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COLLEGE OF NATURAL AND COMPUTITIONAL SCIENCE

DEPARTMENT OF STATISTICS

A

Thesis

On

Analysis of Multi-environmental Trial Data Using AMMI and GGE Biplot on Barley Genotypes Evaluated in Tigray

Submitted to the Department of Statistics in Partial Fulfillment of the Requirements for the Degree of Master of Science in Statistics (Biometry Stream)

BY:

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APPROVAL SHEET

MEKELLE UNIVERSITY

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"***Analysis of Multi-environmental Trial Data Using AMMI and GGE Biplot on Barley Genotypes Evaluated in Tigray***"

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Declaration

I, declare that this Thesis entitled **"*Analysis of Multi-environmental Trial Data Using AMMI and GGE Biplot on Barley Genotypes Evaluated in Tigray*"** is my original work and has not been presented for any other award, and that all sources of materials used in this Proposal are duly acknowledged. This Proposal was carried out under the supervision of my principal advisor **Mr. Said Mussa**, Department of Statistics, College of Natural and Computational Sciences, Mekelle University in the academic year of 2023.

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Acronyms

AEA	Average Environment Axis
AEC	Average Environment Coordination
AMMI	Additive Main effects and Multiplicative Interaction
ANOVA	Analysis Of Variance
ASV	AMMI Stability Value
CSA	Central Statistical Agency
CV	Coefficient of Variation
GEI	Genotype by Environment Interaction
GGE	Genotype plus Genotype by Environment interaction
LSD	Least Significance Difference
PCA	Principal Component Analysis
SNNP	South Nation and Nationality People
SAS	Statistical Analysis Software
METs	Multi-Environmental Trials
YSI	Yield Stability Index

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Abstract

Barley (Hordeum vulgare L.) was one of the first plants people grew for food, and now it's grown all over the world and it has a special role in Ethiopian agriculture. However, production is affected by environment interaction and lack of stable genotypes across locations. The presence of genotype-environment interaction (GEI) influences production making the selection of cultivars in a complex process. Since, this experiment were conducted for forty barley genotypes by Alpha lattice design using two replications at three locations in Tigray during 2017 and 2018 cropping seasons considering each year-location combination as a different environments. The study carried out with objectives to estimate magnitude of genotype by environment interaction, comparing AMMI and GGE to evaluate stability of genotypes and identifying superior genotypes. We observed significance effects in all sources of combined ANOVA, since the grain yields of all 40 barley genotypes were significantly affected by environment, which accounted for 40.6 % of the total variation, whereas genotype and genotype-environment interaction accounted for 21.12 % and 23.07 %, respectively. The two most used methods to analyze GEI and evaluate genotypes are AMMI and GGE Biplot, being used for the analysis of multi environment trials data (MET).Both models were equivalent for the data's evaluation, but GGE permitting increased reliability in the selection of superior cultivars (Which-won-where pattern) and test environments (discrimitiveness vs. representativeness).Wricke's ecovalence, Finley-Wilkinson, Shukla's stability, Lin&Binns cultivar superiority measure, AMMI Stability Value (ASV), and YSI stability analysis measures also used to identify stable genotypes, and G19, G36, G5 are the most stable genotypes in almost the stability analysis measures, since they are superior genotypes with all test environments. While the genotypes G33, G32, G12 and G18 also the instable genotypes in the test environments.

GGE Biplot view of relation among test environments of this study showed that; Among the testing environments Hagereselam 2018 is an ideal testing location to identify stable and high yielding genotypes followed by Ayba 2018, since Hagereselam 2018 and Ayba 2018 are most applicable test locations for identifying stable and high yielding barley genotypes for the region. Mean performance and stability of GGE biplot indicated that G24 had the ideal genotype with highest mean yield as well as stability with desirable genotypes G20, G19, G5, G36, while G33 and G30 had the lowest mean yield and less stability genotypes in all the six test environments.

Key Words: *Barley (Hordeum vulgare L.), METs, GEI, combined ANOVA, Stability Analysis, AMMI Model, ASV, GGE biplot*

CHAPTER ONE

1. INTRODUCTION

1.1. Background of the study

Barley (*Hordeum vulgare L.)* was one of the first plants people grew for food, and now it's grown all over the world. Barley is a very important crop that is grown for food worldwide. It was the fourth largest in terms of how much cereal crops it made and how much land was used to grow them compared to wheat, rice, and maize in world. A lot of countries grow barley as a crop that they sell for money. Russia, Canada, Germany, Ukraine, and France are the biggest barley producers, together making up almost half of the world's total production (Smith, 1992).

Barley is currently the fifth most significant cereal crop in Ethiopia after maize, tef, sorghum, and wheat by area covered and productivity. Barley is a major crop farmed by highland farmers above 1800m mainly under rain fed circumstances and may be grown in the highlands, on steep slopes, degraded areas, and with low inputs. It is also one of the oldest crops still being grown there and With its quick growth and distinguishable physical and genetic features, it is a valuable plant for scientific studies (Birhanu et al., 2020).

Barley has a special role in Ethiopian agriculture, where it has been grown for at least 5000 years according to a number of sources. Ethiopian barley research and development The Agew people are said to have been the first Ethiopians to plant barley in about 3000 BC (Flood, 2013).

Barley is grown on 950,742.01 hectares of land in Ethiopia, with an annual yield of roughly 23,780,102.92 quintals and a productivity of 25.01 quintal ha^{-1} in the main cropping season of 2019/20(CSA, 2020). Hence in the Tigray region, barley is the crop that is most widely grown and consumed, followed by sorghum, tef, and wheat. In addition, barley is produced on a total of 85,431.88 hectares, with 1,606,888.13 production in quintals with an average yield of 18.81 quintal ha^{-1} (CSA, 2020). A staple meal for highlanders, barley is used to make "injera," bread, soup, porridge, alcoholic and nonalcoholic drinks, as well as other dishes. The social and dietary habits of people depend on it. (Ganewo et al., 2022)However, barley growing was done with little to no external inputs in the highland elevations of Ethiopia, particularly in the Tigray region. Therefore, it is crucial to find genotypes in the northern part of Ethiopia that can generate large yields of barley under a variety of conditions (Gebremedhin et al., 2014). Changes in the relative behavior of the genotype in different environments are usually observed. This phenomenon is called genotype by environment interaction (GxE) (Kandus et al., 2010).

In crops like barley, where we test different materials in various areas, the way the genes and the environment interact is very important. We need to consider this interaction using statistical approaches when choosing the best types of barley to grow (Peixoto et al., 2022).

Successful barley genotypes that exhibit excellent performance for yield and other crucial agronomic features are desired by farmers and studies. Their advantage should remain true not only over long periods of time but also in a variety of environmental circumstances. The occurrence of genotype-environment interactions (GEI) is the fundamental reason for variations in genotypes' yield stability.

Genotype–environment interaction (GEI) is an age-old, universal issue that relates to all living organisms and interacts to produce an array of phenotypes. GEI is the variation caused by the joint effects of genotypes and environments (Kang, 2020).

Genotype by environment interaction (GxE) means that different types of genes respond differently in different environments. Living things are not defined by just their genes or just their surroundings. The way they are formed is a result of the interaction between their genes and environment. A genotype x environment interaction is when the performance of different genetic traits is affected by different environments they are tested in (Okonkwo JC. Begna Temesgen, 2013).

The GxE interaction makes it difficult to select genotypes that produce high yields and that are more stable in breeding programs. This, of course, reduces the selection progress. When choosing the best cultivars (or agronomic techniques) to use in subsequent years in various places, as well as when determining a cultivar's stability across environments prior to its commercial release, multi-environment trials are crucial. Grain yield is one of the most crucial cultivar qualities to take into account when comparing the performance of cultivars across locations. Different cultivars respond differently to environmental changes when cultivated in many environments (Vargas et al., 1999).

G X E can also be viewed as an evaluation of the genotypes' flexibility in terms of how specific phenotypes will manifest themselves when different environmental circumstances are at influence. Information on the adaptability and stability of the varieties to be released is important from the evaluation of genotypic performances in multi-location trials (Goa et al., 2022).

Breeders and biometricians have long encountered GxE and yield stability because they make it more difficult to choose superior genotypes by slowing down genetic advancement. A G x E is crucial to reduce the utility of genotype means across locations or environments for selection and moving superior genotypes to the next stage of selection. Through the organized processes of plant breeding, plant breeders have controlled these interactions over the course of recent history as well as the history of crop domestication, improvement, and dissemination. It may be erroneous to use several statistical methods that take into account all phenotypic variance (i.e., means across habitats). In addition to the test

environment changing, the growing season in each habitat could also pose a threat to the variety's stability .The term "genotype by environment interaction (G x E) " describes how various genotypes respond differently to different environment. The recurring G x E interactions has significance for the particular breeding strategy because they alter the order of genotypes across environments. Numerous statistical models have been applied to comprehend how various crops interact in order to find the best genotypes (Teressa et al., 2021).

To understand how various crops interact and find the best genotypes, many statistical models have been applied. The complexity of the GEI has been examined using a variety of statistical methods. One of those approaches, the bi-plot methodology, presents the intricate GEI in an easy-to-understand graphical format. The most frequently utilized bi-plot kinds to fully comprehend GEI are AMMI (Additive Main-effect and Multiplicative Interaction) and GGE (Genotype + Genotype by Environment Interaction). A genotype evaluation model should simultaneously contain G and GEI (Verma et al., 2016).

1.2. Statement of problem

Despite the significant research on barley genotypes, no comprehensive analysis that incorporates data from several environmental trials has been done. This makes it more challenging to determine which genotypes of barley are best suited for the region's specific environmental conditions. Therefore, a statistical analysis that integrates statistical data from numerous experiments carried out in varied environmental conditions is required in order to offer insightful information about the performance and stability of barley genotypes. With the aim of comparing stable genotypes using statistical measures and identifying superior genotypes that consistently perform well under a variety of environments in the local region, this study attempts to fill the gap by conducting more statistical analysis of multi-environmental trials on barley genotypes.

It is reasonable to predict that the interactions between genotype and environment will vary and be significant in a variety of conditions. As a result, while one cultivar may yield the most in one area, another may perform better in the same environment. It was important to conduct research on genotypes by environment interaction to estimate the amount of interactions in the selection of genotypes across various settings and to ascertain the average performance of the genotypes under consideration.

Effectively interpreting and visualizing GxE data can be challenging due to the complexity of the interactions. Developing intuitive graphical representations and statistical summaries that facilitate meaningful interpretation is essential for researchers and stakeholders.

1.3. Significance of the study

The study holds significant importance in the field of agricultural research and crop improvement. The use of advanced statistical methods such as AMMI (Additive Main Effects and Multiplicative Interaction) and GGE (Genotype and Genotype by Environment) analysis allows for a comprehensive evaluation of genotypes across different environmental conditions.

By employing these analytical techniques, the study can provide valuable insights into the performance of barley genotypes in diverse environments, helping to identify varieties that exhibit stability and high yield potential across varying growing conditions. This information is crucial for breeders and farmers in Tigray, as it can guide the selection and deployment of barley genotypes that are well-suited to the region's specific agro-ecology conditions.

Furthermore, the findings of this study may contribute to the development of improved barley cultivars with enhanced adaptability and resilience, ultimately leading to increased agricultural productivity and food security in Tigray, Ethiopia. Overall, the research has the potential to make a significant impact on the local agricultural sector by informing decision-making processes related to crop selection, methods for evaluating genotypes and environments for researchers and breeders.

Therefore, an improvement in barley production would boost farmers' incomes, resulting in increased food security for the region and the country. Both breeders and researchers (Biometrician's) can use it as a starting point for future references.

1.4. Objectives

1.4.1. General Objective

The general objective of the study is to conduct a statistical analysis on multi-environmental trials on barley genotypes using AMMI and GGE bi-plot methods used to identify more stable barley genotypes.

1.4.2. Specific Objectives

- To estimate the magnitude of genotype x environment interaction for grain yield performance.
- To compare the multivariate statistical methods AMMI and GGE biplots for selecting stable genotypes and estimated environments.
- To identify stable and superior barley genotypes in each test environment.

1.5. Research Question

This study answers the following questions:

- What is the magnitude of genotype x environment interaction in a barley grain yield performance?
- How does the AMMI model compare to the GGE model for selecting stable genotypes in different environments?
- What are the most statistical models for identifying stable and superior genotypes in diverse environmental conditions?

CHAPTER TWO

2. LITERATURE REVIEW

2.1. Barley crop and its production

Barley is an important grain crop and a source of food security in Ethiopia. It is grown in a variety of ecologies from 1800 to 3400 m altitude during the mild seasons, and it thrives in temperatures between 15 and 30 ^{0}C, while it can withstand higher temperatures in production systems where the humidity is low. With around 26% of the continent's total barley production (Saverus, 2019).

Ethiopia is now the second-largest producer of the grain after Morocco (Saverus, 2019) and it is ranked twenty-first in the world for the production of barley With a 1.2% proportion of global output. For Ethiopian highlanders specifically, barley is a staple food grain. It matures quickly, which helps to fill the important food gap that arises before other crops are ready for harvest in October. Especially when combined with the country's commercial brewing and value-added companies, it is a crop with a lot of growth potential and may be extremely profitable (Kifle, 2022).

Barley is an important crop in Tigray, a region in northern Ethiopia. It is grown by smallholder farmers for both food and feed purposes. The crop is well adapted to the region's semi-arid climate and is able to tolerate drought and high temperatures.

Tigray produces barley compared to other parts of Ethiopia Tigray is fourth after Oromo, Amara, SNNP and is the region that produces most barley in the nation, as was already mentioned. Tigray produced 20,268,653.53 quintals of barley in 2019/20, which accounted for 6.05% of the nation's overall barley production, according to the Central Statistical Agency of Ethiopia. In Tigray highlands, where the climate is ideal for its cultivation, barley is mostly grown. The area is located between 1,500 and 4,500 meters above sea level, and its average annual temperature is between 10 and 25°C (Gebremedhin et al., 2014). The cool weather and high altitude are ideal for the development and growth of barley.

Plant breeders have employ meta-analysis of multi-environment trials to find stable genotypes that can perform well in a variety of conditions, improving barley production in Tigray. This makes it possible for farmers to get high-yielding, hardy varieties that can endure the difficulties caused by climate change and other stressors.

2.2. Genotype x Environment Interaction

Crop cultivars are grown in a variety of environments. They come into contact with various types of soil, levels of soil fertility, moisture content, temperatures, and cultural practices. The environment can be referred to as a collective term for all the factors that agricultural production must take into account. When

cultivars are compared in various conditions, their performance may not be the same relative to one another. In some situations, one cultivar might produce the most yields, while another cultivar might perform best. Genotype x Environment interaction describes changes in the relative performance of genotypes in various settings (Saverus, 2019).

In other words, a cultivar may function best in one environment while being subpar in another. Another way to put this is to say that genotype performance varies across different settings. A varied genotypic expression in various environments is known as GEI. This interaction has the result of reducing the correlation between phenotype and genotype. This brings up the crucial problem of adaptability because a breeder's selection of superior performers in one environment might not hold true in another environment. When breeders are evaluating enhanced varieties, interactions between genotype and environment have a significant impact (HAILEMARIAM, 2017). The breeder will be better equipped to choose the appropriate breeding strategy to employ in order to create the genotype that is most adapted to the target region by assessing the GEI.

The term "genotype-environment interaction," or GxE, refers to how two different genotypes respond to environmental change in various ways. A "norm of reaction" is a graph that shows how genes and the environment interact when phenotypic differences are continuous (Campbell, 1996).

G X E can also be viewed as an evaluation of the genotypes' flexibility in terms of how specific phenotypes will manifest themselves when different environmental circumstances are at influence. Information on the adaptability and stability of the varieties to be released is important from the evaluation of genotypic performances in multi-location trials (Goa et al., 2022).

To understand how various crops interact and find the best genotypes, many statistical models have been applied. The complexity of the GEI has been examined using a variety of statistical methods. One of those approaches, the bi-plot methodology, presents the intricate GEI in an easy-to-understand graphical format. The most frequently utilized bi-plot kinds to fully comprehend GEI are AMMI (Additive Main-effect and Multiplicative Interaction) and GGE (Genotype + Genotype by Environment Interaction). A genotype evaluation model should simultaneously contain G and GEI (Verma et al., 2016).

In coordinated trials, genotype by environment interaction (GxE interaction) is unavoidable given that diverse genotype responses have been seen in various contexts. For the purpose of selecting optimal genotypes, many statistical models have been utilized to comprehend complex GxE interactions of various crops. Multi-location data are typically studied using analysis of variance (ANOVA), principal component analysis (PCA), and linear regression analysis (LR). As a multiplicative model, PCA does not represent the additive main effects, whereas the widely used approach ANOVA can only describe

the genotypic main effects since it is an additive model. The AMMI model, which combines additive main effects and multiplicative interaction, adequately explains GxE interaction (Purchase et al., 2000).

G X E can also be conceptualized as a measurement of the relative plasticity of genotypes in terms of the expression of specific phenotypes in the context of variable environmental influences(Zakir, 2011).The intricate GxE interaction is explained graphically in a much simpler way using the bi-plot methodology.

When genotype performance is plotted against an environmental gradient, the slope of the line represents a conceptual G X E relationship. Lines that are not parallel but do not intersects show that cultivar performance is constant across settings. The optimal cultivar will depend on the environment, and lines that intersect show a change in cultivar rank across settings. Almost all decision-making processes involved in plant breeding programs are impacted by G X E, including selecting the most appropriate testing conditions, allocating resources within a breeding program, and selecting a breeding strategy (Zakir, 2011).

2.3. The Analysis of GxE Intersection

The very success of a scientific crop improvement effort connected to genetic stability is highlighted by the G x E interaction. Additionally, it affects the adoption assessment of enhanced strains prior to their distribution for industrial production. Because they lower genotypic stability values across a variety of conditions, GEI are crucial for the development and evaluation of plant varieties (Self-control, n.d.).

The varying performance of the genotypes under various sites or settings is a challenge to barley breeding with a focus on creating high-yield and allowably stable genotypes. Due to the interaction of genotypes with the environments makes difficult to identify the best performing genotype, genotype evaluation in multiple environments and the identification of the best performing genotype lack efficient selection.

The investigation of GEI and phenotypic stability has been approached in a variety of ways. In the Multi-environment Trials (METs), the additive main effects and multiplicative interaction (AMMI) approach is frequently utilized for GEI inquiry. By evaluating a cultivar's stability across environments prior to its commercial release, multi-environment trials (MET) play a crucial role in choosing the appropriate cultivars and/or agronomic approaches to utilize in subsequent years at various locations. To find barley genotypes that produce a high yield and consistently perform in varied environments (Abdipur & Vaezi, 2014).

The most stable genotypes were those that performed better in terms of yield. The most stable genotypes in the environment were those with the best values for IPCAs and the AMMI stability measure (HAILEMARIAM, 2017).

Data analysis by researchers and farmer assessments provide information for designing and developing practical methods to enhance or choose varieties that are better suited to the particular environment. They also provide a functional understanding of relevant mechanisms to support future crop and product development in an environmentally conscious way (Guade, 2017).Thus the GxE interaction analysis is more applicable for choosing the varieties better stable and adaptable in the given environment by using statistical analysis .

2.4. Stability Analysis for G XE Interaction

Univariate stability analysis focuses on evaluating the performance of a single trait, such as grain yield, across multiple environments. It aims to identify genotypes or treatments that consistently perform well or poorly across different conditions. This analysis helps breeders or researchers select genotypes that exhibit stable performance, regardless of the specific environmental conditions.

The plant breeder is always interested in the stability of performance for the characters which are of economically important. The desirable hybrids should have low GxE interactions for important characters, so as to get desirable performance of hybrids over wide range of environmental conditions. Genotype x environment interactions are of common occurrence and often creates manifold difficulties in interpreting results and thus hamper the progress of breeding programs aiming at further genetic improvement in crop plants. Under the biological concept stable genotype is one, whose phenotype shows little deviation from the expected character level when performance of genotype is tested over a number of environments.

A univariate nonparametric stability methods are not affected by data distribution and these methods are based on rank order of genotypes, a genotype is considered stable if its ranking is relatively constant across environments. Analysis of interaction of genotypes with locations and other agro-ecological conditions would help in getting information on adaptability and stability of performance of genotypes An ideal genotype should have both high mean yield performance and high stability across environments (Mulugeta et al., 2014).

Wricke's proposed Ecovalence (W_i) is measure of genotypic stability across environments. Ecovalence is the contribution of each genotype to the GEI sum of squares. It is generally expressed in percentage. The genotypes with Low value of W_i are less stability performance and the genotypes with highest value of W_i are more stability performance for the given environments.

Finlay and Wilkinson's (1963) regression coefficient (b_i) is based on the analysis of variance and focuses on the genotype-environment interaction. It provides estimates of genotypic and environmental effects, as well as the interaction effect.

Therefore, the genotypes with regression coefficients greater than one would be more adapted to favorable growth conditions; those with regression coefficients less than one would be instable environmental conditions, and those with regression coefficients equal to one would have an average stability to all environments. Thus, genotypes with regression coefficients greater than 1 would have high stability, whereas those with a regression greater than one with greater mean yield would have stable and adapted to all environments and it is superior used for future farming (Hailemariam & Tesfaye, 2019).

Genotypes with regression coefficients above one would be better adapted to favorable growth conditions; those with regression coefficients below one would be better adapted to unfavorable environmental conditions, such as; water stress environments; and those with regression coefficients at or near one would be averagely adapted to all environments. As a result, genotypes with variances in regression deviations equal to zero would have high stability, whereas those with variances in regression deviations larger than zero would have low stability. To determine the genotype that is stable, several stability models have been created (Abuali et al., 2014).

Since the existence of GEI causes the relative performance ranking to alter between contexts, complicating the evaluation of genotypes, multi environment trial studies are crucial. If GEI didn't exist, one genotype would dominate in every environment, thus selecting the optimal genotypes would need just one trial(Neisse et al., 2018).

Multivariate stability analysis considers multiple traits simultaneously to assess the overall stability of a genotype or treatment. It takes into account the correlation between different traits and evaluates how well a genotype performs across different environments for all the considered traits. This analysis helps in identifying genotypes that not only have stable performance for a specific trait but also exhibit consistent performance across multiple traits.

Breeders who want to choose genotypes that perform better in various situations may run into issues as a result of ineffective approaches for genotype-environment interaction study.

The two most popular Multivariate statistical methods for assessing GEI are AMMI (Additive Main-effects and Multiplicative Interaction) and GGE (Genotype main effects and Genotype-Environment interaction effects) model. Due to the fact that they apply to any two-way data matrices and that such data come from a variety of trials, these two statistical analyses (AMMI and GGE) are more pertinent for agricultural researchers than other statistical methods.

The AMMI model, a hybrid model that incorporates both additive and multiplicative components of a two-way data structure, allows a breeder to correctly forecast genotypic potentiality and environmental impacts on it. Ordinary ANOVA is used by AMMI to assess the major effects (additive portion) and principal component analysis (PCA) is used to study the residual that is non-additive after ANOVA. An illustration was given by Zobel et al. (1988) with regards to the application of AMMI in METs (Multi-environmental Trials) data analysis, which divides the GEI matrix into unique genotypic and environmental scores(SOLONECHNYI et al., 2018).

Purchase et al. (2000) developed a quantitative stability value to rank genotypes through the AMMI model, namely the AMMI Stability Value (ASV). AMMI Stability Value (ASV) is useful in plant breeding and variety selection programs as it helps breeders identify genotypes that perform consistently well across diverse environments. Genotypes with high stability values are desirable as they exhibit less interaction with environmental factors, making them suitable for cultivation in various locations and under different growing conditions.

GGE (genotype and genotype-environment interaction), which is used for GEI analysis, is a variation of the traditional AMMI approach developed by Yan et al. in 2000. Principal component analysis is applied to these effects after the genotype effect (G) and the multiplicative effect (GE) is combined in the GGE analysis. This bi-plot is known to be a GGE bi-plot, according to Yan et al. (2000).

GGE bi-plot has some graphical visualization features, including the ability to show how a genotype performs in a given environment, how adaptable a genotype is to different environments, how two genotypes compare to one another in various environments, how to show which genotypes perform best in each environment, how to show an environmental group for a particular genotype or genotypes, how to show genotype average performance and stability .These features contribute to the GGE bi-plot's status as a most complete tool for quantitative genetics and plant breeding(Yan & Hunt, 2001).

To comprehend GEI, its causes, and effects better, the AMMI model employs analysis of variance and principal component analysis. Both genotype main effects and GEI effects are essential for the study according to GGE bi-plot analysis. Only the early analysis steps where GGE examines G plus GE while AMMI separates G from GEI and the final analysis steps where the bi-plots for the interpretation of the genotype environment interaction are built distinguish these two models from one another(Neisse et al., 2018).

A graphical analysis of the GGE bi-plot was created and utilized to investigate and understand the performance of the genotypes, environmental variables, and their interaction effects. Variety placement in a certain area or setting might demonstrate a successful performance. A genotype that is positioned at the top of the multi-dimensional graphic is the optimal genotype for that area (Arshadi et al., 2018).

2.5. Impact of GxE Interaction on crop improvement

The ability of a genotype to respond to environmental variables, which is defined by the genotype's genetic makeup, affects grain yield stability. When proposing cultivars for certain cropping situations, the adaptability and stability of a genotype are useful indicators. The degree to which a genotype is suited to its environment directly affects how productive a plant is. Therefore, useful phenotypic characterization is site-specific and reflects the fusion of the plant's complete lifespan and the local environmental factors. Accurately predicting the performance of certain genotypes across a wide variety of changeable settings will be a crucial aspect of truly increasing agricultural production efficiency (Zakir, 2011).

The farmers require cultivars that perform well in terms of yield and other crucial agronomic characteristics. Their superiority ought to hold true over a variety of environmental factors and for many years. The occurrence of genotype-environment interaction (GEI) is the fundamental reason for variations in how genotypes perform across contexts (Gedif & Yigzaw, 2014).

It is reasonable to predict that the interactions between genotype and environment will vary and be significant in a variety of conditions. As a result, while one cultivar may yield the most in one area, another may perform better in the same environment. GxE studies help breeders identify genotypes that exhibit stable performance across multiple environments. This means that even if there are variations in environmental conditions, these genotypes consistently produce high yields. This helps to mitigate the risk of crop failure due to unpredictable environmental fluctuations. It was important to conduct research on genotypes by environment interaction to estimate the amount of interactions in the selection of genotypes across various settings and to ascertain the average performance of the genotypes under consideration(Patel & Patel, 2015).

Among various statistical techniques used for evaluating GEI, the two most frequently used are AMMI (Additive Main-effects and Multiplicative Interaction) and GGE Biplot. Several researchers have used the GGE model as an effective method for analyses of GEI (Yan et al., 2007), compared the AMMI and GGE methods using simulated and real data and found that the GGE method was more effective in identifying stable genotypes, and

Gauch et al. (2008) also compared the two methods using maize yield and found that the GGE method is effective in identifying mega-environments). The AMMI model uses analysis of variance and principal component analysis to achieve a better understanding of GEI, and the GGE Biplot analysis, which considers both genotype main effects and GEI effects as important for the analysis. The only difference between these models is in the initial steps of the analysis, where GGE analyzes G plus GE (or GEI) while AMMI separates G from GE; and at the final steps where the biplots for the interpretation are built(Neisse et al., 2018).

CHAPTER THREE

3. METHODS

3.1. Study area & period

The field experiment was conducted at three test locations in Tigray, northern Ethiopia during 2017 and 2018 main cropping seasons. The locations were selected by their potential for barley production and contrasting growing conditions. These locations represent the varying agro ecologies of the major barley growing areas of Tigray, northern Ethiopia. Namely: Ayba in Amba-alaje wereda of north Tigray, Mekelle Enderta wereda and Hagereselam in Degua-temben wereda of north east Tigray given in **Table 1**.

Table 1: the name and code of the testing environments

No.	Location	Year	Environment
1.	Mekelle	2017	E1
		2018	E2
2.	Hagereselam	2017	E3
		2018	E4
3.	Ayba	2017	E5
		2018	E6

3.2. Sampling procedures

The tested barley genotypes were sampled for adaptation and performance in the Tigray region by local checking of main cropping seasons. A sample of 40 genotypes coded as 1 to 40 used in this study.

3.3. Study design

The alpha lattice design with two replications was used for the experiments in this study to evaluate the performance of barley genotypes under different given environments. It involves arranging experimental units in a square or rectangular lattice, with each genotype represented once in each row and column.

3.4. Source of Data

The data is secondary data and collected primarily by Dr. Yemane Tsehaye (Collage of Dryland Agriculture and Natural Resources).Who is well experienced researcher of plant breeding in Mekelle University collected the experiments at farming areas in years of 2017 and 2018 cropping seasons.

3.5. Statistical analysis

The data obtained from the multi-environmental site can be evaluated through suitable statistical software like: Genstat, R-Software, and Minitab software's. Analysis of variance was for each environment.

The Bartlett's test was made to test the homogeneity of error variance across all the environments. However, the valid standard error was used to estimate the least significant difference (LSD) to compare each pair-wise genotype means.

Combined analysis of variance will done for each trait to obtain estimates of environmental (location &year), genotype and GEI source of variation by using MINITAB and Genstat software's.

A regression model will used to produce the best linear unbiased predictors (BLUPs) for genotypes, locations, years and their interactions using Genstat.

The multivariate analytical tools, AMMI and GGE bi-plots, and other stability measurements were also used to get insights on the significant of GxE interaction and determine the most stable genotypes.

3.6. Analysis of Variance

Perform an ANOVA analysis on the combined dataset to assess the variability in performance among different barley genotypes across different environments. This will allow determining if there are significant differences in performance between genotypes and if these differences are influenced by environmental factors.

Statistical computation and estimation were carried out using R and Genstat software's. Each location in a given year was considered as an individual environment.

Data obtained from each location was initially analyzed separately by running a single ANOVA and thereafter data were pooled to perform the combined analysis of genotypes across locations. Analysis of variance was carried out to partition the variance due to genotype, environment and genotype by environment interaction. . Similarly, homogeneity of error variance was tested using Bartlett's test to determine the validity of the combined analysis of variance.

The combined ANOVA model is:

$$Y_{ijr} = \mu + g_i + e_j + \rho_{r(j)} + \varepsilon_{ijr}$$

Where: Y_{ijk} observed value of genotype i environment j and replicate r within environment j, μ is grand mean of the experiment, g_i is effect of genotype *i*, e_j is the effect of environment j , $\rho_{r(j)}$ is replicate r within environment effect and ε_{ij} is random error.

Table 2: outline of analysis of variance for combined environments

Source of Variation	Degree of Freedom	Sum of Squares	Mean Sum Square	F-ratio
Genotype(g)	$g-1$	SSg	MSg	
Rep($environment$)	$e(r-1)$	SSb	MSb	
Environment	$e-1$	SSE	MSE	F_0
Genotype(g) *Environment(e)	$(g-1)(e-1)$	SSg	MSg	
Error	$e(g-1)(r-1)$	$SSerror$	$MSerror$	
Total	$ger-1$	SS_T		

N.B: r is number of replication, e number of environments, g is total genotypes, SS & MS are the Sum and mean squares respectively.

3.7. Stability Analysis

3.7.1. Wricke's Ecovalence (W_i)

Ecovalence measures the contribution of a genotype to the GEI. The Ecovalence (W_i) or stability of the genotype is its interaction with the environments, squared and summed across environments, and expressed mathematically as: $$W_i = \sum_{j=1}^{e}\left[y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} - \bar{y}_{..}\right]^2$$

Where: y_{ij} = is the mean performance of the genotype i in the j^{th} environment;

$\bar{y}_{i.}$ = the marginal mean of the ithgenotype;

$\bar{y}_{.j}$ = is the marginal mean of the jth environment;

$\bar{y}_{..}$ = *is the grand mean*

The interpretation of genotype with low value has smaller deviations from the overall mean across environments and they are more stable. Since the ecovalence strongly depends on the environments included in the test and the breeder can manipulate the ecovalence by choosing specific location. A genotype with high ecovalence = 0 is regarded as stable in all environments.

3.7.2. Finlay-Wilkinson (b_i) Analysis

Finlay and Wilkinson's (1963) regression coefficient (b_i) is based on the analysis of variance and focuses on the genotype-environment interaction. It provides estimates of genotypic and environmental effects, as well as the interaction effect.

Environmental indices, which are the difference between the marginal means of the environments and the overall mean, are regressed on the observed data. The procedure principally defines stability as the sensitivity of a genotype to changing environments, and this is measured and reflected by the regression coefficient (b) of joint regression analysis(Purchase et al., 2000). They discovered that a genotype with poor stability (unstable) has a regression coefficient greater than 1, and that a value less than 1 is indicative of greater stability. A regression coefficient of exactly 1 (b_i=1) indicates well-adapted genotype across environments.

According to Finlay and Wilkinson (1963), a genotype with a $b_i$value less than 1.0 has above average stability and is especially adaptable to low-performing environments and if it is greater than 1.0 the genotype has below average stability and is especially adaptable to high performing environments. Whereas, a genotype with b_i value equals to 1.0 is adapted to the wide range of environments or an indication of its average stability. When this value is associated with high mean yield it indicates a genotype's good general adaptability; and when it is associated with low mean yield it shows the genotype's poor adaptability to all environments. Hence, in most cases the deviation from regression (S_{di}^2) is taken as a parameter for stability rather than which is more about the responsiveness of genotypes.

3.7.3. Shukla's Stability Variance ($\delta_i{}^2$)) Analysis

Shukla's (1972) stability variance ($\delta_i{}^2$) measures the stability of genotypes across environments by estimating the variance of the genotype-environment interaction. It provides a measure of the stability of genotypes and helps identify genotypes with consistent performance across different environments.it is based on the residuals in a two-way classification; the variance of a genotype across environments is the stability measure.

Shukla's stability variance ($\delta_i{}^2$) is the contribution of a genotype to the GEI sums of squares after adjusting for the average genotypic contribution to the GEI sums of squares.

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

Where: Y_{ij} is the mean of the i^{th}genotype in the j^{th}environment, Y_i is the mean of i^{th} genotype in all environments, $Y_{.j}$ is the mean of all genotypes in the j^{th} environments and $\bar{\boldsymbol{Y}}_{..}$ is the mean of all genotypes in all environments. A genotype is called stable if its stability variance (δ^2) is equal to environmental variance ($\delta_e{}^2$) .

3.7.4. Lin and Binns Cultivar Superiority Measure (P_i)

Lin and Binns (1988) defined the superiority measure (P_i) of the genotype as the mean square of the distance between the genotype and the genotype with maximum response. According to Lin and Binns (1988) for cultivar superiority measure (P_i) analysis, the genotype with low or small (P_i) value is considered to be more stable.

3.7.5. AMMI Stability Value (ASV)

AMMI Stability Value (ASV) is stability value based on the AMMI models IPCA1 APCA2 values for each genotype and each environment, it was calculated according to (Farshadfar et al., 2011).

AMMI Stability Value (ASV) is the effect of distance from the coordinate point to the origin in a two dimensional scatter diagram of IPCA1 scores against IPCA2 scores. IPCA1 score contributes more to the GxE interaction Sum of squares, and a weighted value is required. This weight is calculated according to the relative contribution of IPCA1 to IPCA2 to the interaction Sum Squares calculated as:

$$\text{ASV} = \sqrt{\left[\frac{IPCA1\text{SumSqusare}}{IPCA2\text{SumSqusare}}(IPCA1_{score})\right]^2 + (IPCA2_{score})^2}$$

Where: $\frac{IPCA1SumSqusare}{IPCA2SumSqusare}$ = is the weight derived from dividing the sum of IPCA1 squares by the sum of IPCA2 squares. The larger the absolute value of IPCA, the greater the adaptability of a specific variety for a certain environment. Conversely, genotypes with lower values of the ASV are considered to be more stable in different environments.

3.7.6. Yield Stability Index (YSI) Analysis

Yield Stability Index (YSI) is a Selection of stability and will not necessarily lead to the best genotype (in terms of performance). Thus, the GSI for each genotype was computed via the sum of the rank of the genotype grain yield (RY) and the rank of the genotype ASV (RASV) (Farshadfar et al., 1995).

The genotype Selection index was calculated using the equation:

YSI = RASV + RY

The terms RASV and RY in this context stand for genotype mean yield ranking across environments and AMMI Stability value ranking, respectively. The YSI combines stability and mean yield into a single criterion, with a low score suggesting stable genotypes with high mean yield. Therefore it is assumed that the YSI with the lowest value is the most stable. A genotype is better suited to particular surroundings when it has a higher IPCA score, whether positive or negative.

3.8. Additive Main effects and Multiplicative Interaction (AMMI) Analysis

3.8.1. AMMI Analysis of variance

The AMMI analysis is analysis of variance (ANOVA) followed by a principal component analysis applied to the sums of squares allocated by the ANOVA to the genotype x environment interaction.

The AMMI Model Equation is:

$$Y_{ij} = \mu + \alpha_g + \beta_e + \sum_{n=1}^{N} \lambda_n \gamma_{gn} \delta_{en} + \theta_{ge} + \varepsilon_{ge}$$

Where: $Y_{ij} = the\ mean\ yield\ of\ genotype\ g\ in\ environment\ e; \mu = the\ grand\ mean;$

$\alpha_g = the\ deviation\ of\ the\ genotype\ mean\ from\ the\ grand\ mean$;

$\beta_e = the\ deviation\ of\ the\ environment\ mean\ from\ the\ grand\ mean;$

$\lambda_n = the\ singular\ value\ for\ the\ n^{th}\ IPCA; \gamma_{gn} = the\ PCA\ score\ of\ a\ genotype\ for\ PCA\ axis\ n;$

$\delta_{en} = the\ environmental\ PCA\ score\ \ for\ PCA\ axis\ n;$

$\theta_{ge} = the\ \ residual\ GxE\ interaction\ or\ AMMI\ residual; \varepsilon_{ge} = the\ residuals\ ; and$

$N = the\ number\ of\ Principal\ Components\ retained\ in\ the\ model$

The sum of squares of the G×E interaction was divided into an n singular axis or Interaction Principal Component Axis (IPCA), which reflects the standard portion in which each axis corresponded to a particular AMMI model.

The degrees of freedom (df) for IPCA axes were calculated based on the following method (Zobel et al., 1988): $df = G + E - 1 - 2n$

Where: $G = the\ number\ of\ genotypes; E = the\ number\ of\ environments$ and n is the n^{th} axis of IPCA.

3.8.2.AMMI bi-plot analysis

To investigate the yield stability of the genotypes using bi-plot graphs. Bi-plot graph interpretation is based on the variation of the additive main effects (genotype and environment) and the multiplier effect of the G×E interaction. The abscissa represents the main effects (average of varieties evaluated), and the ordinate the interaction among the axes (IPCA). In this case, the lower the IPCA value (absolute value) the lower the contribution of the G×E interaction and the greater the genotype stability. An ideal genotype is one with a high yield and IPCA values close to zero. An undesirable genotype is one with low stability, which is associated with low yields. The average predictions were estimated according to the AMMI model. All statistical analyses will perform by using the meta-analysis procedure in Genstat.

3.9. GGE biplot multi-environmental trials

Yield data from multi-environment trials comprises an environmental effect (E), a genotype effect (G), and an interaction term of genotypes and environments (GEI). In the framework of recommendation trials, however, only G and GE are important for identification of superior cultivars. Yan et al. (2000) proposed a graphical interpretation of G + GE based on a bi-plot technique referred to as GGE bi-plot. To that end, the environment-centered matrix, containing the GGE data, is subjected to singular value decomposition, so that each element in the matrix is estimated as:

$$Y_{ijr} = \mu + e_j + \sum_{k=1}^{x} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ijr}$$

Where: $Y_{ijr} = observation\ of\ replicate\ r\ of\ genotype\ i\ in\ the\ environment\ j$; μ is the overall mean, $e_j = mean\ effect\ of\ environment\ j, x$ =is the number of principal components (PC) needed to provide an adequate description of G + GE.

λ_k is the singular value for the k[th] principal component,α_{ik} $is\ the\ eigen\ vector\ score\ for\ genotype\ i\ and\ component\ k$, γ_{jk} $is\ the\ eigen\ vector\ scores\ for\ environment\ j\ and\ component\ k$ and ε_{ijr} is the error for genotype i environment j and replicate r.

3.10. Combined Comparison of stability analysis procedures

To compare the stability analysis procedures, spearman's coefficient of rank correlation (r_s) was employed. This is because spearman coefficient of rank correlation works to the data in the forms of ranks. After computing the stability values according to the procedure and definition used were then ranked to determine Spearman's rank correlation coefficient between different procedures.

Procedurally, by assuming n genotypes are arranged in the same following order according to two stability parameters, and indicates the ranking order of the genotype for the first parameter, while indicates the ranking number of the genotypes of the second parameter, then $d_i = x_i - y_i$ (i $= 1, 2, \ldots \ldots,$ n) and spearman's rank correlation coefficient (r_s) can be described as:

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

The significance of $r_s$can be tested by means of student's *t* test, where $t = \frac{r_s\sqrt{n-2}}{\sqrt{1-r_s^2}}$ with n-2 degrees of freedom. If t ≥ t (0.01: n-2), the null hypothesis is discarded and r_s is described as highly significant.

CHAPTER FOUR

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance and estimation of variance components

Before data analysis, homogeneity of error variance was determined by Bartlett's test (Steel and Torrie, 1980) and the data collected was homogenous. Bartlett's test indicated homogenous error variance for the grain yield. In addition, normality test was also computed using Shapiro-Wilk normality test, and the data had confirmed that it came from normal distribution.

To describe the main effect and quantify the interactions among and within the source of variations combined analysis of variance was performed. The combined analysis of variance of grain yield (tones) of 40 barley genotypes tested in three locations for consecutive two years is presented in **Table 3**. The combined analysis of variance is performed on Multi-Environmental Trials (METs) data before to identify the significance of different effects, such as; Location, Year, Genotype and all interactions .The Experiment were conducted in three locations over a period of two years. Before considering each year-location combination as a different environment, we can identify the combined analysis of variance (**Table 3**) showed that the barley yield of 40 genotypes is highly significantly affected ($p<0.01$, $p<0.05$) by main effects of variation (Genotype, location, year) and interaction effect source of variation (Location*year, Genotype*year, Genotype*Location*year). The interaction of Genotypes by years had no significant effect on the barley grain yields .Highly significance differences in Locations, years, and Genotypes may be given to changes in environment conditions that differ from one environment to the next. The Location*year interaction explains 19.37 % of the total sum squares of the barley genotypes tested across three Locations and Two years while the main source of variations Location and year explains

By considering each year-location combination as a different environment, we can identify the combined analysis of variance to show the Environment, Genotype and the Genotype by Environment interaction (GEI) effect for the 40 barley genotypes grain yield as given in **Table 4**.

The analysis showed that barley grain yield was significantly ($p < .01$) affected by Genotype, Environment, and Genotype by environment interaction effects. The significance of GEI indicated that the relative performances of the genotypes were not consistent across the test environments and the environments had different effects on the yield potential of the genotypes.

Environmental effect explains 40.6% of the total sum of squares of the 40 barley genotypes grain yield investigated in Six Environments. While the Genotypic and GEI explains 21.12% and 23.07% respectively. The higher proportion of the sum of squares suggests that the environment plays a stronger

role in influencing the response variable (grain yield) compared to the genotypes and the genotype and environment interaction with the Environment. In agreement with this finding, (*Ageyeman,A.&Parks*,E. 2015) and (SOLONECHNYI et al., 2018) reported significant effects of genotype, environment, and genotype by environment interaction on cassava and spring barley grain yield respectively.

This, in turn, suggested the need to conduct further analysis on genotype by environment interaction to understand the nature of the interaction, and to identify stable genotypes.

Table 4 : ***Combined Analysis of variance for grain yield of 40 barley genotypes considering each Locations–year combination as Environment***

Source	DF	SS	MS	SS %	F-Value	P-Value
GENOTYPE	39	81.166	2.0812	21.12	8.94	0.000
REP(Environment)	6	3.991	0.6652	1.04	2.86	0.011
Environment	5	156.065	31.2129	40.60	134.02	0.000
GENOTYPE*Environment	195	88.670	0.4547	23.07	1.95	0.000
Error	234	54.498	0.2329	14.17		
Total	479	384.391				

4.2. Stability Analysis

4.2.1. Univariate Stability measures

Univariate stability measures in GxE data analysis are used to assess the performance and stability of genotypes across different environments. In this study of METs data the univariate stability measures was determined for grain yields of 40 Barley genotypes at six environments.

The estimates of stability measures are given in the output **Table: 5**. The Mean in the table indicates the average yields of a genotype in the Six Environments. Taking the mean grain yield as a reference; G24, G20, G19, G5, and G36 are the first five barley Genotypes with high average or consistence performance across all the six environments from the 40 barley genotypes that used for this experiment, while G30, G33, G32, G11, and G16 had the greater variability in performance across the environments.

4.2.1.1. Wricke's Ecovalence Analysis (W_i)

Ecovalence was described by Wricke's in 1962 as the genotype's stability in its interaction with environments, squared and summed over environments. Because they fluctuate less in different locations genotypes with the lowest ecovalence are thought to be more stable than others.

Wricke's Ecovalence had determined for grain yields of 40 Barley genotypes at six Environments as given in **Table 5**. G10, G19, G29, G5 and G35 with lowest stability ecovalence value were the five most stable

genotypes. The genotypes G20, G12, G18, G32 and G33 had the highest ecovalence values and ranks 36^{th}- 40^{th} respectively. This result shows that the unstable genotypes contribute the highest amount of variation to the total GEI variance and this lead the genotype unstable.

4.2.1.2. Finley & Wilkinson stability Analysis

Finlay and Wilkinson (1963) principally defines stability as the sensitivity of a genotype to changing environments, and this is measured and reflected by the regression coefficients (bi) of joint regression analysis.

According to Finlay and Wilkinson (1963) **Table 5** showed genotypes G30, G36, G31, G27, and G7 as the genotypes with greater stability and consistent performance because of their regression coefficients (bi) value significantly lower than 1. G30 is associated with lower mean yield with lower regression coefficient and it especially indicates a cultivar with poor adaptability in the test environments. However, G5 is associated with higher mean yield and adapted better of the test environments.

Genotypes G2, G5, G13, , G8, and G20 possesses average stability due to their regression coefficients near to 1.0 and G20 & G5 be consider as well adapted cultivars across the environments because their good mean yield .

Genotypes G12, G15, G16, G22 and G9 with regression coefficients (b_i) >1 are the most instable genotypes and considered responsive to good environments (had below average stability) from the 40 barley genotypes for the given environments.

4.2.1.3. Shukla's Stability Variance Analysis ($\delta_i{}^2$)

Shukla's (1972) stability variance ($\delta_i{}^2$), the amount of genotype by environment variance associated with genotypes *i*. This stability variance is a linear function of with the Wricke's ecovalence. However, Shukla's model differs in the ranking of the genotypes from Wricke (1962) when covariates (locations means) were considered. A genotype is described as stable if the stability variance ($\delta_i{}^2$) is close to zero (smaller), relatively large value of ($\delta_i{}^2$) indicates greater instability of the genotype. The most stable genotypes as indicated by this stability parameter given in **Table 5** were G30, G36, G27, G31, and G7. In terms of Shukla's stability the stable genotypes G36 and G7 have highest yielding genotypes. The genotypes G12, G33, G18, G15, and G16 were with poor stabilities ranked 36^{th}-40^{th}.

4.2.1.4. Lin and Binns cultivar superiority measure (Pi)

According Lin and Binns cultivar superiority measure (Pi) the lowest values are considered as the most stable genotypes. From the result of cultivar superiority measure in **Table 5** the most stable genotypes were G24, G20, G19, G5, and G36 arranged from the 1^{st} to 5^{th} superior cultivars since the genotype G24 may perform similarly to the other genotypes under similar environmental conditions and genetic makeup.

However, the genotypes G25, G3, G32, G30, and G33 were the most unstable genotypes according this measure. The Lin and Binns procedure thus appears to be a genotype performance measure, rather than a stability measure over sites.

4.2.2. AMMI Stability Value (ASV)

The ASV measure was developed by (Purchase et al., 2000) to address this issue since the AMMI model does not include a quantitative stability measure, which is necessary to rank genotypes based on their yield stability. A two-dimensional scatter plot of IPCA1 (interaction principal component analysis axis 1) scores vs. IPCA2 scores really measures ASV as the distance from zero. **Table 6** shows the average grain yield, IPCA score, ASV and GSI of each genotypes in the test environments.

According to the ASV, the five superior stable genotypes were G10 > G26 > G29 > G19 and G6. These genotypes had the highest stability and the lowest role in GxE. The genotypes G33, G32, G18, G20, and G11 have high ASV values and those are suggested as unstable genotypes from those of 40 barley genotypes in the six test environments.

4.2.3. Yield Stability Index (YSI)

Stability should however not be the only parameter for selection because the most stable genotypes would not necessarily give the best yield performance, hence there is a need for approaches that incorporate both mean yield and stability in a single index .in this regard ,as ASV takes in to account both IPCA1 and IPCA2 that justify most of the variation in the GE interaction, therefore the rank of ASV and yield mean in such a way that summed in a single simultaneous selection index of yield and the yield stability called as: yield stability index (YSI). The least YSI is considered as the most stable with high grain yield.

According the YSI in **Table 6** G19, G5, G35, G26, and G6 are the five most stable genotypes ranked 1^{st} - 5^{th} from the 40 barley genotypes in the six test environments, since genotypes G19 and G5 are the most stable with high grain yields. However the genotypes G33, G32, G11, G18, and G12 are the most unstable genotypes with lower grain yields.

Table 5: Estimates of stability coefficient measures for 40 barley genotypes yield across six environments

Genotype	Mean	Rank	Finley& Wilkinson	Rank	Cultivar superiority	Rank	Shukla's stability	Rank	Wricke's Stability	Rank
1	2.659	27	1.1605	33	1.0249	29	0.5773	33	0.3382	27
2	2.593	33	0.9972	19	1.1289	37	0.4405	22	0.2877	23
3	2.91	9	1.1014	29	0.7032	12	0.5088	26	0.2254	17
4	2.909	10	0.8196	7	0.7436	13	0.3246	7	0.3951	31
5	3.352	4	1.0252	23	0.2758	4	0.4242	20	0.0904	4
6	2.834	15	0.9353	13	0.7492	14	0.3593	11	0.1035	6
7	2.996	7	0.7167	5	0.5829	7	0.2459	5	0.3753	29
8	2.701	22	1.0209	22	0.9514	25	0.4313	21	0.1419	9
9	2.616	31	1.2129	36	1.0729	33	0.5973	35	0.2328	18
10	2.646	28	1.0347	25	0.9934	28	0.417	18	0.0123	1
11	2.551	37	1.0693	27	1.1122	35	0.5348	28	0.449	35
12	2.589	34	1.3275	40	1.0601	32	0.7526	40	0.5396	37
13	2.718	19	0.9906	18	0.881	18	0.4193	19	0.1829	12
14	2.69	23	1.113	30	0.921	22	0.5303	27	0.2617	20
15	2.845	14	1.2717	39	0.7691	15	0.6498	37	0.2683	22
16	2.578	36	1.2565	38	1.112	34	0.6295	36	0.2237	16
17	2.671	25	0.872	8	0.9575	26	0.3759	13	0.4188	32
18	2.615	32	1.2071	35	1.0273	30	0.6714	38	0.5946	38
19	3.44	3	0.9823	16	0.1987	3	0.3836	14	0.0429	2
20	3.528	2	1.0182	21	0.1361	2	0.4983	25	0.4632	36
21	2.643	29	1.0807	28	0.982	27	0.4901	24	0.1938	15
22	2.718	19	1.2303	37	0.9007	20	0.5927	34	0.1372	8
23	2.906	11	0.8943	10	0.697	11	0.3272	8	0.1155	7
24	4.037	1	1.1216	31	0	1	0.5377	29	0.2664	21
25	2.587	35	0.9574	14	1.1193	36	0.3903	15	0.1893	14
26	2.884	13	0.9838	17	0.6945	10	0.411	17	0.1834	13
27	2.622	30	0.7003	4	1.0383	31	0.2312	3	0.3661	28
28	2.67	26	0.8873	9	0.9446	23	0.3514	10	0.2419	19
29	2.705	21	0.9152	12	0.9127	21	0.3311	9	0.0451	3
30	2.444	40	0.6059	1	1.3233	39	0.1475	1	0.3227	26
31	2.686	24	0.6931	3	0.9461	24	0.2392	4	0.4335	33
32	2.546	38	1.028	24	1.2553	38	0.5701	32	0.8298	39
33	2.517	39	1.0635	26	1.3801	40	0.7259	39	1.4796	40
34	2.801	16	0.9076	11	0.8536	17	0.3733	12	0.2995	24
35	3.064	6	1.1782	34	0.4988	6	0.5446	30	0.0975	5
36	3.191	5	0.6921	2	0.4007	5	0.2267	2	0.3826	30
37	2.765	18	1.1384	32	0.8935	19	0.5544	31	0.311	25
38	2.793	17	0.9793	15	0.7816	16	0.4055	16	0.1585	10
39	2.885	12	0.8084	6	0.6855	8	0.2766	6	0.1769	11
40	2.955	8	0.9974	20	0.6879	9	0.4726	23	0.4486	34

Table 6: Grain yield average, IPCA scores, ASV and GSI of each genotype in the test environments.

Genotype	Mean	Rank	IPCAg1	IPCAg2	ASV	Rank	YSI	Rank
G1	2.659	27	0.29676	0.09743	1.109421	31	58	33
G2	2.593	33	0.28976	-.09072	1.082873	29	62	35
G3	2.91	9	0.27164	0.06531	1.013693	24	33	15
G4	2.909	10	0.26128	-0.29356	1.016326	26	36	18
G5	3.352	4	0.13117	-0.00802	0.488543	8	12	2
G6	2.834	15	-0.07077	-0.10076	0.282152	5	20	5
G7	2.996	7	-0.2474	-0.32444	0.976774	23	30	13
G8	2.701	22	0.13532	-0.0388	0.505423	9	31	14
G9	2.616	31	0.21263	0.21145	0.819581	17	48	26
G10	2.646	28	0.00983	0.03348	0.049608	1	29	12
G11	2.551	37	-0.37338	0.16204	1.399877	36	73	38
G12	2.589	34	-0.29635	0.43415	1.185932	32	66	36
G13	2.718	19	-0.23989	0.03628	0.894087	20	39	19
G14	2.69	23	-0.24815	0.16169	0.938149	22	45	23
G15	2.845	14	0.22801	0.27803	0.893469	19	33	15
G16	2.578	36	0.19107	0.26179	0.758175	15	51	29
G17	2.671	25	-0.35761	-0.11052	1.336318	35	60	34
G18	2.615	32	-0.38776	0.29707	1.474259	38	70	37
G19	3.44	3	-0.06823	-0.04112	0.257394	4	7	1
G20	3.528	2	-0.38338	0.08746	1.430383	37	39	19
G21	2.643	29	-0.15956	0.17807	0.62031	11	40	21
G22	2.718	19	0.1004	0.25161	0.450667	7	26	10
G23	2.906	11	0.16544	-0.1533	0.634884	12	23	8
G24	4.037	1	-0.2405	0.19242	0.916059	21	22	7
G25	2.587	35	0.19155	-0.05242	0.715256	13	48	26
G26	2.884	13	0.02298	0.04544	0.096893	2	15	4
G27	2.622	30	-0.25877	-0.32033	1.015505	25	55	31
G28	2.67	26	-0.27584	-0.07333	1.029842	27	53	30
G29	2.705	21	-0.04284	-0.05842	0.169896	3	24	9
G30	2.444	40	-0.10746	-0.4181	0.578751	10	50	28
G31	2.686	24	-0.31482	-0.26698	1.202404	33	57	32
G32	2.546	38	0.48767	0.00188	1.816084	39	77	39
G33	2.517	39	0.70543	-0.0361	2.627269	40	79	40
G34	2.801	16	0.29191	-0.17919	1.101742	30	46	24
G35	3.064	6	0.05387	0.22495	0.301409	6	12	2
G36	3.191	5	-0.19699	-0.25173	0.775579	16	21	6
G37	2.765	18	0.28938	0.10438	1.082694	28	46	24
G38	2.793	17	-0.22145	0.01133	0.824758	18	35	17
G39	2.885	12	-0.19481	-0.20006	0.752552	14	26	10
G40	2.955	8	0.34985	-0.11835	1.308206	34	42	22

4.2.4. Combined Comparison of stability analysis procedures

Spearman's rank correlation was computed for the various stability measures of grain yield and is presented in (**Table 7**). The mean grain yield had a strong negative correlation with Lin&Binns Cultivar superiority and YSI, but a non-significant negative correlation with the rest procedures ASV, Finley&Wilkinson, Shukla's stability, and Wricke's stability. As grain yield is one of the most important cultivar performance trait, stability parameters that positively associated with grain yield seems the appropriate stability parameter that helps identify both high yielding and relatively stable genotypes. However, there is not appropriate stability parameter significant and positive association with grain yield. Therefore, it seems the stability parameter that can't provide genotypes that are both high yielding and relatively stable.

Shukla's stability has strong positive correlation with Finley &Wilkinson's stability, since it is meant the stable genotypes in Finley&Wilkinson are similar ranked to Shukla's stability. However, positive but non-significant correlation with the Mean grain yield, Wricke's, ASV, YSI, and cultivar superiority stability measures.

The ASV had strong positive correlation with Wricke's and YSI indicating that there is similarity in the ranking of genotypes made based on these stability indices. Though there seems a difference in the value of the other stability parameters.

YSI have strong positive correlation with Cultivar superiority, ASV, and Wricke's stability but strong negative correlate with Mean grain yield, but non-significance correlation with Finley-Wilkinson and Shukla's stability.

Table 7: Spearman's rank correlation coefficients for different GEI stability statistical methods for mean grain yield of 40 barley genotypes grown in six environments of Tigray.

Mean yield	**1.000**						
Shukla's stability	**-0.259**	**1.000**					
Wricke's stability	**-0.313**	**0.198**	**1.000**				
YSI	**-0.799**	**0.312**	**0.736**	**1.000**			
ASV	**-0.275**	**0.286**	**0.896**	**0.782**	**1.000**		
Cultivar superiority	**-0.989**	**0.269**	**0.326**	**0.810**	**0.298**	**1.000**	
Finley& Wilkinson	**-0.163**	**0.957**	**-0.008**	**0.131**	**0.073**	**0.170**	**1.000**
	Mean yield	Shukla's stability	Wricke's stability	YSI	ASV	Cultivar superiority	Finley& Wilkinson

Wricke's Stability given in **table 7** indicated the strong positive correlation with ASV and YSI. But not correlated with Finley&Wilkinson stability analysis and less correlated with cultivar superiority, Shukla's stability and Wricke's stability.

Lin&Binns cultivar superiority is highly correlated with Mean yield (negatively) and YSI (positively) and non-significant correlation with the other stability measures given in this data set analysis.

Finley&Wilkinson stability analysis is highly positive correlation with Shukla's stability measure, but no correlation with Lin&Binns cultivar superiority measure and ASV.

The correlations of the stability parameters with it selves are given 1.00 in all, this indicated that the perfect correlations.

4.3. Additive main effects and multiplicative interaction (AMMI) analysis model

AMMI model introduced by Gauch (1992), and contains the additive main effects (G and E) and multiplicative interaction (GEI) model, or it combines ANOVA and PCA in a single model. In the case of AMMI analysis, principal component analysis is applied to the GEI effects only after some preliminary verifications are made based on ANOVA analysis.

4.3.1. AMMI Analysis of variance

AMMI analysis combines the ANOVA and PCA in a single model and helps in the visual interpretation of complex multi-environment data in a graphical visual comprehension. According to AMMI analysis for grain yield **Table 8**, there is highly significant variation ($P<0.001$) b/n main sources genotype, environment, and the interaction effect of genotype and environment in the grain yield. The environment, genotype and the GEI accounted for 67.53%, 20.22%, and 10.7% of the total sum of squares in the case of grain yield performance, respectively. The main factor environment is highly affects the grain yield performance.

It can be seen from the table, the mean square of the two IPCA were highly significant ($p<0.001$). AMMI multiplicative component further partitioned the GE interaction into two interaction principal component axes (IPCAs). However, the two axes showed a significant contribution to the GEI in the AMMI model.

The IPCA 1 and IPCA2 had very highly significant ($P \leq 0.001$) for grain yield. IPCA 1 and IPCA 2 axes explained 67.99% and 18.23% of the total GEI, respectively. This showed that the first two interaction principle components have taken the largest portions (86.22%) of the interaction sum squares with 67.99% and 18.23% and 43 and 41 degree of freedom respectively of the 40 barley genotypes in the six test environments.

Table 8: AMMI analysis of variance of grain yield of 40 barley genotypes on six environments.

Source	df	SS	MS	SS %	GEI %	P value
Genotypes	39	23.22	0.595	20.22		<0.001
Environments	5	77.53	15.506	67.53		<0.001
Interactions	195	12.33	0.063			
IPCA 1	43	8.38	0.195	7.3	67.99	<0.001
IPCA 2	41	2.25	0.055	1.96	18.23	<0.001
Residuals	111	1.70	0.015			

4.3.2. AMMI biplots Analysis

The AMMI analysis permits the estimation of interaction effects of genotype in each and it helps identify the genotypes best suited for specific environments. Selection of genotypes can be obtained with the aid of bi-plot analysis.

The AMMI biplot analysis for barley grain yield grown in six environments is given in **Figure 1, t**he AMMI1 model is the most well-known AMMI model; its abscissa represents the main effects (G and E), and its ordinate represents the PC1 scores. An AMMI1 biplot have used to evaluate genotypes and environments in terms of their mean production, and at their stability in terms of GEI with PC1.it illustrates that the superior genotype had a higher grain yield (x-axis) and had a minimum value of the IPCA1(y-axis) and near to zero. A Consideration must be given to stable genotypes in addition to good grain performance.

The vertical line that splits the horizontal axis in half represents the mean of grain yield, and the genotypes on the right side had a larger grain yield than the average. Conversely, the zero line for IPC1 is the horizontal line that split the vertical axis into two sections. Since, the stable genotypes have a minimal GxE interaction and are located close to this line. Although the genotypes with low grain yield performance (below average) might be suggested for weak and poor environments, but their IPC1 value should have be positive.

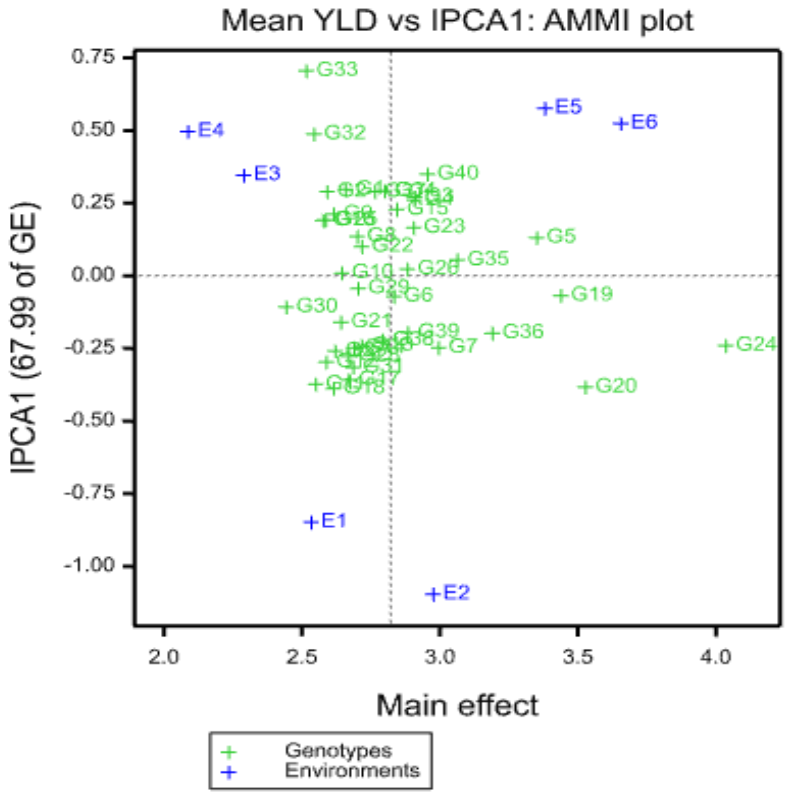

Figure 1: the AMMI1 biplot mean yield vs. IPCA1

The genotypes and environments average was 2.822 tons. The superior genotypes were G24, G19, G5, G36, G35 and G7 and were located on the right side of the graph and close to zero in terms of the IPCA1 .the most unstable genotypes and the lowest grain yield genotypes had G33, G32, G16, G18, G30, and G12 had the least GxE interaction in the environments E1, E3, and E4.

Genotypes (environments) with large IPCA1 score (either positive or negative) have high interactions whereas genotypes (environments) with IPCA1 score near to zero have small interactions. The genotypes having a zero IPCA1 score are less influenced by the environments and adapted to all environments. Since G10, G26, G35, G19, G29, G6, and G22 were most stable genotypes that across these environments because their IPCA1 scores were close to zero. However the genotypes G19, G26, G6 and G35 are more preferable since it had a mean grain yield above average, but the rest genotypes G10, G29, and G22 have grain mean yield below average. In summary, a stable genotype might not be the highest yielding. These results are in line with (Zeleke, 2016).

The environments having a small score had small interaction effects indicating all genotypes performed well in these environments. Hagereselam 2017(E3) was relatively close to zero than other environments, hence it was more stable environment. But its mean yield is fifth (before last) compared with the rest environments; it might not be the best location with respect to yield.

The graph space Figure 1 are divided into four quadrant from lower yielding environments in quadrant I and IV to high yielding in quadrants II and III. In Addition, quadrant II considered as ideal environment that have high yielding genotypes with stable environments and are consistently perform well across different conditions. So, from the graph in Figure 1, Ayba (E5 & E6) which is in quadrant II are ideal environments, while quadrant III characterizes in high yielding environment with unstable genotypes, in this quadrant Mekelle 2018 (E2) is found. Similarly Hagereselam 2017(E3) and Hagereselam 2018(E4) in quadrant I are characterized as stable genotypes and lower yielding and in contrast quadrant IV unstable genotype with the low yielding environment and Mekelle 2017 (E1) is found.

As for AMMI2, its x-axis represents the IPCA1 scores and its y-axis the IPCA2 scores the average values are crossed at the origin. In this way we can evaluate genotypes in terms of their stability and specific adaptability to environments, and vice versa and helps in the visual interpretation of the GEI pattern and identify genotypes or environments that exhibit low, medium, or high level of interaction effects (Zeleke, 2016).

IPCA1 and IPCA2 of grain yield accounted for 67.99% and 18.23% of interaction respectively. The stability of a genotype or an environment is determined by the end point of its vector from the origin. Genotypes near the origin are non-sensitive to environmental interactive forces, hence may be considered stable ones and those distant from origin are sensitive and have large interactions. Genotypes G19, G29, G5, G8, G10, and G26 were closer to the origin than any of other genotypes, hence they are most stable (Figure 2). However G12, G18, G33 and G32 are considered the unstable genotypes.

In AMMI 2 biplot, the environment scores are joined to the origin by the vector lines. Environments with short lines have strong interaction effects. Mekelle 2018 (E2), Hagereselam 2018 (E4), and Ayba 2017 (E5) having longer vector lines had high interaction while Mekelle 2017 (E1), Hagereselam 2017 (E3), and Ayba 2018 (E6) having shorter spokes produce a relative weak interaction.

As for specific adaptations, Figure 2 showed G33 with high yield performance in environments Hagereselam 2018(E4) and Ayba 2018 (E6) while performing poorly in Mekelle (E1 & E2). Mekelle 2017 (E1) had genotypes G17, G28 and G31 and Mekelle 2018 (E2) had genotypes G18, G11, and G20 with high performance due to specific adaptations; G15 and G16 also adapted well in Ayba 2017 (E5). The environment Ayba 2018(E6) had G9, G37 and G32 as the genotypes with the highest performance due to specific adaptation, but these genotypes had low performance in Mekelle 2017 (E1).

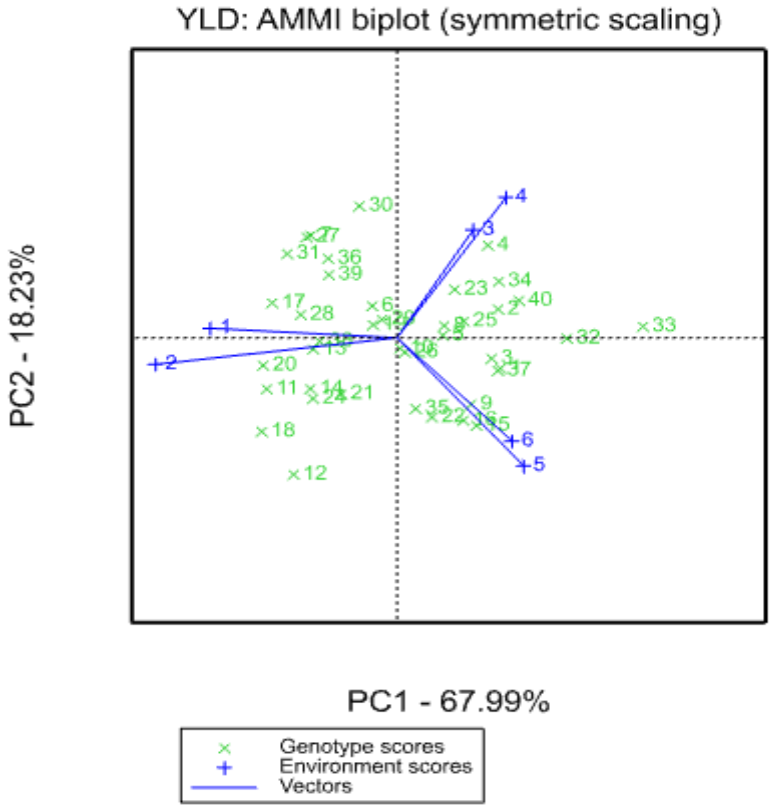

Figure 2: AMMI2 biplot of IPCA1 vs. IPCA2 of 40 barley genotypes on six environments

4.3.2. AMMI selections for the highest four yielding genotypes across six environments

The AMMI model selected four best genotypes for each environment and illustrated in **Table 9**. The genotype G24 is the first highest yielding genotype in the six test environments, which is followed by; G19, G5, and G20. The genotypes G24, G19, and G20 are appeared in the top four high grain yield genotypes in at least six environments, which is followed by; G5 in four environments and G36 in two environments. The pair environments with the same ranking genotypes are in one location with two years considering the year vs. location as environment. Since the locations give same higher grain yield genotypes within two consecutive years. G24, G20, G19, G5, and G36 are the genotypes with ranks of mean grain yields 1st, 2nd, …, and 5th respectively.

Table 9: AMMI selections of first four highest yielding genotypes per environment

Number	Environment	Mean (tone/ha)	IPCA Score	Ranking Genotypes			
				1st	2nd	3rd	4th
5	Ayba 2017	3.382	0.5768	G24	G5	G19	G20
6	Ayba 2018	3.657	0.5245	G24	G5	G19	G20
4	Hagereselam 2018	2.088	0.4964	G24	G19	G5	G20
3	Hagereselam 2017	2.291	0.3465	G24	G19	G5	G20
1	Mekelle 2017	2.535	-0.8480	G24	G20	G19	G36
2	Mekelle 2018	2.977	-1.0961	G24	G20	G19	G36

4.4. GGE bi-plot Analysis

The GGE Biplot model (Yan et. al., 2000) was introduced based on biplots, which are an effective tool for visualizing two-way data, and are frequently used for the analysis of MET data. A GGE biplot is able to simultaneously display genotype main effects (G) and genotype × environment effects (GE) from a two-way data table (Yan et. al., 2000). Its first component, when highly correlated with genotype main effect (G), represents the proportion of production attributed to the genotype effect. The second represents the proportion explained by GEI. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also sources of variation in GEI analysis of METs data (Yan et al., 2007).

4.4.1. GGE biplot for evaluation of genotypes and environments interaction

GGE biplots is a multi-faceted tool originated with Gabriel (1971), and it has strongly captured the imagination of plant breeder and production agronomist. GGE biplot analysis is increasingly being used in the GEI interaction data analysis in agriculture (Daemo et al., 2023; Hailemariam & Tesfaye, 2019; Tier, 2014; Yan et al., 2007; Yan & Kang, 2017).

GGE biplots is one of the statistical tools with various uses, i.e., Mega-environment analysis (e.g. "Which- won- where" pattern), whereby specific genotypes can be recommended to specific mega-environments; genotype evaluation based on their mean performance and stability across mega environments, and test-environmental evaluation based on their discriminating ability and representativeness (Yan & Hunt, 2001).

The partitioning of GGE through GGE biplot analysis showed that PCA1 and PCA2 accounted 66.73% and 22.40% of the GGE sum squares respectively for the grain yield of the 40 barley genotypes,

explaining 89.13% of the total GEI variation as shown in **Figure 3**. This showed that the first two principal components were adequate for visually representing the data 89.13%.

In this case GGE is greater efficient by retaining most of the variation in the first two IPCAs i.e. 89.13%, which is by far greater comparing with AMMI that is around 86.22%. This GGE result greater than that of AMMI is also observed by (Daemo et al., 2023; Rad et al., 2013; Semahegn & Gebreyohannes, 2020; Zeleke, 2016).

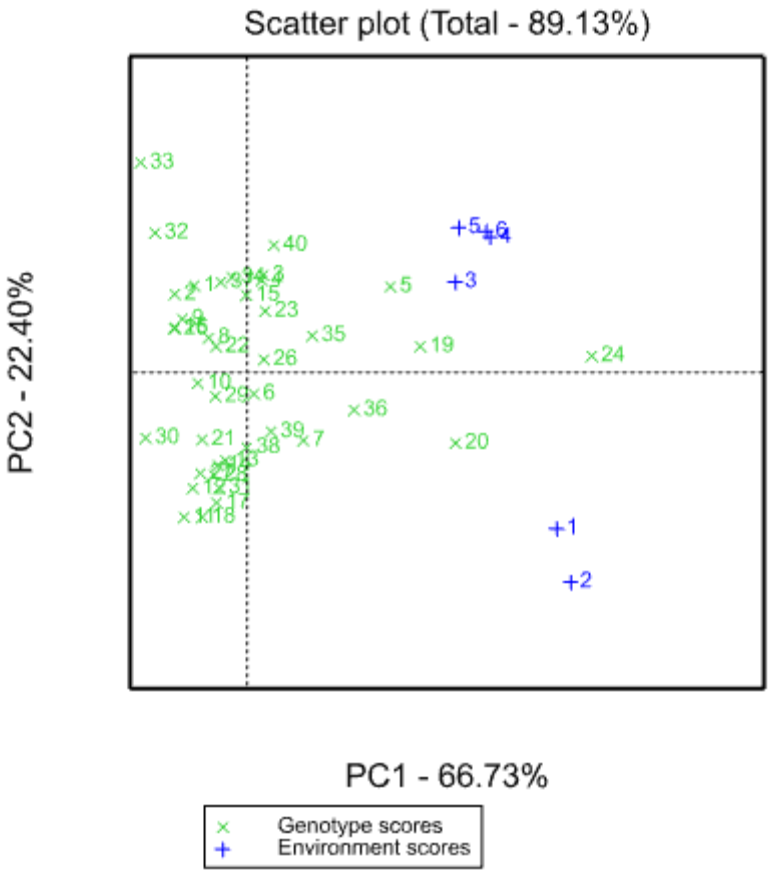

Figure 3: The GGE biplot Showing the performance of 40 barley genotypes on six test environments

4.4.2. The "which won where " pattern and mega environments

The polygon view of a GGE biplot explicitly displays the "which-won-where" pattern and /or it indicates the best genotypes in each environment and group of environments, hence, it shows a short summary of the GEI pattern of a MET data set (**Figure 4**). In this situation, the polygon is formed by connecting the genotypes that are far away from the origin of the biplot and all of the other genotypes are contained inside the polygon.in this case, the polygon connects all the farthest genotypes, and a rays (lines) that are perpendicular to the polygon had divide the polygon in to sectors. The sectors can help to visualize the mega environments. This means the best (winning) genotypes of the sectors are placed at the vertex in that sector. The vertex genotypes in this investigation were G24, G33, G30, G11, and G20.Thus, the vertex genotypes for each sector indicates the highest yield for the environments that lie within that sector.

The rays in **Figure 4** are 4 lines that are perpendicular to the sides of the polygon and divide the biplot into 4 sectors .But the environments fall into only one of the sectors and the genotypes G24, G20, G19,G5, G36, G35,G7, and G26 have located in the given sector and they are given higher yield in all the six test environments, while G24 and G20 are located at the vertex in this sector indicates the highest grain yield compared to the other genotypes in all the six test environments in this study.

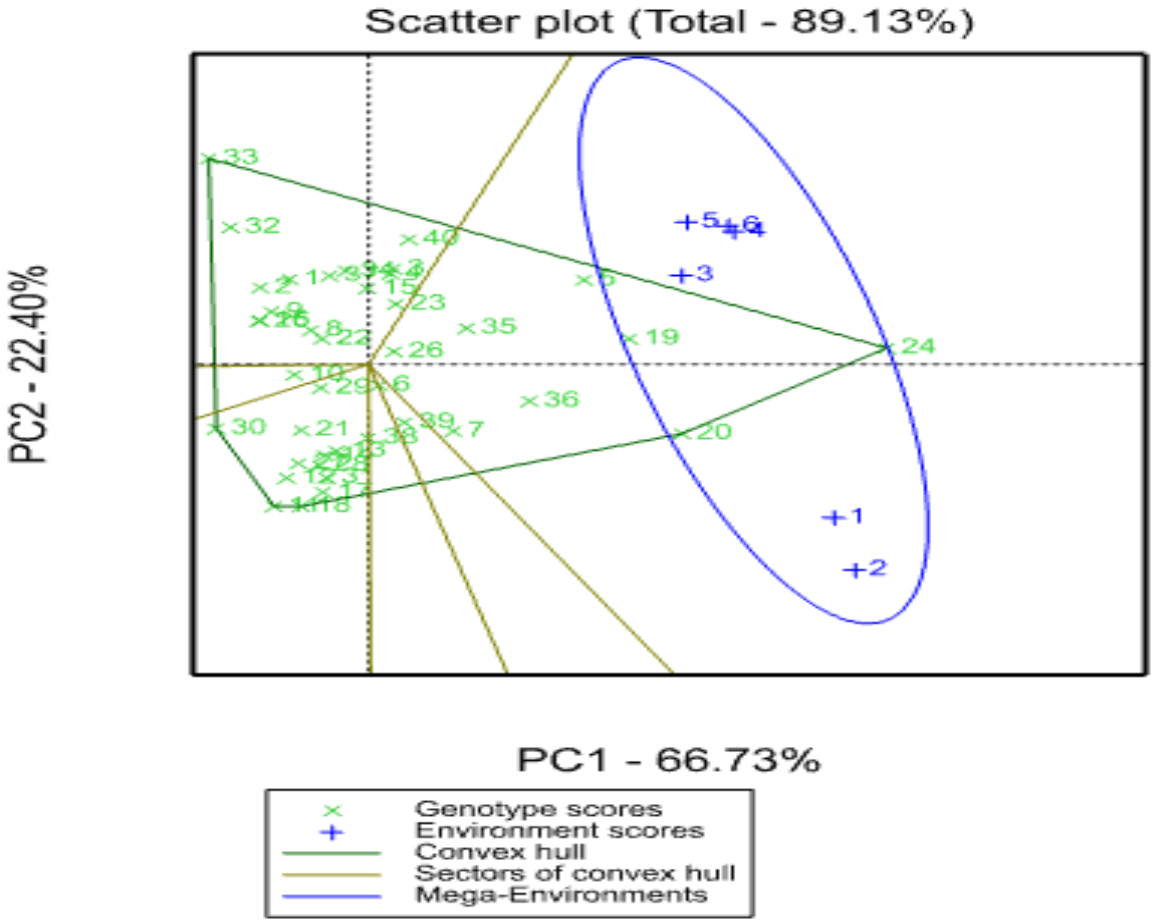

Figure 4: "Which-won-where" pattern of GGE biplot based on 40 barley genotypes evaluated in six environments of Tigray

Another important feature of this biplot is that it indicates environmental groupings, which suggestes a possible existence of different mega-environments. Visualization of the "which-won-where" pattern of METs data is important for studying possible existence of different mega-environments (ME) in a region (Yan & Hunt, 2001 ;Gauch, 2016) .

In case of this study there is only one mega-environment based on the analysis of the six environments of the data, since there is similarities between the testing environments and the highest yielding (vertex) in the mega-environment are the genotypes G24 and G20 . the other vertex genotypes G33,G30, and G11 are poor performing in all the six environments.

4.4.3. Mean yield and Stability performance of genotypes

The yield stability of genotypes was evaluated by the average environment coordination (AEC) method (Yan and Hunt, 2001). In this method, the average principal components will be used in all environments, as given in **Figure 5**. A line drawn through this average environment and the biplot origin is called the average environment axis and serves as the abscissa of the AEC. Unlike to abscissa of AEC, The greater GEI effect and reduced stability indicates when far from the AEC ordinate in either directions of the plot. The AEC (y-axis) separates genotypes with below-average means from those with above-average means. The Genotypes G24, G20, G19, and G5 had the highest mean yields, and genotypes G30, G33, G32, and G11 had the lowest mean yields. The yield of genotype G33 was the most variable (far from AEC abscissa), while G19, G24, G26, and G35 were highest stabilities.

An ideal genotype is one that has both high mean yield performance and high stability. In this case, it is defined by a projection onto the mean-environment axis that similar the longest vector of the genotypes that had above-average mean yields and zero variability across all environments. Thus, varieties G30, G33, G32, and G11 which had fell below the AEC ordinate, showed below average grain yield performance, whereas varieties G24, G20, G19, G5, G36, G35, G7, and G26 fells above the AEC ordinate, performed above average grain yield average performance.

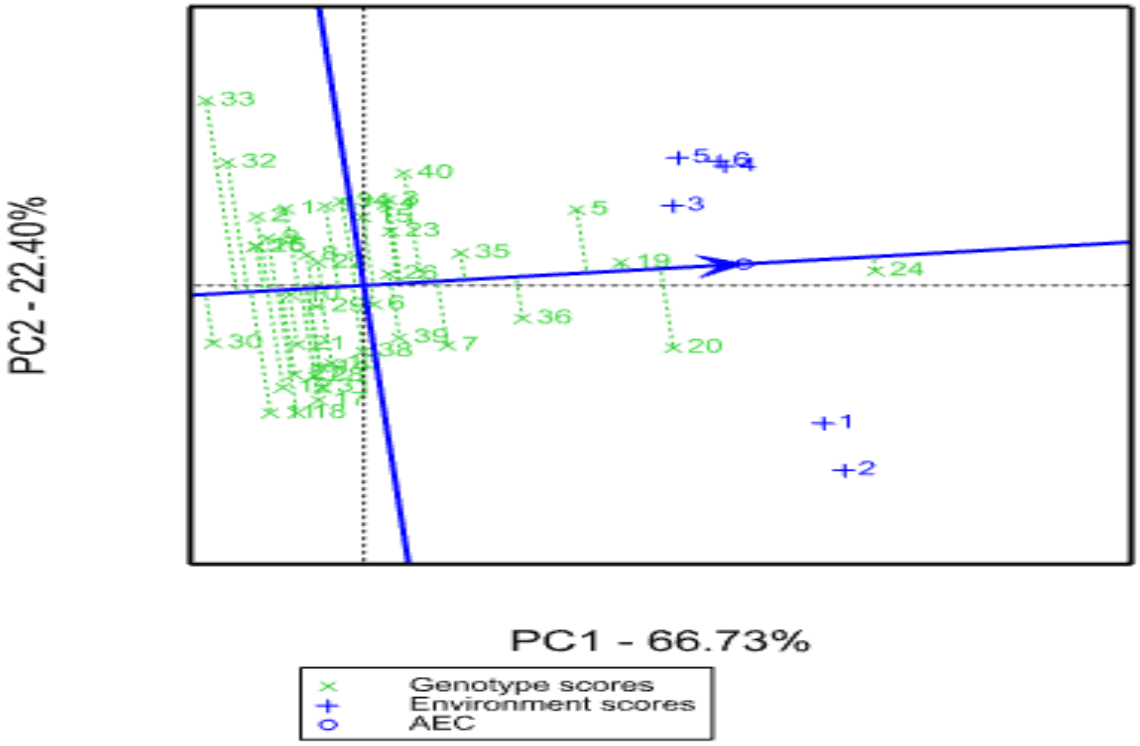

Figure 5: AEC views of the GGE biplot for the mean performance and stability of 40 barley genotypes in six test environments

4.4.4. Evaluation of genotypes based on the ideal genotypes

An ideal genotype has the highest mean grain yield and is stable across environments (Bacha, 2015; Tulu & Wondimu, 2019) .The ideal genotype is located in the first concentric circle in the biplot. Desirable genotypes are those located close to the ideal genotype. Thus, starting from the middle concentric circle pointed with arrow concentric circles was drawn to help visualize the distance between genotypes and the ideal genotype (Yan & Tinker, 2006).

The ideal genotype can be used as a reference for selection. Genotypes that are close to the ideal genotype can be considered in further tests since they are desirable genotypes, while genotypes far away from the ideal genotype can be minimize for breeding cycle from the given environments because they have poor performance.

G24 is the ideal genotype, since it is located at the first concentric (center) circle in the biplot given in **Figure 6**. The genotypes G20, G19, G5, G36, and G35 are located near to the ideal genotype, and considered they are desirable genotypes. However, the genotypes G33, G32, G30, and G11 are undesirable genotypes were they are far from the first concentric circle (ideal genotype). This result is in line with those by (Tulu & Wondimu, 2019) and (Mehari et al., 2015).

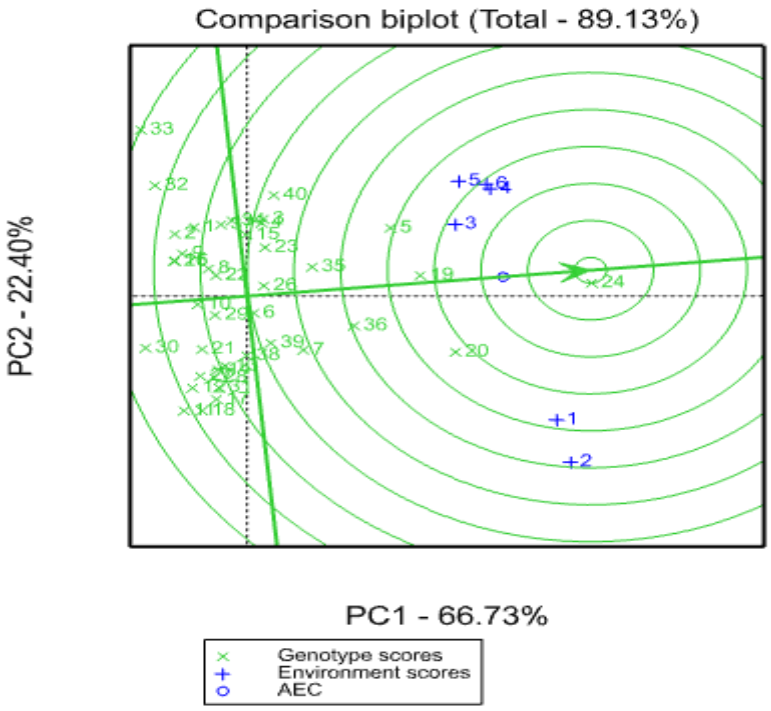

Figure 6: GGE biplot with scaling focused on genotypes, for the evaluation based on the ideal genotype of 40 barley genotypes across six test environments

The distance between two genotypes approximates the Euclidean distance between them, which is a measure of the overall dissimilarity between them (Yan *et al*., 2006). In this case, G26, G35, and G5 are

quite similar, whereas G24 and G11 are very different. This implies that the dissimilarity is because of the variation in interaction with the environments (GEI).

4.4.5. Test environments evaluation for selecting generally adapted genotypes

The ideal environment is representative and has the highest discriminating power(Yan & Kang, 2017). The ideal environment is located in the first concentric circle in the environment-focused biplot, and it is a point on the Average Environment Coordinate in the positive direction ("most representatives") with a distance to the biplot origin equal to the longest vector of all environments. The desirable environments are close to the ideal environment. Nearest to the first concentric circle, Environment E4 (Hagereselam 2018) was the ideal environment (**Figure 7**); therefore, it should be regarded as the most suitable to select widely adapted genotypes. Since the environments E6 (Ayba 2018) and E3 (Hagereselam 2017) are located near to the ideal environment and they are desirable environments. In contrast to the six test environments E2 (Mekelle 2018) is poorest (undesirable) for selecting genotypes adapted to the whole region (all environments).

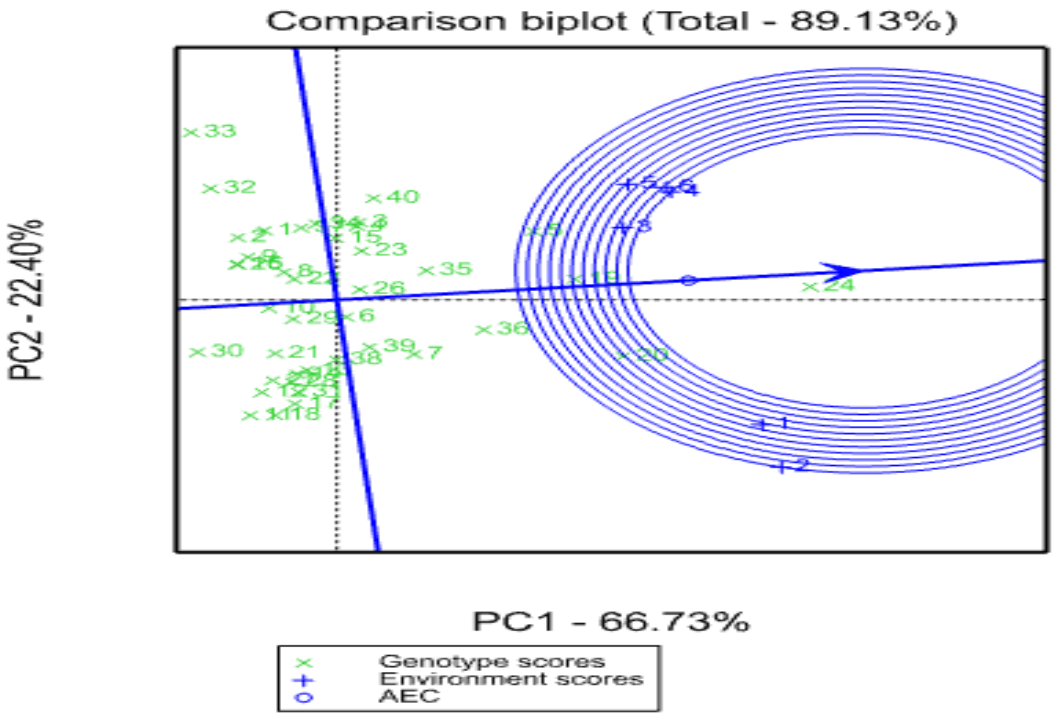

Figure 7: GGE biplot with scaling focused on environments, for the evaluation based on the ideal environment of 40 barley genotypes across six test environments

4.4.6. Discriminating ability and representativeness of environments

The lines connecting the environments to the biplot origin are called environmental vectors, and the length of the environmental vectors is proportional to their standard deviation which is a measure of the descriminating ability of the environments .Similarly the angele between two environments measure their

correlation coefficient between the test environments . According to Kroonenberg (1995) and Yan (2002) the cosine angle between the vectors of two environments approximates the correlation coefficient between them. When the angle between the environments is acute angle ($< 90^0$) , the environments have strong postive correlation ,if the angle is aptuse angle ($>90^0$) there is strong negative correlation , and if the angle is right angle($=90^0$) there is no correlation between the environments. In this case, all the six test environments had stong postive correlations.Espetially Ayba 2018 (E6) and Hagereselam 2018 (E4) have highly correlated environments (**Figure 3**).

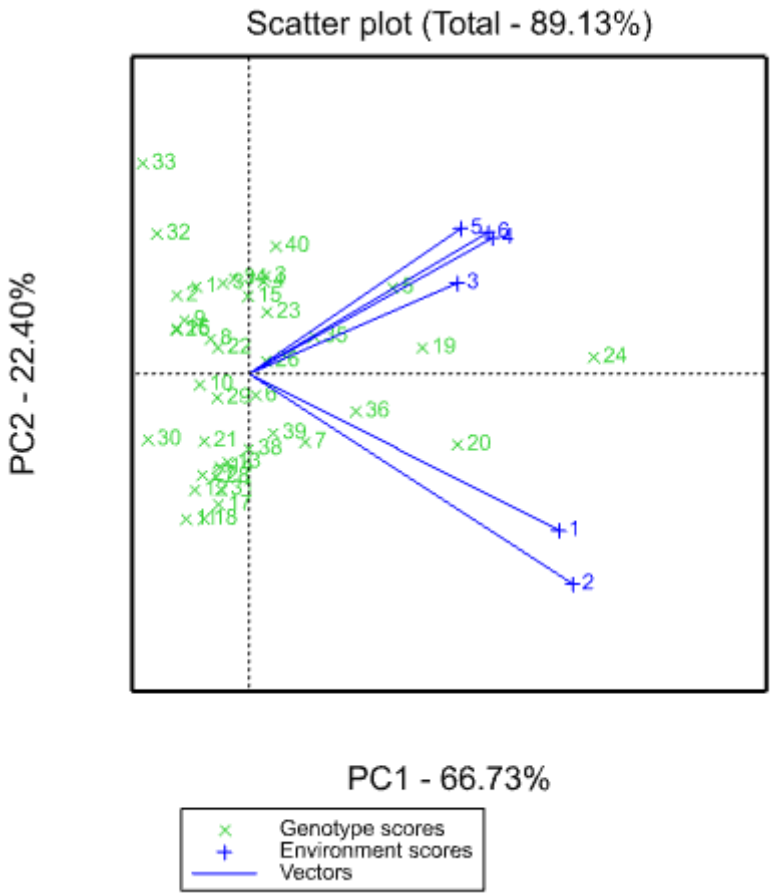

Figure 8: GGE biplot to show Discriminating power and representativeness of the six environments

The discriminating power vs. representativeness view of the GGE biplot as shown in **Figure 8** showed that the test environments E4 (Hagereselam 2018) and E6 (Ayba 2018) with the longest projection from the biplot origin were found more discriminating of the genotypes, i.e., they provided much information about the differences among genotypes. On the other hand, E3 (Hagereselam 2017), with its shortest vector from the biplot origin, was found less discriminating of the test genotypes. Test environments E3 (Hagereselam 2017), E4 (Hagereselam 2018) and E6 (Ayba 2018) were found to be more representative of other test environments due to the fact that they have smaller angles with the average environment axis(AEAs). E4 (Hagereselam 2018) was therefore identified as an ideal environment that has both discriminating ability of the genotypes and representative of the other test environments. Therefore,

environment E4 (Hagereselam 2018) can be used to effectively select superior barley genotypes that can perform consistently across environments, and most representative and desirable of all.

4.5. Comparison of AMMI and GGE Biplot analyses

The AMMI (Additive Main effects and Multiplicative Interaction) and GGE (Genotype plus Genotype by Environment interaction) biplot methods are the two most frequently used methods in the analysis of genotype by environment (GxE) data. Both methods aim to visualize the interaction between the genotypes and environments and identify the stable genotypes across environments. AMMI and GGE biplot which are both based on the statistical model of principal component analysis (PCA) (Semahegn & Gebreyohannes, 2020).

The AMMI model Proposed by (Gauch et al., 2008)uses analysis of variance and principal component analysis to achieve a better understanding of GEI, its causes and consequences. Yan et al. (2000) proposed the GGE Biplot analysis, which considers both genotype main effects and GEI effects as important for the analysis.

GGE biplot analysis integrates some features from AMMI. It allows visual interpretation of GxE interaction:

1. The analysis AMMI model applies only to GEI effect, while GGE biplot considers G plus GEI .but this difference is not to make either of the methods superior. Nevertheless, GGE Biplot presents some features based on the presence of G in the analysis, which naturally the AMMI model does not offer(Neisse et al., 2018).
2. The AMMI and GGE biplots may explain differently the sum square of GEI effect, since the GGE may explain more or less than that of AMMI biplot. In this case, GGE biplot is greater efficient by retaining most of the variation in the first two IPCAs i.e. 89.13%, which is by far greater comparing with AMMI that is around 86.22%. GGE biplot analysis is based on environment-centered PCA, whereas AMMI analysis is referred to double center PCA (Kroonenberg, 1995).
3. The which-won-where view of the GGE biplot is superior to the AMMI graph for mega-environment analysis in that it explains more G+GE, it is easier to construct, and it is easier to visualize the which-won-where patterns, especially for large MET data sets. However, AMMI could be misleading (Yan & Tinker, 2006).
4. The mean vs. stability view of the GGE biplot is superior to the AMMI biplot for genotype evaluation because it explains more G+GE, it has the same units on both axes, and it has an objective shape that inherently results from the data , whereby it shows the relative importance of G vs. GE in the data. Furthermore, the GGE biplot has the inner product property of a biplot; it shows not only the mean

performance and stability of each genotype, but also the relative performance of each genotype in each environment.

5. The discriminating power vs. representativeness view of the GGE biplot is an effective tool for test-environment evaluation, which can lead to the identification of a minimum set of discriminating and representative test environments. Test-environment evaluation has not been a research topic in AMMI analysis.

6. Genotype evaluation is meaningful only for a specific mega-environment, and an ideal genotype should have both high mean performance and high stability within a mega-environment. Assuming that the mega-environment differentiation in **Figure 4**, since genotype evaluation should be conducted for each mega-environment. **Figure 5** is the "Average Environment Coordination" (AEC) view (Yan & Hunt, 2001)of the GGE biplot involving the six environments (Yan et al., 2007).

Superior to AMMI, the GGE biplot has many visual interpretations that an AMMI does not have, particularly allows visualization of any crossover GxE interaction. This part of GxE interaction is usually essential to breeding program. In addition, comparing with different AMMI family models (AMMI0, AMMI2, …, AMMI k) GGE biplot is always close to the best AMMI models in most cases.

Moreover, GGE biplot is more logical and biological for practice than AMMI in terms of explanation of PC1 score (GEI effect), which represents genotypic effect rather than additive main effect. This is in line with the ideas of (*AMMI and GGE Biplot Analysis of Root Yield Performance of Cassava Genotypes in the Forest and Coastal Ecologies*, 2015; Hailemariam & Tesfaye, 2019; Tier, 2014; Yan et al., 2007)

CHAPTER FIVE

5. CONCLUSION and Recommendation

This study indicated that the genotype, environment and genotype-by-environment interaction were highly significant effect ($p<0.001$) for grain yield of barley genotypes tested in cropping seasons studied in Tigray, Ethiopia. The contribution environment accounted for 40.6 %, while the genotype-by-environment interaction and genotype are 23.07% and 21.12% of the variation in grain yield respectively.

Among various statistical techniques used for evaluating GEI, the two most frequently used are AMMI (Additive Main-effects and Multiplicative Interaction) and GGE (Genotype plus Genotype by environment interaction) Biplot. In case of this study the GGE model is an effective method for analyses of GEI; in explanation of the total sum squares, in identifying superior genotypes for each mega environments (which-won-where pattern), in identifying most discriminating and representative environments The polygon views of the GGE biplot pointed out that there existed only one mega-environment, while GGE is more applicable for diverse environments.

Various stability models were used in the measurement of genotype stability such as; Wricke's, Finley-Wilkinson, Shukla's, Lin&Binns cultivar superiority, AMMI Stability Value (ASV), YSI, AMMI and GGE biplots. G19, G36, G5 are the most stable genotypes in almost the stability analysis measures, since they are superior genotypes with all test environments. While the genotypes G33, G32, G12 and G18 also the instable genotypes in most of the genotype stability measurements.

GGE Biplot view of relation among test environments of this study showed that; among the testing environments Hagereselam 2018 is an ideal testing location to identify stable and high yielding genotypes, since Hagereselam and Ayba are most efficient test locations for identifying stable and high yielding barley genotypes for the region. Mean performance and stability biplot of tested genotypes across test environments indicated that G24 had the ideal genotype with highest mean yield as well as stability with desirable genotypes G20, G19, G5, G36, while G33 and G30 had the lowest mean yield and less stability undesirable genotypes in all the six test environments.

Recommendations

This study recommends that:

- The genotypes G24, G19, G5 and G36 are recommended for breeders and researchers to use for improving production and for farther experimental analysis in addition for other environments.
- Environments E4 and E6 had recommended environments for experiments of barley genotypes.
- A statistical method GGE biplot is recommended to use in genotypes and environments yield and stability evaluations of multi-environmental trial data analysis.
- To use multiple environments (more than six) with a lot of years in experiments of multi-environmental trial data analysis is recommended.

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