



Application of Genotype by Environmental Interaction in Crop Plant Enhancement

Temesgen Begna*

Ethiopian Institute of Agricultural Research, Chiro National Sorghum Research and Training Center, Chiro, Ethiopia

***Corresponding Authors:** Temesgen Begna, Ethiopian Institute of Agricultural Research, Chiro National Sorghum Research and Training Center, Chiro, Ethiopia

Abstract: The difference in genotype response to different environments is referred to as genotype-by-environment interaction. Due to scaling or re-ranking effects, there are two basic types of genotype-by-environment interaction. The scaling effect is linked to the variance of characteristics in different environments. The assessment of genetic correlations between performances in different environments is a measure of the re-ranking genotype-by-environment interaction effect. The presence of genotype-by-environment interaction indicates that the phenotypic manifestation of a character is influenced by both environmental factors and the genotype. The presence of genotype-by-environment interactions has long presented a serious impediment to gaining a better understanding of the genetic control of variability. They have made it difficult to evaluate evolutionary trends and have inhibited the rationalization of breeding strategies and methods for improved commercial crop performance. The genetic variation in phenotypic plasticity is known as genotype-by-environment interaction, and it is a key concept in ecology and evolutionary biology. A genotype-by-environment interaction has far-reaching implications for trait development and determining how varieties will respond to changes in the environment. Interactions between genotypes and their environments impact the genetic architecture of quantitative traits and are confounding factors in genetic investigations. In general, the presence of genotype-by-environment interaction makes choosing superior genotypes more difficult. The presence of genotype-by-environment interaction makes superior genotype selection more difficult, and understanding the environmental and genotypic causes of considerable genotype-by-environment interaction is critical at all phases of plant breeding. In-plant breeding, genotype-by-environment interaction is a key factor in producing superior genotypes for specific environments. In-plant breeding, the presence of genotype-environment interaction manifests itself as either inconsistent responses of some genotypes relative to others as a result of genotypic rank change or changes in the absolute differences between genotypes without rank change. A plant breeding program's success is determined by its ability to provide farmers with genotypes that are guaranteed to perform best in terms of production and quality under a variety of environmental conditions. The expression of a phenotype is determined by the genotype, the environment, and the genotype by environment interaction, which is defined as the differential responsiveness of specific genotypes to different environments. Genotype by environment interaction is a statistical decomposition of variance that assesses the relative performance of genotypes produced in various environments.

Keywords: Genotype \times environment interaction; Environment; Phenotype; Genotype; Interaction; Variation

1. INTRODUCTION

The differential in response of two genotypes to environmental variation is known as genotype by environment interaction (Yan *et al.*, 2007). The genotype of a crop variety and the environment in which it is grown help to determine its performance. Inconsistency in genotype performance or a change in the magnitude of the difference between genotypes under a variety of environments is referred to as genotype by environment interaction. Plant breeders must consider genotype-environment interactions while generating improved cultivars (Kan, A and Kaya, M, 2010). When unpredictable environments and/or reduced genetic variance increase selection in one direction, the genotype by environment interaction has implications for genotype adaptation and evaluation. For breeders, the genotype by environment interaction is undesirable since it complicates genotype evaluation (Yan and Tinker, 2006).

Identification of phenotypic stability and control of adapted genes are critical requirements for improving plant adaptation (Farshadfar *et al.*, 2012). Variations in the phenotypic composition of the

yield, while the genotypic composition remains stable are referred to as phenotypic stability (Becker and Leon, 1988). Plant breeding programs are focused on selecting superior genotypes in specific environments. Growers use a target environment to produce their crops (Jat P and Serre M.L, 2016). Plant breeders undertake trials across places and years, especially during the last stages of cultivar development, in order to identify superior genotypes across multiple environments. When genotype performance changes across environments, there is said to be genotype-by-environment interaction. Because of the effect of environment on trait expression, genotype performance can vary substantially across environments. Cultivars with high and consistent yields are difficult to find, but they are extremely valuable (Dia *et al.*, 2012).

Plant breeders use their own multiple-environment trials, or test environments, to undertake indirect selection because testing genotypes in all target environments is difficult. The interaction between genotype and environment reduces the predictability of genotype performance in target environments based on genotype performance in test environments (Kumar *et al.*, 2013). The selection of proper test locations is an important component in plant breeding because it compensates for genotype by environment interaction and increases selection gain (Yan *et al.*, 2011). Crop adaptation to local environments is influenced by developmental responses to weather, photoperiod, nutrition availability, and abiotic and biotic stresses, all of which differ between growing regions (Adee *et al.*, 2016). A cultivar superiority index (Pi) evaluates the adaptability of superior cultivars to specific conditions, with a lower value indicating general adaptation and a greater value indicating specific adaptation (Lin and Binns, 1988).

When genotypes differ with how their trait values vary across environments, this is known as genotype by environment interaction. Understanding the genetic basis of trait variation relies on genotype by environment interaction, which has applications in genomics, evolutionary biology (Via and Lande, 1987), and ecology (Miner *et al.*, 2005). Quantitative trait phenotypic variance (δ^2P) can be broken into genotypic (δ^2G), environmental (δ^2E), and genotype-by-environment (G x E) interactions ($\delta^2G \times E$) components (Gage *et al.*, 2017). This interaction accounts for the varying reaction of distinct genetic backgrounds to the settings they encounter, and it constitutes a fraction of the phenotypic variance that impedes broad-scale adaptation but can be utilized for environment-specific adaptation (Gage *et al.*, 2017). Although experimental assessment of the higher-order variance components is sometimes challenging and not always attainable, depending on the mating and experimental designs used, the genotypic variance can be further partitioned into additive (δ^2A), dominance (δ^2D), and epistatic genetic variance components.

The overall $G \times E$ variance can be partitioned into additive-by-environment interaction, dominance-by-environment interaction, and epistatic-by-environment interaction variances in the very same fashion. Understanding how phenotypic variance is broken down into its constituent components for each trait can help breeders make better decisions about the best breeding methods and individuals to use as breeding parents for the next generation, as well as the best combination of current breeding lines to produce hybrids for production in hybrid crops. When the breeding goal is to generate cultivars with consistent performance across a wide range of environments, $G \times E$ interactions hamper both the early- and late-generation evaluation phases of cultivar development, and they are generally considered as a nuisance factor to be reduced (Rogers *et al.*, 2021). Understanding the relative relevance of $G \times E$ interactions can help in breeding scheme optimization. Crop breeders typically test a large number of novel breeding materials in one or a few environments, followed by more extensive testing of a small number of selected breeding lines in a variety of environments.

To analyze multi-environment trial data and choose superior genotypes for specific or broad adaptation, several methods have been applied. For examining $G \times E$ in genotype evaluation, methods such as additive main effects and multiplicative interaction (AMMI) (Gauch, 2006) and the genotype, genotype by environment (GGE) biplot technique (Yan *et al.*, 2007) have been recommended. GGE biplot is based on principal component analysis, while AMMI model combines analysis of variance and principal component analysis (Yan *et al.*, 2007). The primary effects are considered as additive effects in the AMMI model, whereas the GEI is treated as a multiplicative effect (Annicchiarico P, 1997). Yan *et al.* (2007) also found that both GGE and AMMI analyses were capable of separating genotype and genotype by environment in mega-environment analysis, GGE biplot was superior to AMMI graph in mega-environment analysis. The GGE biplot displays the effective perspective of a multi-environment experiment using principal component scores to indicate "which-won-where" (Yan

et al., 2007). GGE biplot is a good tool for visual data interpretation, according to various researches (Akter *et al.*, 2015). The interaction of genotype and environment is crucial in determining the relationship between traits such as linear and non-linear regression (Mungra *et al.*, 2011).

In Africa, where agricultural productivity is insufficient, the growth in population and the resulting increase in demand for agricultural products is predicted to be greater. It is impossible to overestimate the importance of increasing agricultural production. Given the restricted potential for extending cultivated land globally, this embodies challenges to developing systems, and must mostly come from increasing yield per unit area. To accommodate this demand, several crop enhancement programs have been launched around the world. Every year, promising genotypes are tested for performance at a number of sites that represent the crop's main growing area as part of every crop development program. This is to find genotypes that have both high yield and resistance to severe environmental changes. It has been discovered that a specific variance in environment can result in genotype disparity. Genotype environment interaction refers to the interaction of genetic and non-genetic factors that cause genotypes to function differently in different environments. As a result, a genotype-environment interaction can be defined as a change in the relative performance of two or more genotypes in two or more environments. The objective of the paper was to understand the application of genotype by environment interactions in crop plant enhancement for desired traits.

2. ORIGIN OF GENOTYPE × ENVIRONMENT INTERACTIONS

There are two different conceptions of the origin of genotype × environment interaction. The two concepts are referred to as biometric and developmental interaction (Tabery J, 2007) or statistical and common sense interaction (Sesardic N, 2005). Fisher introduced the biometric concept of genotype × environment interaction, whereas Lancelot Hogben introduced the developmental concept of genotype × environment interaction (Tabery J, 2007). The biometric (statistical) concept of genotype × environment interaction has its origins in research programs that seek to measure the relative proportions of genetic and environmental contributions to phenotypic variation within populations. In population genetics and behavioral genetics, biometric gene-environment interaction is particularly important (Tabery J, 2007). Developmental geneticists and developmental psycho-biologists are more likely to use the term "developmental genotype-environment interaction." The developmental interaction is expressed in the causal interaction of genes and environments in producing an individual's phenotype, not just as a statistical phenomenon (Tabery J and Griffiths PE, 2010). Fisher and Lancelot Hogben's concepts have substantially influenced subsequent research on genotype-environment interaction (Tabery J, 2007).

An individual's phenotype is determined by genetics, environment, and any genotype-environment interactions. When genotypes' relative performance varies depending on the environment, such interactions are said to exist. In one environment, a genotype's performance may be superior, whereas, in another, it may be lower. The genotype-environment interaction can be divided into two types: (1) rank-change interaction, in which genotypes are ranked in different orders in different environments; and (2) level-of-expression interaction, in which the expression of genotypic differences (the spread of the breeding values) varies across environments without necessarily changing the order of genotype rankings. In order to obtain the best genetic gain for crop enhancements, breeders must first determine the patterns and magnitude of GE (Muir *et al.*, 1992). Breeders are more concerned with rank-change interaction since they are primarily concerned with evaluating and selecting candidate genotypes. While level-of-expression interaction isn't as significant in breeding as it is in other fields, it could be crucial in determining which genetic material to use in specific growing environments and for specific end-products.

The relationship between genotype and environment is a fundamental element limiting germplasm selection and the discovery of superior genotypes for use in plant breeding programs. As a result, a genotype-environment interaction can be defined as a change in the relative performance of two or more genotypes in two or more environments. Researchers typically undertake multiplication experiments to examine new or enhanced genotypes across several environments (locations and years) before recommending them for release and commercialization. The difference in genotype responses to different environments is referred to as genotype by environment interaction (Falconer and Mackay, 1996). The effects of genotype, environment, and genotype-environment interaction impact phenotypic performance as well as general and particular adaptability to various environments

(Falconer and Mackey, 1996). This information is critical for developing better selection strategies and determining the ideal environment in which to choose genotypes for grain yield (Kang, 1997).

2.1 Types of Variation in Genotypes x environment (GxE) interactions and Its Components:

Any observable difference between individuals of the same population produced by genetic differences, environmental variations, or phenotypic differences is referred to as variation. A variation is classified into the following types.

2.1.1 Variation Due to Genotype

Variation (due to underlying heritable genetic variation); is a sufficient prerequisite for natural selection evolution. Natural selection can use genetic variation to raise or decrease the frequency of alleles already present in the population, which is a powerful factor in evolution. Mutation (that can produce entirely new alleles in a population), random mating, random fertilization, and recombination between homologous chromosomes during meiosis (which reshuffles alleles within an organism's offspring) can all contribute to genetic variation. Genetic variation is beneficial to a population because it allows certain individuals to adapt to their environment while still allowing the population to survive. The genetic variation within a population is a measure of the genetic differences that exist. Genetic variation refers to a specie's genetic variance as a whole. Individual differences in DNA segments or genes are referred to as genetic variations, and each variation of a gene is referred to as an allele.

Genotypic variation occurs as a result of variances in the genetic makeup of individuals in a population. To address the greatest genetic production potential of crops and harness this variation through effective selection for development, plant breeding is mainly dependent on the availability of substantial genetic variation. Plant breeders improve crops by identifying genetic variation sources for desired characteristics. The rates of genetic gain in plant breeding are determined by the genetic diversity for a specific trait in the breeding population. The magnitude of genetic variation in plants will help in the creation of optimal breeding strategies for maximal genetic gain (Kai Luo *et al.*, 2016). There are three components of genetic variation. 1. Additive genetic (genes which are 100% transmitted from parent to offspring). 2. Dominant gene action and 3. Epistatic gene components (when one gene masks the effect of another gene). These three components are used for variety development. $V_P = V_G + V_E = V_D + V_H + V_I + V_E$, where V_P = Total phenotypic variance, V_G = Genotypic variance, V_D = Additive gene, V_H = Dominance gene and V_I = Epistatic, $V_I = i, j$ and l .

2.1.2 Variation Due Phenotype: Variation (due to underlying heritable genetic variation); is a necessary condition for natural selection evolution. The external appearance of an individual or plant that distinguishes it from other species of plants is called the phenotype. The genetic makeup of the plant, its environment, and the interaction between its genetic constitution and the environment determine the phenotypes. The combination of genotypic traits and environmental conditions produces a plant phenotype. Plant phenotype is determined not only by the genetic composition of the plant and environmental conditions but also by their interaction (GxE), which is commonly characterized by the linear model $P=G+E+GxE$ (Visscher *et al.*, 2008). This model can be written from statistical standpoint as $P_{ij} = u+G_i+E_j+(GE)_{ij}$, where u is the overall mean, G is the effect of genes of the i th genotype and E is the effect of environment at j th location. It follows from the model that, for a given genotype, there can be many phenotypes depending up on the E and G .

As a result, in a breeding program, variety trials are frequently undertaken in multiple environments to reduce the risk of rejecting genotypes that may perform well in some but not all environments (El-Soda *et al.*, 2014). In general, the narrow-sense heritability of a trait is estimated using main effects to anticipate the genotypic response to selection across environments. It is essential to evaluate genotypes in many environments to get insight into the magnitude of GxE (El-Soda *et al.*, 2014), and crop breeders are interested in determining how much selection progress made in one environment may be carried over to other environments (El-Soda *et al.*, 2014).

2.1.3 Variation Due Environment: Environmental variation is a difference that occurs as a result of environmental factors and changes depending on the circumstances. Variations in the environment can be produced by a single component or a combination of factors, such as climate, food supply, and the actions of other organisms. The error means variance is used to quantify this uncontrolled

variation. We grow genetically homogeneous genotypes in different environments because it is non-heritable and observes environmental variation (Bernardo R, 2008).

Heritability: The proportion of observed variability that really is due to hereditary variables, with the rest due to environmental impacts, is known as heritability. It's the percentage of overall variance that may be attributed to average genetic effects. There are two types of heritability. 1. Broad sense heritability is the proportion of phenotypic variance due to genotypic variance i. e $H^2 = V_G/V_P \times 100$. 2. Narrow sense heritability is the proportion phenotypic variance due to additive genetic variance i. e $h^2 = V_D/V_P \times 100$.

Phenotyping Plasticity: A genotype's able to develop different phenotypes in different environments (even if it is the same genotype). When faced with changing environmental conditions, a plant cannot move, which means it must cope with environmental heterogeneity by adapting to the new or changing environment. It can do so by altering phenotypic expression, a process known as phenotypic plasticity (El-Soda *et al.*, 2014). Changing gene expression and plant physiology in response to environmental factors is a common example of plasticity (Juenger T.E, 2013). The impact of the environment on different plant genotypes has long been recognized and taken into account in crop breeding programs. The focus of plant breeding research has shifted from the creation of molecular markers, which is no longer a concern, to high-throughput, automated phenotyping, due to technological advances in genotyping technologies. With these advancements, determining the effect of the environment on the phenotypic should become easier (El-Soda *et al.*, 2014).

2.2. Genotype x environment interaction

The difference in response of two genotypes to environmental variation is known as genotype by environment interaction (Yan *et al.*, 2007). When unpredictable environments and/or reduced genetic variance increase selection in one direction, the genotype by environment interaction has an impact on the genotype's adaptation and evaluation. For breeders, the genotype-by-environment interaction is undesirable since it complicates genotype evaluation (Yan and Tinker, 2006). Identification of phenotypic stability and control of adapted genes are critical requirements for improving plant adaptation (Farshadfar *et al.*, 2012). Variations in the phenotypic composition of the yield while the genotypic composition remains stable are referred to as phenotypic stability (Becker and Leon, 1988). To analyze multi-environment trial data and choose superior genotypes for specific or broad adaptation, several methods have been applied. For examining G x E in genotype evaluation, methods such as additive main effects and multiplicative interaction (AMMI) (Gauch, 2006) and the genotype, genotype by environment (GGE) biplot technique (Yan *et al.*, 2007) have been recommended.

GGE biplot is based on principal component analysis, while AMMI model combines analysis of variance and principal component analysis (Yan *et al.*, 2007). The primary effects are considered as additive effects in the AMMI model, whereas the GEI is treated as a multiplicative effect. Yan *et al.* (2007) also found that while both GGE and AMMI analyses could differentiate genotype and genotype-by-environment in mega-environment analyses, GGE biplot was superior to AMMI1 graph in mega-environment analysis. The GGE biplot displays the effective perspective of a multi-environment experiment using principal component scores to show "which-won-where" (Yan *et al.*, 2007). GGE biplot is a good tool for visual data interpretation, according to various researches (Aker *et al.*, 2015). The high-yielding and stable genotypes were identified using GGE biplot analysis of the study. The G x E interaction is critical for finding the link between traits in linear and non-linear regression (Mungra *et al.*, 2011).

Because abiotic and biotic factors are more variable in semi-arid tropics, this interaction is greater. However, a cultivar superiority index (Pi) assesses the adaptability of superior cultivars to specific environments, with a lower value indicating general adaptation and a larger value indicating specific adaptation (Lin and Binns, 1988). This index can be used to assess a cultivar's performance and stability based on its characteristics, allowing for a greater selection. The approach the breeder takes to find and choose superior genotypes based on the traits of interest determines whether or not the breeding program's goals are achieved.

2.3 Categorization of Genotype-by-Environmental Interaction

Interactions between genotype and environment can be divided into three categories. (1) 'No' G-E interaction, (2) Non-crossover interaction, and (3) Crossover interaction. The number of possible G-E

interactions increases exponentially as the number of environments and genotypes increases. At least four different types of interactions are possible with only two Gs and two Es and a single criterion. With ten Gs and ten Es, 400 different types of interactions are possible, making their implications and interpretation more difficult to grasp (Allard R.W, 1999).

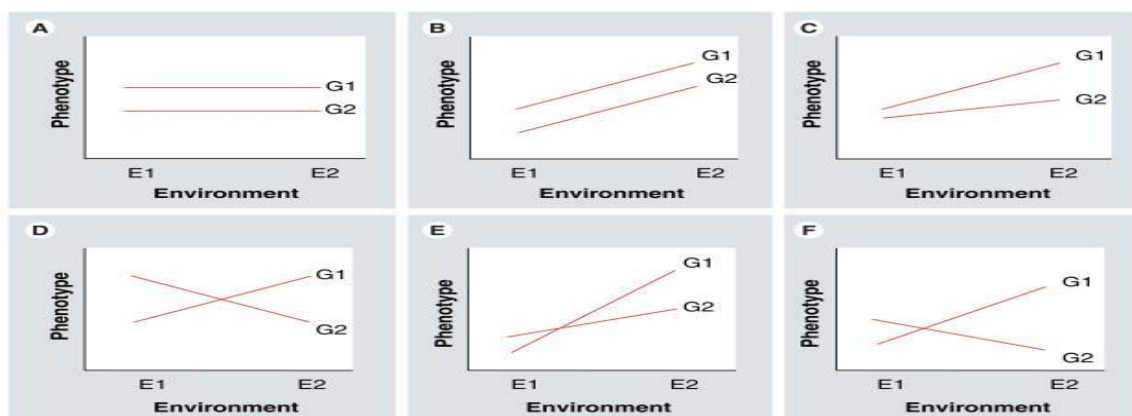


Figure 1 : Graphical representation of the ‘no’ interaction, no crossover interaction and crossover interaction types of genotype-environment interactions

2.3.1 No G-E interaction

When there is no G-E interaction, each risk factor's effect is consistent (homogeneous) across levels of the other risk factors. When one genotype (G_1) consistently surpasses the other genotype (G_2) by approximately the same number across both environments, it is said to have a 'no' G-E interaction. When there is no genotype by environment interaction, each risk factor's effects are consistent (homogeneous) across levels of the other risk factors. When one genotype (G_1) consistently outperforms the other genotype (G_2) by approximately the same number through both environments, this is called a 'no' genotype by environment interaction. When the relative performance of genotypes remains constant across settings, there is no genotype by environment interaction.

The GxE (VGE) graph depicts two components: homogeneity vs. heterogeneity of genetic variance (VG) and correlation between performances across environments. (A) Homogeneity of VG and no correlation between environments; (B) Heterogeneity of VG in different environments and no correlation between environments; (C) Crossover interactions are caused by imperfect correlations between genotypic performance across environments and homogeneous VG; (D) VGE is caused by a combination of heterogeneous VG and an imperfect correlation between genotypic performance across environments.

2.3.2 Non-crossover (Quantitative) G x E Interaction

When one G (G_1) consistently outperforms another (G_2) across the test E, it is said to have a non-crossover G-E interaction. The Gs G_1 and G_2 react to the two Es in distinct ways, but their ranks remain the same. The two Gs' responses are not additive under different Es, the quantity of inter-genotypic variance increases, and the two Gs' modifications are in the same direction.

The non-crossover interaction represents a change in genotype performance magnitude (quantitative), but the genotype rank order across environments remains unchanged. Genotypes that are superior in one environment maintain their supremacy in other environments as a result of this interaction (Zakir M, 2018). Non-crossover interactions could indicate genotypes that are genetically heterogeneous but test environments that are more or less homogeneous, or genotypes that are genetically homogeneous but environments that are heterogeneous. The performance of all identical genotypes produced in the same (ideal) environment should be consistent. When one genotype (G_1) consistently outperforms another genotype (G_2) across the test environment, it is considered to be a non-crossover genotype via environmental interaction.

2.3.3 Crossover (qualitative) G x E interaction

When the ranks of G change or shift from one E to another, the differential and the non-stable response of Gs to different Es is referred to as a crossover interaction. Crossover interaction is the

differential response of cultivars to various settings, and during crossover interaction, cultivar ranks shift from one environment to another. Crossover interaction is characterized by intersecting lines in a graphical representation. There is no crossover interaction if the lines do not connect (Kang, 1997).

Crossover interactions are more important in crop breeding than non-crossover interactions, because the presence of a cross-over interaction has significant implications for breeding for specific adaptation, and it is critical to estimate the frequency of crossover interactions (Singh *et al.*, 1999). Variation in phenotypic sensitivity to the environment among genotypes may necessitate the development of specifically adapted varieties (Falconer, 1952). If no single genotype is superior in all environments, genotype-environment interaction shows the possibility of genetic divergence among populations subjected to long-term selection in many environments (Via, 1984).

Crossovers or qualitative interaction are the varying responses of genotypes to different environments when genotype rankings change from one environment to another. A crossover interaction occurs when the rankings of genotypes vary or switch from one environment to another, resulting in a divergent and non-stable response of genotypes to various environments. No genotype is superior in multiple environments due to crossover interaction (Via, 1984).

2. 4 Statistical Methods Used For Genotype × Environment Interaction and Stability Analysis

In plant breeding multi-environment trials (MET), the presence of genotype-environment interaction is expressed as either inconsistent responses of some genotypes compared to others due to genotypic rank change or changes in the absolute differences between genotypes without rank change (Crossa *et al.*, 2002). If the GEI variance is significant, one or more of the many approaches for determining genotype stability can be used to identify stable genotypes as well as the optimum variety for limited conditions (Which-won-where). The most often used statistical tools to determine the pattern of genotypic responses across environments were reviewed below, among the several stability parameters created by different investigators.

2.4.1 Additive Main Effects and Multiplicative Interaction (AMMI) Model

AMMI (additive main effects and multiplicative interaction) is a model that combines additive and multiplicative components into a single, powerful analysis to provide plant breeders and other plant scientists with a powerful statistical tool for multi-location trial analysis (Zobel *et al.*, 1988). Plant breeders' ultimate goal is to create high-yielding genotypes that are adaptable to a wide range of conditions. However, GEI makes achieving this goal more difficult (Gauch and Zobel, 1996). According to Zobel *et al.* (1988), traditional models such as analysis of variance (ANOVA) and principal component analysis (PCA) fail to identify and separate significant genotype and environment main effects, and linear regression models account for only a small portion of the interaction sum of squares. However, AMMI research reveals an extremely important interaction component with apparent agronomic implications and no explicit design requirements other than a two-way data structure. The AMMI model is used primarily for three objectives.

The first is model diagnostics; AMMI is better for initial statistical analysis of yield trials because it gives an analytical tool for identifying other models as sub cases when they are better for certain data sets. Second, AMMI explains the GEI and highlights genotype and environment patterns and interactions (Zobel *et al.*, 1988). The third application is to increase yield estimation accuracy. Gains in the accuracy of genotype yield estimations have been attained, which are comparable to increasing the number of replicates by a factor of two to five (Zobel *et al.*, 1988). Similar benefits could be utilized to lower cultivar testing costs by reducing the number of replications, to include more treatments in studies, or to increase the efficiency of genotype selection.

The AMMI model combines genotype and environment main effects analysis of variance with GEI principal components analysis. It's proved to be beneficial in understanding complex GE relationships. It also incorporates analysis of variance (ANOVA) and additive and multiplicative parameters into a single model. The AMMI principal component analysis divides GEI into multiple orthogonal axes, while the interaction principal component analysis divides GEI into several orthogonal axes (IPCA). Because AMMI features a biplot feature, genotypes and environments are shown on the same diagram, allowing inference about specific genotype-environment interactions based on the sign and magnitude of IPCA 1 values. Any genotype with an IPCA 1 value close to zero has adapted to the tested environments in general. With IPCA 1 values of the same sign, a large genotypic PCA1 score indicates more particular adaptability to environments. The genotypes can be grouped based on how comparable they perform across environments when biplot display and

genotypic stability statistics are combined. Plant breeders may readily pick genotypes that are high yielding and stable (with low interaction with sites) from a bi-plot, as well as entries that yield well at specific sites, from a bi-plot (Yau, 1995).

2.4.2 Genotype Main Effect and Genotype x Environment Interaction (GGE) Biplot analysis

Another important model for evaluating genotype performance across testing environments is genotype main effect and GEI biplot analysis, which allows for visual evaluation of genotype, environment, and GEI in a multi-environment experiment. The GGE biplot is created by plotting the genotypes' and environments' first principal component scores against their respective second principal component scores resulting from SVD (singular value decomposition) of environments centered or environment standardized environments. GGE biplots are also useful for genotype evaluation, determining mean performance and stability, and environmental evaluation (the capacity to distinguish between genotypes in a given environment) (Yan and Kang, 2003). Furthermore, while the AMMI biplot (Zobel *et al.*, 1988) is the most well-known, the polygon view of a biplot is the most effective approach to depict genotype-environment interaction patterns and to properly analyze a biplot (Farshadfar *et al.*, 2013). As a result, visualizing the "which-won-where" pattern of MET data is critical for determining whether or not various mega-environments exist in a given location.

2.4.3 Superiority Index (Pi)

The superiority measure (Pi) introduced by Lin and Binns (1988) is defined as the distance mean square between the genotype response and the maximum response. They explained that the cultivar superiority metric entails calculating the mean square difference between a genotype's performance and the best genotype's performance within a particular environment (across environments). It measures both average performance and stability at the same time. The closer a genotype is to the genotype with the highest yield, the smaller its Pi value is, and the better the genotype is (Crossa, 1990).

2.4.4 Static Stability Coefficient (SSC)

The variance around the genotype's phenotypic mean across all environments is known as the static stability coefficient. This provides a measure of genetic consistency without taking performance into account. It is based on environmental variances or the variation in genotype yields across test conditions (Becker and Leon, 1988). This coefficient has a lower value (near to zero) when a genotype fits the static stability concept better.

2.4.5 Wricke's Ecovalence (W^2i)

The stability of a genotype, defined ecovalence as the contribution of each genotype to the GEI sum of squares. The *i*th genotype's ecovalence (W^2i), or stability, is its interaction with environments squared and summed across environments. W^2i genotypes with a lower value can be deemed stable, whilst W^2i genotypes with a greater value can be considered unstable. The W^2i , like static stability, does not take genotype performance into account.

2.4.6 AMMI Stability Value (ASV)

In a two-dimensional plot of IPCA1 scores vs. IPCA2 scores in the AMMI model, the AMMI Stability Value (ASV) is the distance from the coordinate point to the origin. A weighted value is required since the IPCA1 score contributes more to the GEI sum of squares. The relative contribution of IPCA1 to IPCA2 to the interaction sum of squares was used to obtain this value for each genotype and environment. Lower ASV genotypes are thought to be more stable than genotypes with higher ASV. In circumstances where the two first IPCAs accounted for a significant percentage of genotype x environment interactions, the ASV, which employs two IPCA scores to construct a balanced assessment between them, can be valuable (Anley *et al.*, 2013).

2.4.7 Yield Stability Index (YSI)

This parameter was generated by (Farshadfar *et al.*, 2011). However, stability should not be used as the sole criterion for selection, as the most stable genotypes may not always produce the best yields (Mohammad *et al.*, 2007). As a result, techniques that combine both mean yield and stability in a single index are needed, which is why different authors developed different selection criteria for simultaneous yield and stability selection. In this sense, ASV considers both IPCA1 and IPCA2, which account for the majority of the variation in the GE interaction. The lowest ASV is given the rank one, while the highest yield mean is given the rank one, and the ranks are then added together to

form a single simultaneous yield and yield stability selection index called yield stability index (YSI). The lowest YSI is said to be the most stable, with the highest yield production, and vice versa.

2.5 Importance of Genotype by Environment Interaction

Because genotypic-stability values are reduced under a variety of conditions, genotype x environment (GxE) interactions are crucial in the production and evaluation of plant varieties (Hébert *et al.*, 1995). The genotype-environment interaction phenomenon describes how genotypes behave differently in different contexts, affecting the effectiveness of selection in a breeding program. Genotypes x environment interactions develop as a result of genotype sensitivity to various environmental situations being different. Crops must be evaluated in a variety of environments to assess their specific and wide adaptation in order to mitigate the effect of G x E interaction. Plant productivity is directly proportional to how effectively an individual's genotype is adapted to the surrounding environment.

Plant breeders are interested in genotype-by-environment interaction for a number of reasons (Fehr, 1987). Living organisms are made up of genes whose expressions are influenced by their environments; thus, the genotypic expression of a phenotype is influenced by the environment. Because elite varieties developed for one region may not perform the same in multiple locations, the genotype environment interaction effect challenges breeders' selection of acceptable variety. Crop breeding involves a variety of genetic materials with diverse properties that are affected by environmental factors. Plant breeders have established ways to ensure progress in selection efficacy by mitigating the confounding effect of G E interaction on selection efficiency. Understanding genotype stability across environments aids in determining their suitability for the expected fluctuations in growing conditions, integrating multi-environment trial data, pedigree information, and genotypic data of cultivars, and improving accuracy and precision in the assessment of both genetic and environmental influences.

Plant breeders have developed and used a number of strategies to explain the genotype-environment interaction at the end of breeding programs. To choose high-yielding and stable cultivars, cultivar development based on phenotypic values of different genotypes under varying environmental conditions is required (Marfo and Padi, 1999). However, because of variances in responsiveness to factors such as soil fertility and pathogen prevalence, genotypes evaluated in different locations or years often give significantly varied outcomes in performance (Padi 2008). This difference in performance referred known as genotype-environment (G E) interaction, might make it more difficult for a genotype to demonstrate superior performance in different environments (Romagosa *et al.*, 2009). As a result of the genotype-environment interaction, there may be a low correlation between phenotypic and genotypic values, causing heritability estimates to be skewed and selection progress to be slowed (Romagosa *et al.*, 2009).

Essentially, the G E interaction decides the best breeding technique to use (Romagosa *et al.*, 2009). The ability of a genotype to react to environmental conditions, which is governed by the genotype's genetic composition, has an impact on yield stability (Ulaganathan *et al.*, 2015). The occurrence of genotype-environment interaction is the primary cause of differences in genotype performance across environments (Gedif and Yigzaw, 2014). It's reasonable to predict that genotype-environment interactions will vary and be plentiful in different environments. As a result, one cultivar may produce the best yield in one environment while excelling in another. This prompted the investigation of genotype-environment interactions in order to determine the extent of interactions in genotype selection across several environments, as well as compute the average performance of the genotypes under consideration (Chandrakanth *et al.*, 2016).

3. CONCLUSION

Because of the world's growing population, increasing crop productivity per unit of land and per unit of time will be a big challenge in the future. Breeders have focused on the production of cultivars with higher yield and yield stability, as well as increased resistance/tolerance to abiotic stressors, to fulfill the increasing food need of a growing population. The interaction between genotype and environment is one of the primary variables contributing to the crop's low yield and productivity. The presence of a genotype x environment interaction contributes to crop production inconsistency across a wide variety of conditions. In the absence of genotype x environment interaction, the superior genotype in one environment may be considered the superior genotype in all, whereas the existence of genotype x environment interaction confirms a genotype's superiority in a specific environment. As a result, it's

critical to understand the nature of genotype x environment interactions before choosing a genotype for a specific cultivation area.

The principal challenges for crop improvement in the decades ahead, which are linked to demographic trends and climate change, require a more efficient use of plant genetic resources in breeding programs targeted at generating more stable varieties. Genotype by environment interactions are situations in which environmental factors affect different people differently based on their genotype, while genetic factors have a different effect depending on environmental characteristics. Understanding complicated trait variation requires an understanding of genotype-environment interactions. A genetic variation's genotype by environment interaction effect on a quantitative trait could result in changes in trait variance among groups of individuals with different variant genotypes. Genotype by environment interaction refers to the comparative performances of genotypes that differ among environments, indicating differences in genotype ranks or levels of expression of genetic differences. Unless breeding programs are structured to target multiple categories of environments, genotype-by-environment can lower heritability and overall genetic gain. Understanding the influence of genotype by environment interaction, the function of environments in generating genotype by environment interaction, as well as the issues and opportunities, is critical for effective breeding program design and genetic material deployment.

The change of genetic factors by environmental factors, as well as the role of genetic factors in determining genotype performance in various environments, is referred to as genotype x environmental interaction. A change in the relative performance of a character of two or more genotypes measured in two or more environments is referred to as a genotype-environment interaction. Its origins can be traced back to two ideas: biometrics and developmental interaction. Variations in genotype order between environments, as well as changes in the absolute and relative magnitude of genetic, environmental, and phenotypic variances between environments, may be involved in interactions. The presence of the genotype x environment interaction effect makes selecting superior genotypes for a target environment even more challenging. As a result, testing in multiple environments to identify stable genotypes and environments using the most efficient stability estimating models is required before deciding on any variety to use in broader agro-ecology. Because genotype x environment interactions can have a big impact on the potential for evolutionary responses to selection, this knowledge is crucial.

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