost, I would like to thanks to the almighty God for giving me the blessing and strength for finishing this thesis. I would like to express my sincere gratitude to Professor M. K. Sharma my thesis advisor for his valuable and constructive comments and encouragements throughout my study.

Very special thanks are extended to my friend Zelalem Tazu for his great help in getting the data for this thesis and for his encouragement and support.

A large degree of emotional support and encouragement has been received from the many friends I have made during my stay at the University. Many thanks to Yohannes for the help he gave me. Also I am grateful to all of those who supported me in any respect during the completion of my study

I would like to express my regards and thanks to the Department of Statistics Addis Ababa University and staff members, especially Ato Mekonnen Taddesse (Asst. Prof.) and Professor Eshetu Wencheko for all their encouragements and cooperation.

Finally, and most importantly, I wish to thank my parents and friends for their love and encouragement.

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ACRONYMS

AMMI	Additive Main Effect and Multiplicative Interaction
ANOVA	Analysis of Variance
ASV	AMMI stability values
BLUP	Best linear unbiased predictors
CIMMYT	International Maize and Wheat Improvement Center
CSA	Central Statistical Agency
CV	Coefficient of Variation
DF	Degrees of Freedom
EIAR	Ethiopian Institute of Agricultural Research
ESE	Ethiopian Seed Enterprise
GE (G×E)	Genotype by Environment
GEI	Genotype by Environment Interaction
IPCA	Interactions of Principal Component Analysis
JLR	Joint linear regression
LR	Linear Regression
MET	Multi-environment Trial
MSE	Mean square error
NID	Normally and Independently Distributed
PCA	Principal Components Analysis
RCBD	Randomized Complete Block Design
REML	Restricted maximum likelihood
RS	Rank sum
SAS	Statistical Analysis System
SS	Sum of Squares

1: INTRODUCTION

1.1 BACKGROUND OF THE STUDY

Ethiopia is the largest producer of wheat in sub-Saharan Africa. Wheat occupies about 1.8 million hectares annually and ranks 4th in area and 2nd in productivity among the cereals CSA (2012). Bread and durum wheat are the major types of wheat grown. Bread wheat is of recent introduction; durum wheat is indigenous to the Ethiopia which is considered ‗the secondary center of diversity for tetraploid wheat'.

Wheat is one of the major cereal crop grown in the Ethiopian highlands, which lie between 6 and 16 degree North and 35 and 42 degree East at altitudes ranging from 1500 to 3000. The most suitable areas for wheat production, however, fall between 1900 and 2700 meter. In the highlands, rainfall distribution is by modal and ranges between 600 and 2000 mm/annum. The rainy season divided in to the short rains (bulg) following from February to April and the main rain (meher) following from June to September.

Farmers and scientists want successful wheat genotypes that show high performance for yield and other essential agronomic traits. Their superiority should be reliable over a wide range of environmental conditions but also over years. The basic cause of differences between genotypes in their yield stability is the occurrence of genotype-environment interactions (GEI).

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 × environment (G×E) interaction is one of the main complications in the selection of broad adaptation in most breeding programs. 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×E system could have a large impact on plant breeding (Magari and Kang, 1993; Basford and Cooper, 1998). G×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 effect of G×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).

When environmental differences are large like in Ethiopia, it may be expected that the interaction of G×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).

One of the most challenging issues in plant breeding process to accurately analyze genotype × environment interaction (GEI) is based on data from multi-environment trials. GEI is a universal issue that relating to all living organisms, from humans to plants and bacteria (Kang, 1998). Usually GEI is the nonadditive component of two or more experiments with the same genotypes combined over environments. The process for selecting high yield and stable genotypes usually involves three stages of experimentation: At stage-1, genotypes are tested at a single location; at stage-2, the selected genotypes are tested in a multi-location trials (genotype × location); and finally at stage-3, the most promising genotypes with new set of genotypes are tested for several years under a range of locations (genotype × location × year) (Linn & Binns, 1994).

Wheat genotypes are generally evaluated in multi-environment trials (MET) to test their performance across environments and to select the best genotypes for specific environments. In most cases, GEI is significant, complicating yield improvement studies, but the release of a genotype with consistent performance over a wide range of environments should lead to stability in production. However, a measure of the relative yield stability of wheat genotypes under a wide range of environmental conditions is needed for determining the efficiency of a genotype evaluation program. In light of these considerations a number of statistical procedures have been applied to estimate the stability of genotypes and related interactions.

There are two major approaches to studying genotype by environment interactions and determining the adaptation of genotypes (Hühn, 1996). The most common approach is parametric analyses, which are based on statistical assumptions about the distribution of genotypic, environmental and GEI effects. Another approach is nonparametric or analytical clustering, which makes no specific modeling assumptions when relating environments and phenotypes relative to biotic and abiotic environmental factors. Parametric measures of phenotypic stability are mostly related to variance components or related statistics. These stability estimates have good properties under certain statistical assumptions, based on the normal distribution of errors and interaction effects, but may not perform well if these assumptions are violated by factors such as the presence of outliers (Hühn, 1990a). Due to the fact that parametric tests for the significance of variances and variance related measures can be very sensitive to the underlying statistical assumptions an alternative approach is to use techniques such as non-parametric measures that are more robust to departures from the assumptions used in parametric analysis (Adugna and Labuschagne, 2003).

The univariate parametric stability statistics are commonly used by plant breeders to analyze GEI. The essential ideas of stability analysis are described in Lin et al., (1986); Hussain et al., (2000) and Backer & Leon (1988) are concerned with describing as to how a genotype responds to differing environmental conditions. The parametric stability methods have good properties under statistical assumptions of a normal distribution of independent errors with homogenous variance and no outliers. However, many of these measures may not perform well if any or all of these assumptions are violated, specifically the assumptions of homogeneity of mean square errors (MSEs), nonmixture of normal distributions and data having no outliers (Hühn, 1990). Due to GEI the relative differences among genotypes render performance over environments inconsistent. MSEs are rarely homogeneous in multi-environment or regional yield trials. MSEs are influenced by specific circumstances and tend to be lower in low yielding environments (Bowman & Watson, 1997).

A number of parametric statistical procedures have been developed over the years to analyze genotype × environment interaction and especially yield stability over environments. A number of different approaches have been used, for example joint regression analysis and multivariate statistics, to describe the performance of genotypes over environments. To date considerable differences of opinion still exist between the leading protagonists of the different statistical approaches as to the best and most suitable procedure to be used for a specific data set or production region.

Thus it is advisable to search for alternative approaches such as nonparametric methods that are more robust and are valid in the absence of variance homogeneity, no outliers and normality assumptions. The importance of nonparametric methods in modern statistics has been growing dramatically since their inception in the mid-1930s. Requiring few or no assumptions about the populations from which the data is obtained, nonparametric methods emerged as a very useful methodology among statisticians and researchers performing data analyses. Today, these techniques are being applied to an ever-growing variety of experimental designs in the social, behavioral, biological and physical sciences (Hollander & Wolfe, 1999). These methods are based on the ranks of original observations or residuals of combined ANOVA model.

Several procedures have been proposed based on comparing ranks of genotypes in each environment, with genotypes with similar ranking across environments being considered stable (Hühn, 1979; Nassar and Hühn, 1987; Kang, 1988; Ketata et al., 1989; Fox et al., 1990). The following four nonparametric measures of phenotypic stability have been proposed by Hühn (1979) and Nassar and Hühn (1987): $S_i^{(1)}$, the genotype absolute rank difference mean as tested over n environments; $S_i^{(2)}$, the between- ranks variance over the n environments; $s_i^{(3)}$, the sum of the absolute deviations of the squares of ranks for each genotype; and $s_i^{(6)}$, the sum of the squares of ranks for each genotype relative to the mean of ranks. See also Sabaghnia et al. (2006). It is possible to not only assign mean yield ranks, with the genotype with the highest yield being ranked 1, but also ranks for the Shukla stability variance (Shukla, 1972) in which the lowest estimated yield value is ranked 1 (Kang 1988), with the sum of these two sets of ranks resulting in an index in which the genotype with lowest rank-sum is considered to be the most desirable. In addition, a nonparametric superiority measure for general adaptability has been suggested based on stratified ranking of the cultivars in each separate environment, with the proportion of sites at which a specific cultivar occurred in the top third of the ranks (the TOP value), the middle third of the ranks (the MID value) and the lower third of the ranks (the LOW value) being calculated, a genotype with a high TOP value (i.e., occurring principally in the top third of the ranks) being considered as a widely adapted genotype (Fox et al., 1990).

According to Hühn (1990) the nonparametric procedures have a number of advantages over parametric stability methods e.g., they reduce the bias caused by outliers, no assumptions are needed about the distribution of the observed values, they are easy to use and interpret, and additions or deletions of one or few genotypes do not cause much variation in the results. There is theoretical justification for the use of nonparametric methods in the assessment of yield stability analysis of combined heteroscedastic and nonnormal ANOVA. The parametric procedures are not robust specifically when the distribution of data is nonnormal, heteroscedastic and mixture of normal distributions. It is a known fact that the parametric methods have large power values than their nonparametric counterparts when all classical assumptions hold. But the adequate application of parametric methods need fulfillment of some strict statistical assumptions.

Genotype performance trials are usually analyzed by various ANOVA models which are based on assumptions that may often not be satisfied. Departure from one or more assumptions can affect both the type-1 error and the sensitivity of F or t tests. Excellent and detailed discussions about assumptions, the consequences, their invalidates and remedial steps involved for ANOVA are described by some classic papers (Eisenhart, 1947; Cochran, 1947).

Many statistical procedures have been proposed to study G×E interactions (Westcott, 1986; Crossa, 1990; Lin and Binns, 1994; Kang and Gauch, 1996). Most of these procedures, however, fail to distinguish between significant crossover and noncrossover (usual) interactions (Baker, 1990). Nonparametric statistical procedures for the test of crossover interactions have been developed in the field of medicine and can be applied to G×E interactions in Multi-environment Trial (METs) (Truberg and Hühn, 2000). Nonparametric measures for the test of interactions provide a useful alternative to parametric methods such as the ANOVA currently used, which is based on original data values. Hühn and Leon (1995) compared four nonparametric analyses of interactions and grouped them into two different concepts of interactions. While the Bredenkamp, Hildebrand, and Kubinger procedures depend on usual interactions, the van der Laan–de Kroon method depends on crossover interactions. Truberg and Hühn (2000) studied five statistical methods for the analysis of G×E interactions and suggested that for analysis of usual non crossover interactions, the methods of Hildebrand and Kubinger are closely connected with the ANOVA. If some of the necessary assumptions are violated, the validity of the inferences obtained from the standard statistical techniques, for example, ANOVA, may be questionable or lost. In such cases, however, the results of nonparametric estimation and testing procedures, which are based on ranks, can be more reliable (Truberg and Hühn, 2000).

Multivariate statistical methods are appropriate for analyzing two-way layouts of genotypes and environments in multi-environment trials. The response of a special genotype in various test environments may be conceived as a pattern in multi-dimensional space, with the coordinates of an individual axis being that of yield or another trait. Cluster analysis (Abou-El-Fittouh et al., 1969), principal components analysis (Freeman and Dowker, 1973), principal coordinates analysis (Mungomery et al., 1974), factor analysis (Peterson and Pfeiffer, 1989), the additive main effect and multiplicative interaction (Zobel et al., 1988), shifted multiplicative model (Cornelius et al., 1992), site regression biplot (Yan et al., 2000) are the most common multivariate statistical methods used for investigation of the G×E interaction and yield stability analyses. Many studies have used multivariate stability statistics to analyze the G×E interaction in agricultural trials. There is increasing global interest in using these statistics by plant breeders due to potential high returns relative to stability parameters.

Stability analysis is only relevant if GEI is present (Hussain et al., 2000). Basically there are two broad categories of GEI: crossover and non-crossover (usual) interaction. A crossover interaction (discordance) exists if the ranking of the genotypes is not identical in different environments. If the ranking is identical, crossover interaction is nonexistent (concordance) (de Kroon & Laan 1981; Truberg & Hühn, 2000). Measures of GEI and stability are common tools applied by biometricians who have developed numerous methods to analyze it (Lin et al., 1986; Becker & Leon 1988; Flores et al., 1998; Mohammadi & Amri, 2008).

1.2 STATEMENT OF THE PROBLEM

Ethiopia is known for its diverse/heterogeneous agro-ecology ranging from 100m below sea level in the Danakil depression to 4620m above sea level at mount Ras Dashan that contributes further to the problem of selecting stable wheat varieties for wider adaptation. To reduce the effect of genotype by environment interaction, crop improvement programs 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 genotype by environment interaction on the Ethiopian wheat varieties using parametric methods. Interestingly, it was not much done in analyzing GEI and stability on multi-environmental crop data using nonparametric methods in Ethiopia. Most stability analysis methods used in Ethiopia was based on Shukla, ecovalence, joint linear regression of genotype yield on an environmental index derived from the average performance of all genotypes in an environment (Finlay & Wilconsin, 1963; Eberhart & Russell, 1966) used by Khan et al., (1988); Sial et al., (2000) and Javaid et al., (2006). Thus, this thesis was conducted to show the application of nonparametric methods to measure genotype × environmental interaction and stability of wheat genotype in comparison with the parametric methods. And also this thesis attempted to compare these different methods.

1.3 OBJECTIVE OF THE STUDY

GENERAL OBJECTIVE

The general objective of this study is to analyze genotype by environment interaction and stability of the Ethiopian bread wheat genotype for grain yield across the target environments with different statistical methods and to compare the relationships between the different stability tests.

The specific objectives of this study were:

- To assess Ethiopian wheat genotype for adaptation using multivariate statistical analysis (AMMI), parametric analysis and nonparametric analysis.
- To evaluate the adaptability of 20 bread wheat genotypes and to identify the best performing ones for future uses.
- To study the different stability statistics and measures and determine suitable method for a wide range of wheat genotypes and environments in Ethiopia,
- To compare the different stability parameters with Spearman‘s rank correlation and identify the significant correlation.

2: LITERATURE REVIEW

2.1 BASIC CONCEPTS

2.1.1 GENOTYPE BY ENVIRONMENT INTERACTION

The importance of GEI is highlighted by Gauch and Zobel (1996):

> *"Were there no interaction, a single variety of wheat (Triticum aestivum L.) or corn (Zea mays L.) or any other crop would yield the most the world over, and furthermore the variety trial need be conducted at only one location to provide universal results. And were there no noise, experimental results would be exact, identifying the best variety without error, and there would be no need for replication. So, one replicate at one location would identify that one best wheat variety that flourishes worldwide."*

Genotype by Environment interaction is a common phenomenon in agricultural research. Differences between genotypic values may increase or decrease from one environment to another which might cause genotypes to even rank differently between environments. The Genotype by Environment interaction studies are somewhat complicated as they require integrated approaches which combine many fields including agriculture, biology, statistics, computer, and genetics.

A genotype or the genetic makeup of an organism is defined by Falconer and Mackay (1996) as the combination of alleles at a single autosomal locus in a diploid organism. The physical or visible characteristics resulting from the interaction between the genetic makeups and the environments are referred to as phenotype. Phenotype can be observed, measured, classified or counted. 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) Microenvironment 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. Environmental factors (non genetic factors) such as locations, growing seasons, years, rainfall, the amount of precipitation received in each season, temperature, etc. may have positive or negative impact on genotypes. Mather and Jinks (1982), Mukai (1988), and Wu and OiMalley (1998) report on two types of environmental variations: (1) micro environmental which cannot easily be identified or predicted (e.g., year-to-year variation in rainfall, drought conditions, extent of the insect damage) and (2) macro-environmental variances which can be identified or predicted (e.g., soil type, management practices, controlled temperatures). According to these investigators, the G×E interaction variance can only be estimated for the macro-environmental condition indicating that some variables that explain experiment differences are often unknown or can't be measured.

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 favorable direction is desirable to obtain maximal performance (Chahal and Gosal, 2002).

The association between the environment and the phenotypic expression of a genotype constitute the G×E interaction. The G×E interaction determines if a genotype is widely adapted for an entire range of environmental conditions or separate genotypes must be selected for different sub environments (Bondari K.). When G×E interaction occurs, factors present in the environment (temperature, rainfall, etc.), as well as the genetic constitution of an individual (genotype), influence the phenotypic expression of a trait. The impact of an environmental factor on different genotypes may vary implying that the productivity of an animal or plant may also vary from one environment to the next. Breeding plans may focus on the G×E interaction to select the best genotype for a target population of environments.

A basic principle indicated by the G×E interaction is that even if all animals or plants were created equal (same genotypes), they will not necessarily express their genetic potential in the same way when environmental conditions (drought, temperature, disease pressure, stress, etc.) vary (Bondari K.). This important concept may require genetic engineering of plants or animals specifically tailored to their environmental conditions.

Breeders/agronomists usually test a diverse array of genotypes in diverse environments, which implies that GEI is to be expected. According to Haldane (1947), GEI is important only if genotypes switch ranks from one environment to another. GEIs can be grouped into two broad categories: crossover and non-crossover interactions; a brief discussion of each follows.

Crossover (qualitative) interaction

The differential response of cultivars to diverse environments is referred to as a crossover interaction when cultivar ranks change from one environment to another. A main feature of crossover interaction is intersecting lines in a graphical representation. If the lines do not intersect, there is no crossover interaction (Kang, 1998).

In crop breeding, the crossover interaction is more important than non-crossover interaction (Baker, 1990). Since the presence of a crossover interaction has strong implications for breeding for specific adaptation, it is important to assess the frequency of crossover interactions (Singh et al., 1999). According to Gregorius and Namkoong (1986), crossover interaction is not only non-additive in nature but also nonseparable.

Variation among genotypes in phenotypic sensitivity to the environment (GEI) may necessitate the development of locally adapted varieties (Falconer, 1952). If no one genotype has superiority in all situations, GEI indicates the potential for genetic differentiation of populations under prolonged selection in different environments (Via, 1984).

Non-crossover (quantitative) interaction

These interactions represent changes in magnitude of genotype performance (quantitative), but rank order of genotypes across environments remains unchanged, i.e. genotypes that are superior in one environment maintain their superiority in other environments. Non-crossover interactions mean that genotypes are genetically heterogeneous but test environments are more or less homogeneous or that genotypes are genetically homogeneous but environments are heterogeneous. All identical genotypes grown in constant (ideal) environments should perform consistently. Any departure from the ideal environment leads to GEI (Kang, 2002).

2.1.2 INTERACTION ILLUSTRATION

Statistically, G×E interactions occur if the performance of genotypes varies significantly across environments or when differences between genotypes are not the same in all locations within and across years (Edmeades et al., 1989). Agricultural researches have demonstrated that a genotype resulting in a good phenotype in one environment might not necessarily result in a good phenotype in another environment. The presence of G×E interaction indicates the inconsistency of relative performance genotypes over environments (Hill et al., 1998).

For two genotypes A and B, and two environments X and Y, the basic types of relationships between genotype × environment interactions and changes of rank orders are demonstrated schematically in Figure1.

Some authors introduced the terms qualitative interactions (crossover interactions) and quantitative interactions (noncrossover interactions). For noncrossover interactions, the true treatment differences vary in magnitude but not in direction, whereas for crossover interactions, the direction of true treatment differences varies. Although these terms and the corresponding tests of significance for these effects have been developed in the field of medicine, they can be appropriately applied to questions concerning genotype environment interactions in crop improvement (Hühn 1996).

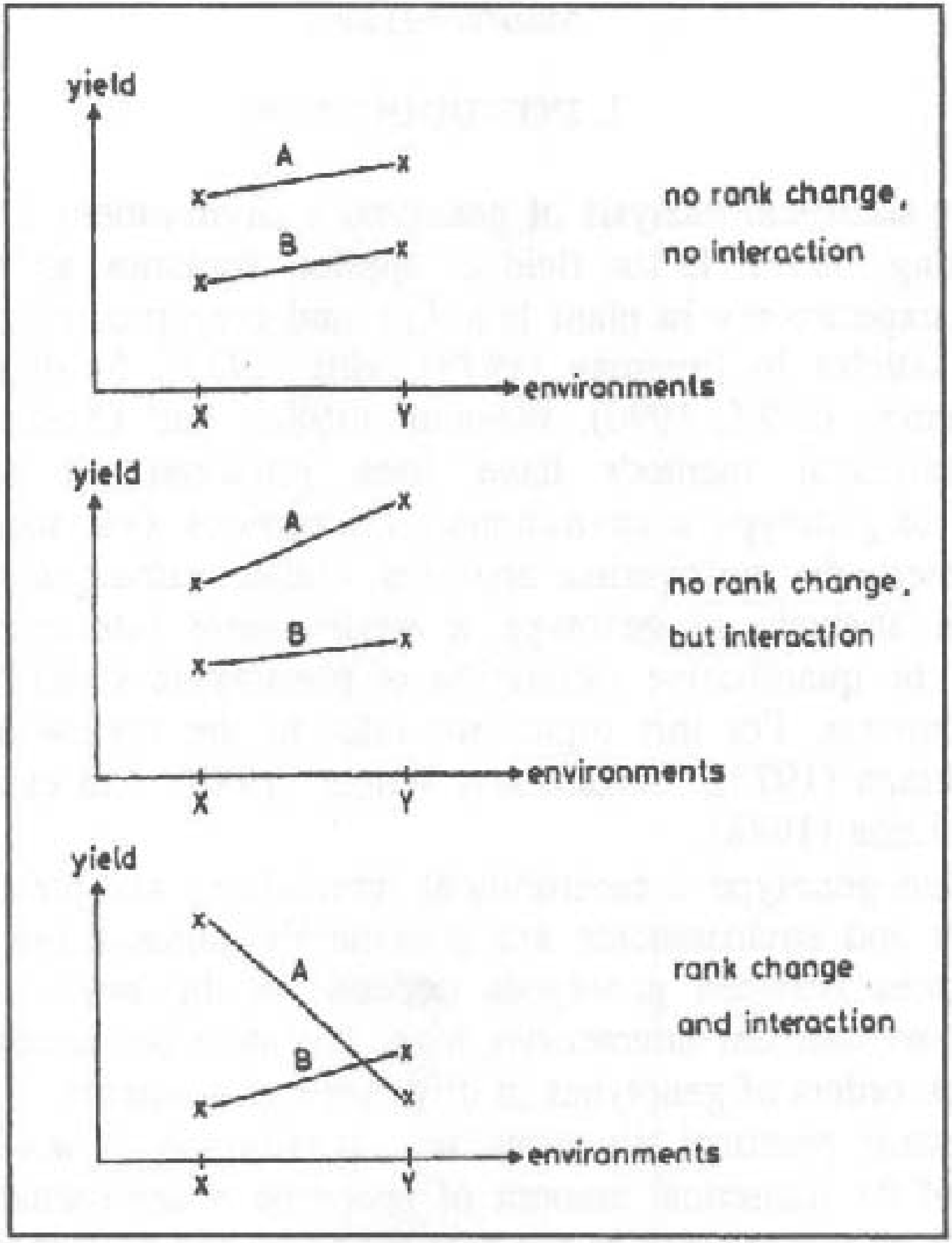


Figure2. 1 Genotype environment interactions and changes of rank orders - different type of relationships (for two environments X and Y and two genotypes A and B) (modified from Wricke, 1965 by Hühn (1996)).

2.1.3 SIGNIFICANCE OF G × E INTERACTION

What breeders can do to overcome the problem of G×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×E analysis of variance may be partitioned into components due to G×L, G×Y and G×L×Y. Significance of mean square for G×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×Y interaction is very different from G×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.

According to DeLacy et al. (1996), 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×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×E interactions complicates the identification of superior genotypes for a range of environments. G×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 Leon (1988), cultivar rank changes are of greater importance than scale change interactions in cultivar trials conducted over a series of environments. Hence, G×E interaction is critical only if it involves significant crossover interactions (significant reversal in genotypic rank across environments) (Becker and Leon, 1988).

The statistical analysis of G×E is important in applied statistics as well as for the analysis of experiments in plant breeding and crop production (Kang, 1996). Different statistical methods such as variance components, regression models, and multivariate analysis and cluster techniques have been proposed for the estimation and partitioning of G×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×E interaction per se, but interested in the existence (or non-existence) of different rankings of genotypes. This concept of G×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.

2.2 CONCEPTS OF STABILITY

Stability is a central keyword for plant breeders analysing GE data. A simple corresponding statistical term is ‗dispersion around a central value' (Denis et al., 1996). There are two concepts of stability: static and dynamic. The static concept means that a genotype has a stable performance across environments and there is no among environment variance. This would mean that a genotype would not respond to high levels of inputs, such as fertilizer. This type of stability would not be beneficial for the farmer, and it has been referred to as the biological concept of stability (Becker, 1981), which is equivalent to Lin et al.'s (1986) type 1 stability. In type 1 stability, a genotype is regarded as stable if its among environment variance is small.

The dynamic concept means that a genotype has a stable performance, but, for each environment, its performance corresponds to the estimated level or predicted level. There would be agreement between the estimated or predicted level and the level of actual performance (Becker and Leon, 1988). This concept has been referred to as the agronomic concept (Becker, 1981), which is equivalent to Lin et al.'s (1986) type 2 stability. In type 2, a genotype is regarded as stable if its response to environments is parallel to the mean response of all genotypes in a test.

Stability has been described in many different ways over the years and there have also been different concepts of stability (Lin et al., 1986). The terms phenotypic stability, yield stability and adaptation are often used in quite different senses. Different concepts and definitions of stability have been described over the years (Lin et al., 1986; Becker and Léon, 1988).

Lin et al. (1986) identified three concepts of stability:

Type 1: A genotype is considered to be stable if its among-environment variance is small. Becker and Léon, (1988) called this stability a static, or a biological concept of stability. A stable genotype possesses an unchanged performance regardless of any variation of the environmental conditions. This concept of stability is useful for quality traits, disease resistance, or for stress characters like winter hardiness. Parameters used to describe this type of stability are coefficient of variability (*CV*) used by Francis and Kannenburg (1978) for each genotype as a stability parameter and the genotypic variances across environments (*S*).

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

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

Methods to describe type 3 stability are the methods of Eberhart and Russell (1966) and Perkins and Jinks (1968). Becker and Leon (1988) stated that all stability procedures based on quantifying GEI effects belong to the dynamic concept. This includes the procedures for partitioning the GEI 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 analyses.

Lin et al. (1986) defined four groups of stability statistics. Group A is based on deviation from the average genotype effect (DG), group B on the GEI term (GEI) and groups C and D on either DG or GEI. The formulae of groups A and B represent sums of squares and those of groups C and D represent a regression coefficient or deviation from regression. They integrated type 1, type 2 and type 3 stabilities with the four groups: group A was regarded as type 1, groups B and C as type 2, and group D as type 3 stability. In type 3 stability, a genotype is regarded as stable if the residual mean square from the regression model on the environmental index is small (Lin et al., 1986).

Group A:	DG (Deviation of average genotype effect)	SS (sum of squares)
Group B:	GE (GE interaction term)	SS
Group C:	DG or GE	Regression coefficient
Group D:	DG or GE	Regression deviation

Lin and Binns (1988) proposed the type 4 stability concept on the basis of predictable and unpredictable non-genetic variation: the predictable component is related to locations and the unpredictable component is related to years. Lin and Binns (1988) suggested the use of a regression approach for the predictable portion and the mean square for years within locations for each genotype as a measure of the unpredictable variation. The latter was called the type 4 stability statistic.

2.3 REVIEW OF LITRETURES SPECIFIC TO THE STUDY

Multi-environment bread wheat yield trial comprised of 18 cultivars along with the standard check HAR1899 was conducted at three locations, Ineway, Molale and Mehalmeda during main seasons, July to December in 2001-2004 by Kemelew M. et al. (2012). The objective of the experiment was to identify stable and high yielding bread wheat cultivar suitable for the rainfall wheat production system in Ethiopia. Analysis of variance using grain yield data from twelve environments made of three locations and four years revealed that both the main and interaction components were significant at (P < 0. 01%),suggesting that no matter how productive cultivars may be, selection of cultivars based on grain yield is not reliable if the cultivar × environment interaction is statistically significant. Additive main effect and multiplicative interaction analysis of grain yield combined over ten environments showed that some of the tested bread wheat cultivars were most stable and high yielding, some were less stable and high yielding and one cultivars was stable and low yielding cultivars. The result demonstrated that application of Additive main effect and multiplicative interaction analysis is important in handling the cultivar × environment interaction component and developing specific and widely adapted wheat varieties.

In an attempt to identify suitable bread wheat varieties for the Tigray Region of Northern Ethiopia, six early type varieties namely HUW-468, HI-1418, DL-788-2, GW-273, local and standard check were tested in six drought prone areas of Tigray Region by Hintsa G. et al. (2012). The study was conducted in farmers‘ fields using the mother-baby trial approach with an objective of identifying high yielding with broadly and specifically adapted varieties for drought prone areas of the Tigray region. Results of the analysis of variance for AMMI model showed significant differences among the genotypes and locations, but were not significant for G×L interaction. Similarly, the regression analysis showed that regression coefficients (b_i) of the tested genotypes were not significantly different from unity. Based on deviation from linear regression and over all mean grain yield, HUW-468 was the best performing genotype yielding 2.375 t/ha. In a similar manner, the IPCA1 (interaction principal component analysis) for this variety had the lowest score (0.47), indicating its stability in all environments. Besides, HI-1418 was also a good yielder in both relatively better locations like Illalla and Atsbi with an annual rainfall of 433 and 411 mm, respectively and in less favored locations of Enderta and Wukro with environmental mean yield of less than 1 t/ha. Although it is difficult to conclude the adaptability and stability of the candidate varieties in one year trial, all of the varieties showed a wide adaptation across the tested locations that indicated the change in environment had negligible effect on their grain yield. The local and standard checks were relatively sensitive to variation across locations. This indicate that these check varieties lack wider adaptability even within the drought prone areas of the region and a higher yield is expected, especially from the standard check in relatively better environments. Since the varieties HUW-468, HI-1418 showed an excellent performance over the local and standard checks, they can be recommended to moisture stressed wheat growing areas of Northern Ethiopia.

Genotype × Environment interactions and correlation among some stability parameters of yield was observed by Letta (2007) in durum wheat genotypes. Twenty genotypes of durum wheat genotypes were tested over 15 environments during 2003-2005 cropping seasons in south east Ethiopia. Location within year and year variability were dominant sources of interactions. Nearly all the sources of variation in the combined analysis were highly significant except for genotype-year interaction and the analysis of AMMI showed that the four interactions of principal component analysis were highly significant. The stability analysis identified genotype 3 and 4 as more stable genotypes and recommended for commercial production in the south east Ethiopia. Highly significant rank correlation were found among $S^2_{d_i}$, W_i, $S^2_{x_i}$ and ASV implying their close similarity and effectiveness in detecting stable genotypes and they are equivalent in measuring stability.

Fifteen maize genotypes were tested by Solomon et al. (2008) at nine different locations in 2005 under rainfed condition to determine stable genotypes for grain yield and determine genotypes with high yield and from homogeneous grouping of environments and genotypes. There was considerable variation among genotypes and environments for grain yield. Stability was estimated using the Additive Main Effects and Multiplication Interactions (AMMI). Based on stability analysis, genotypes 30H83, BH-540, Ambo Synth-1 AMH-800 and BHQP-543 were found to be stable for grain yield. The first two Interaction Principal Component axis (IPCA1 and IPCA2) were significant ($p<0.01$) and cumulatively contributed 70.27% of the total genotype by environment interaction. The coefficient of determination (R^2) for genotypes 30H83 was as high as 0.92, confirming its high predictability to stability. Among the genotypes, the highest grain yield was obtained from genotype 30H83 and BH-541 (8.98 and 8.05 t ha^{-1}) across environments. The authors also further categorized the locations into three classes based on estimates of environmental indices, hence Bako, Hawassa and Hirna under favorable environments, Arsi-Negele and Areka under intermediate environments and Awada, Gofa and Jinka under unfavorable environments for maize cultivation.

Mosisa et al. (2008) evaluate Twenty maize cultivars at nine locations in Ethiopia (1100. 2240 masl) in randomized complete block design with three replications for two years to study the nature and magnitude of genotype x environment (G x E) interaction and phenotypic yield stability of the cultivars. Analysis of variance and stability analysis were computed. Variances due to genotypes, years, locations, genotype x year, genotype x location and genotype x year x location interaction were significant ($P<0.01$). Most of the cultivars had significant deviation mean square (S2di), implying that these cultivars had unstable performance across the testing environments. However, Additive Main Effect and Multiplicative Interaction (AMMI) analysis showed Gibe-1 (mean yield 7.40 t ha^{-1}) had relatively stable performance across the environments. None of the cultivars were the best for grain yield in all environments. BH-660 (mean grain yield 8.14 t ha-1) had a relatively good performance in the mid-to high-altitude (1650-2240 m above sea level) areas whereas BH-140 (mean grain yield 6.65 t ha-1) had good performance in the low-mid to mid-altitude (1100-1650 m above sea level) areas, indicating the possibility of developing specific cultivars adapted to mid- and high- or low-mid and mid-altitude areas.

Bogale et al. (2008) evaluate eight drought tolerant maize lines and their 28 crosses with two local hybrids separately in 12 environments to estimate the magnitude of genotype x environment interaction (GEI) and relationships between parents and progenies in stability. An additive main effects and multiplicative interaction (AMMI) model was used to analyze the grain yield data. The first two IPCAs of the AMMI 2 analysis accounted for 56 % of the GEI sum squares in trials of the hybrids. High yielding hybrids like O, P, S, Z, U, G and one of the checks (BH140) showed minimum GEI, indicating wide adaptation of these varieties over environments. In contrast, high yielding hybrids such as A, D and J adapted to unfavorable environments and K and T to favorable environments. Most of the crosses from drought tolerant parents were better than the check (BH540) in mean grain yield and stability.

Mohammed et al. (2012) tested grain yield of 15 durum wheat (Triticum durum Desf.) genotypes, consisting of four cultivars and 11 advanced lines in a randomized complete block design, with three replications, across nine environments of southeastern Ethiopia During the 2007-2009 bona crop season, and analyzed using three parametric stability measures. The objectives were to assess genotype × environment interactions (GEI), determine stable genotypes, and compare mean grain yield with the parametric stability parameters. To quantify yield stability, three stability statistics were calculated: regression coefficient (β_i), deviation from regression ($\mathrm{S}^2_{\mathrm{d_i}}$), and ecovalence ($\omega_i^2$). Durum wheat genotypes KUCUK CD1B2620-G-8M-030Y-030M-2, Dire, Cit-71/DUKEM/DON87CD86772-DZ2491, GOBDER20/TOB//SOAA/2 *PLATA-12CDSS98B01116T-0TOPYOB-OKQ-OSDZ, Yerer, and Englize were the most stable genotypes, which all scored fully on the three stability statistics used. Among these genotypes, KUCUK CD1B2620-G-8M-030Y-030M-2Y… and Dire had grain yield greater than the grand mean yield. The magnitude of GEI for grain yield of durum wheat genotypes tested across nine rainfed environments in the highlands of southeastern

Ethiopia was larger than that of the genotype main effect, but smaller than that of environment main effect. The genotypes studied exhibited both crossover and non-crossover types of GEI. The Former led to differential rankings of genotypes across test environments, thereby making genotypic selection difficult for the rainfed conditions of the highlands of Bale, Southeastern Ethiopia.

In order to investigate efficient use of existing technologies outside their original recommendation domains, the Eastern Africa Agricultural Productivity Project (EAAPP) assembled 21 commercial rust resistant bread wheat varieties released by various research centers in the country and conducted a countrywide evaluation to estimate the magnitude of G×E interaction and yield stability of bread wheat varieties under different agro-ecologies. The varieties were tested at 30 different environments in the main cropping season of 2011–2012 Zerihun et al. (2012). The experiment was laid out in a randomized complete block design with two replications. Additive main effect and multiplicative interaction (AMMI) and AMMI stability values (ASV) were computed. The combined ANOVA showed that the main effects of environments, genotypes and genotype by environment (G×E) interactions were highly significantly ($p<0.01$) different for grain yield and accounted for 87%, 0.90%, and 7% of the total sum of squares variations, respectively. The highest environmental and genotype by environment (G×E) interactions effect indicated the major influence that environment had on performance of the genotypes and that the performance of the genotypes were inconsistent across testing environments. The mean grain yield of the varieties across the 30 environments was 3.08t/ha, within a range of 0.66-8.19t/ha. The overall mean grain yield of the varieties across environments indicated that ‗Shorima‘, ‗Mada-walabu‘, and ‗Gasay‘ were the best performing varieties, with mean grain yields of 3.35, 3.31, and 3.28t/ha, respectively. The stability statistics, AMMI, showed that the first six IPCA were highly significant (p≤0.01) and explained 94% of the total G×E interactions. Based on IPCA and ASV, ‗Mada-walabu‘, ‗Senkegna‘, ‗Alidoro‘, and ‗Shorima‘, in that order, were stable genotypes across locations. ‗Hawii‘, ‗Huluka‘, and ‗Bolo‘ were not broadly adapted varieties. However, recently released varieties ‗Danda‘a‘, ‗Huluka‘, and ‗Digelu‘ were relatively good yielders in high yielding environments, and ‗Kakaba‘, ‗Hawii‘, and ‗Pavon-76‘ were good yielders in moisture deficit areas. Despite the high contribution of environment to the total variations of the varieties performance across locations, this study identified some widely adapted commercial varieties: ‗Mada-walabu‘, ‗Senkegna‘, ‗Alidoro‘, and ‗Shorima‘, for efficient use in wider environments than in their original recommendation domains.

To determine stable bread wheat genotypes with high kernel yield, a field experiment was conducted with 19 bread wheat genotypes by Mizan et al. (2012) in a randomized complete block design with 3 replications tested at 6 locations of major wheat growing areas of Tigray, northern Ethiopia, in the 2009-2010 main cropping seasons. An additive main effect and multiplicative interaction (AMMI) analysis was conducted. The first three interaction principle component axes of AMMI analysis accounted for 93.8% of the G×E interaction sum of squares. Both the AMMI and AVS Analyses revealed that genotype CARSME-37 (a) is stable because of its limited interactions combined with above average kernel yield performance. Additionally, AMMI showed that environments are highly variable both for main and interaction effects. Korem proved to be a favorable environment, while Adi-ahferom, Wukro and Alaje are medium-yielding, and Quiha and Lmichew are low-yielding environments for majority of the traits.

Kılıç H. (2012) evaluated Twenty five bread wheat genotypes in a randomized complete block design with 4 replications. The objectives of this research were to assess genotype-environment interaction (GEI) and to determine stable bread wheat (Triticum aestivum L.) genotypes for grain yield in the South-Eastern Anatolia region of Turkey during the 2004-2007 growing seasons. Genotypes, environments main effects and GEI were significant at P < 0.01. Both parametric (b_i, $\mathrm{S}^2_{\mathrm{d_i}}$, R_i^2, W_i^2, S_i^2, CV_i, σ_i^2, P59, α_i, λ_i and P_i) and non-parametric ($S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(6)}$, TOP and RS) univariate stability statistics were used to determine stability of the bread wheat genotypes. Genotypes G16, G6, G3, G5 and G20 were the most stable based on parametric and non-parametric stability measures used. The level of association among the stability measures was assessed using Spearman's rank correlation. The rank correlation matrix indicated that most non-parametric measures were significantly inter-correlated with parametric measures and therefore can be used as alternatives.

Akçura M. et al. (2009) evaluated 20 durum wheat genotypes at fourteen environments in the Central Anatolian Region of Turkey for two years. Six stability measures consisting of 4 parametric and 2 nonparametric were used to evaluate the genotype by environment interaction (GEI). The experimental layout was a randomized complete block design with three replications. Genotypes, environments main effects and GEI were significant at P < 0.01. Both parametric (b_i, $\mathrm{S}^2_{\mathrm{d_i}}$, R_i^2, P_i) and nonparametric ($S_i^{(1)}$, $S_i^{(2)}$) univariate stability statistics were used to determine stability of the durum wheat genotypes. Genotypes 20, 13 and 12 were most stables based on genotypes according to six stability measures. The level of associations among the stability measures was assessed using Spearman's rank correlation. Regression coefficient (b_i) was negatively and significantly correlated (P < 0.01) with superiority index (P_i). On the other hand, $S_i^{(1)}, S_i^{(2)}$ and $\mathrm{S}^2_{\mathrm{d_i}}$ were positively and significantly correlated with P_i . As a result, these relationships reveal that only one of them could be sufficient to select genotypes of interest in a durum wheat breeding program.

Reza M. et al. (2007) evaluated grain yields of 15 durum wheat genotypes selected from Iran/ ICARDA joint project grown in 12 environments during 2004–2006 in Iran. The objective of this study was to compare nonparametric stability procedures and apply different nonparametric tests for genotype by environment (G×E) interactions. Results of nonparametric tests of G×E interaction and a combined ANOVA across environments indicated the presence of both crossover and non-crossover interactions, and genotypes varied significantly for grain yield. In this study, high values of TOP (proportion of environments in which a genotype ranked in the top third) and low values of sum of ranks of mean grain yield and Shukla's stability variance (ranksum) were associated with high mean yield. The other nonparametric stability methods were not positively correlated with mean yield but they characterized a static concept of stability. The results of correlation analysis indicated that only TOP and rank-sum methods would be useful for simultaneous selection for high yield and stability. These two methods identified lines Mrb3/Mna-1, Syrian-4 and Mna-1/Rfm-7 as genotypes with dynamic stability and wide adaptation. According to static stability parameters, the genotypes 12AMar8081 and

19A-Mar8081 with lowest grain yield were selected as genotypes with the highest stability.

Kaya et al. (2002) suggested that the interaction of the 20 genotypes with six environments was best predicted by the first two principal components of genotypes and environments. Also, they proposed that bi-plots generated using genotypic and environmental scores of the first two AMMI components can be used by breeders and have an overall picture of the behavior of the genotype, the environment and GEIs. At the same time, Kaya et al. (2006) also evaluated bread wheat genotypes in multi-environment yield trials by using GGE bi-plot analysis and they determined that there were two proper rain fed mega environments in the Central Anatolian Plateau, also they recommended that two mega environments should be used by rain fed wheat improvement programs in order to enhance yield based selection gain in multi-environment yield trials.

Mut Z. et al. (2009) evaluated 25 bread wheat genotypes (20 advanced lines and 5 cultivars) in 7 environments during 2003-2005 in the central Black Sea region of Turkey. The objectives of this study were to compare nonparametric stability measures, and to identify promising high-yield and stable bread wheat (Triticum aestivum L.) genotypes. The experimental layout was a randomized complete block design with 4 replications. Three nonparametric statistical tests of significance for genotype × environment (GE) interaction and 10 nonparametric measures of stability were used to identify stable genotypes in 7 environments. Combined ANOVA and nonparametric tests (Kubinger, Hildebrand, and De Kroon/Van der Laan) of genotype × environment interaction indicated the presence of significant crossover and non-crossover interactions, as well as significant differences between genotypes. In this study high TOP values (proportion of environments in which a genotype ranked in the top third) and low rank-sum values (sum of ranks of mean yield and Shukla‘s stability variance) were associated with high mean yield. Nonetheless, results of the other nonparametric tests were negatively correlated with mean yield. In the simultaneous selection for high yield and stability, only the rank-sum and TOP methods were useful in terms of the principal component analysis (PCA) results, and correlation analysis of nonparametric stability statistics and yield. According to these stability parameters (TOP and rank-sum) G7, G9, G20, and G21 were the most stable genotypes for grain yield. The results also revealed that based on nonparametric test results stability could be classified into 3 groups, according to agronomic and biological concepts of stability.

3: METHODOLOGY

3.1 MATERIAL

Twenty wheat genotypes, listed in Table 3.1, were evaluated over a period of two years from 2007 to 2008 in 4 locations (Table3.2) under irrigated condition. The experimental layout was a randomized complete block design (RCBD) with four replications. Planting method was on 30 cm apart at a seed rate of about 120 kg/ha. Plots were managed conventionally and followed the established local practices but usually the plot area ranged from 10 to 15m^2.

Table 3.1 Genotype codes of 20 wheat genotypes.

No.	Genotype code	No.	Genotype code	No.	Genotype code
1.	G1	8.	G8	15.	G15
2.	G2	9.	G9	16.	G16
3.	G3	10.	G10	17.	G17
4.	G4	11.	G11	18.	G18
5.	G5	12.	G12	19.	G19
6.	G6	13.	G13	20.	G20
7.	G7	14.	G14		

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

The trials were conducted under irrigated conditions and fertilization at each site and other management activities were done according to the practices of each farmer (co-operator) for his farm and the specific field. The whole plot was harvested to estimate grain yields and to reduce border effects, data were recorded from the two central rows of each plot. Grain yields are expressed in kg/ha at 12.5 moisture content.

The locations where the experiment was conducted were different in soil type, altitude, mean annual temperature and rainfall and considered as individual environment (Table3.2). Also the years differentiated in terms of mean seasonal rainfall. Therefore, locations in each year were considered as different environments. Hence, an environment is defined here as a location-year combination. Consequently, combinations of seasons (Year 1 and Year 2) and four locations were treated as eight environments (E1-E8).

TABLE 3.2 Description of the experimental sites and environments

Year	Locations	Codes	Altitude (masl)*	Soil texture	Agro-ecologies
2007	Adet	E1	2240	Nitosol	Tepid Moist Mid Highlands
	Holeta	E2	2400	Silt clay loam	Tepid Moist Mid Highlands
	Kulumsa	E3	2200	Clay loam	Tepid Sub-Moist Mid Highlands
	Sinana	E4	2400	sandy loam	Cool Sub-humid Mid Highlands
2008	Adet	E5	2240	Nitosol	Tepid Moist Mid Highlands
	Holeta	E6	2400	Silt clay loam	Tepid Moist Mid Highlands
	Kulumsa	E7	2200	Clay loam	Tepid Sub-Moist Mid Highlands
	Sinana	E8	2400	sandy loam	Cool Sub-humid Mid Highlands

* masl = meter above sea level

The data being considered here are obtained from trials conducted by the Ethiopian Institute of Agricultural Research (EIAR).

3.2. STATISTICAL METHODS

3.2.1. PARAMETRIC METHODS

A number of parametric statistical procedures have been developed over the years to analyze genotype by environment interaction and especially yield stability over environment. A number of different approaches have been used, for example, joint regression analysis and multivariate statistics, to describe the performance of genotypes over environments.

A combined analysis of variance procedure is the most commonly used method to identify the existence of GEI from replicated multi-location trials. The analysis of multi-environment yield trials is usually complicated by the presence of GEI. If the GEI variance is found to be significant, one or more of the various methods for measuring the stability of genotypes can be used to identify the stable genotype(s).

Conventional analysis of variance

Consider a trial in which the yield of *g* genotypes is measured in *e* environments each with *r* replicates. The classic model for analyzing the total yield variation contained in *ger* observations is the analysis of variance.

In the analysis of combined experiment of data from several environments, the first requirement is to assess the homogeneity of the error variance at the various environments. If the errors are homogeneous, the analysis can proceed. However, if the error variances are heterogeneous, the data will be transformed to produce homogenous variance or the locations may be separated into groups within which the variance is homogenous or, alternatively, inverse of error mean square for each environment could be used as weights in combined analysis. Therefore, in order to combine the data, the error with each mean is measured should be tested for homogeneity, which is one of the basic assumptions of analysis of variance. This can be done first by providing a separate analysis of variance (ANOVA) for each environment. If the individual experiments are laid out as RCBD, separate ANOVA structure with sources of variation and degrees of freedom for each environment is:

Table 3.3: The general separate ANOVA structure for each environment

Source of variation	Df
Genotypes(entries)	*g-1*
Replicates(blocks)	*r-1*
Error	*(g-1)(r-1)*

The statistical model for this design is

$$y_{ij} = \mu + G_i + \beta_j + \varepsilon_{ij} \begin{cases} i = 1,2,\dots,g \\ j = 1,2,\dots,r \end{cases}$$

Where μ is an overall mean, G_i is the effect of the i^{th} genotype, β_j is the effect of the j^{th} block (replication) and ε_{ij} is NID $(0, \sigma^2)$ random error term. Genotype and blocks are considered as fixed factors. Furthermore, the genotype and block effects are defined as deviations from the overall mean so that $\sum G_i = 0$ and $\sum \beta_j = 0$.

Then, quick test for homogeneity of variance is applied using either by F-test or chi-square test depending on the number variances or environments. The F-test for homogeneity of variances is applied whenever there are only two variances, with the F value computed as the ratio of the two variances-the larger variance in the numerator and the smaller variance in the denominator. This is well demonstrated through the standard F-test in the analysis of variance, which is used to test the homogeneity of two error mean squares. The chi-square test, which is commonly known as the Bartlett‘s test, should be used when more than two variances are tested. Since there are more than two environments in the study and hence have more than two variances (or error mean squares), the investigator will use the Bartlett‘s test for testing the equality (or homogeneity) of several variances.

Combined analysis of variance

When data are combined over locations and years for analysis, the analysis of variance structure may take different forms. These are:

- When the same location and randomization is used each year;
- When the same location is used, but different randomization is adopted each Year and
- When different locations are used each year.

The difference among the three ANOVA is mainly on the relationship between replications on one hand, and year and location on the other hand. When the same location and randomization is used each year, then replication is nested under location. But when the same location is used with different randomization, then replication is said to be nested under location by year interaction. When locations are different each year, the test also becomes slightly different.

The investigator will use the second forms of combined analysis, that is, when the same location is used, but different randomization is adopted each year. In this case,

$$SS_E = SS_Y + SS_L + SS_{L\times Y}$$

$$SS_{G\times E} = SS_{Y\times \mathrm{G}} + SS_{L\times \mathrm{G}} + SS_{L\times Y\times \mathrm{G}} \text{ , and}$$

$$SS_{Rep\,(E)} = SS_{Rep\,(L\times Y)}$$

A combined ANOVA can be performed using either plot values or data of genotypes in individual environments that have been averaged across experiment replicates (i.e. genotype environment cell means). To convert the result of an ANOVA performed on the basis of a cell mean in to result on a plot basis, for a constant number of experiment replicates (k), the sum of squares (SS) of effects must be multiplied by k (Cochran and Cox, 1957).

In multi-environment yield trials of l genotypes (i=1,2,…,l), m environments(j=1,2,…m) and k replicates(l=1,2,…,k) arranged in RCBD, the liner model for the conventional analysis variance(ANOVA) is

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

Where

- Y_{ijk} is the observed yield response of the k^{th} plot of the i^{th} genotype at the j^{th} environment.
- μ is the overall mean yield of genotypes at all possible environments.

- G_i is the effect of i^{th} genotype; and $\sum_{i=1}^{l} G_i = 0$
- E_j is the random effect of the j^{th} environment drawn from a population with mean 0 and variance σ_E^2 and E_j is distributed as NID (0, σ_E^2)
- GE_{ij} is the interaction effect of the i^{th} genotype in the j^{th} environment. Since environments are random, this interaction is usually considered to be a random effect with mean 0 and variance $\sigma_{G\times E}^2$
- B_{jk} is the effect of the k^{th} replication in the j^{th} environment, and
- e_{ijk} is the usual random error term with mean 0 and variance σ_e^2 and e_{ijk} is distributed as NID (0, σ_e^2)

The following were determined from the ANOVA analysis, the effects of the genotypes, environments as well as their first order interactions. There are different possibilities for the model

1. Genotypes and locations are random (random-effects model)

Table 3.4: ANOVA table for random-effects model.

Source	df	SS	MS	Expected MS	F
Location(L)	s-1	SS_L	MS_L	$\sigma_e^2 + k\sigma_{L\times G}^2 + l\sigma_{R(L)}^2 + kl\sigma_L^2$	$\frac{MS_L + MS_e}{MS_{R(L)} + MS_{G\times L}}$
Rep(L)	s(k-1)	$SS_{Rep(L)}$	$MS_{R(L)}$	$\sigma_e^2 + l\sigma_{R(L)}^2$	
Genotype(G)	l-1	SS_G	MS_G	$\sigma_e^2 + k\sigma_{L\times G}^2 + ks\sigma_G^2$	$\frac{MS_G}{MS_{G\times L}}$
L×G	(s-1)(k-1)	$SS_{L\times G}$	$MS_{G\times L}$	$\sigma_e^2 + k\sigma_{L\times G}^2$	$\frac{MS_{G\times L}}{MS_e}$
Pooled error	s(k-1)(l-1)	SS_e	MS_e	σ_e^2	

2. Genotypes are fixed, Locations are fixed (fixed-effects model)

Table 3.5: ANOVA table for fixed-effects model.

Source	df	SS	MS	Expected MS	F
Location(L)	s-1	SS_L	MS_L	$\sigma_e^2 + l\sigma_{R(L)}^2 + kl\theta_L^2$	$\frac{MS1}{MS2}$
Rep(L)	s(k-1)	$SS_{\mathrm{Rep(L)}}$	$MS_{R(L)}$	$\sigma_e^2 + l\sigma_{R(L)}^2$	
Genotype(G)	l-1	SS_G	MS_G	$\sigma_e^2 + ks\theta_G^2$	$\frac{\mathrm{MS3}}{\mathrm{MS5}}$
L×G	(s-1)(k-1)	$SS_{L\times \mathrm{G}}$	$MS_{\mathrm{G\times L}}$	$\sigma_e^2 + k\theta_{\mathrm{L\times G}}^2$	$\frac{\mathrm{MS4}}{\mathrm{MS5}}$
Pooled error	s(k-1)(l-1)	SS_e	MS_e	σ_e^2	

Where θ_G is a positive function of the constants G_i.

3. Genotypes are fixed, Locations are random (mixed-effects model)

Table 3.6: ANOVA table for mixed-effects model.

Source	df	SS	MS	Expected MS	F
Location(L)	s-1	SS_L	MS_L	$\sigma_e^2 + l\sigma_{R(L)}^2 + kl\sigma_L^2$	$\frac{MS_L}{MS_{R(L)}}$
Rep(L)	s(k-1)	$SS_{\mathrm{Rep(L)}}$	$MS_{R(L)}$	$\sigma_e^2 + l\sigma_{R(L)}^2$	
Genotype(G)	l-1	SS_G	MS_G	$\sigma_e^2 + k\sigma_{\mathrm{L\times G}}^2 + ks\theta_G^2$	$\frac{MS_G}{MS_{\mathrm{G\times L}}}$
L×G	(s-1)(k-1)	$SS_{L\times \mathrm{G}}$	$MS_{\mathrm{G\times L}}$	$\sigma_e^2 + k\sigma_{\mathrm{L\times G}}^2$	$\frac{MS_{\mathrm{G\times L}}}{MS_e}$
Pooled error	s(k-1)(l-1)	SS_e	MS_e	σ_e^2	

Locations and Years in the same trial can be analyzed as a factorial

Table 3.7: ANOVA structure for Locations and Years in the same trial

Source	df
Years(Y)	y-1
Locations(L)	s-1
Y×L	(y-1)(s-1)
Rep(Y×L)	ys(k-1)

The magnitude of the interactions between genotypes and environments (G x Y, G x L, G x Y x L) can be determined. For a simpler interpretation, consider all year and location combinations as –environments" and use one of the models for multi-location trials are appropriate.

For this thesis genotypes were assumed to be fixed and environment were assumed to be random.

Table 3.8: The general analysis of variance (ANOVA) and mean square expectations

Source	df	SS	MS	Expected MS	F
Environment(E)	m-1	SS_E	MS_E	$\sigma_e^2 + l\sigma_{R(E)}^2 + k\sigma_{\mathrm{G\times E}}^2 + kl\sigma_E^2$	$\frac{MS_E}{MS_{R(E)}}$
Rep(E)	m(k-1)	$SS_{\mathrm{Rep(E)}}$	$MS_{R(E)}$	$\sigma_e^2 + l\sigma_{R(E)}^2$	
Genotype(G)	l-1	SS_G	MS_G	$\sigma_e^2 + k\sigma_{\mathrm{G\times E}}^2 + ks\theta_G^2$	$\frac{MS_G}{MS_{\mathrm{G\times E}}}$
G×E	(m-1)(k-1)	$SS_{\mathrm{G\times E}}$	$MS_{\mathrm{G\times E}}$	$\sigma_e^2 + k\sigma_{\mathrm{G\times E}}^2$	$\frac{MS_{\mathrm{G\times E}}}{MS_e}$
Pooled error	m(k-1)(l-1)	SS_e	MS_e	σ_e^2	

Table 3.9: A comparison of appropriate interaction tests for fixed- and random-effects models

Fixed-Effects Model	Random-Effects Model
$H0$: $GE_{11} = GE_{12} = \cdots = GE_{lm} = 0$	$H0$: $\sigma^2_{\mathrm{G\times E}} = 0$
Ha : At least one of the GE_{ij} differs from the rest	Ha : $\sigma^2_{\mathrm{G\times E}} > 0$
T.S.: $F = \frac{MS_{\mathrm{G\times E}}}{MS_e}$	T.S.: $F = \frac{MS_{\mathrm{G\times E}}}{MS_e}$
R.R.: Based on df_1= (m-1)(k-1), df_2 = m(k-1)(l-1)	R.R.: same

The test for $\sigma^2_{\mathrm{G\times E}}$ is the same in the mixed model as in the random-effects model.

The within-environment residual mean square measures the error in estimating the genotype means due to differences in soil fertility and other factors, such as shading and competition from one plot to another.

The pooled error mean square (MS_e) to be inserted in the ANOVA can be estimated from the experimental errors of individual trials. If there is little variation in residual mean squares from one environment to another and for trials with the number of replicates, the pooled error variance (MSe) is found by averaging the residual mean squares of all environments:

$$MS_e = \frac{\sum_{j=1}^{m} MS_{e(j)}}{m}$$

Where $MS_{e(j)}$ is the residual mean square (MS) for the j^{th} (j=1, 2, … , m) environment.

Analysis of variance of multi-location trials is useful for estimating variance components related to different sources of variation, including genotypes and genotype-environment interaction. In general, variance component methodology is important in multi-location trials, since errors in measuring the yield performance of a genotype arise largely from genotype environment interaction. Therefore knowledge of the size of this interaction is required to (a) obtain efficient estimates of genotype effects and (b) determine optimum resource allocations, that is, the number of plots and locations to be included in future trials.

For balanced multi-location trials, that is, those with the same number of experimental units (genotypes or agronomic treatments) observed per site, estimation of the variance component is accomplished using the analysis of variance method. Each of the mean squares is known to estimate a linear function of the variance component defined in the model. These linear functions are called expected mean squares. By solving simultaneous equations we can obtain each of estimates of the variance components. Genetic and genetic-environment variance components can also be estimated by the restricted maximum likelihood (REML) method. This method is analogous to the analysis of variance, and both produce identical estimators for balanced data.

The ANOVA method for estimating variance components consists of equating mean squares to their expectations and solving the resulting set of simultaneous equations we obtain as follows.

Table 3.10: The general estimates of variance components and methods of determination

Variance component	Method of determination
Environment(σ^2_E)	$\frac{MS_E - MS_{R(E)} - MS_{\mathrm{G\times E}} + MS_e}{kl}$
Replication within environment($\sigma^2_{R(E)}$)	$\frac{MS_{R(E)} - MS_e}{l}$
Genotype(σ^2_G)	$\frac{MS_G - MS_{\mathrm{G\times E}}}{km}$
Genotype × Environment($\sigma^2_{\mathrm{G\times E}}$)	$\frac{MS_{\mathrm{G\times E}} - MS_e}{k}$
Pooled error(σ^2_e)	MS_e

Stability analysis

Stability analysis provides a general summary of the response patterns of genotypes to environmental change. Freeman (1973) termed the main type of stability analysis, joint regression analysis or joint linear regression (JLR). It involves the regression of the genotypic means on an environmental index. Joint regression analysis provides a means of testing whether the genotypes have characteristic linear responses to changes in environments. Joint regression analysis was first proposed by Yates and Cochran (1938) and then widely used and reviewed by various authors (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Perkins and Jinks, 1968; Wright, 1971; Freeman and Perkins, 1971; Shukla, 1972; Hardwick and Wood, 1972; Freeman, 1973; Hill, 1975; Lin et al., 1986; Westcott, 1986, Becker and Léon, 1988; Baker, 1988; Crossa, 1990; Hohls, 1995).

Eberhart and Russell's joint regression analysis

Regression coefficient (*b_i*) and deviation mean square ($s^2_{d_i}$)

Joint linear regression (JLR) is a model used for analysing and interpreting the nonadditive structure (interaction) of two-way classification data. The GEI is partitioned into a component due to linear regression (b_i) of the i^{th} genotype on the environment mean, and a deviation (d_{ij}):

$$(GE)_{ij} = b_i E_j + d_{ij}$$

and thus

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

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×E from analysis of variance is partitioned 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 $S^2_{d_i}$ as a stability parameter. Many scientists consider b_i as a response parameter and $S^2_{d_i}$ 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 3.1.

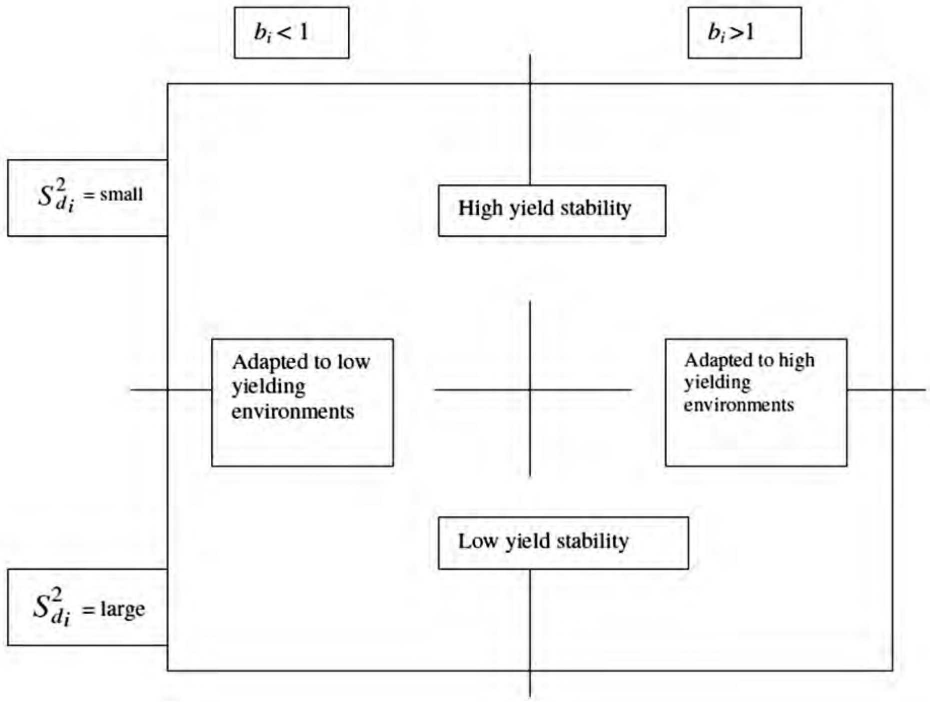


Figure3. 1 Interpretation of parameters $\mathbf{b_i}$ and $\mathbf{S^2_{d_i}}$ for the regression approach, adapted from Haufe and Geidel (1978) as cited by Becker and Léon (1988)

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 3.2 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.

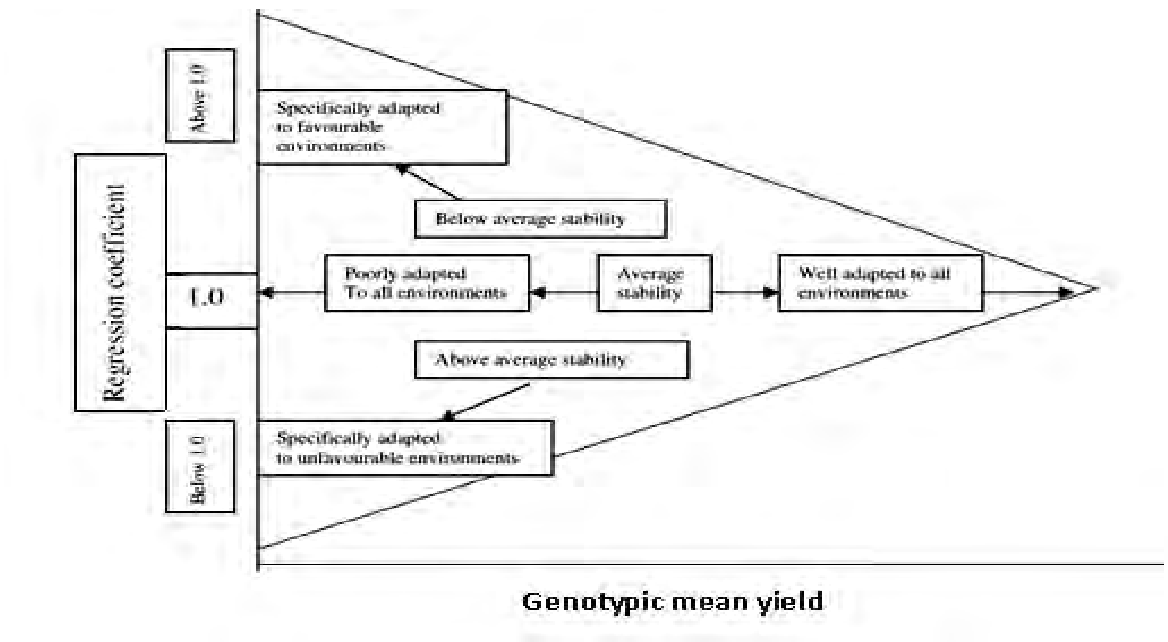


Figure3. 2 A generalized interpretation of the genotypic pattern obtained when, genotypic regression coefficients are plotted against genotypic mean, adapted from Finlay and Wilkinson (1963).

This model uses the marginal means of the environments as independent variables in the regression analysis and restricts the interaction to a multiplicative form.

In effect the residual mean squares from the regression model across environments is used as an index of stability, and a stable genotype is one in which the deviation from regression mean squares ($s^2_{d_i}$) is small.

The deviation sums of squares are the sums of variance due to deviation from regression divided by (E-2), and subtracting pooled error mean square, where E 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.

$$s_{d_i}^2 = \frac{1}{E-2}\left[\sum_{j=1}^{e}(\bar{y}_{ij.} - \bar{y}_{i..} - \bar{y}_{.j.} + \bar{y}_{...})^2 - (b_i - 1)^2 \sum_{j=1}^{e}(\bar{y}_{.j.} - \bar{y}_{...})^2\right]$$

Where b_i is the linear regression coefficient, $\bar{Y}_{ij.}$ is the mean performance of genotype i in the j^{th} environment and $\bar{Y}_{i..}$ and $\bar{Y}_{.j.}$ are the genotype and environment mean deviations, respectively, and $\bar{Y}_{...}$ is the overall mean.

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).

Wricke's ecovalence *(W_i)*

Wricke (1962, 1964) defined the concept of ecovalence as the contribution of each genotype to the GEI sum of squares. The ecovalence (W_i) or stability of the i^{th} genotype is its interaction with the environments, squared and summed across environments, and express as

$$W_i = [\bar{Y}_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} - \bar{Y}_{..}]^2$$

Where $\bar{Y}_{ij}$ is the mean performance of genotype i in the j^{th} environment and $\bar{Y}_{i.}$ and $\bar{Y}_{.j}$ 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 mean across environments and are thus more stable. According to Becker and Léon (1988) ecovalence measures the contribution of a genotype to the GEI, a genotype with zero ecovalence is regarded as stable. 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. 3.3).

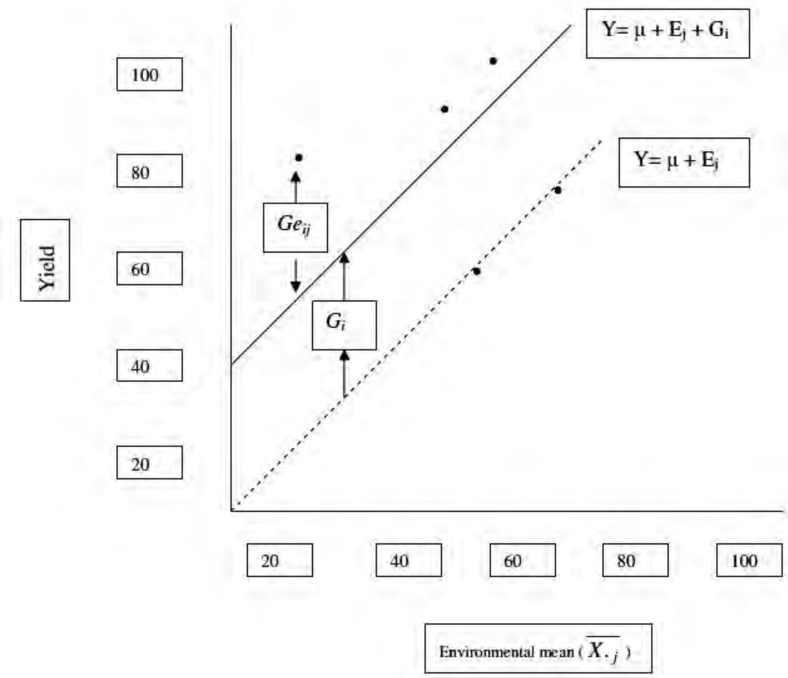


Figure3. 3 Graphical representation of GEI: The stability statistic ecovalence (**W_i**) is the sum of squares of deviations from the upper unbroken line.

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×E interaction effects of genotype I and are summed and squared across environments and constitutes ecovalence.

Shukla's stability variance parameter (σ_i^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" (s_i^2) and is estimated as follows:

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

Where Y_{ij} is the mean yield of the i^{th} genotype in the j^{th} environment, $\bar{Y}_{i.}$ is the mean of the genotype i in all environments, $\bar{Y}_{.j}$ 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_i^2) is equal to the environmental variance (σ_e^2) which means that σ_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 variances 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 s_i^2 are equivalent for ranking purposes (Wricke and Weber, 1980).

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×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×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×E interactions into two dimensions (biplot) and identifying the factor responsible for the interaction.

Additive main effects and multiplicative interaction method (AMMI)

According to Zobel et al. (1988), considering the three traditional models, analysis of variance (ANOVA) it 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. Firstly, to diagnoses the model. The 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×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.

Regarding problems from noise, there exist four basic options: better experiments, more replications, analysis of the experimental design, and analysis of the treatment design (Gauch 1992). First, accuracy can be increased by larger or better controlled yield plots. Second, greater accuracy results from a larger number of replications. Third, accuracy can be increased; relative to a completely randomized (CR) experiment, by a better experimental design, such as randomized complete blocks (RCB) or various incomplete block designs. For example, just 5 replications in a RCB design are often as accurate as 6 or 7 replications in a CR design, so the reward for a better statistical design and analysis is effectively 1 or 2 free replications. Complete block designs can reduce the error mean square and thereby increase statistical significance, whereas incomplete block designs can also adjust the yield estimates (so that an estimate is not simply an average over replications). Fourth, accuracy can be gained, for a regional trial planted in several locations or years, by statistical analysis of the treatment design, namely, a two-way factorial design of genotypes and environments. The total sum of squares (SS) is partitioned into a pattern-rich model and a discarded noise-rich residual, thereby adjusting the yield estimates and gaining accuracy. For example, just 5 replications analyzed by AMMI frequently achieve equivalent accuracy as 10 to 25 replications without AMMI analysis, so the reward for AMMI analysis is effectively 5 to 20 free replications.

The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the G×E interaction. It has proven useful for understanding complex G×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:

$$Y_{ijk} = \mu + G_i + E_j + \sum_{n=1}^{N} \lambda_n \alpha_{in} \gamma_{jn} + e_{ijk}$$

where Y_{ijk} is the yield of the i^{th} genotype in the j^{th} environment and k^{th} replication; μ is the grand mean; G_i and E_j are the genotype and environment deviations from the grand mean, respectively; λ_n is the eigen value of the PCA analysis axis n; α_{in} and γ_{jn} are the genotype and environment principal component scores for axis n; N is the number of principal components retained in the model. There are at most min (l—1, m—1) axes, but usually the number of axes N retained in the model is smaller, producing a reduced model denoted AMMI1 or AMMI2 if retaining 1 or 2 IPCAs, and so on. A reduced model leaves residuals and e_{ijk} is the error term.

The least-squares solution is found for balanced data by ANOVA followed by PCA, as proved by Gabriel (1978). Gauch (1992) gives a worked example.

In the initial analysis of variance, the total variation is partitioned into three sources, namely genotypes, environment and G×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×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×E interactions.

Regarding agricultural problems from G×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.

A special kind of AMMI biplot graph can help researchers comprehend and define mega-environments (Gauch, 1992). To indicate a location's probable position in an AMMI biplot in nature years, circle the points for past results for that location (or give each location a distinctive symbol, or whatever). Various locations will occupy different prediction regions, with a small region indicating high predictability and a large region low predictability. Then superimpose the regions in which various genotypes are winners, which turn out to be horizontal bands in an AMMI1 biplot or polygons in an AMMI2 biplot. Locations situated within a single genotype's winning turf, or which rarely and slightly cross over into another genotype's turf, have an obvious variety recommendation. But locations that straddle genotype boundaries are inherently less predictable and more problematic. In such cases, income stability may be promoted best by planting at least two different varieties to hedge one's bets, rather than by attempting to breed a single genotype with awesome stability. Those genotype turfs that contain numerous locations (or that represent significant crop regions) are candidates for mega-environments.

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×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×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;).

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×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×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×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×E interaction.

The AMMI stability value (ASV)

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):

$$AMMI\ Stabilty\ Value\ (ASV)$$

$$= \sqrt{\left[\frac{IPCA1\ Sum\ of Squares}{IPCA2\ Sumof Squares}(IPCA1\ score)\right]^2 + [IPCA2\ score]^2}$$

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×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×E sum of squares.

3.2.2. NON PARAMETRIC METHODS

Nonparametric measures for phenotypic stability based on ranks provide a useful alternative to parametric measures currently used which are based on absolute data. Some advantages of nonparametric stability statistics compared to parametric measures are: Hühn (1990)

1. Reduction or even avoidance of the bias caused by outliers.
2. No assumptions are needed about the distribution of the phenotypic values.
3. Stability parameters based on ranks are easy to use and to interpret.

4. Additions or deletions of one or a few genotypes or another grouping of the material are not as likely to cause great variations in the estimates as would be the case for parametric stability parameters.
5. For many applications, for example selections in breeding and testing programs, the rank orders of the genotypes are the most essential information. An estimation of phenotypic stability by using only this rank-information, therefore, seems to be an appropriate approach.

Three groups of methods based on non parametric statistics were applied:

– Test of G×E interaction;
– Genotype stability estimation;
– Relationship between non parametric estimators of genotype stability.

1. Test of *G×E* interaction

Test of genotype × environment (G×E) interactions were performed using non parametric statistic after HÜHN (1996):

1.1) Hildebrand's method (HÜHN, 1996):

a) Transformation of original data for grain yield

y_{ijk} (i=1,2,…,l; j=1,2,…,m; k=1,2,…,n) in value of y^*_{ijk} performed by formula:

$$y_{ijk} - \bar{y}_{i..} - \bar{y}_{.j.} + 2\,\bar{y}_{...} = y^*_{ijk}$$

$\bar{y}_{i..}$ - Average grain yield of genotype;

$\bar{y}_{.j.}$ - Average grain yield of environment;

$\bar{y}$ - Average grain yield over all;

y_{ijk} - Grain yield of genotype “i” in “j” environment and “k” repetition.

b) Transformation of y^*_{ijk} values in R_{ijk} ranks

$$R_{ijk} \; : \; y^*_{ijk} \; \rightarrow \; R_{ijk}$$

c) Statistic test of genotype × environment interaction significance were calculated by formula:

$$\frac{12}{l\, m\,(N+1)} \sum_{i=1}^{l} \sum_{j=1}^{m} (\bar{R}_{ij\,.} - \bar{R}_{i..} - \bar{R}_{.j\,.} + \bar{R}_{...})^2 \quad \sim \quad \chi^2 \text{ with } (l - 1)\ (m - 1)$$

degrees of freedom

N = *nlm*

l - number of genotypes;

m - number of environments;

$\bar{R}_{ij\,.}$ - rank average per genotype/environment;

$\bar{R}_{i..}$ - genotype rank average;

$\bar{R}_{.j\,.}$- environment rank average;

$\bar{R}_{...}$- average rank overall (HILDEBRAND, 1980; KUBINGER, 1986).

1.2) Kubingers method (HÜHN, 1996):

a) Transformation of original data for grain yield:

y_{ijk} (i =1,2,…,l; j=1,2,…,m; k=1,2,…,n) in ranks:

$$R_{ijk} \; : \; y^*_{ijk} \; \rightarrow \; R_{ijk}$$

b) Transformation of rank sum for genotype ~~i~~”, environment ~~j~~” and repetition ~~k~~”, (R_{ijk}) in R^*_{ijk} by formula

$$R_{ijk} \; \rightarrow \; {R_{ijk}}^* = R_{ijk} - \bar{R}_{i..} - \bar{R}_{.j\,.}$$

$\bar{R}_{i..}$ - genotype rank average;

$\bar{R}_{.j.}$- environment rank average.

c) Transformation of R_{ijk}^{*} values in R_{ijk}^{**} ranks: (rank the R_{ijk}^{*} values)

$$R_{ijk}^{**} : R_{ijk}^{*} \rightarrow R_{ijk}^{**}$$

d) Statistic test of genotype × environment interaction significance were calculated by formula:

$$\frac{12}{l\,m\,(N+1)} \sum_{i=1}^{l} \sum_{j=1}^{m} (\bar{R}_{ij.}{}^{**} - \bar{R}_{i..}{}^{**} - \bar{R}_{.j.}{}^{**} + \bar{R}_{...}{}^{**})^2 \sim \chi^2 \text{ with } (l - 1)\,(m - 1)$$

degrees of freedom

$\bar{R}_{ij.}{}^{**}$ - rank average of genotype "i" in particular environment "j";

$\bar{R}_{i..}{}^{**}$- rank average of genotype;

$\bar{R}_{.j.}{}^{**}$ - rank average of environment;

$\bar{R}_{...}{}^{**}$ - rank average over all.

For original data set, effects of genotype (G), environment (E) and G×E interactions are commonly calculated by combined analysis of variance (ANOVA) techniques, leading to an estimated variance component for G, E and G×E interactions. Statistical tests of significance for G, E and G×E were determined by F-test of ANOVA. Two nonparametric statistical methods in comparison with ANOVA method were applied to test the significance of G, E and G×E interaction. The first was Bredenkamp method (Bredenkamp 1974; Hühn and Leon 1995) based on the usual model for interactions. In this method interactions are defined as deviations from the additivity of main effects. The second was the van der Laan–de Kroon method (de Kroon and van der Laan 1981; Hühn and Leon 1995) which used the crossover G×E interactions. The test statistics of the above methods are approximately χ^2-distributed with *(l*–1*) (m*–1*)* degrees of freedom, where *l* = number of genotypes and *m*= number of environments (for detail, see Huehn and Leon (1995)).

The two nonparametric methods transform the original data into ranks and analyze the rank orders. The value of genotype *i* in environment *j* and replication *k* is denoted by y_{ijk} (i = 1,2,…,l; j = 1,2,…,m; k = 1,2,…,n).

1.3) Bredenkamp method:

Interactions detected by this method correspond to usual crossover interactions of parametric methods. In this method y_{ijk}-values for all environments and for all genotypes are transformed into ranks R_{ijk} of one single rank order (Hühn and Leon 1995).

Test of genotypes

The test statistic for testing genotypic differences was calculated as follows:

$$\chi^2_{(G)} = \frac{12l}{N^2(N+1)}\sum_{i=1}^{l} R_{i..}^2 - 3(N+1)$$

That is approximately χ^2-distributed, with *l*–1 degrees of freedom and N = lmn. $R_{i..}$ is rank average of genotype.

Test of environments

The test statistics for a test of environmental differences as follow is approximately χ^2-distributed, with *m*–1 degrees of freedom.

$$\chi^2_{(E)} = \frac{12m}{N^2(N+1)} \sum_{j=1}^{m} R^2_{.j.} - 3(N+1)$$

Test of interaction effects (non-crossover interaction)

The statistic for a test of G×E interaction differences is approximately χ^2-distributed, with *(l*–1*) (m*–1*)* degrees of freedom.

$$\chi^2_{(G\times E)} = \frac{12lm}{N^2(N+1)} \sum_{i=1}^{l} \sum_{j=1}^{m} \left(R^2_{ij.} - \frac{1}{m^2} R^2_{i..} - \frac{1}{l^2} R^2_{.j.} \right) + 3(N+1)$$

1.4) Van der Laan–de Kroon method

Interactions detected by this method correspond to crossover interactions of parametric methods (Baker 1988). That means that interactions are used only insofar as they lead to different rankings of genotypes and/or environments. Therefore, this method requires rank orders for each environment or for each genotype separately (Hühn and Leon 1995).

Test of genotypes

The y_{ijk}-values are ranked for each environment separately into the ranks R_{ijk}. The test statistic for a test of genotypes differences is approximately χ^2-distributed, with *l*–1 degrees of freedom.

$$\chi^2_{(G)} = \frac{12}{lmn^2(ln+1)} \sum_{i=1}^{l} R^2_{i..} - 3m(ln+1)$$

Test of environments

The y_{ijk} values are ranked for each genotype separately into the ranks R_{ijk}. The test statistic for a test of environmental differences is approximately χ^2-distributed, with *m*–1 degrees of freedom.

$$\chi^2_{(E)} = \frac{12}{lmn^2(mn+1)} \sum_{i=1}^{m} R^2_{.j.} - 3l(mn+1)$$

Test of interaction effects (Crossover interactions)

The y_{ijk}-values are ranked for each environment separately into ranks R_{ijk}. The test statistic for the hypothesis of no rank changes of genotypes between environments (crossover interaction) is approximately χ^2-distributed, with (*l*–1) (*m*–1) degrees of freedom.

$$\chi^2_{(G\times E)} = \frac{12}{ln^2(ln+1)} \left(\sum_{i=1}^{l} \sum_{j=1}^{m} R^2_{ij.} - \frac{1}{m^2} R^2_{i..} \right)$$

The hypothesis of no environmentally caused changes in rank orders (within genotypes) can also be tested using this method (de Kroon and van der Laan 1981).

2. Nonparametric Genotype stability estimation

We denote: y_{ij} = phenotypic value of the i^{th} genotype in the j^{th} environment (i = 1, 2, . . ., L; j = 1, 2, . . ., M) . In this two-way table with L rows (genotypes) and M columns (environments) one ranks the L phenotypic values y_{ij} within each column = environment separately (lowest value = rank of 1 and highest value = rank of L). Let r_{ij} be the rank of genotype *i* in environment *j*.

The following concept of phenotypic stability seems to be practicable: A genotype *i* is stable over environments if its ranks are similar over environments, i.e. maximum stability = equal ranks over environments Hühn (1990).

Each statistic which measures the similarity or dissimilarity of the ranks for each row = genotype can be used as an appropriate stability parameter. The statistics based on yield ranks of genotypes in each environment are expressed as follows:

2.1) <u>Average rank differences in different environments</u>, $S_i^{(1)}$. Mean of the absolute rank differences of a genotype *i* over the M environments. Genotypes ranking were done for each environment separately:

$$s_i^{(1)} = \frac{\sum_{j<j'}\left|r_{ij} - r_{ij'}\right|}{\binom{m}{2}} = \frac{2}{m(m-1)}\sum_{j}^{m-1}\sum_{j'=j+1}^{m}\left|r_{ij} - r_{ij'}\right|$$

2.2) <u>Rank of variance</u>, $S_i^{(2)}$ across “m” environments: common variance of the ranks

$$s_i^{(2)} = \frac{1}{m-1}\sum_{j=1}^{m}(r_{ij} - \bar{r}_{i.})^2$$

$$\bar{r}_{i.} = \frac{1}{m}\sum_{j=1}^{m} r_{ij}.$$

$\bar{r}_{i.}$ was interpreted as estimation of each “r_{ij}” under hypothesis of maximal stability (equal ranks). For a genotype “i” with maximum stability one obtains $s_i^{(1)} = s_i^{(2)} = 0$. Both stability parameters have been frequently used in the field of practical applications (SKRØPPA, 1984). In both cases, environmental factors have no effects on stability, but the differences among genotypes can affect stability measures and lead to differences in stability among genotypes when there is no genotype × environment interaction. Due to it, the transformed values are used if there is an intention to measure phenotypic yield stability independent from the yield level. Genotype effects are considered as fixed ones, while the remaining effects are defined to be random (PIEPHO and LOTITO, 1992). The null-hypothesis of no genotype × environment interaction effects implies ―all genotypes are equally stable" (with maximum stability). Tests of significance for both stability measures were done according to the following formula (HÜHN and NASSAR, 1989; 1991):

$$Z_i^{(v)} = \frac{\left[s_i^{(v)} - E\left\{s_i^{(v)}\right\}\right]^2}{var\left\{s_i^{(v)}\right\}}, v = 1,2$$

has an approximate χ^2 distribution with 1 degree of freedom.

2.3) <u>Relative deviation in relation to the average rank</u>, $s_i^{(3)}$ (HÜHN, 1979): sum of the absolute deviations of the r_{ij}'s from maximum stability expressed in $\bar{r}_{i.}$ units

$$s_i^{(3)} = \sum_{j=1}^{m} \frac{|r_{ij} - \bar{r}_{i.}|}{\bar{r}_{i.}}$$

This parameter expresses stability in the units of yield. It expresses a sum of absolute deviations of ranks r_{ij} from their average rank $\bar{r}_{i.}$, where deviations are expressed in the $\bar{r}_{i.}$ units. The numerator measures stability (= variability of ranks $\bar{r}_{i.}$), while the denominator implies the yield level (= average values of ranks r_{ij}).

This set encompasses other measures, but the measure $s_i^{(3)}$ is the simplest and mostly used.

2.4) The sum of squares of rank for each genotype relative to the mean of ranks: $s_i^{(6)}$

$$s_i^{(6)} = \sum_{j=1}^{m} \frac{(r_{ij} - \bar{r}_{i.})^2}{\bar{r}_{i.}}$$

Tests of significance

One of the most crucial points in developing new stability parameters must be the availability of efficient tests of significance

1) For testing the stability of a single genotype and

2) For testing stability comparisons between certain genotypes.

The statistical properties of $s_i^{(1)}$ and $s_i^{(2)}$ have been investigated by Nassar & Hühn (1987). Approximate tests of significance based on the normal distribution are developed for these two nonparametric measures:

$$Z_i^{(v)} = \frac{\left[s_i^{(v)} - E\left\{s_i^{(v)}\right\}\right]^2}{var\left\{s_i^{(v)}\right\}}, v = 1,2 \qquad (1)$$

would have an approximate chi-squared distribution with one degree of freedom and, similarly, the statistic

$$s^v = \sum_{i=1}^{k} Z_i^{(v)}, v = 1,2 \qquad (2)$$

may be approximated by a chi-squared distribution with L degrees of freedom with E($s_i^{(v)}$) = expectation (= mean) of $s_i^{(v)}$ and V($s_i^{(v)}$) = variance of ($s_i^{(v)}$) .

Under the null hypothesis that all genotypes are equally stable the means $E(s_i^{(v)})$ and variances $V(s_i^{(v)})$ may be computed from the discrete uniform distribution (1, 2, . . ., L). The following explicit formulae are derived and explained in Nassar and Hühn (1987):

$$E(s_i^{(1)}) = \frac{L^2-1}{3l}$$

$$E(s_i^{(2)}) = \frac{L^2-1}{12}$$

$$V(s_i^{(1)}) = \frac{(L^2-1)\left[(L^2-4)(M+3)+30\right]}{45L^2M(M-1)}$$

$$V(s_i^{(2)}) = \frac{(L^2-1)\left[2(L^2-4)(M-1)+5(L^2-1)\right]}{36M(M-1)}$$

With this global test based on (2) with *L* degrees of freedom an efficient statistical test is available to decide whether or not there are significant differences in stability between the genotypes. To test the stability of a single genotype *i* expression (1) can be applied in the form of a chi-squared test with one degree of freedom.

If the global chi-squared test based on (2) is significant, one may look for stability differences among genotypes using standard procedures for multiple comparisons among the observed $s_i^{(v)}$-values. Here, the number of degrees of freedom should be infinity since the variance of $s_i^{(v)}$) is known and is not being estimated (see : Nassar and Hühn, 1987) .

Kang‘s (1988) rank-sum is another nonparametric stability procedure where both yield and Shukla‘s (1972) stability variance were used as selection criteria. This index assigns a weight of one to both yield and stability statistics to identify high-yielding and stable genotypes. The genotype with the highest yield is given a rank of 1 and a genotype with the lowest stability variance is assigned a rank of 1. All genotypes were ranked in this manner, and the ranks by yield and by stability variance are added for each genotype. The genotype with the lowest rank-sum is the most desirable one.

The stratified ranking technique of Fox et al. (1990) consists of scoring the number of environments in which each genotype ranked in the top, middle and bottom thirds of trial entries. A genotype that occurred mostly in the top third (high TOP value) was considered a widely adapted cultivar.

Thennarasu (1995) proposed another set of nonparametric statistics ($NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$), based on ranks of adjusted means of the genotypes in each environment, and defined stable genotypes as those whose position remained unaltered in relation to the others in the set of environments assessed. These were calculated as follows:

$$NP_i^{(1)} = \frac{1}{n}\sum_{j=1}^{n}\left|r_{ij}^{*} - M_{di}^{*}\right|$$

$$NP_i^{(2)} = \frac{1}{n}\left(\sum_{j=1}^{n}\frac{\left|r_{ij}^{*} - M_{di}^{*}\right|}{M_{di}}\right)$$

$$NP_i^{(3)} = \frac{\sqrt{\sum\left(r_{ij}^{*} - \bar{r}_{i.}^{*}\right)^2/n}}{\bar{r}_{i.}}$$

$$NP_i^{(4)} = \frac{2}{n(n-1)}\left[\sum_{j=1}^{n-1}\sum_{j'=j+1}^{n}\frac{\left|r_{ij}^{*} - r_{ij'}^{*}\right|}{\bar{r}_{i.}}\right]$$

The adjusted rank, r_{ij}^*, is determined on the basis of the adjusted phenotype values ($y_{ij}^* = y_{ij} - \bar{y}_{i.}$), where $\bar{y}_{i.}$ is the mean performance of the i^{th} genotype. The ranks, obtained from these adjusted values (y_{ij}^*), depend only on G×E interaction and error effects.

In the above formulas, r_{ij}^* is the rank of y_{ij}^*, and $\overline{r_{i.}^*}$: and M_{di}^* are the mean and median ranks for adjusted values, where $\bar{r}_{i.}$ and M_{di} are the same parameters computed from the original (unadjusted) data.

3. Relationship between non parametric estimators of genotype stability

Comparison between the investigated estimators was calculated by rank correlation coefficient (r_s), after Spearman: Spearman‘s coefficient of rank correlation (r_s) was employed [RGD Steel (1980)] to statistically compare the stability indices used in this study. 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:

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

d_i = difference between two ranks of investigated trait;

n = number of correlated pairs.

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.

4: RESULT AND DISCUSSION

4.1 PARAMETRIC METHOD

4.1.1 PARAMETRIC G×E INTERACTION ANALYSIS

The statistical analyses presented in this thesis were done using the software's SAS for parametric analysis, Microsoft Excel for all nonparametric analysis and GenStat Discovery Edition 4 for AMMI analysis.

The usual diagnostic plots-including a normal probability plot of residuals (i.e. for separate ANOVA for each environment Fig A.1 and for combined ANOVA Fig A.3 of Appendix), a histogram of residuals, plot of residuals versus fitted values, plot of residuals versus level of regressor variable and formal statistical procedures to assess model assumptions for the individual ANOVAs (i.e. for yield data at each environment), and the separate LR models (for each genotype yield) were performed. Examination of the results do not reveals any serious violations of the assumptions that errors are normally and independently distributed with mean zero and constant variance. In the Shapiro-Wilk (W) test for normality, the p-value is based on the assumption that the distribution is normal. In this study, the p-value for each of the separate ANOVA model is very large (>0.05), indicating that we cannot reject the hypothesis that the residual is normally distributed (see the output of the proc univariate in Table A.3 of Appendix). For homogeneity of residual variance, in each of the separate ANOVA, the investigator uses the Bartlett's test by considering genotype as a group. Based on this, the p value for each of the separate ANOVA is much greater than 0.05 (see Table A.2 in Appendix) indicating the hypothesis that the residual variances in each of the separate ANOVA are homogeneous cannot be rejected. Thus, the residuals have constant variance. Plots of residual versus the fitted value for each of the separate ANOVA are given in Fig A.1 of Appendix. There should be no relationship between the size of the residual and the fitted values. These plots reveal nothing of unusual interest. Thus, the usual interpretation for each of the separate ANOVA is valid since all assumptions concerning the data are met.

Separate analyses of variance (ANOVA) were first done with the classical RCBD model with replications (block) at each environment. Summary results of the separate analysis are given in Table A.1 of appendix. In the analysis of combined experiment of data from several environments, the first requirement is to assess the homogeneity of the error variance at the various environments. If the error variances are homogeneous, the analysis can proceed with the original data. This can be done by importing error mean square and degree of freedom for error from the individual analysis of variance. Then we apply Bartlett's chi-square test for testing Homogeneity of error variance. Here null and alternate hypothesis are

$H_o: \sigma_1^2 = \sigma_2^2 = \cdots = \sigma_p^2$ against the alternate hypothesis

H_o: at least two of the σ_i^2's are not equal, where σ_i^2 is the error variance for the i^{th} environment.

Let $s_{e_1}^2, s_{e_2}^2, \ldots, s_{e_p}^2$ are the MSE of p environments respectively and $n_1, n_2, \ldots, n_p$ are the df for p environments, respectively. Then the test statistics for testing homogeneity of variance is

$\chi_{p-1}^2 = \frac{\sum n_i \log \bar{s}_e^2 - \sum n_i \log s_{e_i}^2}{1+\frac{1}{3(p-1)}(\sum \frac{1}{n_i} - \frac{1}{\sum n_i})}$, where $\bar{s}_e^2 = \frac{\sum n_i s_{e_i}^2}{\sum n_i}$ and if $n_i = n$

$$\chi^2_{p-1} = \frac{n\left[p \log \bar{s}^2_e - \sum \log s^2_{e_i}\right]}{1 + \frac{p+1}{3np}}$$

Where χ^2_{p-1} follows χ^2distribution with *p-1* df. If the calculated value of χ^2_{p-1} is greater than tabulated χ^2_{p-1}value at *p-1* df then the null hypothesis of homogeneity of variance is rejected and the data is heterogeneous in different environments, otherwise it is homogeneous.

Table 4.1: Error mean squares and their logarithms of each of the separate ANOVA model Environment Error mean square (MSE) log(MSE)

Environment	MSE	log(MSE)
1.	485943.88	5.686586117
2.	217170.16	5.336800151
3.	133636.19	5.125924085
4.	574896.92	5.759589982
5.	123295.46	5.090947085
6.	197121.67	5.29473437
7.	502225.07	5.700898388
8.	366847.15	5.564485149

Where log refers to logarithm base 10.

For our data set, the computed chi-square value (χ^2_{cal} =9.99) is smaller than the corresponding tabular chi-square value (χ^2_{tab}) with (8-1) =7 df and at the 1% level of significance of 18.47. Thus, the hypothesis that the eight error variances are homogenous cannot be rejected. Therefore, a combined analysis of variance (ANOVA) was performed on the original (untransformed) yield data for the complete set of trials. The p-value based on the Shapiro-Wilk (W) test of normality for the combined ANOVA is 0.9929, which is very large, indicating the residuals in the combined ANOVA model are normally distributed. The Bartlett's chi-square test for the combined data is 28.5742 with p-value is 0.0730, indicating constant error variance. The plot of residuals versus the fitted values for the combined ANOVA model is shown in Fig A.2 of Appendix. There is no severe indication of dependency between the size of the residuals and the fitted values.

4.1.1.1 Analysis of variance and estimation of variance components.

The relative performance of genotypes based on the mean grain yield environments are presented in Table 4.2. Yield performances are ranked. Grain yield is given in kg ha^{-1}.

Table 4.2: Mean grain yield (kg/ha) of 20 bread wheat genotypes over 8 test environments.

genotype	Mean grain yield	Rank
G1	3853.23	1
G2	3570.28	6
G3	3673.42	3
G4	3593.33	4
G5	3186.36	15
G6	3329.14	12
G7	3313.60	13
G8	3513.09	7
G9	3456.28	9
G10	3048.72	16
G11	3034.36	18
G12	3030.58	19
G13	3454.74	10
G14	3273.31	14
G15	3577.59	5
G16	3438.62	11
G17	3465.84	8
G18	3048.49	17
G19	3759.88	2
G20	2759.81	20

The first ranked genotype for grain yield is G1 with G19 ranked second and G3 ranked third. The genotype with the lowest mean grain yield was G20, G12 and G11. Means across environments are adequate indicators of genotypic performance only in the absence of G×E. If G×E is present, means across environments does not tell us how genotypes differ in relative performance over environments.

The combined analysis of variance (ANOVA) is shown in Table 4.3 and it revealed that there were significant differences among environments ($p<0.01$) and genotypes ($p<0.01$) for grain yield indicating the presence of variability in genotypes as well as diversity of growing conditions at different locations. The G×E interaction was highly significant ($p<0.01$) reflecting the differential response of genotypes in various environments (Zubair et al., 2001). The total variation explained (%) is 77.9% for environment, 3.78% for genotype and 5.66% for G×E. The high percentage of the environment is an indication that the major factor that influence yield performance of bread wheat genotypes in Ethiopia is the environment. The relatively large proportion of Genotype × Environment variance, when compared to that of genotypes as a main effect, is a very important consequence.

Table 4.3: Combined ANOVA for yield and the percentage sum of squares of the 20 hybrids tested at 8 environments over a period of two years.

Source	DF	Sum of Squares	**%SS**	Mean Square	F Value	Pr > F
Env(E)	7	999543941.9	77.9	142791991.7	439.17	<.0001
Location (L)	3	623756478.2		207918826.1	639.47	<.0001
Year (Y)	1	5160646.2		5160646.2	15.87	<.0001
L×Y	3	370626817.5		123542272.5	379.96	<.0001
Rep(env)	24	14149904.6	1.1	589579.4	1.81	0.0112
Genotype(G)	19	48459603.8	3.78	2550505.5	7.84	<.0001
Env*genotype	133	72644063.7		546196.0	1.68	<.0001
G×L	57	35364200.2		620424.6	1.91	0.0002
G×Y	19	8002038.5		421159.9	1.30	0.1808
G×L×Y	57	29277825.0		513646.1	1.58	0.0064
Error	456	148264845	11.56	325142		
Corrected Total	639	1283062422				

The combined analysis of variance across locations and years showed highly significant differences among locations (L), year (Y) and genotypes (G) and their interaction (L×Y, G×L, G×L×Y). However, the interaction G×Y was not significant.

The high mean square values for locations indicated that the performance was affected significantly by variations among locations (Table 4.3). From Table 4.3 we also show that locations contributed the major share (48.61%) of variability followed by location by year interaction (28.89%). Location was the most important source of yield and yield components variation. The interaction G×L was significant and constitute 2.76% of the total variability and 48.68% of the G×E interaction.

The restricted maximum likelihood (REML) estimates of variance components for environment, genotype and genotype × environment interaction are shown in Table 4.4. Estimated variance component due to environment ($\hat{\sigma}_E^2 = 1774767.5$) made the greater contribution to the total estimated variance for grain yield. Genotype × Environment interaction and residual components of variance were 55263.4 and 325142.1 respectively.

When individual estimates of variance for grain yield (Table 4.4) were expressed as a percent of the total variation ($\sigma_G^2 + \sigma_{G\times E}^2 + \sigma_e^2$), the σ_G^2 component accounted for 14.14% of the total variation. The $\sigma_{G\times E}^2$ was 12.47% of the total variation, indicating that the genotypes were less consistent over environments. This means that location selection needs more effort. All of the variance components were highly significant (p<0.01), and the importance of the $\sigma_{G\times E}^2$ component indicates that factors such as rainfall, temperature, and disease incidence can result in conditions unique to each year location combination and that the genotypes respond differently to these conditions.

Table 4.4: Estimates of variance components for grain yield, genotypes and their interactions.

Variance Component	Estimate	% variance component
Var(env) $\hat{\sigma}_E^2$	1774767.5	
Var(rep(env)) $\hat{\sigma}_{R/E}^2$	13221.9	
Var(genotype) $\hat{\sigma}_G^2$	62634.7	14.14
Var(env*genotype) $\hat{\sigma}_{G\times E}^2$	55263.4	12.47
Var(Error) $\hat{\sigma}_e^2$	325142.1	73.39

The GEI is highly significant ($p<0.01$) accounting for 5.66% of the sum of squares implying the need for investigating the nature of differential response of the genotypes to environments. Presence of the GEI indicates that the phenotypic expression of one genotype might be superior to another genotype in one environment but inferior in a different environment. In other words, when significant G×E interaction is present, the effects of genotypes and environments are statistically nonadditive (or the differences between genotypes depend on the environment). The presence of a significant G×E interaction complicates interpretation of the results. That means, it is difficult to identify superior genotypes across environments when G×E interaction is highly significant.

From the combined ANOVA in Table 4.3, G×E interaction is highly significant and hence superiority of genotypes across environments cannot be identified by considering their mean yield performance (see Table 4.2). Furthermore, the traditional analysis of variance determines the values of each variance source and the significance of the contribution of each component, but it does not partition the interaction in to several components and thus other types of analyses should be performed. Hence, such multi-location trial data along with a highly significant G×E interaction requires measures of stability analysis.

4.1.2 PARAMETRIC STABILITY ANALYSIS

4.1.2.1 Eberhart and Russell's joint regression analysis

Eberhart and Russell's (1966) procedure involves the use of joint linear regression where the yield of each genotype is regressed on the environmental mean yield. This stability is the most widely used in plant breeding for providing the genotypic stability. The genotype's performance is generally expressed in terms of three parameters, mean yield (Y), regression coefficient (b_i) and the deviation ($S^2_{d_i}$) from the regression. According to this model a stable genotype should have a high mean yield, b_i = 1 and $S^2_{d_i}$ = 0. It is however specifically the deviation from the regression ($S^2_{d_i}$) which is used as a measure of a genotype's stability across environments.

Table 4.5: Genotype mean grain yield, regression coefficient (b_i) and deviation from regression $S^2_{d_i}$ for the 20 wheat genotypes at 8 environments.

genotype	environmental_ mean (qt/ha)	Rank	Betai(b_i)	$S^2_{d_i}$	Ran k
G1	38.5323	1	1.15221	14.8229	8
G2	35.7028	6	1.00187	31.1914	13
G3	36.7342	3	1.08743	18.1041	11
G4	35.9333	4	1.00859	37.8399	16
G5	31.8636	15	1.03931	7.4371	4
G6	33.2914	12	0.98777	7.1108	3
G7	33.1360	13	1.13589	8.9777	6
G8	35.1309	7	1.23703	15.4147	9
G9	34.5628	9	0.84846	32.8621	15
G10	30.4872	16	1.04088	4.4499	2
G11	30.3436	18	0.92841	4.1229	1
G12	30.3058	19	0.89369	32.2332	14
G13	34.5474	10	0.96193	10.4573	7
G14	32.7331	14	1.07642	17.5357	10
G15	35.7759	5	1.00154	8.6727	5
G16	34.3862	11	0.95156	45.1729	17
G17	34.6584	8	1.08446	28.7490	12
G18	30.4849	17	0.90825	75.3256	19
G19	37.5988	2	1.05179	147.7119	20
G20	27.5981	20	0.60251	67.5409	18

Results from the Eberhart and Russell regression model for the 20 wheat genotypes are summarized in Table 4.5. It is evident that G19, G18, and G20 with their very high $S^2_{d_i}$ have low yield stability and b_i greater than one for G19 implied that it was adapted to high yielding environments and b_i less than one for G18 and G20 implied that it was adapted to low yielding environments. However, a low $S^2_{d_i}$; and b_i less than one indicates that G11 and G6 were the most stable genotypes and are well adapted to low yielding environments and a low $S^2_{d_i}$; and b_i greater than one indicates that G10 was the most stable genotypes and are well adapted to high yielding environments.

4.1.2.2 Wricke's ecovalence (W_i)

Wricke's ecovalence (1962) is an alternative method that is frequently used to determine stability of genotypes based on the G×E interaction effects. It indicates the contribution of each genotype to the G×E interaction. The cultivars with the lowest ecovalence contributed the least to the G×E interaction and are therefore more stable.

The most stable genotypes according to the ecovalence method of Wricke (1962) were G10, G5 and G11. These genotypes were not the best ranked for mean yield, being 16th, 15th and 18th respectively.

The most unstable hybrids according the ecovalence method, higher W_i values were G20, G16 and G2 these hybrids were ranked 20th, 11th and 6th for mean yield respectively (Table 4.6).

Table 4.6: Wricke's ecovalence value for 20 the hybrids at 8 environments.

genotype	environmental_mean	Rank	Ecovalence ($\mathbf{W_i}$)	Rank
G1	3853.23	1	538363.71	10
G2	3570.28	6	1786429.07	18
G3	3673.42	3	1130443.87	16
G4	3593.33	4	946303.10	15
G5	3186.36	15	302434.95	2
G6	3329.14	12	426586.25	8
G7	3313.60	13	450989.95	9
G8	3513.09	7	1601020.69	17
G9	3456.28	9	929789.55	14
G10	3048.72	16	286221.53	1
G11	3034.36	18	311294.11	3
G12	3030.58	19	635894.48	12
G13	3454.74	10	382220.02	5
G14	3273.31	14	384437.43	6
G15	3577.59	5	365884.53	4
G16	3438.62	11	2733767.87	19
G17	3465.84	8	420613.95	7
G18	3048.49	17	576063.53	11
G19	3759.88	2	894997.34	13
G20	2759.81	20	3057255.53	20

4.1.2.3 Shukla's stability variance procedure (σ_i^2).

Shukla's (1972) stability variance values and the stability ranking as well as the mean yield with its ranking are given in Table 4.7. The most stable wheat genotypes as indicated by this stability parameter were G10, G5 and G11. The genotypes with a poor stability according this procedure were G20, G16 and G2.

Table 4.7: Genotype mean grain yield and Shukla's stability variance (σ_i^2) for the 20 Bread wheat varieties.

genotype	environmental_mean	Rank	stability_variance	Rank
G1	3853.23	1	80379.35	10
G2	3570.28	6	278484.96	18
G3	3673.42	3	174360.32	16
G4	3593.33	4	145131.63	15
G5	3186.36	15	42930.34	2
G6	3329.14	12	62636.89	8
G7	3313.60	13	66510.50	9
G8	3513.09	7	249055.06	17
G9	3456.28	9	142510.43	14
G10	3048.72	16	40356.78	1
G11	3034.36	18	44336.55	3
G12	3030.58	19	95860.42	12
G13	3454.74	10	55594.63	5
G14	3273.31	14	55946.60	6
G15	3577.59	5	53001.70	4
G16	3438.62	11	428856.20	19
G17	3465.84	8	61688.91	7
G18	3048.49	17	86363.44	11
G19	3759.88	2	136987.86	13
G20	2759.81	20	480203.44	20

4.1.2.4 The environmental variance

The environmental variance (s_i^2) is one of the major stability measures for the static stability concept, i.e., the variance of genotype yields recorded across test environments. The smaller the s_i^2, the more stable the ith genotype.

Genotype's variance across environments and coefficient of variation are listed in Table 4.8. Based on these two measures, genotypes G20, G9 and G12 can be considered relatively more stable. Among these genotypes, G9 have mean grain yield of 3456.28 which is slightly above the grand mean, while genotypes G12 and G20 have respectively mean yield of 3030.58 and 2759.81 which are less than the grand mean. Relatively, genotypes G8, G1 and G7 can be regarded as unstable genotypes (see Table 4.5.). A problem with this method is that, in general, genotypes with high phenotypic stability measured through the environmental variance show low yield. For instance, according to the environmental variance G20 and G12 were the most stable genotypes with low mean yield. These genotypes were not the best ranked for mean yield, being 20th and 19th respectively. In consequence, plant breeders do not use this method to evaluate yield stability across environments.

Table 4.8: Genotype mean grain yield, environmental variance (s_i^2), and coefficient of variation (CV_i) for the 20 bread wheat varieties.

genotype	environmental_mean	Rank	environmental_variance	Rank	CV_i
G1	3853.23	1	2405185.03	19	40.2484
G2	3570.28	6	2046790.55	13	40.0714
G3	3673.42	3	2258509.74	17	40.9110
G4	3593.33	4	1950761.93	9	38.8692
G5	3186.36	15	1968419.49	10	44.0316
G6	3329.14	12	1802192.15	7	40.3245
G7	3313.60	13	2334427.18	18	46.1095
G8	3513.09	7	2859762.45	20	48.1366
G9	3456.28	9	1376777.48	2	33.9487
G10	3048.72	16	1971708.36	11	46.0579
G11	3034.36	18	1573821.98	5	41.3439
G12	3030.58	19	1496225.77	3	40.3620
G13	3454.74	10	1703592.37	6	37.7805
G14	3273.31	14	2112633.36	15	44.4042
G15	3577.59	5	1842655.07	8	37.9430
G16	3438.62	11	2002503.27	12	41.1531
G17	3465.84	8	2146490.02	16	42.2723
G18	3048.49	17	1539659.50	4	40.7031
G19	3759.88	2	2097619.78	14	38.5202
G20	2759.81	20	802702.02	1	32.4637

4.2 ADDITIVE MAIN EFFECTS AND MULTIPLICATIVE INTERACTION (AMMI) MODEL

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×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 GenStat Discovery Edition 4. Biplot of the first two principal components were constructed 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. 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 20 wheat genotype evaluated over two years and across four locations according to the AMMI model are presented in Table 4.10. The ANOVA indicated highly significant differences ($P < 0.01$) for environments, genotypes and genotypes × environment interaction. The IPCA are ordered according to decreasing importance. The F-test was highly significant (P < 0.01) for the first two IPCA axes and significant (P < 0.05) for the third IPCA.

Table 4.9 Analysis of variance (ANOVA) based on the AMMI model for grain yield (kg ha^{-1}) for the two years (2007-2008)

Source	df	SS	MS	F	F_prob	Total variation Explained (%)	G × E Explained (%)	Cumulative (%)
Total	639	1283062539	2007923	-	-			
Treatments	159	1120647854	7048100	21.68	0.00000			
Genotypes	19	48459604	2550505	7.84	0.00000	3.78		
Environments	7	999544204	142792029	242.19	0.00000	77.90		
Reps within Env. (Block)	24	14149905	589579	1.81	0.01117			
Interactions G × E	133	72644046	546196	1.68	0.00005	5.66		
IPCA 1	25	23438053	937522	2.88	0.00001**		32.26	32.26
IPCA 2	23	17702491	769674	2.37	0.00042**		24.37	56.63
IPCA 3	21	12908381	614685	1.89	0.01023*		17.77	74.4
IPCA 4	19	9872819	519622	1.60	0.05258		13.59	87.99
IPCA 5	17	5677587	333976	1.03	0.42656		7.816	95.81
IPCA 6	15	1998751	133250	0.41	0.97632		2.751	98.56
Residuals	13	1045965	80459	0.25	0.99690			
Error	456	148264780	325142	-	-			

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

Grand mean = 3369.032 R-squared= 0.874501 C.V. =17.24566%

The total variation explained (%), ranged from 3.78% for genotypes, 77.90% for environments and 5.66% for G×E. The high percentage of the environment is an indication that the major factor that influence yield performance of wheat in Ethiopia is the environment. Out of the total eight IPCA, the three IPCA axes explained 74.4% of the G×E interaction. The first IPCA captured 32.26% of the total interaction sum of squares in 19% of the interaction degrees of freedom. The second IPCA also explained 24.37% of the interaction sum of squares in 17 % of the interaction degrees of freedom (Table 4.10).

The first two IPCA explained only 56.63% of the G×E interaction, which indicate the G×E interaction effect is still complex. Thus, AMMI biplot was not enough to explain the G×E interaction, so further technique need to be applied to disaggregate the GEI component.

Table 4.11 and Table 4.12 present the AMMI analysis data with the IPCA1 and IPCA2 scores for the genotypes and the environments. The tables also show the names and graph ID of the genotype and the environments. In Figure 4.1 the IPCA1 scores for both the genotype and the environments were plotted against the mean yield for the genotypes and the environments respectively.

Table 4.10 IPCA1, IPCA2 scores and graph ID for the 20 wheat genotypes on mean yield and evaluated in eight environments.

Genotype	Genotype mean	IPCA 1	IPCA 2
G1	3853	7.21379	9.49195
G2	3570	-14.23447	13.78071
G3	3673	0.40226	2.60547
G4	3593	-14.40887	7.65245
G5	3186	-2.74489	3.19634
G6	3329	-11.43273	4.89232
G7	3314	1.21947	10.05481
G8	3513	8.85011	18.08441
G9	3456	-12.86274	-9.03752
G10	3049	6.09173	-0.67620
G11	3034	1.41815	-3.62202
G12	3031	1.19780	-4.23959
G13	3455	2.95747	-1.90659
G14	3273	1.20037	7.13527
G15	3578	6.49709	-5.02418
G16	3439	24.85984	-20.08422
G17	3466	6.97929	5.84181
G18	3048	3.05275	-12.80126
G19	3760	10.22350	-3.17157
G20	2760	-26.47995	-22.17241

Table 4.11 The IPCA1, IPCA2 scores and the graph ID for the eight environments, on environmental mean yield

Environment	Environmental mean	IPCA 1	IPCA 2
E1	4091	32.34405	9.25409
E2	2160	4.62382	-21.47754
E3	2488	-5.59216	-11.42495
E4	5096	-5.33133	24.19281
E5	5409	16.57043	10.02760
E6	2076	-23.93305	-2.51294
E7	3207	-20.99327	14.70052
E8	2425	2.31150	-22.75959

By plotting both the genotype and the environments on the same graph, the associations between the genotype 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 E1, E4 and E5. The lower yielding environments were E2, E3, E6, E7 and E8. Therefore, Adet was generally categorized under high yielding wheat environment as compared to the three relatively categorized under low yielding environments (Holeta, Kulumsa and Sinana). It is further noted that E1 (Adet 2007) was the most favorable season and E6 (Holeta 2008) was less favorable among the eight 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 favorable environments with above-average means were G1, G3, G8, G13, G15, G16, G17 and G19 among them G3 is found to be more stable. Genotypes grouped under low yielding environments are shown at the lower left quadrant of the biplot which are G5, G6 and G20. Generally G20 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 genotype G11 and G12 showed similar performance as they are close to each other.

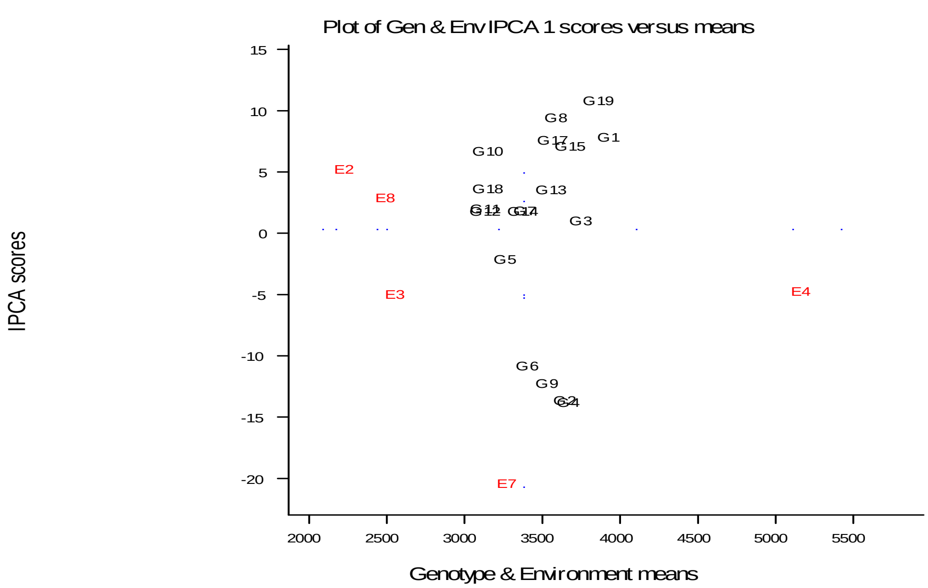


Figure 4. 1 AMMI 1 biplot for grain yield of wheat genotypes showing means of genotypes and environments plotted against their IPCA1 scores (genotypes/environments in place of others with similar means are not shown)

The three 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×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). The biplot showed that E1 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 genotypes. However, due to its high IPCA score, genotype variability at this environment may not exactly reflect the average genotypes performance across environments.

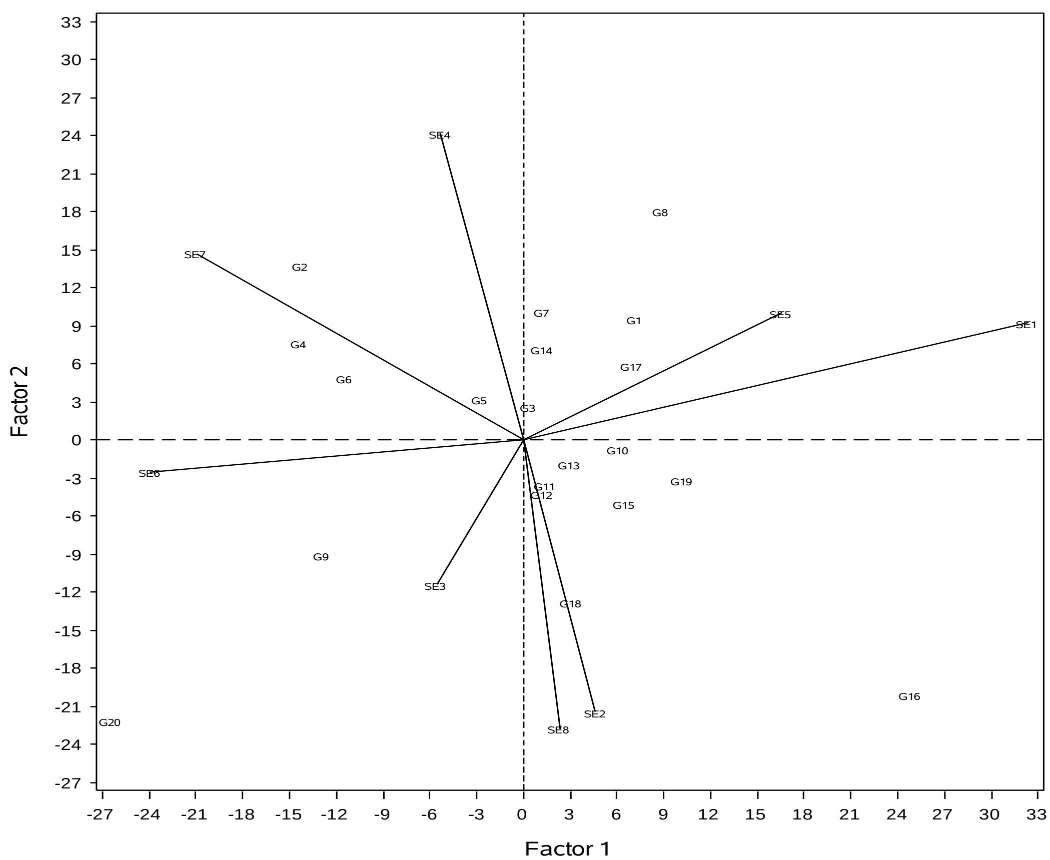


Figure 4. 2 AMMI 2 biplot for grain yield of wheat genotypes showing the plotting of IPCA1 and IPCA2 of genotypes and environments with vectors. The angle and the projection of the vectors indicate the association among the environments

The AMMI 2 biplot also indicated the relationship among the wheat genotypes. G20 and G16 were different from the other genotypes as they are located far apart from the other genotypes in the biplot. They are also the unstable genotype. Genotype G3, G5, G13, G11 and G12 were positioned closer to the origin of the biplot which indicates their stability in performance across environments, while the direction of G5 shows the genotype‘s stability in the low yielding environment. G9 was more adapted to low yielding environment. Generally genotypes 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.

4.1.2.5 The AMMI stability value (ASV)

The ASV as described by Purchase (1997) was calculated for each genotype. Genotypes with lower ASV values are considered more stable than genotypes with higher ASV.

According to the ASV ranking the most stable genotypes were G3, G11 and G13. G3 was the third highest yielder based on the mean yield value (Table 4.9). However, G1 and G19 which was the highest for mean yield first and second, ranked twelfth and thirteenth for the ASV. The most unstable genotypes according to the ASV were G20, G16 and G2 and this result is relatively similar with most of the stability procedures.

Table 4.12 AMMI stability value (ASV) and ranking with the IPCA 1 & 2 scores for the 20 bread wheat varieties.

genotype	environmental_mean	Rank	IPCA1	IPCA2	ASV	Rank
G1	3853.23	1	7.21379	9.49195	13.46549	12
G2	3570.28	6	-14.23447	13.78071	23.34727	18
G3	3673.42	3	0.40226	2.60547	2.659347	1
G4	3593.33	4	-14.40887	7.65245	20.55489	16
G5	3186.36	15	-2.74489	3.19634	4.839855	5
G6	3329.14	12	-11.43273	4.89232	15.90788	14
G7	3313.60	13	1.21947	10.05481	10.18362	9
G8	3513.09	7	8.85011	18.08441	21.54869	17
G9	3456.28	9	-12.86274	-9.03752	19.27967	15
G10	3048.72	16	6.09173	-0.67620	8.093731	7
G11	3034.36	18	1.41815	-3.62202	4.079769	2
G12	3030.58	19	1.19780	-4.23959	4.526494	4
G13	3454.74	10	2.95747	-1.90659	4.355187	3
G14	3273.31	14	1.20037	7.13527	7.310124	6
G15	3577.59	5	6.49709	-5.02418	9.961879	8
G16	3438.62	11	24.85984	-20.08422	38.55815	19
G17	3465.84	8	6.97929	5.84181	10.93228	10
G18	3048.49	17	3.05275	-12.80126	13.42418	11
G19	3759.88	2	10.22350	-3.17157	13.90249	13
G20	2759.81	20	-26.47995	-22.17241	41.48224	20

4.3 NONPARAMETRIC METHOD

4.3.1 NONPARAMETRIC ANALYSIS OF G × E INTERACTIONS

The numerical values of the test statistic for the different statistical procedures to determine the effects of G×E interaction on grain yield of bread wheat genotypes are presented in Table 4.2. χ^2-values with (l–1) (m–1) degrees of freedom for the methods of Hildebrand, Kubinger, Bredenkamp and van der Laan–de Kroon at the indicated levels probability were tested (Table 4.13). The null hypothesis for Bredenkamp is no noncrossover G×E interactions and for van der Laan–de Kroon is no crossover G×E interaction. The results indicated that significant interactions were found according to Hildebrand and Kubinger. In comparing the result of ANOVA with nonparametric analysis procedures, we found that both methods were in agreement, but nonparametric analysis provided more specific information about the nonexistence of crossover and noncrossover G×E interactions. For the de Kroon/van der Laan approach exceeding probabilities larger than 5% were obtained implying No cross-over interactions were therefore detected by the de Kroon/van der Laan procedure and also for Bredenkamp approach exceeding probabilities larger than 5% were obtained implying No noncrossover interactions were therefore detected.

Table 4.13 Analysis of GEI using different nonparametric tests on 20 wheat genotypes grown in 8 environments.

Nonparametric tests	df	Statistic χ2	P-value
Bredenkamp	133	42.1193	0.9999
Hildebrand	133	187.7588**	0.0013
Kubinger	133	177.73416**	0.0058
de Kroon-van der Laan	133	148.5966	0.168

** Significant at the 0.01 level

4.3.2 NONPARAMETRIC STABILITY ANALYSIS

Hühn (1979) and Nassar and Hühn (1987) proposed four non-parametric measures of phenotypic stability.

1. Mean of the absolute rank differences $S_i^{(1)}$ of a genotype and variance among the ranks $S_i^{(2)}$ over the environments

Non-parametric methods are based on the ranks of the genotypes across locations. They give equal weight to each location or environment. Genotypes with less change in ranks are expected to be more stable. The mean absolute rank difference $S_i^{(1)}$ estimates all possible pair wise rank difference across locations for each genotype. The $S_i^{(2)}$ estimates are simply the variance of ranks for each genotypes over environments. For the variance of ranks $S_i^{(2)}$, smaller estimates may indicate relative stability. Often, $S_i^{(2)}$ has less power for detecting stability than $S_i^{(1)}$.

Table 4.14 Mean absolute rank difference ($S_i^{(1)}$) and variance of ranks ($S_i^{(2)}$) for mean yield of 20 bread wheat varieties.

	mean	Rank	$s_i^{(1)}$	Rank	$Z_i^{(1)}$	$s_i^{(2)}$	Rank	$Z_i^{(2)}$
G1	3853.23	1	4.392857	6	2.934521	17.69643	8	1.621303
G2	3570.28	6	7.178571	17	0.160926	38.55357	18	0.188513
G3	3673.42	3	7.321429	18	0.259668	38.26786	17	0.168749
G4	3593.33	4	5.178571	13	1.24709	19.41071	12	1.283605
G5	3186.36	15	4.107143	4	3.724456	12.26786	4	2.950553
G6	3329.14	12	5.214286	14	1.187285	19.42857	13	1.280294
G7	3313.60	13	4.892857	11	1.778415	18.26786	11	1.504359
G8	3513.09	7	7.821429	19	0.790407	43.125	19	0.653549
G9	3456.28	9	6.535714	16	0.007523	30.69643	16	0.043702
G10	3048.72	16	3.785714	2	4.725544	10.85714	2	3.360648
G11	3034.36	18	3.25	1	6.658507	8.982143	1	3.946997
G12	3030.58	19	4.785714	10	2.001908	17.71429	9	1.617581
G13	3454.74	10	4.642857	9	2.320468	14.85714	5	2.267266
G14	3273.31	14	4.964286	12	1.636767	18.125	10	1.533185
G15	3577.59	5	4.464286	7	2.751729	15.26786	7	2.167138
G16	3438.62	11	9.178571	20	3.682725	63.41071	20	6.09659
G17	3465.84	8	4.571429	8	2.488564	15.07143	6	2.214743
G18	3048.49	17	4	3	4.044928	11.42857	3	3.19132
G19	3759.88	2	4.285714	5	3.219727	21.92857	14	0.859026
G20	2759.81	20	5.785714	15	0.430263	26.21429	15	0.331757
	$E(s_i^{(1)})$	$V(s_i^{(1)}$	$E(s_i^{(2)})$	$V(s_i^{(2)}$	S^1	S^2	Tab. χ^2_1	Tab. χ^2_{19}
	6.65	1.7361	33.25	149.2	46.051421	37.280878	3.84	30.14

The $S_i^{(1)}$ may loose power when genotypes are similar in their interactions with the environments. Two rank stability measures proposed by Huehn (1979) were worked out and expressed as $S_i^{(1)}$ and $S_i^{(2)}$ are presented in Table 4.14 The genotypes G11, G10 and G18 had the lowest value of $S_i^{(1)}$ and ranked 18th, 16th and 17th for grain yield. G1 and G19 had higher grain yield as compared to overall mean yield, However, genotype G11, G10 and G18 were stable although it had the lowest mean yield. The highest $S_i^{(1)}$ mean absolute rank was observed for genotype G16, G8 and G3 indicating to be highly unstable genotypes. Since S^1 = 46.05 was higher than the critical value of χ^2 = 30.14, there were significant differences in rank stability for grain yield among 20 wheat genotype grown in 4 locations during 2007-2008 (Table 4.14). And S^2= 37.28 were higher than the critical value χ^2 = 30.14, significant differences in rank stability among 20 wheat genotype grown in 4 locations during 2007-2008 (Table 4.14).

2. Relative deviation in relation to the average rank $s_i^{(3)}$ of a genotypes and the sum of squares of rank for each genotype relative to the mean of ranks $s_i^{(6)}$

The Y_{ij} values must not be corrected for the genotypic effects before ranking because information about trait level would be lost. Hühn (1979) proposed two non-parametric statistics for the simultaneous estimation of performance and stability which are $s_i^{(3)}$ and $s_i^{(6)}$. These statistics measure stability in units of the mean rank of the *ith* genotype using $s_i^{(3)}$, the differences between rank and mean rank are weighted with themselves avoiding the possibility that a lot of smaller rank differences may lead to the same $s_i^{(3)}$ value as a few larger differences. These $s_i^{(3)}$ and $s_i^{(6)}$ non-parametric measures were worked out by using the ranks which were assigned to genotypes on the basis of original mean data within environment and presented in Table 4.15.

Table 4.15 The sum of the absolute deviations of rank ($S_i^{(3)}$) and the sum of squares of rank ($S_i^{(6)}$) for mean yield of 20 bread wheat varieties.

	Mean	Rank	$s_i^{(3)}$	Rank	$s_i^{(6)}$	Rank
G1	3853.23	1	5.081081	18	26.78378	15
G2	3570.28	6	4.852459	17	35.39344	18
G3	3673.42	3	5.830508	19	36.32203	19
G4	3593.33	4	3.491525	13	18.42373	13
G5	3186.36	15	1.652174	4	5.973913	4
G6	3329.14	12	2.727273	9	12.36364	10
G7	3313.60	13	1.978495	6	11	7
G8	3513.09	7	4.051948	15	31.36364	16
G9	3456.28	9	3.915493	14	24.21127	14
G10	3048.72	16	1.225806	2	4.903226	2
G11	3034.36	18	1.212598	1	3.96063	1
G12	3030.58	19	1.870968	5	8	5
G13	3454.74	10	3	11	13	11
G14	3273.31	14	2.371134	8	10.46392	6
G15	3577.59	5	3.017544	12	15	12
G16	3438.62	11	5.844156	20	46.11688	20
G17	3465.84	8	2.742857	10	12.05714	9
G18	3048.49	17	1.333333	3	5.333333	3
G19	3759.88	2	4.842105	16	32.31579	17
G20	2759.81	20	2.098361	7	12.03279	8

The results of $s_i^{(3)}$ and $s_i^{(6)}$ indicated that the genotypes G11, G12 and G18 ranked first, second, and third respectively. According to $s_i^{(3)}$ and $s_i^{(6)}$ G11, G12 and G18 were found to be stable and adapted to all environments. But they occupied 18th, 16th and 17th position in mean yield which implies stable genotypes with low yield.

According to $s_i^{(3)}$ and $s_i^{(6)}$, genotype G16 was found to be most unstable followed by genotype G3. Hühn (1990) used three non-parametric measures $S_i^{(1)}$, $S_i^{(2)}$ and $s_i^{(3)}$ for phenotypic stability of winter wheat grain yield in Germany. He concluded that one is interested in a simultaneous consideration of both stability and yield, $s_i^{(3)}$ can be applied and used on original (Uncorrected yield) data, because correction eliminates the genotypic effects from the data. Sabaghnia et al. (2006) worked out all four non-parametric stability measures for lentil genotypes in Iran and interpreted the similar type of results. $s_i^{(3)}$ measure was used to find the stable cowpea (Vigna unguiculata L.) genotypes by Aremu et al. (2007).

The nonparametric superiority parameter of Fox et al. (1990) consists of scoring the percentage of environments in which each genotype ranked in the top, middle and bottom third of trial entries. A genotype usually found in the top third of entries across environments can be considered relatively well adapted and stable. Thus, G19 was an adapted genotype, because it ranked in the top third of genotypes in a high percentage of environments (high top value, 87.5%), and was followed by G1 (75%) (Table 4.16). The undesirable genotypes identified by this method were G10, G11, G12 and G18.

Kang‘s (1988) nonparametric stability parameter (rank-sum) uses both yield and Shukla‘s stability variance (Shukla 1972). The genotypes with the lowest rank-sum are the most favorable ones. According to the rank-sum statistic G15 had the lowest values for rank-sum and therefore were stable genotypes with high yield, followed by G1 and G17 (Table 4.16). According to the rank-sum statistic, the undesirable genotypes were G20, G12 and G16. The results of this method for stable genotypes are relatively in agreement with the TOP procedure.

Table 4.16 Genotype mean grain yield, Kang's rank-sum and TOP values with ranks for the 20 Bread wheat varieties.

	environmental_mean	Rank	stability_variance	Rank	Kang's rank-sum	Rank	TOP (%)	MID (%)	LOW (%)	rank of top
G1	3853.23	1	80379.35	10	11	2	75	25	0	2
G2	3570.28	6	278484.96	18	24	15	50	37.5	12.5	3
G3	3673.42	3	174360.32	16	19	7	50	25	25	3
G4	3593.33	4	145131.63	15	19	8	50	37.5	12.5	3
G5	3186.36	15	42930.34	2	17	6	0	62.5	37.5	16
G6	3329.14	12	62636.89	8	20	10	12.5	50	37.5	12
G7	3313.6	13	66510.5	9	22	13	12.5	75	12.5	12
G8	3513.09	7	249055.06	17	24	15	25	50	25	11
G9	3456.28	9	142510.43	14	23	14	37.5	50	12.5	8
G10	3048.72	16	40356.78	1	17	6	0	37.5	62.5	16
G11	3034.36	18	44336.55	3	21	12	0	25	75	16
G12	3030.58	19	95860.42	12	31	19	0	37.5	62.5	16
G13	3454.74	10	55594.63	5	15	3	37.5	62.5	0	8
G14	3273.31	14	55946.6	6	20	10	12.5	37.5	50	12
G15	3577.59	5	53001.7	4	9	1	50	50	0	3
G16	3438.62	11	428856.2	19	30	18	50	12.5	37.5	3
G17	3465.84	8	61688.91	7	15	3	37.5	50	12.5	8
G18	3048.49	17	86363.44	11	28	17	0	37.5	62.5	16
G19	3759.88	2	136987.86	13	15	3	87.5	0	12.5	1
G20	2759.81	20	480203.44	20	40	20	12.5	37.5	50	12

Results of Thennarasu's (1995) nonparametric stability statistics, which are calculated from ranks of adjusted yield means, are shown in Table 4.17, with the ranks of genotypes according to these parameters. According to the first method ($NP_i^{(1)}$), genotypes G15, G14 and G10 were stable in comparison with the other genotypes. The unstable genotypes based on $NP_i^{(1)}$ were G20 and G16 followed by G3. Genotype G11 had the lowest value of $NP_i^{(2)}$ and was stable, followed by G10 and G12. Because of the high values for $NP_i^{(2)}$, the stabilities of G19 followed by G16 and G3 were low, although they had the highest mean yield (Table 4.17). $NP_i^{(3)}$, like $NP_i^{(2)}$, identified G11 as the most stable genotype, although it had the lowest mean yield. The next most stable genotypes were G10 and G5 both of which had low mean yield performances. The unstable genotypes based on $NP_i^{(3)}$ were G19 followed by G1 and G3, which had the highest mean yield. Thus $NP_i^{(3)}$ had a negative relationship with yield (P < 0.01).

Stability parameter $NP_i^{(4)}$ identified G11 as a stable genotype, followed by G10 and G5; but like $NP_i^{(2)}$ and $NP_i^{(3)}$, identified G19, G1 and G3 as unstable. The results of three NPs $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$) were very similar to each other and identified G19, G1 and G3 as unstable, although they had the highest mean yield performances.

Table 4.17 Genotype mean grain yield and Thennarasu's nonparametric stability value for the bread wheat varieties.

	Mean	Rank	$NP_i^{(1)}$	Rank	$NP_i^{(2)}$	Rank	$NP_i^{(3)}$	Rank	$NP_i^{(4)}$	Rank
G1	3853.23	1	4.5	7	1.285714	19	1.081081	19	1.343629	19
G2	3570.28	6	4.5	7	0.642857	14	0.747656	15	0.946136	15
G3	3673.42	3	6	18	1	17	0.924001	18	1.191283	18
G4	3593.33	4	4.25	5	0.653846	15	0.748838	16	0.949153	16
G5	3186.36	15	4.5	7	0.346154	6	0.350856	3	0.447205	3
G6	3329.14	12	4.75	11	0.475	9	0.499483	8	0.623377	8
G7	3313.60	13	4.25	5	0.369565	7	0.431717	7	0.55914	7
G8	3513.09	7	5.75	16	0.638889	13	0.70657	14	0.90538	14
G9	3456.28	9	5.75	16	0.71875	16	0.687116	13	0.885312	13
G10	3048.72	16	3.875	3	0.242188	2	0.309303	2	0.394009	2
G11	3034.36	18	4	4	0.228571	1	0.272309	1	0.346457	1
G12	3030.58	19	4.5	7	0.257143	3	0.367445	4	0.456221	4
G13	3454.74	10	4.875	14	0.609375	12	0.659775	12	0.852679	12
G14	3273.31	14	3.625	2	0.258929	4	0.393242	6	0.474227	5
G15	3577.59	5	3.25	1	0.5	10	0.639329	11	0.79198	10
G16	3438.62	11	7.375	19	1.229167	18	0.833499	17	1.03525	17
G17	3465.84	8	4.75	11	0.527778	11	0.618095	10	0.8	11
G18	3048.49	17	4.75	11	0.306452	5	0.368179	5	0.47619	6
G19	3759.88	2	4.875	14	1.392857	20	1.133413	20	1.43609	20
G20	2759.81	20	7.375	19	0.460938	8	0.512606	9	0.639344	9

4.4 RANK CORRELATION AMONG STABILITY STATISTICS AND YIELD

The results of the Spearman‘s rank correlation coefficient among the 15 parametric and non-parametric stability statistics and mean yield are presented in Table 4.18. Mean yield performance across environments was significantly positively correlated with RS and TOP measures (P<0.05 and P<0.01 respectively), but it was not correlated with Wi, $S_i^{(1)}$, $S_i^{(2)}$ and $NP_i^{(1)}$. However, there were significant negative correlations between mean yield and $s_i^{(3)}$, $s_i^{(6)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ (P<0.01). The high correlation between mean yield and stability measures is expected as the values of these statistics were higher for high yielding genotypes. The non-significant correlation and negative significant correlation between yield and stability parameters suggest that stability parameters provide information that cannot be gleaned from average yield alone (Mekbib 2002).

Relationship among parametric and non-parametric methods

Ecovalance (W_i) was perfectly positively associated with Shukla and positively associated with s_i^2, $S_i^{(1)}$, $S_i^{(2)}$, $s_i^{(3)}$, $NP_i^{(2)}$ and $NP_i^{(3)}$ (P<0.01) and with $s_i^{(6)}$ and $NP_i^{(1)}$ (P<0.05). Environmental variance (s_i^2), is significantly correlated with $s_{d_i}^2$ (P<0.01) and with the methods of $s_i^{(3)}$ (P<0.05). Stability variance (σ_i^2) had negative and significant correlations with, $S_i^{(2)}$ and $NP_i^{(2)}$ (P<0.05). The non-parametric method of $S_i^{(1)}$ was significantly positively correlated with $S_i^{(2)}$, $s_i^{(3)}$ and $s_i^{(6)}$ (P<0.01) and with the methods of $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ (P<0.05). $S_i^{(2)}$ had positive and significant correlations with $s_i^{(3)}$, $s_i^{(6)}$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ (P<0.01) and negative and significant correlation with RS ($P<0.05$). $s_i^{(3)}$, as well as $s_i^{(6)}$ parameters were negatively correlated with TOP ($P<0.01$). TOP was negatively and significantly associated with $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ ($P<0.01$).

The most stable genotype according to the parametric methods was G11, G10, G5 and G12 while G11, G10, G5, G18 and G12 were stable according to the nonparametric methods. The most unstable genotype according to the parametric methods was G20, G16 and G2 while G3, G16, G19, G1 and G20 were unstable according to the nonparametric methods. The result shows that both the parametric and nonparametric methods gave a relatively similar result. This implied that the nonparametric stability measurements are useful alternatives to parametric measurements.

Table 4.18 Spearman‘s rank correlation coefficients between different parametric and nonparametric stability parameters for grain yield of 20 bread wheat varieties.

	Y	W_i	σ_i^2	S_i^2	ASV	$S_{d_i}^2$	$S_i^{(1)}$	$S_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	RS	TOP	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$
W_i	-0.24	1.00													
σ_i^2	-0.24	1.00**	1.00												
S_i^2	-0.58*	0.05	0.05	1.00											
ASV	-0.19	0.69**	0.69**	0.01	1.00										
$S_{d_i}^2$	-0.54*	-0.12	-0.12	0.95**	-0.1	1.00									
$S_i^{(1)}$	-0.25	0.77**	0.77**	0.17	0.52*	0.01	1.00								
$S_i^{(2)}$	-0.39	0.86**	0.86**	0.25	0.64**	0.08	0.91**	1.00							
$S_i^{(3)}$	-0.83**	0.62**	0.62**	0.46*	0.43	0.3	0.64**	0.75**	1.00						
$S_i^{(6)}$	-0.79**	0.67**	0.67**	0.41	0.48*	0.25	0.69**	0.81**	0.98**	1.00					
RS	0.56*	0.56*	0.56*	-0.42	0.38	-0.55*	0.43	0.38	-0.2	-0.13	1.00				
TOP	0.86**	-0.38	-0.38	-0.33	-0.29	-0.2	-0.33	-0.5*	-0.81**	-0.79**	0.38	1.00			
$NP_i^{(1)}$	-0.1	0.67**	0.67**	-0.06	0.39	-0.18	0.56*	0.6**	0.47*	0.53*	0.31	-0.15	1.00		
$NP_i^{(2)}$	-0.85**	0.58*	0.58*	0.38	0.46*	0.27	0.48*	0.65**	0.94**	0.93**	-0.29	-0.81**	0.53*	1.00	
$NP_i^{(3)}$	-0.86**	0.63**	0.63**	0.42	0.45*	0.31	0.52*	0.68**	0.95**	0.95**	-0.3	-0.84**	0.48*	0.98**	1.00
$NP_i^{(4)}$	-0.85**	0.64**	0.64**	0.42	0.46*	0.3	0.5*	0.66**	0.94**	0.94**	-0.26	-0.8**	0.51*	0.98**	0.99**

Critical value of the Spearman‘s rank correlation coefficients for n=20, a=0.05 is ±0.450 and for a=0.01 is ±0.591

4.5 DISCUSSION

Breeders can use stability analysis methods to identify cultivars that have predictable performance and that respond positively to improvements in environmental conditions. Currently, plant breeders have a full hand of methods for the analyses of genotype yield adaptability and stability to help in the difficult task of identifying superior cultivars in the presence of significant GEI (Eskridge, 1990). However, they frequently have difficulty in choosing the most suitable method for use in different situations. However, the choice of the best methodology depends on some factors, such as the number of genotypes and environment available, environmental variation, mathematical model fit to the data set, stability concept adopted and the facility to apply and interpret the results. Besides, some methodologies are alternative while others are complementary, being able to be used jointly (Marcus et al., 2008).

Genotype × environment interactions are important sources of variation in any crop and the term stability is sometimes used to characterize a genotype, which shows a relatively constant yield, independent of changing environmental conditions. On the basis of this idea, genotypes with a minimum variance for yield across different environments are considered stable. This idea of stability may be considered as a biological or static concept of stability (Becker and Léon, 1988). This concept of stability is not acceptable to most breeders and agronomists, who would prefer an agronomic or dynamic concept of stability; therefore they prefer genotypes with high mean yields and the potential to respond to agronomic inputs or better environmental conditions (Becker, 1981; Becker and Léon, 1988; Robert, 2002).

In the dynamic concept of stability, it is not required that the genotype response to environmental conditions should be equal for all genotypes (Becker and Léon 1988). The measure of dynamic stability depends on the specific set of tested genotypes, unlike the measure of static stability (Lin et al., 1986). Static stability may be more useful than dynamic stability in a wide range of situations especially in developing countries (Simmonds, 1991). The parameter TOP was related to the dynamic concept of stability. Additionally, Sabaghnia et al. (2006) and Mohammadi and Amri (2008) pointed out that the TOP procedure was associated with mean yield and the dynamic concept of stability, therefore these parameters could be used to recommend cultivars adapted to favorable conditions.

According to Hühn (1990a), non-parametric stability analysis procedures have the following advantages: they reduce the bias caused by outliers, no assumptions are needed about the distribution of observed values, they are easy to use and interpret and additions or deletions of one or a few genotypes do not cause much variation of results. As a result, many researchers applied different non-parametric statistics to evaluate stability (Scapim et al., 2000; Yaksel et al., 2003; Solomon et al., 2007; Mevlut and Yuksel, 2008; Kan et al., 2010; Zali et al., 2011). Huehn (1990 a, b) suggested for a cultivar with maximum stability, $S_i^{(1)}$ = $S_i^{(2)}$ = $s_i^{(3)}$. $S_i^{(1)}$ and $S_i^{(2)}$ are based on ranks of the genotypes across environments and they give equal weight to each environment. $S_i^{(1)}$ estimates are based on all possible pair-wise rank differences across environments for each genotype, whereas $S_i^{(2)}$ is based on the variance ranks for each genotype across environments (Nassar and Hühn, 1987). In this experiment, classification of genotypes based on these parameters was similar. This agrees with the earlier findings of Scapim et al. (2000), Sabaghnia et al. (2006) and Yaksel et al. (2003).

According to Hühn (1990b) $S_i^{(1)}$ and $S_i^{(2)}$ are functions only of the stability measurements whereas numerical values of $s_i^{(3)}$ and $s_i^{(6)}$ combine yield and stability based on yield ranks of genotypes in each environment. The results of this experiment showed that these parameters were significantly (P<0.05) and positively correlated with each other. Flores et al. (1998) also reported significant and positive association between $S_i^{(1)}$ and $S_i^{(2)}$. Scapim et al. (2000) also found high significant correlation among $S_i^{(1)}$, $S_i^{(2)}$ and $s_i^{(3)}$. This suggests that one of the three statistics could be used to assess stability. All of these statistics were negatively correlated with grain yield. Nassar and Hühn (1987) indicated that $S_i^{(1)}$ and $S_i^{(2)}$ are associated with the static biological concept of stability, as they define stability in the sense of homeostasis. Sabaghnia et al. (2006) also reported that $S_i^{(1)}$ and $S_i^{(2)}$ represent static concept of stability. Thus, $S_i^{(1)}$ and $S_i^{(2)}$ could be used as a compromise method that select genotypes with moderate yield and yield stability. Distinct clustering of $S_i^{(1)}$ and $S_i^{(2)}$ also confirms that these two non-parametric statistics can define stability in terms of static or biological concept and hence would have little relevance in selecting genotypes that can respond to changing environmental conditions. $s_i^{(3)}$ and $s_i^{(6)}$ were strongly correlated to Thennarasu's non-parametric statistics. Sabaghnia et al. (2006) and Solomon et al. (2007) also found similar association between $s_i^{(3)}$ with $\mathrm{NP}_\mathrm{i}^{(1)}$ and $s_i^{(6)}$ with ($\mathrm{NP}_\mathrm{i}^{(2)}$, $\mathrm{NP}_\mathrm{i}^{(3)}$ and $\mathrm{NP}_\mathrm{i}^{(4)}$ and pattern of grouping based on principal component analysis.

Thennarasu's (1995) non-parametric stability statistics uses ranks from adjusted yield. According to these procedures, stable genotypes are those whose adjusted ranks remain unaltered in relation to the other in the set of environments assessed. $\mathrm{NP}_i^{(3)}$ and $\mathrm{NP}_i^{(4)}$ express stability in units of mean ranks; therefore they are very much similar to $s_i^{(3)}$ and $s_i^{(6)}$. $s_i^{(6)}$, $\mathrm{NP}_i^{(2)}$, $\mathrm{NP}_i^{(3)}$ and $\mathrm{NP}_i^{(4)}$ were grouped in the same group and showed high correlations. These suggest that Thennarasu's non-parametric stability estimates did not add important information to those statistics obtained by Nassar and Hühn (1987). Thus, the use of Hühn (1990b) stability parameters could be a method of choice as there is a statistical procedure available to test the significance of $S_i^{(1)}$ and $S_i^{(2)}$. However, Thennarasu's (1995) non-parametric stability estimates would be important alternatives to parametric models.

In our study, the highly positive significant correlation between TOP and mean yield ($P < 0.01$) indicated that TOP was the best parameter to identify high yielding genotypes. Rank-sum (RS) is another parameter that was positively correlated with adjusted mean yield. A low value of RS indicates the combination of high yield and high stability. Considering these two parameters (TOP and RS), G19, G1 and G15 were the best genotypes. Consequently, we recommend use of TOP and RS as the best parameters to select superior genotypes. However, due to the simple calculation of TOP and the high significant positive correlation with mean yield, we consider it as the parameter of choice. To discriminate between two genotypes with the same TOP value, we then chose the one with the lowest RS.

The result shows that both the parametric and nonparametric methods gave a relatively similar result. Nonparametric stability measurements are thus useful alternatives to parametric measurements (Yue et al. 1997).

5. CONCLUSION AND RECOMMENDATION

The selection process of good performing and stable genotypes is mainly complicated by the phenomenon of genotype by environment (G×E) interaction. G×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×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×E interactions on variety evaluation, which will help to apply appropriate analytical methods and wise application of resources. It was the objective of this study to analyze genotype by environment interaction and stability of the Ethiopian wheat genotype for grain yield across four different wheat growing regions of Ethiopia for two consecutive years.

Twenty bread wheat genotypes were evaluated for grain yield in a mid altitude areas of Ethiopia, for a period of two years across four locations. The genotypes were planted in a completely randomized block design.

A significant genotype environment interaction were detected by the methods of Hildebrand, Kubinger and combined analysis of variance, also from this analysis the effects environment and genotype were highly significant. From the result it was concluded that the major factor that influence yield performance of bread wheat in Ethiopia is the environment. In particular, the GEI was highly significant implying the need for investigating the nature of differential response of the genotypes to environments. No cross-over interactions were detected by the de Kroon/van der Laan procedure and no noncrossover interactions were detected by the Bredenkamp procedure.

Among the restricted maximum likelihood (REML) estimates of variance components, the estimated variance component due to environment made the greater contribution to the total estimated variance for grain yield. All of the variance components were highly significant, and the importance of the $\hat{\sigma}^2_{G\times E}$ component indicates that factors such as rainfall, temperature, and disease incidence can result in conditions unique to each year-location combination and that the genotypes respond differently to these conditions.

The AMMI model provides a useful technique in diagnosing genotype × environment interaction patterns. It enables clustering of genotypes based on similarity of response characteristics and identifying potential trends across environments. The number of PCA axes retained for most applications is usually s≤3, which is intended to reduce the dimension of the system and provide a more parsimonious description of the underlying interaction structure. The AMMI model provides easily interpretable information as well as the correlation between a genotype and environment.

The analysis of variance for the AMMI model indicated highly significance differences between genotypes and environments as main effects and the interaction effect of G×E was also highly significant. The first three interaction principal component axes (IPCA) of the AMMI model together accounted for 74.4% of the G×E interaction sum of squares for grain yield. The first three IPCA axes were highly significant and hence, the AMMI-3 model was used as the best fit for the bread wheat data.

The following major findings emerged for the multi-environment yield trial data set analyzed here.

- Significant variation existed for environment, genotype and genotype × environment interaction.
- According to Nassar and Huehn nonparametric procedure $S_i^{(1)}$ and $S_i^{(2)}$ there were significant differences in rank stability for grain yield among 20 wheat genotype grown in 4 locations during 2007-2008.
- Genotype G11, G10, G5 and G12 were stable in comparison with the other genotypes and genotypes G16, G3, G20 & G1 were unstable according to the parametric methods.
- The most stable genotype according to the nonparametric methods was G11, G10, G5, G18 and G12. While G3, G16, G19, G1 and G20 were unstable genotypes.
- According to the biplot, Adet was generally categorized under high yielding wheat environment as compared to the three relatively categorized under low yielding environments (Holeta, Kulumsa and Sinana). It is further noted that E1 (Adet 2007) was the most favorable season and E6 (Holeta 2008) was less favorable among the eight environments.
- The different stability measurements (parametric and non-parametric) used in this study demonstrated association and dissociation (no association) among them in ranking of the genotypes based on stability.
- Mean yield performance across environments was significantly positively correlated with RS and TOP measures. Due to highly positive significant

correlation between TOP and mean yield, TOP was the best parameter to identify high yielding genotypes.

- There was perfect correlation between Wricke‘s and Shukla indicates that the two procedures are equivalent for ranking purposes. Also Wricke‘s procedure of stability statistic indicated significant positive correlation with all Thennarasu‘s and Nassar and Hühn‘s (1987) nonparametric stability statistics.
- From the result it was concluded that nonparametric stability measurements was useful alternatives to parametric measurements.

RECOMMENDATION

- From this study we recommend use of TOP procedure as the best parameters to select superior genotypes.
- This study recommends genotypes G19, G1 and G15 as superior genotypes in favorable environment conditions.

REFERENCE

ABOU-EL-FITTOUH, H.A., Rawlings, J.O. & Miller, P.A. (1969): Classification of environments to control genotype by environment interactions with an application to cotton. Crop Sci. 9, 135–140.

ADUGNA,W., and Labuschagne M.T. (2003). Parametric and nonparametric measures of phenotypic stability in linseed (Linum usitatissimum L.). Euphytica 129: 211-218.

AKÇURA, M., Y. Kaya and S. Taner (2009). Evaluation of durum wheat genotypes using parametric and non parametric stability statistics. Turkish J. of Field Crops 14(2):111-122.

ALLARD, R.W. and Bradshaw, A.D., (1964). Implications of genotype-environment interactions in applied plant breeding. Crop science 4:503-508.

AREMU, C. O., Ariyo, O. J. and Adewale, B. D. (2007). Assessment of selection techniques in genotype × environment interaction in cowpea (Vigna unguiculata L. Walp). African Journal of Agricultural Researh 2(8):352-355.

BAKER RJ (1990). Crossover genotype–environmental interaction in spring wheat. In: Kang MS (ed) Genotype-by-environment interaction and plant breeding. Department Of Agronomy, Louisiana Agric Exp Stn, Baton Rouge, LA, USA, pp 42–51

BARIL, C.P., Denis, J.B., Wustman, R. and Van Eeuwijk, F.A., (1995). Analyzing genotype-byenvironment interaction in Dutch potato variety trials using factorial regression. Euphytica 82: 149-155.

BASFORD, K.E. and Cooper, M., (1998). Genotype × environment interactions and some considerations of their implications for wheat breeding in Australia. Australian Journal of Agricultural Research 49: 154-174.

BECKER, H. C. (1981). Correlations among some statistical measures of phenotypic stability. Euphytica 30, 835–840.

BECKER, H.C. and Léon, J. (1988). Stability analysis in plant breeding. Plant Breed. 101: 123.

BOGALE G., Van Rensburg J.B.J. and Van Deventer C.S. (2008). AMMI Analysis of Genotype x Environment Interaction for Grain Yield in Drought-Tolerant Maize (Zea mays L.). East African Journal of Sciences. 2 (1): 1-6

BONDARI K. Statistical Analysis of Genotype X Environment Interaction in Agricultural Research. Experimental Statistics, Coastal Plain Station, University of Georgia, Tifton, GA 31793-0748

BOWMAN, D.T. and C.E. Watson. (1997). Measures of validity in cultivar performance trials. Agron. J., 89: 860-866.

BREDENKAMP, J. (1974). Nonparametrische Pru¨ fung von Wechselwirkungen. Psychologische Beitra¨ge 16, 398–416.

CECCARELLI, S. (1989). Wide adaptation. How wide? Euphytica 40, 197–205.

CHAHAL, G.S. and Gosal, S.S., (2002). Principles and procedures of plant breeding: Biotechnological and conventional approaches. Narosa publishing House. New Delhi, India.

COCHRAN, W.G. (1947). Some consequences when the assumptions for the analysis of variance are not satisfied. Biometrics, 4: 22-38.

COMSTOCK, R.E and Moll, R.H., (1963). Genotype –environment interactions. In: statistical Genetics and plant Breeding. NAS-NRC.pp.164-196.

CORNELIUS, P.L., M.S. Seyedsadr J.Crossa (1992): Using the shifted multiplicative model to search for "separability" in crop cultivar trials. Theoretical Applied Genetics 84: 161–172.

COX, D.R. (1984). Interaction. Int.Statist.Rev. 52: 1-31.

CROSSA, J. (1990). Statistical analysis of multilocation trials. Adv. Agron. 44: 55-85.

CROSSA,J,, Gauch, H.G and Zobel, R.W., (1990). Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. Crop science 30:493-500.

CRUZ, R.M., (1992). More about the multiplicative model for the analysis of genotype-environment interaction. Heredity 68: 135-140.

CSA, (2012). Central Statistical Agency. Addis Ababa, Ethiopia.

DABHOLKAR, A.R., (1999). Elements of biometrical genetics. Concept Publishing Company. New Delhi, India.

DE KROON, J. and P. van der Laan. (1981). Distribution-free test procedures in two-way layouts: a concept of rank-interaction. Stat Neeri, 35:189-213.

DELACY, I.H., Cooper, M. and Basford, K.E., (1996). Relationships among analytical methods used to study genotype-by-environment interactions and evaluation of their impact on response to selection. In: Kang, M.S. and Gauch, Jr. H.G. (eds.). Genotype-by- Environment Interaction, CRC press: Boca Raton, New York. pp. 51-84.

DENIS, J.-B., and Gower, J. C. (1996). Asymptotic confidence regions for biadditive models: Interpreting genotype-environment interactions. Appl. Statist. 45, 479-493.

EBERHART, S.A. and W.A. Russell (1966): Stability parameters for comparing varieties. Crop Sci., 6: 36–40.

EDMEADES, G.O., Bolanos, J., Lafitte, H.R, Rajaram, S., Pfeiffer, W.H. and Fisher, R.A., (1989). Traditional approaches to breeding for drought resistance in cereals. In: Baker, F.W.G. (ed.). Drought resistance in cereals. ICSU press. CAB International. Mallingford. pp. 27- 52.

EISENHART, C. (1947). The assumptions underlying the analysis of variance. Biometrics, 3: 1-21.

ESKRIDGE KM (1990) Selection of stable cultivars using a safety-first rule. Crop Sci 30: 369-374

FALCONER, D.S. (1952). The problem of environment and selection. Am. Nat. 86:293-298.

FALCONER, D.S. and Mackay, T.F.C. (1996). Introduction to quantitative genetics. 4th edition, Longman, New York, P.132-133.

FEHR, W.R., (1991). Principles of cultivar development theory and technique. IOWA State University, USA. pp. 247-260.

FINLAY, K.W. and G.N. Wilkinson. (1963). The analysis of adaptation on a plant breeding programme. Aust. J. Agric. Res., 14:742-754.

FLORES, F., M.T. Moreno and J.I. Cubero. (1998). A comparison of univariate and multivariate method to analyze environments. Field Crops Res., 56: 271-286

FOX PN, Skovmand B, Thompson BK, Braun HJ, Cormier R (1990) Yield and adaptation of hexaploid spring triticale. Euphytica 47: 57-64

FRANCIS, T.R., and L.W.Kannenberg. (1978). Yield stability studies in short-season maize. I. Adescriptive method for grouping genotypes. Canadian Journal of Plant Science 58: 1029-1034.

FREEMAN, G.H., and J.M. Perkins. (1971). Environmental and genotype-environmental components of variability. VIII. Relations between genotypes grown in different environments and measures of these environments. Heredity 27:15–23.

FREEMAN, G.H. & Dowker, B.D. (1973): The analysis of variation between and within genotypes and environments. Heredity 30, 97–109.

FREEMAN, G.H., (1973). Statistical methods for the analysis of genotype by environment interactions. Heredity 31:339-354.

FREEMAN, G. H., (1985): The analysis and interpretation of interactions. J. Appl. Statist. 12, 3Ð10.

FREEMAN, G. H., (1990): Modern statistical methods for analyzing genotype × environment interactions. In: M. S. Kang (ed.), Genotype_Environment Interaction and Plant Breeding, pp. 118-125. Louisiana State University Agricultural Center, Baton Rouge, LA.

GABRIEL, K.R. 1978. The biplot graphic display of matrices with application to principal component analysis. Biometrika 58:453–467.

GAUCH, H.G. Jr. (1988). Model selection and validation for yield trials with interaction. Biometrics 44:705–715.

GAUCH, H.G. 1992. Statistical Analysis of Regional Yield Trials: AMMI Analysis of Factorial Designs. Elsevier, Amsterdam, The Netherlands.

GAUCH HG, Zobel RW (1996) AMMI analysis of yield trials. In: Kang MS, Gauch HG(eds) Genotype by environment interaction. CRC Press. Boca Raton, FL.

GAUCH, H.G. and Zobel, R.W., (1997). Identifying mega-environments and targeting genotypes. Crop Science 37(2): 311-326.

GREGORIUS, H.R., and G. Namkoong. (1986). Joint analysis of genotypic and environmental effects. Theoretical and Applied Genetics 72:413–422.

HALDANE, J.B.S. (1946). The interaction of nature and nurture. Ann. Eugenics. 13:197-205.

HARDWICK, R.C, and J.T, Wood. (1972). Regression methods for studying genotype-environment interactions. Heredity 28:209–222.

HILDEBRAND, H., (1980). Asymptotosch Verteilungsfreie Rangtests in linearen Modellen. Med. Inform. Stak. 17: 344-349.

HILL, J. (1975). Genotype-environment interactions - a challenge for plant breeding. Journal of Agricultural Science 85: 477-493.

HILL J, Becker HC, Tigerstedt PMA (1998). Quantitative and ecological aspects of plant breeding. Chapman and Hall, London.

HINTSA, G., Abraha H. and Tesfay B. (2011): Genotype by environment interaction and grain yield stability of early maturing bread wheat (Triticum aestivum L.) genotypes in the drought prone areas of Tigray region, northern Ethiopia. Ethiop. J. Appl. Sci. Technol. 2(1): 51 - 57

HOHLS, T., (1995). Analysis of genotype-environment interactions. S. Afr. J. Sci. 91: 121-124.

HOLLANDER, M. and D.A. Wolfe. (1999). Nonparametric Statistical Methods. 2nd. ed J. Wiley, New York.

HÜHN M., (1979): Beiträge zur Erfassung der phänotypischen Stabilität. I. Vorschlag einiger auf Ranginformationen beruhenden Stabilitätsparameter. EDV in Medizin und Biologie 10: 112-117.

HÜHN, M. & NASSAR, R. (1989): On tests of significance for nonparametric measures of phenotypic stability. Biometrics 45: 997-1000.

HÜHN, M. (1990): Nonparametric estimation and testing of genotype × environment interaction by ranks. In: M.S. Kang (eds.) Genotype-by-Environment Interaction and Plant Breeding.

HÜHN, M., (1990a). Non-parametric measures of phenotypic stability. Part I: Theory. Euphytica 47:189-194.

HÜHN, M., (1990b). Non-parametric measures of phenotypic stability: Part II. Applications. Euphytica 47: 195-201.

HÜHN, M., and R.Nassar. (1991). Phenotypic stability of genotypes over environments: On tests of significance for two nonparametric measures. Biometrics 47: 1196-1197.

HÜHN M., J. LÉON, (1995). Nonparametric analaysis of cultivar performance trials: experimental results and comparison of different procedures based on ranks. Agron. J. 87: 627-632.

HÜHN, M. (1996): Nonparametric analysis of genotype_ environment interactions by ranks. In: Louisiana State University Agricultural Center. USA. p. 69-93.

HUSSEIN, M.A., A. Bjornstad and A.H. Aastveit. (2000). SASG X ESTAB: A SAS program for computing genotype X environment stability statistics. Agron. J., 92: 454-459.

JAVED, H.I., M.A. Masood, S.R. Chughtai, H.N. Malik, M. Hussain and A. Saleem. (2006). Performance of maize genotypes on the basis of stability Analysis in Pakistan. Asian J. Plant Sci., 5: 207-210.

KANG, M.S. (1988). A rank-sum method for selecting high-yielding, stable corn genotypes. Cereal Res. Commun. 16:113–115.

KANG, M.S., (1990). Genotype-by-environment interaction and plant breeding. Louisiana State University, Baton Rouge, LA, USA.

KANG, M.S., (1996). Using genotype by environment interaction for crop cultivar development. Advances in Agronomy 62: 199-252.

KANG, M. S., and H. G. Gauch, Jr(eds), (1996): Genotype-by-Environment Interaction. CRC Press, Boca Raton, LA.

KANG, M.S. (1998). Using genotype-by environment interaction for crop cultivar development. Adv. Agron., 62: 199-253.

KANG, M.S. (2002). Quantitative genetics, genomics, and plant breeding. CABI Publishing. p. 222

KAYA Y, Taner S (2002). Estimating genotypes ranks by nonparametric stability analysis in bread wheat (Triticum aestivum L.). J Cent Europ Agric 4:47-53.

KAYA, Y., Akcura, M., Taner, S., (2006). GGE –biplot analysis of multi environment yield trials in bread wheat. Turk.J.Agric.For. 30:325-337.

KEMELEW, M. and Alemayehu A. (2011): Genotypes × environment interaction in bread wheat (Triticum aestivum L.) cultivar development in Ethiopia. International Research Journal of Plant Science Vol. 2(10) pp. 317-322

KETATA, H., S.K. Yau and M. Nachit. (1989). Relative consistency performance across environments. International symposium on physiology and breeding of winter cereals for stressed Mediterranean environments. Montpellier, pp. 391-400.

KHAN, I.A., B.A. Malik and M. Bashir. (1988). Investigation of genotype × environment interaction for seed yield in chickpea (Cicer arietinum L.). Pak. J. Bot., 20: 201-204.

KILIÇ, H. (2012): Assessment of parametric and non-parametric methods for selecting stable and adapted spring bread wheat genotypes in multi – environments. J. Anim. Plant Sci. 22(2).

KUBINGER, K.D. (1986). A note on non-parametric tests for the interaction on two-way layouts. Biometrical J. 28: 67-72.

LETTA, T., (2007). Genotype by environment interactions and correlation among some stability parameters of yield in durum wheat (Triticum, durum Desf) genotypes grown in south east Ethiopia. African crop science conference. vol 8. pp. 693-698.

LIN, C.S., M.R. Binns and L.P. Lefkovitch. (1986). Stability analysis: where do we stand? Crop Sci., 26: 894-900.

LIN, C.S. and Binns, M.R. (1988). A superiority measure of genotype performance for genotype x location data. Can. J. Plant Sci. 68: 193198.

LIN, C.S. and M.R. Binns. (1994). Concepts & Methods for Analyzing Regional Trial Data for Cultivar & Location selection. In: Jules J. Plant Breed. Review, 12: 271-297.

MAGARI, R., (1989). Stability of some Albanian maize local varieties and hybrids (in Albania). Bull Agric. Sci. 4:123-129.

MAGARI, R. and Kang, M.S., (1993). Genotype selection via a new yield-stability statistics in maize yield trials. Euphytica 70:105-111.

MARCUS V K, Pedro Soares V F, Carlos Alberto S, Maria CGV, Edvaldo S, Manoel GP, Mevlut A, Yuksel K (2008) Nonparametric stability methods for interpreting genotype by environment interaction of bread wheat genotypes (Triticum aestivum L.). Genet and Mol Biol 31: 906-913

MATHER, K. and J.L.Jinks. (1982). Biometrical Genetics /The study of continuous variation. Chapman and Hall, London, New York, 396pp.

MEKBIB, F. (2002). Simultaneous selection for high yield and stability in common bean (Phaseolus vulgaris L.) genotypes. The Journal of Agricultural Science, Cambridge 138, 249–253.

MEVLUT A. and Yuksel K. (2008). Nonparametric stability methods for interpreting genotype by environment interaction of bread wheat genotypes. Genetics and Molecular Biology, 31, 4, 906-913

MIZAN T., Sentayehu A., and Mandefro N. (2012): Environment Interaction of Bread Wheat (Triticum aestivum) Genotypes in Northern Ethiopia. Book of abstracts of wheat for food security in Africa. p-48

MOHAMMADI, R. and A. Amri. (2008). Comparison of parametric and nonparametric methods for selecting stable and adapted durum wheat genotypes in variable environments. Euphytica, 159: 419-432.

MOHAMMED A., Tesfaye L., Ayalneh T., Mulusew F., Amare B., and Tilahun B.(2012): Yield Performance and stability analyses of durum wheat genotypes under southeastern Ethiopian conditions. Book of abstracts of wheat for food security in Africa. P-17

MOSISA, W. and Z. Habtamu. 2008. Genotype × environment interaction and yield stability of maize. East African Journal of Sciences 2(1) 7–12.

MUKAI, T. (1988). Genotype by environment interaction in relation to the maintenance of genetic variability in populations of Drosophila melanogaste proceedings of the 2nd International conference on quantitative Genetics (Editors:B.S.Weir, E.J.Eisen, M.M.Goodman, and G.Namkoong): 21-31.

MUNGOMERY, V.E., Shorter, R., and E. Byth. (1974). Genotype × environment interactions and environmental adaptation.I. Pattern analysis-applications to soybean population. Australia Journal Agriculture. Res. 25: 59-72.

MUT, Z., N. Aydın, H. O. Bayramoğlu and H. Özcan (2009). Interpreting genotype × environment interaction in bread wheat (Triticum aestivum L.) genotypes using non-parametric measures. Turk J Agric., 33: 127-137.

NASSAR, R. & HUHN, M . (1987): Studies on estimation of phenotypic stability: Tests of significance for nonparametric measures of phenotypic stability. Biornetrics 43: 45-53.

PERKINS, J.M. & Jinks, J.L. (1971): Analysis of genotype × Environment interaction in triple test cross data. Heredity 26, 203–209.

PETERSON, C.J., & Pfeiffer, W.H. (1989): International winter wheat evaluation: relationships among test sites based on cultivar performance. Crop Sci. 29, 276–282.

PIEPHO, H.P. and S. Lotito, (1992). Rank correlation among parametric and nonparametric measures of phenotypic stability. Euphytica. 64: 221-225.

POLIGNANO G.B., Uggenti P. & Perrino P. (1989): Pattern analysis and genotypic × environmental interactions in faba bean (Vicia faba L.) populations. Euphytica 40, 31–41.

PURCHASE, J. (1997). Parametric analysis to describe genotype × environment interaction and yield stability in winter wheat. PhD thesis, University of the Free State: South Africa.

REZA M., Abdolvahab A., Reza H. and Mohammad A. (2007): Interpreting genotype × environment interactions for durum wheat grain yields using nonparametric methods. Euphytica 157:239–251

ROBERT N (2002) Comparison of stability statistics for yield and quality traits in bread wheat. Euphytica 128: 333–341

SABAGHNIA, N., H. Dehghani and S.H. Sabaghpour. (2006). Nonparametric methods for interpreting genotype × environment interaction of lentil genotypes. Crop Sci., 46: 1100-1106.

SCAPIM CA, Oliveira VR, Bracinill AL, Cruz CD, Andrade CAB, Vidigal MCG (2000). Yield stability in maize (Zea mays L.) and correlations among the parameters of the Eberhart and Russell, Lin and Binns and Huehn methods. Genet. Mol. Biol. 23: 387-393.

SHUKLA, G.K. (1972). Some statistical aspects of partitioning genotype environmental components of variability. Heredity 29:237–245.

SIAL, M.A., M.A. Arain and M. Ahmad (2000). Genotype × environment interaction on bread wheat grown over multiple sites and years in Pakistan. Pak. J. Bot., 32: 85-91.

SIMMONDS, N.W. (1991). Selection for local adaptation in a plant breeding programme. Theor. Appl. Genet. 82: 363-367.

SINGH, M., Ceccarelli, S. & Grando, S. (1999). Genotype × environment interaction of cross-over type: detecting its presence and estimating the crossover point. Theoretical and Applied Genetics, 99: 988‐995.

SKRØPPA, T. (1984). A critical evaluation of methods available to estimate the genotype × environment interaction. Studia Forestalia Suecica 166: 3-14.

SOLOMON, A. Mandefero, N. and Habtamu, Z. 2008. Genotype – environment interaction and stability analysis for grain yield of maize (Zea mays L,.) in Ethiopia. Asian Journal of Plant Science 7: 163–169.

SOLOMON KF, Smith HA, Malan E, DuToit WJ (2007) Comparison study using rank based non-parametric stability statistics of durum wheat. WJAS 3: 444-450

STEEL RGD, Torrie JH (1980) Principles and procedures of statistics, a Biometrical Approach. 2nd edition. McGraw-Hill, New York, 633 pp

SUZUKI, D., Griffiths, A. and Lewontin, R., (1981). An introduction to genetic analysis. W.H. Freeman and Company. San Francisco, USA.

THENNARASU K (1995). On certain non-parametric procedures for studying genotype-environment interactions and yield stability. Ph.D. Thesis. P. J. School, IARI, New Delhi

TRUBERG B., M. HÜHN, (2000) Contributions to the analysis of genotype × environments interactions: Comparison of different parametric and non-parametric tests for interactions with emphasis on crossover interaction. J. Agron. Crop Sci. 185: 267-274.

TSIGE, G.K., (2002). Genetic diversity analysis and genotype × environment interaction in Ethiopian Mustard. Ph.D. Thesis, Department of Plant Sciences / Plant Breeding, Faculty of Natural and Agricultural Sciences. University of the Free State, Bloemfontein, South Africa.

VAN EEUWIJK, F.A., (1995). Multiplicative interaction in generalised linear models. Biometrics 51: 1017-1032.

VAN EEUWIJK, F. A., Denis, J.-B., and Kang, M. S . (1996). Incorporating additional information ongenotypes and environments in models for two-way genotype by environment tables. In ―Genotypeby- environment interaction" (M. S. Kang and H. G. Gauch, Jr., eds.), pp. 1549. CRC Press, Boca Raton, FL.

VARGAS, W., Crossa, J., Van Eeuwijk, F.A., Ramirez, M.E. and Sayre, K., (1998). Using partial least square regression, factorial regression and AMMI models for interpreting genotypeby environment interaction. Crop Science 39: 955-967.

VIA, S. (1984). The quantitative genetics of polyphagy in an insect herbivore. I. Genotype-environment interaction in larval performance on different host plant species. Evolution 38,881-895.

WESTCOTT, B. (1986). Some methods of analyzing genotype × environment interaction. Heredity 56: 243-253.

WRICKE, G. (1962). Über eine Methode zur Erfassung der ökologischen Streubreite in Feldversuchen. Z. Pflanzenzücht. 47:92–96.

WRICKE, G., (1964). Zur berechnung der ökovalenz bei sommerweizen und hafer. Z. Pflanzenzüchtg. 52: 127-138.

WRICKE, G. and Weber, W.E., (1980). Erweiterte analyse von wechselwirkungen in versuchsserien. In: Biometrie-heute and morgen. kopcke and uberla.(eds.). Springervelag, Berlin.

WRIGHT, A.J., (1971). The analysis and prediction of some two factor interactions in grass breeding J. Agric. Sci. 76: 301-306.

WU, R.L. and D.M. OiMalley. (1998). Non linear genotypic response to macro and micro- environments. Theoretical and applied genetics 96:669-687.

YAKSEL K, Seyfi T, Sait C (2003) Nonparametric stability analysis of yield performances in Oat (Avena sativa L.) genotypes across environments. AJPS 2: 286-289

YAN, W., Hunt, L.A., Sheng, Q. & Szlavnics, Z. (2000): Cultivar evaluation and megaenvironment investigation based on the GGE biplot. Crop Sci. 40, 597–605.

YATES, F. and W.G. COCHRAN (1938): The analysis of groups of experiments. J. Agric. Sci. 28: 556–580.

YAU, S.K. (1995). Regression and AMMI analyses of genotype × environment interactions: An empirical comparison. Agronomy Journal 87:121-126.

YUE GL, Roozeboom KL, Schapaugh WT Jr, Liang GH (1997). Evaluation of soybean cultivars using parametric and non-parametric stability estimates. Plant Breeding 116: 271-275.

ZALI H, Farshadfar E, Sabaghpour SH (2011) Non-parametric analysis of phenotypic Stability in chickpea (Cicer arietinum L.) genotypes in Iran. Crop Breed 1: 89-100

ZAVALA-GARCIA, F., P.J. Bramel-Cox, and J.D. Eastin. (1992). Potential gain from selection for yield stability in two grain sorghum populations. Theoretical and Applied Genetics 85:112-119.

ZERIHUN T., Firdissa E., Fekadu F., Kebede T., Mathewos A., Mohamed A., Mizan T., Muluken B., Yosef G/H., Alemayehu A., and Birhanu B. (2012): Exploiting yield potential of Ethiopian commercial bread wheat (Triticum aestivum L.) varieties outside their original recommended domains. Book of abstracts of wheat for food security in Africa. P-47

ZOBEL RW, Wright MJ, Gauch HG (1988) Statistical analysis of a yield trial. Agron J. 80: 388-393.

ZUBAIR, M. and Ghafoor, A. (2001). Genotype × Environment interaction in mung bean. Pak. J. Bot. 33(2): 187-190.

APPENDIX

Table A.1 Individual (separate) analyses of variance (RCB design) for a trial with 20 genotypes and four replications, by environment**.**

Environment	Sources of variation	Degree of freedom	Sum of squares	Mean squares
1.	Replication	3	911451.90	303817.30
	Genotype	19	23447395.23	1234073.43
	Error	57	27698801.25	485943.88
2.	Replication	3	1872851.38	624283.79
	Genotype	19	10888312.31	573069.07
	Error	57	12378698.93	217170.16
3.	Replication	3	147301.334	49100.445
	Genotype	19	5131004.336	270052.860
	Error	57	7617262.98	133636.19
4.	Replication	3	2960607.67	986869.22
	Genotype	19	20594592.71	1083925.93
	Error	57	32769124.21	574896.92
5.	Replication	3	4317283.39	1439094.46
	Genotype	19	19868804.89	1045726.57
	Error	57	7027841.01	123295.46
6.	Replication	3	2227983.262	742661.087
	Genotype	19	7686009.276	404526.804
	Error	57	11235935.45	197121.67
7.	Replication	3	935675.59	311891.86
	Genotype	19	20295738.81	1068196.78
	Error	57	28626828.93	502225.07
8.	Replication	3	776750.05	258916.68
	Genotype	19	13191792.03	694304.84
	Error	57	20910287.38	366847.15

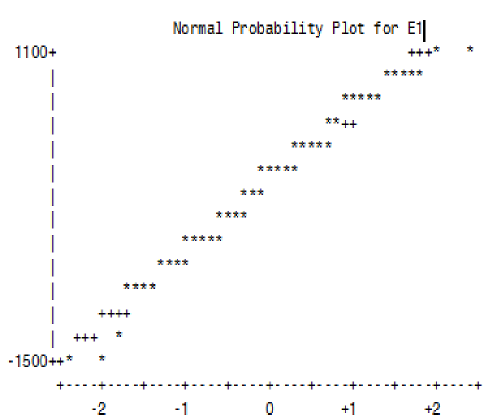
Table A.2: Bartlett's test for homogeneity of residual variance using genotype as a group in each of the separate ANOVA.

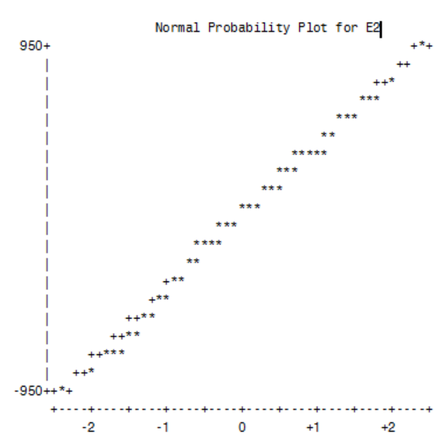
Environment	Source	DF	Chi-Square	Pr > Chi-Square
1.	Genotype	19	14.1906	0.7725
2.	Genotype	19	12.7759	0.8498
3.	Genotype	19	20.7092	0.3531
4.	Genotype	19	25.1756	0.1548
5.	Genotype	19	17.8538	0.5322
6.	Genotype	19	17.3993	0.5628
7.	Genotype	19	18.5856	0.4837
8.	Genotype	19	23.3652	0.2216

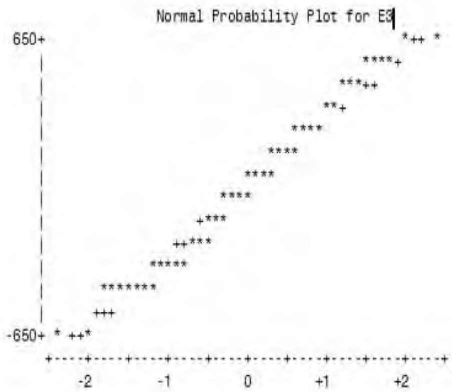
Table A.3: Test for Normality of residuals in each of the separate ANOVA model using the Shapiro-Wilk (W) statistic**.**

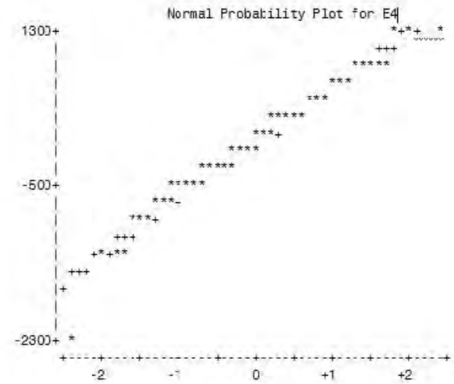
Environment	Value of W	P-value=Pr<W
E1	0.984037	0.4207
E2	0.988484	0.6968
E3	0.98672	0.5804
E4	0.980998	0.2803
E5	0.987432	0.6269
E6	0.983928	0.4148
E7	0.993185	0.9520
E8	0.987091	0.6045

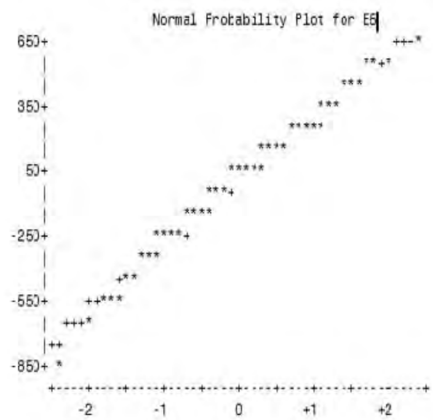
Figure A.1: Normal probability plot of residuals for each environment from the separate ANOVA.

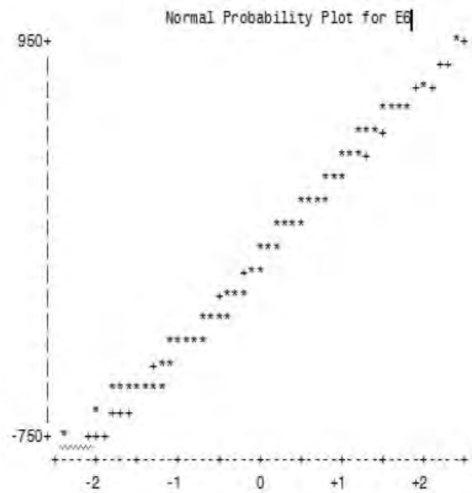


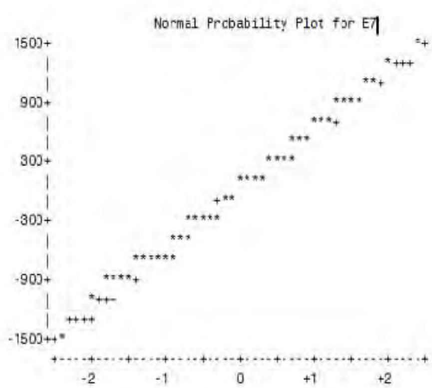



Normal Probability Plot for E3
650+
-650+
-2
-1
0
+1
+2


Normal Probability Plot for E4
1300+
-500+
-2300+
-2
-1
0
+1
+2


Normal Probability Plot for E5
650+
350+
50+
-250+
-550+
-850+
-2
-1
0
+1
+2


Normal Probability Plot for E6
950+
-750+
-2
-1
0
+1
+2


Normal Probability Plot for E7
1500+
900+
300+
-300+
-900+
-1500+
-2
-1
0
+1
+2

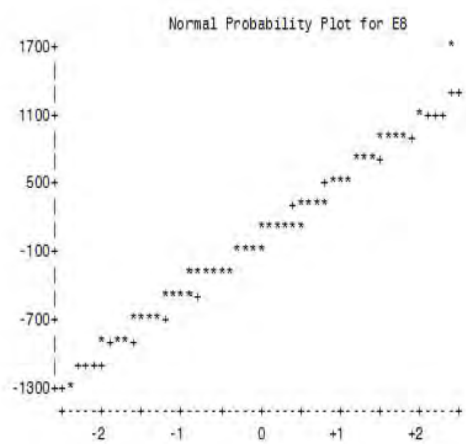
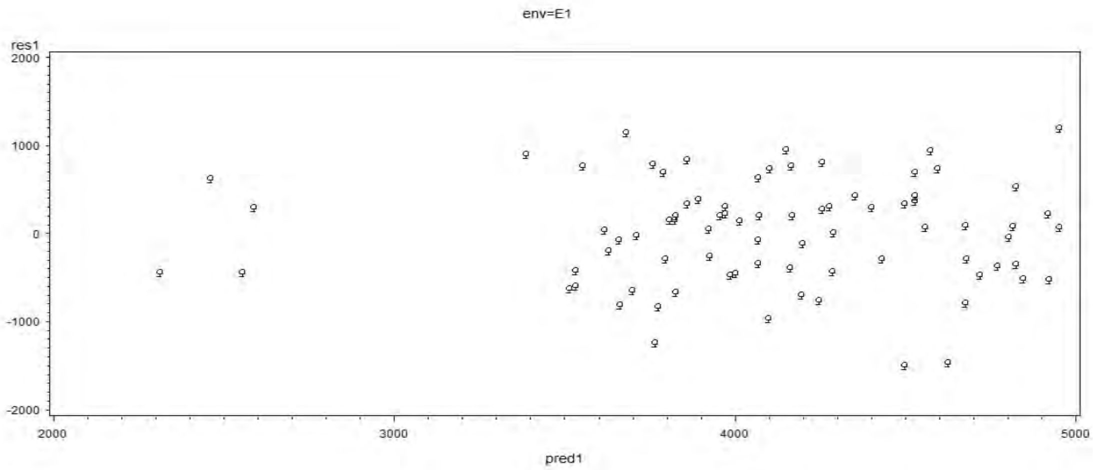
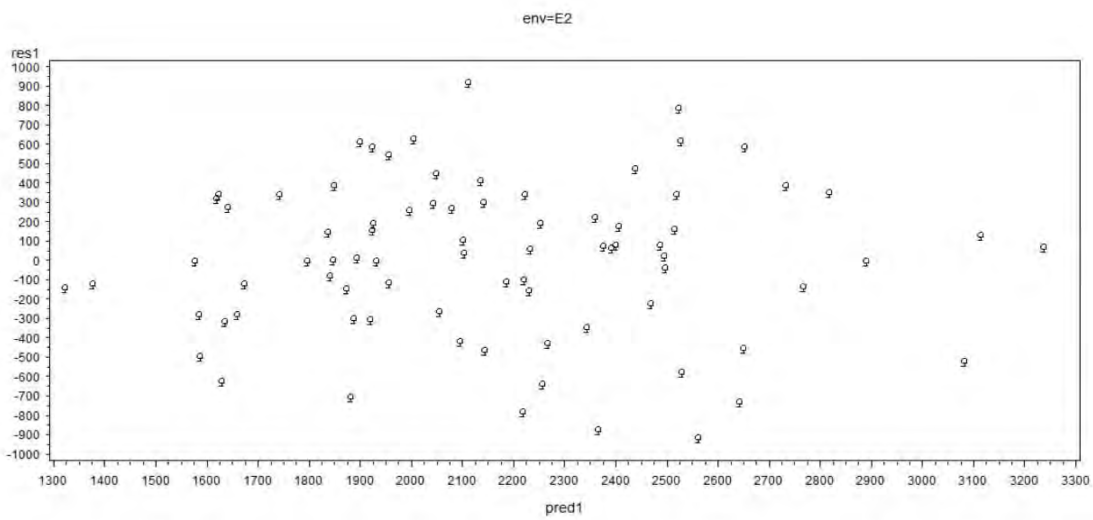
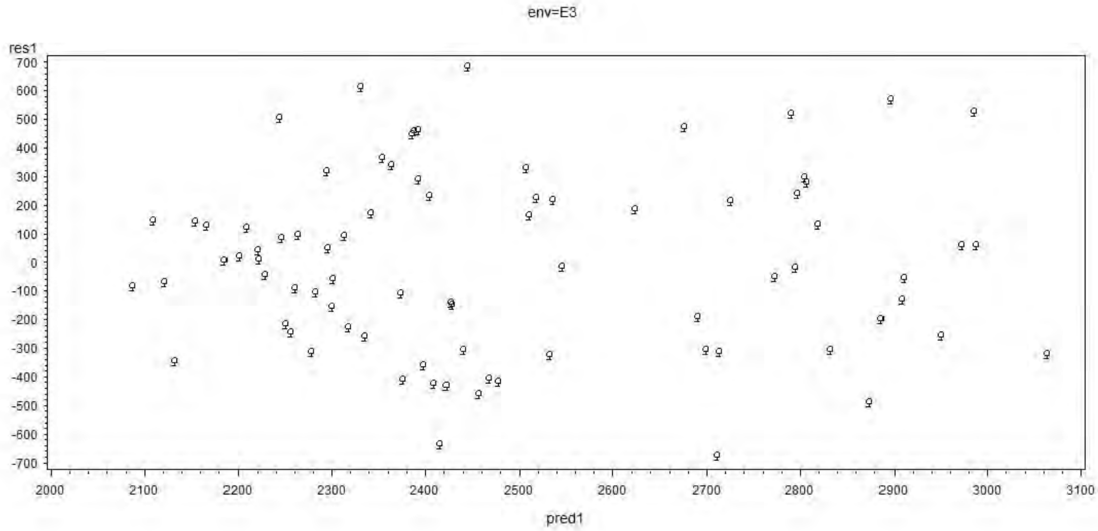
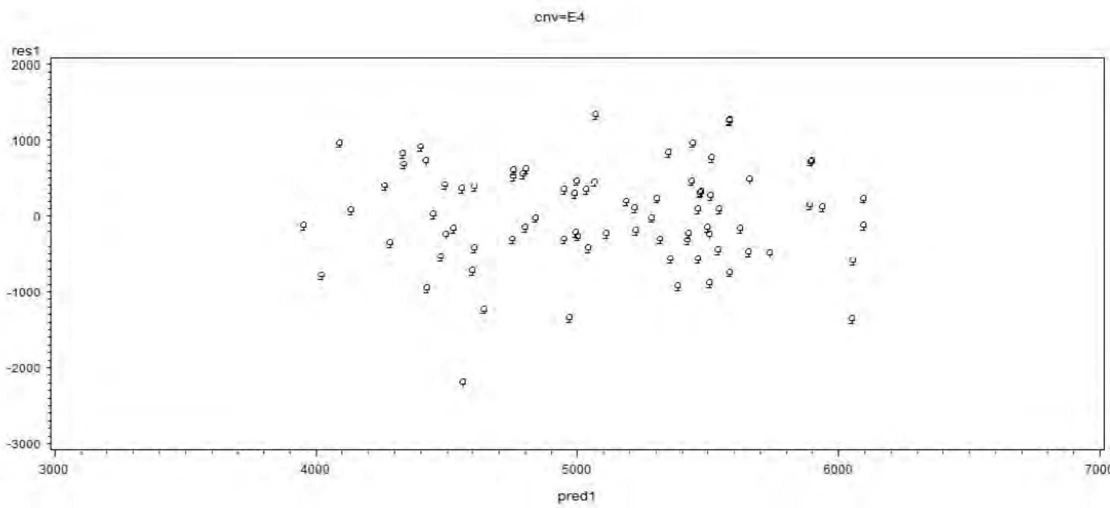

Normal Probability Plot for E8
1700+
1100+
500+
-100+
-700+
-1300+
-2
-1
0
+1
+2

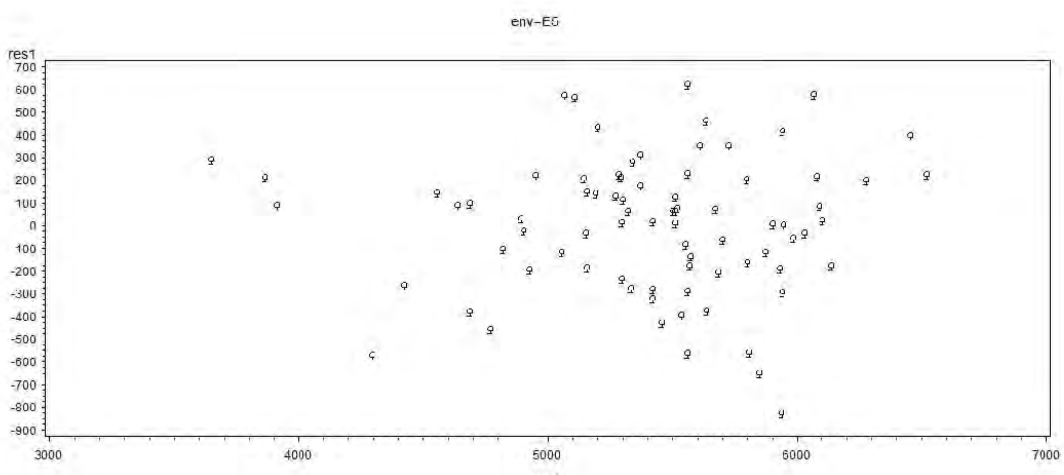
Figure A.2: Plot of residuals against the predicted value in each of the separate ANOVA model.

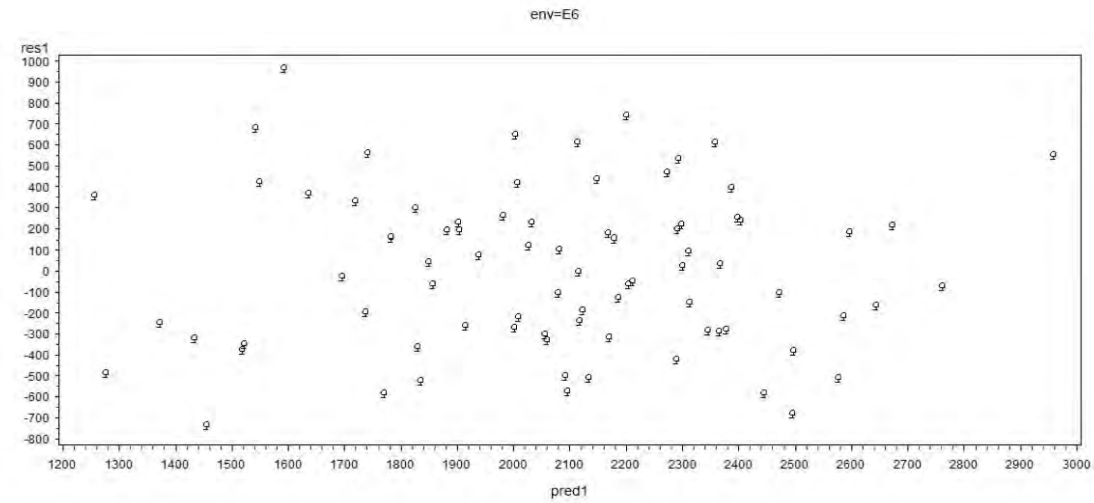


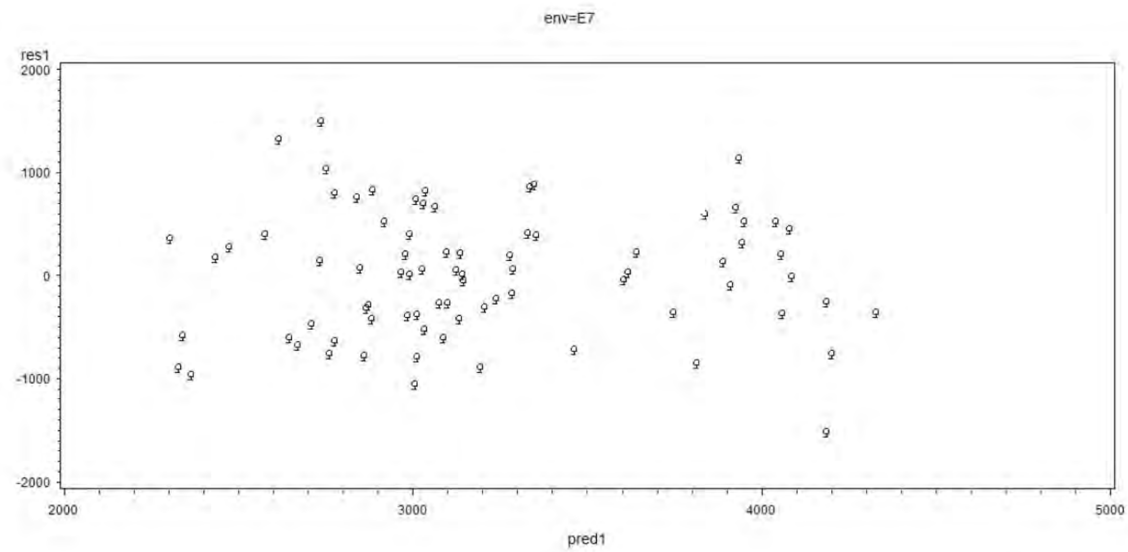


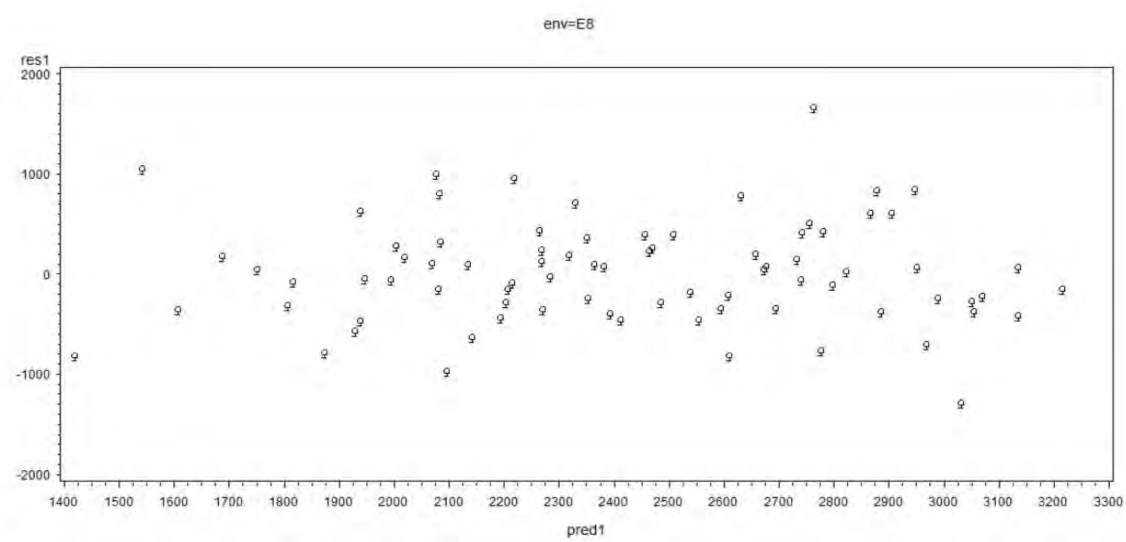

env=E3
res1
pred1


env=E4
res1
pred1


env=E5
res1
pred1


env=E6
res1
1000
900
800
700
600
500
400
300
200
100
0
-100
-200
-300
-400
-500
-600
-700
-800
1200 1300 1400 1500 1600 1700 1800 1900 2000 2100 2200 2300 2400 2500 2600 2700 2800 2900 3000
pred1


env=E7
res1
2000
1000
0
-1000
-2000
2000 3000 4000 5000
pred1

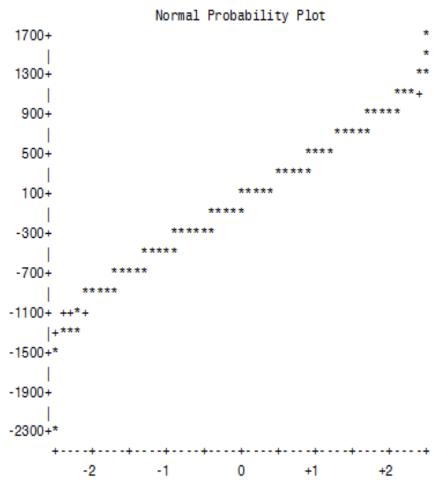

env=E8
res1
2000
1000
0
-1000
-2000
1400 1500 1600 1700 1800 1900 2000 2100 2200 2300 2400 2500 2600 2700 2800 2900 3000 3100 3200 3300
pred1

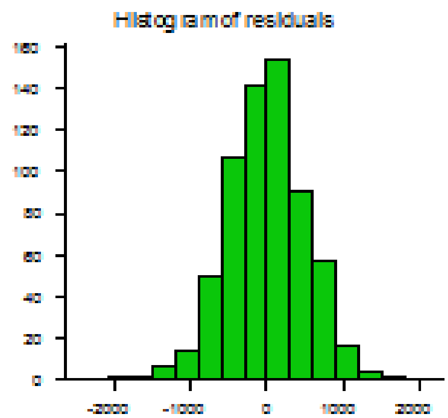
```
                    Tests for Normality

Test                  --Statistic---    -----p Value------

Shapiro-Wilk          W      0.992933   Pr < W      0.0041
Kolmogorov-Smirnov    D      0.030646   Pr > D      0.1489
Cramer-von Mises      W-Sq   0.105868   Pr > W-Sq   0.0956
Anderson-Darling      A-Sq   0.702222   Pr > A-Sq   0.0702
```

Figure A.3: Normal probability plot and histogram of residuals for the combined ANOVA.





Bartlett's Test for Homogeneity of res2 Variance

Source	DF	Chi-Square	Pr > ChiSq
genotype	19	28.5742	0.0730

Figure A.4: Plot of residuals against the predicted value in the combined ANOVA