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Advancement of Analytical Models quantifying G × E Interactions and Stability analysis in Multi-Environment Trial

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Abstract **– The genotypes showed different performances in a different environment known as genotype-environment interaction. This genotype by environment interaction (GEI) is a critical concern to agricultural researchers to improve crop varieties. The existence of G×E interaction makes it difficult to select best performing genotypes during testing of a large number of genotypes and environments over the season and multiple testing sites. The phenotypic response occurs in unpredictable ways across diverse and changing environmental conditions due to the complexity of mechanisms and processes. GEI can be better understood by breeders with the help of analytical tools. In order to make more informed breeding decisions, it is important to use appropriate strategies to analyze genotype by environment interactions. Predicting genotype performance as accurately as possible requires the use of good analytical methods. By modeling the GE interaction, phenotypic stability can be measured in several ways. Methods such as univariate (parametric and non-parametric) and multivariate analysis can be used in these studies. Additive Main Effects and Multiplicative Interactions (AMMI) models combine analysis of variance with principal component analysis for genotype and environment effects. Comparatively to other types of biplots, the GGE biplot displays the Genotype plus Genotype by Environment (GGE) part of a MET data set. Cultivar evaluation requires the use of GGE biplots to display information relevant to the evaluation of cultivars. AMMI and GGE Biplot provide information about genotypes with a broad range of adaptability, as well as the additive main effect and multiplicative interaction (AMMI) methodology. By displaying mega-environments and adaptive responses graphically, AMMI provides greater opportunities than other similar tools. In this review, we evaluated different stability models as well as conventional and new analytical methodologies used to measure genotype by environment interaction.**

Keywords **– AMMI, GGE Biplot, Multi-Environment, Statistical Model, Stability.**

I. INTRODUCTION

The genotypes of organisms showed different performances in a different environment known as genotype-environment interaction. Genotype by environment interaction is also defined as the difference between the phenotypic value and the value expected from the corresponding genotypic and environmental values (Yan and Hunt, 2002). Phenotype results from the interaction of genotype and environments. Currently, breeders and genetics substantially attempt to improve the hereditary of crop species to avert difficulties associated with genetic susceptibility. According to the definition of Kang (2002) focusing on improving the genetic base and unpredictable climatic factors encountered at different locations and years, this differential response is generally called genotype-environment interactions. This genotype-environment interaction (G×E) is a critical concern to agricultural researchers to improve crop varieties (Eberhart and Russell, 1966).

The existence of G×E interaction makes it difficult to select best performing genotypes during testing of a large number of genotypes and environments over the season and multiple testing sites Ebrehart and Russel (1996) stated that G EI commonly occurs in the pure line, single, or double-cross hybrids, top cross, or other breeders working activities Finlay and Wilkinson, 1963 stated, the aim of agronomist or plant breeder has been,

the response of a cultivar, genotype, or generally crop varieties performed very well over diverse environmental situations. Although breeders and agronomists have been aware of genetic variability in multi-environment trial data the genotypes have been masked due to predictable and unpredictable environmental factors to show their genetic potential. It has been known for many years that genotype-environment interactions play important role in crop improvement (Eberhart and Russel 1966).

The relative ranking of genotypes and the magnitude of differences between genotypes are well documented in the presence of G×E. genotype-environment interactions complicate the comparison of genotypes' performance across environments, particularly if there are many genotypes and environments. Thus, in order to select superior cultivars that have high yields and stability, various statistical methods must be used to measure and assess genotypic performance in various environments (Eberhart and Russel 1966; Finlay and Wilkinson, 1963).

Genotype by environment interaction analysis is crucial for recommending novel selections for large-scale production. The interaction between genotype, environment, genotype, and environment interaction, enables evaluations of genotypic performance and stability for yield and yield-related traits. (Horn et al, 2017). A G×E analysis involves evaluating new selections across representative growing environments allowing breeders to recommend promising genotypes based on their specific or broad adaptations. During the final stage of selecting elite breeding materials, G×E analysis is important. A number of analytical tools have been developed to analyze and interpret G×E data, including regression coefficients (Finlay and Wilkinson, 1963), the sum of square deviations (Ebreart and Russel's 1966), stability variance (Shukula,1972), and recently developed analytical tools AMMI and GGE that quantify G×E interactions differently (Jalata, 2011 and Luel et al,2014). Breeders and agronomists use different analytical models to quantify G×E interactions, characterize their forms, and develop strategies to select stable genotypes through predominantly biometrical models we review some classical and new analytical models to measure genotype by environment interactions and asses different stability parameters in multi-environment trials MET.

II. Basic Concepts of Genotype by Environment Interaction

Dia et al (2017) defines genotype-environment interaction G×E as the modification of genetic factor by environmental factor and the role played by generic factors in genotype performance across environments. Furthermore, they also noted that GEI occurs in animal and plant breeding, genetic, epidemiology, pharmacogenomics, and conservation biology research. Dia et al (2017) describe that, traits such as reproductive fitness, longevity, height, weight, yield, and disease resistance. It has been noted by Ekanayake et al (1999) that yield measurements are affected by more than one factor in some experiments or processes. The G×E interaction occurs when factor interact when yield does not equal the sum of the separate effects. A phenotype (P) is described using an additive linear model in terms of its nature in a single environment as follows.

P = G + E; Where, G is genotype and E is environment, in this model the interaction (G × E) is nested within environment (E). To separate the effect of environment E from the G × E interaction, many trial sites are required. Therefore, the phenotype (P) = G + E + (G × +E). The genotypic performance might vary from environment to environment, as a result the rank of genotypes are different between environments. Since the G × E interaction is to some extent difficult hence, it requires integrated approaches that combine several fields su-

-ch as agriculture, biology, statistics, computer, and genetics (Tazu, 2011 and Bondari, 2015).

The relationships between the environment and the phenotypic expression of a genotype establish the G × E interaction. Genetic adaptation to an entire range of environmental conditions is determined by the G*E interaction, or if separate genotypes are required for different sub-environments. G * E interaction occurs when environmental factors (temperature, rainfall, etc.) and an individual's genetic makeup (genotype) are combined to affect the expression of a trait phenotypically. As different genotypes are affected differently by environmental factors, the productivity of animals or plants may differ as well. As Bondari (2015) stated, breeding strategies may focus on the G×E interaction to select appropriate and elite genotypes for a target environments.

Dia et al. (2017) stated that, "G × E is said to exist when genotype performance differs across environments as a result performance of genotype can vary greatly across environments because of the effect of environment on trait expression". Similarly, Crossa, (2012) analyzed the presence of genotype × environment interaction (GEI) in plant breeding multi-environment trials (MET) is expressed either as variable responses of some genotypes relative to others due to genotypic rank change or as changes in the absolute differences between genotypes without rank change (heterogeneity of within-site variance). Genotypes with high yielder and stable performance are difficult to identify, but it has great value since it is impossible to test genotypes in all target environments plant breeders do indirect selection using their own multiple-environment trials or test environments.

III. GENOTYPE-ENVIRONMENT INTERACTION ANALYSIS

Dia et al (2017) define genotype-environment interaction G × E as the modification of genetic factors by environmental factors and the role played by genetic factors in genotype performance across environments. Furthermore, they also noted that GEI occurs in animal and plant breeding, genetics, epidemiology, pharmacogenomics, and conservation biology research. Dia et al (2017) describe that, traits such as reproductive fitness, longevity, height, weight, yield, and disease resistance. It has been noted by Ekanayake et al (1999) that yield measurements are affected by more than one factor in some experiments or processes. The G×E interaction occurs when factors interact when yield does not equal the sum of the separate effects. A phenotype (P) is described using an additive linear model in terms of its nature in a single environment as follows.

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IV. GENOTYPE-ENVIRONMENT INTERACTION ANALYSIS

Classically, a sum of squares is partitioned into components for varieties, environments, and variety-environment interactions to sum up the variation in response to many varieties grown in various environments. This method conveys little information regarding individual response patterns. In addition to grouping varieties or environments to further reduce the interaction sum of squares, further partitioning of the interaction sum of squares may help identify significant sources of interaction, but these groupings are often difficult to interpret biologically and not repeated in subsequent years (Kempton, 1984). A set of genotypes exposed to a range of environmental conditions is required in order to generate data for GEI analysis. Malosetti et al., 2013 propose that genotypes in the population can consist of advanced lines, cultivars, or offspring from specific crosses, such as F2, backcrosses, or recombinant inbred lines (RIL).

To properly analyze and obtain accurate information, it is also necessary to identify appropriate statistical models, such as fixed, random, or mixed effects, in genotype-by-environment interaction analyses. However, the issue of fixed or random effects of genotype and environment has not been resolved for the analysis of G × E interaction. Bondari (2015) describes a sampling consideration for determining whether an experiment contains a representative sample of all possible genotypes and environments (fixed effects) or a representative sample of all possible genotypes and environments (random effects). In some cases, descriptions of the experimental data might prove useful in determining whether the G × E interaction effects should be viewed as fixed or random. Testing across years and sites may be used to assess unpredictable or uncontrollable environmental features from a statistical perspective. Predictable or controlled features of the environment are presented as fixed effects in additive linear models. Therefore, plant breeders always work with mixed models because the environment has specific combinations with predictable and unpredictable features (Ekanayake et al., 1999).

The growing environment usually masks the ability of genetic expression, leading to poor genetic gain from artificial selection, particularly for quantitative traits such as grain yield. Yield trials are conducted with many genotypes grown in a number of environments (year and site combinations), usually with replication. In yield data, we can separate the total sum of squares (SS) into three types, such as genotype main effect, environment main effect, and genotype X environment interaction. By definition, the main effects are additive, interaction

(residual from the additive model), and non-additive commonly, all three sources are statistically significant and ergonomically important (Zobel et al., 1988) a number of analytical tools must be developed to help breeders understand GEI, given the complexity of the mechanisms and processes that contribute to phenotypic variation across diverse and changing environmental conditions.

The use of adequate strategies to analyze GEI is the first and important step toward more informed breeding decisions. Good analytical methods are a prerequisite for predicting the performance of genotypes as accurately as possible ANOVA, multivariate analyses of multi-location trials, linear regression, AMMI, and GGE biplots are commonly applied statistical analyses to yield trials in order to measure consistent performance regarding G * E interaction. For exploring the opportunities and/or limiting the disadvantages of G x E interactions by using proper techniques is generally more useful than ignoring them.

V. Statistical Models for G × E Data

G x E interaction can be addressed by a combination of the linear model, Bi-linear model, and mixed a linear-bilinear model with fixed effects is important for exploratory analyses, but limited by model assumptions (homoscedasticity) and a large number of parameters. However, mixed models are more natural to analyze MET data because of the heterogeneity of variances and covariance in the data (between environments G x E) (Malosetti, et al., 2017). Early approaches to the analysis of GEI included the conventional, two-way fixed effects (FE2W) model, with sum to zero constraints, and the simple linear regression of genotype yields on the environment means.

VI. Analysis of Variance (ANOVA)

The analysis of variance has been widely used to partition total phenotypic variation into components due to genotype, environment and G x E interaction, and error (micro-environmental variation). Quantifying the magnitude of G x E interactions is often done using the relative sizes of their variance components. Cooper and Delacy (1994) state that, the plant breeder faces a problem where the objective is to select genotypes based on G x E interaction. According to Zobel et al. (1988), the ordinary ANOVA is an additive model that does not test the significance of the GE interaction and only describes the main effects. In any case, ANOVA provides no insight into the particular patterns of genotypes or environments that give rise to the interaction In the absence of replication, the interaction effect partitions into two components, an additive genotype-environment main effect and an interaction effect (G x E). Therefore, the analysis of variance of the combined data expresses the observed (Yij) mean yield of the ith genotype at the jth environment as; $Y_{ij} = \mu + G_i + E_j + GE_{ij} + e_{ij}$

Where, μ is the general mean, Gi, Ej, and GEij are the effect of the genotype, environment, and genotype by environment interaction, respectively and eij is the average of the random errors associated with the rth plot that receives the ith genotype in the jth environment. In the equation above, the interaction (GE ij) component implies that the expected value of an ith genotype in a jth environment (Y ij) will depend both on G and E levels separately and on the combination of G and E levels (Crossa, 1990). The presence of a significant genotype by environment interaction complicates the interpretation of the results. However, Crossa mentioned two possible ways of overcoming this problem. The first is to examine the data and see if the interaction is due to one observed outlier. A high residual might be due to a recording error. Therefore, the outlier may be replaced by its expected value, using the additive model without considering the interaction term.

Alternatively, the results can be expressed on a different scale. Usually, the logarithm transformation of the data removes interaction without rank changes and achieves both equalities of variance within treatments and normality of residuals. However, crossover or rank change interactions cannot be removed by log transformation. When genotype-environment interaction exists and is not due to one outlier and cannot be removed by a suitable transformation, it should be assumed that an underlying model equation above is representing the data. The other important aspect of the analysis of variance is variance components related to different sources of variations including genotype, genotype by environment interaction can be estimated. In general variance component methodology is important in multi-location trials because errors mostly arise from G X E interaction in determining genotype performance. As Ferreira et al., 2006 cited from Roemer (1917) proposed, the use of variance of each genotype over the environments to estimate the static phenotype stability of the ith genotype, the following estimator could be used: $S^2{}_i = \frac{\sum_{j=1}^{q}(Y_{ij} - \overline{Y}_{i.})^2}{q-1}$

Where, q environments and $S^2$is genotypic variance.

$\overline{Y}_i$.Represents over all marginal mean of genotypes i.

Y_{ij} is the marginal genotype mean in the**ith** and environments means in the jth.

6.1. *Limitations of ANOVA*

Crossa (1990) described the advantages of analysis of variance to obtain unbiased estimates of the components of genetic variance and genotype-environment interactions. It also identifies some limitations in the characterization of additional structures in non-additive ingredients. In fact, if there is little variation in the mean squared remaining between the media and the experiments of equal size, then the combined error variance is found by averaging the mean squared. rest of all environments. This combined experimental error is used to test the null hypothesis that genotype differences are the same in all environments. However, if the variances of errors are heterogeneous, the F-test of the mean squares of interaction with genotype-environment for composite error variance will favor significant results. One of the main deficiencies of the combined analysis of variance of multi-location yield trials is that it does not explore any underlying structure within the observed nonadditivity (genotype-environment interaction). Analysis of variance fails to determine the pattern of the response of genotypes and environments (Crossa, 1990; Purchase, 1997; Mulualem and Bekeko, 2017). They showed that the valuable information contained in (G-1) (E-1) degrees of freedom is practically wasted if no further analysis is done.

VII. Methods Of Univariate Statistical Analysis

By modeling the GE interaction, one can measure phenotypic stability in several ways. They include a) Univariate parametric methods, such as simple and bi-segmented linear regression, variance components with mixed models, descriptive statistics, and non-linear regression models. b) Non-parametric methods including variance of genotype rank values (Ferreira et al., 2006).

7.1. *Wricke's Stability*

A measure of stability based on the contribution made by each genotype to the G × E interaction sum square. Wricke, (1962; 1964) was discussed and supported by Castelo et al., (2016). The Wricke (1962) methodology,

also known as "Ecovalence" (Wi), is used to evaluate stability based only on ANOVA components. It is suggested that the sum of the squares of the G x E interaction should be decomposed into parts related to genotypes in an isolated manner, which is similar to the model of Plaisted and Peterson -- this method is proposed to use the sum of the square of the GE is; Population effects $\omega = \sum g^2_{ij}$ and a sample estimated as; $\omega i = \sum_{j=1}^{q}(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..})^2$.

This equation implies, for the i^{th} genotype represents the sum of squares of the GE estimate interaction effects. If $\omega_i = 0$, the genotype is considered stable and if it is greater than 0 the genotype is considered unstable. Wricke (1964) called this parameter ecovalency, and referred to it as genotype ability to answer to environmental changes. A high ecovalency implies a low ω i.

7.2. *Shukla's Stability Variance*

Shukla (1972) proposed the variance component as another means of describing phenotypic stability throughout an environment. After removing environmental main effects, Shukla defined stability variance as an unbiased estimate of the variance of genotype i across environments. In a two-way classification, stability variance is based on the residual matrix (GEij+ eij) since the genotype main effect is constant. In this case, the stability statistic is called the stability variance (*i2), and it is estimated as follows. $\delta^2_i = \frac{1}{(G-1)(G-2)(E-1)}[G((G-1)\sum_j(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..})^2 - \sum_i\sum_j(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..})^2]$.

If the stability variance of a genotype (*i2) equals the environmental variance (*02), then *i2=0, and a genotype is stable. In this context, a relatively large value of (*i2) indicates a greater level of genotype (i) instability. It is not uncommon for the stability variance estimates to be negative in variance component problems since it is the difference between two sums of the square. In Purchase's (1997), a negative estimation of (*i2) would be interpreted as zero.

7.3. *Regression Models*

Joint linear regression is another important method for analyzing and interpreting two-way classification data with non-additive structures. Various genotypes and agronomic treatments have been tested using this approach in genetics, plant breeding, and agronomy. (Crossa, 1990) reports that the genotype-environment interaction is partitioned into a component caused by linear regressions (bi) between genotype and environment and a deviation (dij) between genotype and environment.

According to Kempton (1984), alternative methods for analyzing the response of varieties to different environments include comparing the distribution of quantitative scores to each environment according to temperature, soil moisture, sowing date, the yield of previous crops, or a combination of these factors, and then describing the response of varieties to the different environments through linear regression. However, when analyzing variety trials it is more usual to regress the response of a variety onto the mean response of all varieties in each environment rather than use an independent environmental score. This technique is popularly associated with the work of Finlay and Wilkinson (1963). According to Finlay and Wilkinson (1963) stated, the yield of each genotype is plotted against the mean yield of each environment and in which each genotype is represented by a fitted straight line. Philosophically, this type of graphical display of MET data is very attractive, since it clearly indicates differential genotype responses to test environments. The problem with this

method is that the environmental means are not always good, and are frequently a poor measure of environments such that the fitted lines in most cases only account for a small fraction of the total GE (Zoble et al., 1988).

The optimal genotype then becomes the one that features high productivity, associated with a regression coefficient as close as possible to 1, and regression deviations close to 0. Based on Castelo et al., (2016), Stated that there are two important issues in methodologies that are used in the regression analysis first, the means and the coefficients assigned to genotypes tend to be positively correlated, that is, stable genotypes tend to have lower expression of the character in question, second, the assumption of linearity is not usually met. Returning to the analysis of variance model for combined data where the observed mean yield (Y_{ij}) of the i^{th} genotype at the j^{th} environment is expressed as $Y_{ij} = \mu + G_i + E_j + (GE)_{ij} + e_{ij}$ Since the problem lies on the interaction component (GE_{ij}), it is partitioned into components due to linear regression (bi) of the j^{th} genotype on the environmental mean and deviation (d_{ij}). Further details about interaction are obtained by regressing the performance of each genotype on the environmental means.

Eberhart and Russell (1966) proposed pooling the sum of squares for environments and genotype-environment interactions and subdividing it into a linear effect between environments with 1 df, a linear effect for genotype-environment with (G-1) df, and a deviation from regression for each genotype with (E-2) df. Thus, part of the performance of the genotypes across environments or the genotypes stability is expressed in terms of three empirical parameters; mean performance, slope of regression and sum of squared deviation from regression. Conventional interpretation of regression coefficient is used as a measure of genotypic stability across environments. Values of bi close to 1 indicate a relatively stable genotype; this definition is in accordance with the dynamic concept, but which tends to vary less with environmental change. A stable genotype is, thus, characterized by bi close to 1, and deviation from regression close to zero. Several authors have criticized the regression approach (Crossa, 1990, Becker and Leon, 1988), pointing out the following statistical and biological limitations.

7.4. *The Statistical Limitations*

Means of genotypes are not independent of the overall mean of the environment, Errors related to the slopes of genotypes are not statistically independent because sum of squares gives deviations with (G -1) (E-2) df, cannot be an Orthogonal Split between G genotypes and it assumes a linear relationship between environmental media and interactions when this assumption is violated, the efficiency of the analysis is impaired, decrease and the results may be skewed. The environmental index (Ij) is not independent of the response variable (Yij), as it is estimated as the mean environmental response, although the effect of this dependence decreases as the number of genotypes increases. The use of biased estimates of the regression coefficients because the independent variable is measured with error, the deviation depends on the phenotype and the ratio 2e δ2, where 2e is the environmental variance and 2 is residual variance. Therefore, bias decreases as environmental effects increase. Another problem that can affect inference is the violation of the assumption of uniformity of the remaining environmental variances.

7.5. *The Biological Limitations*

The relative stability of the two genotypes depends not only on a particular site but also on all other genotypes

included in the analysis. When only a few sites with very low or high performance are included in the analysis, the fit of the regression may be affected by the genotype performance in some of these extreme environments, which can make wrong conclusion. The coefficient of linear regression (bi) is not a measure of stability but rather additional information about the average response of a genotype to the advantage of environmental conditions. However, the regression method of Eberhart and Russel for stable genotype determination is still widely used. Therefore, the author concludes that regression analysis should be used with caution when the data set includes results from a few locations with extremely low or high performance. The basic difference between the methods proposed by Eberhart and Russel (1966) and Finlay and Wilkinson (1963) is that the former proposes a logarithmic transformation of the data, while the latter uses parameters regression coefficients and deviations to evaluate the stability, adaptability and response patterns of genotypes to the environment. In summary, if one is interested in a few genotypes specifically adapted to extremely low or high yield environments, regression can be very useful. Even small differences in ball value become significant if the environment is used where the performance level is below or above average. There is little reason to reject the popular regression approach, and we find no method for estimating the stability of yield generally preferable because environmental variances do not provide valuable information for most plant propagation purposes.

VIII. CULTIVAR PERFORMANCE MEASURE (PI)

According to Parmar et al. (2016) explain the idea of Lin and Binns (1988) proposed cultivar performance (Pi) as the mean squares of distance between genotypes iand 'i' where 'i' is the genotype with maximum response over all locations. The smaller the value of Pi, the smaller the distance to the genotype with maximum yield, the better the genotype. Pi values were measured on overall location mean; it represents superiority in the sense of general adaptability (wide adaptation). The methodology proposed by Lin and Binns (1988), somewhat differs from the cited ones, since it is not explicitly based on values obtained from the ranking of genotypes, considering that this methodology is based on absolute values obtained for the rated character and not on the numbering of the ranking of genotypes. Lin and Binns proposed obtaining the stability statistics Pi, which is given by the expression: $Pi = \sum_{j-1}^{n}(xij - Mj)^2/2n$

In which, Pi = superiority index of i^{th} cultivar; X_{ij} = productivity of i^{th} cultivar planted in the j^{th} site; Mj = maximum response obtained among all the cultivars in the j^{th} site; n = number of sites. This expression can be developed into: $P_i = \left[\frac{n(\bar{X}i. - \bar{M})^2 + \sum_{j=1}^{n}(Xij - \bar{X}i. - Mj + M^{-2})}{2n}\right]$.

In which: $\bar{X}i$ is the mean of the character obtained in n environments; and$\bar{M}$, the mean of the maximum responses of genotypes in all environments. Such methodologies, despite being considered as alternatives, especially for their lack of robustness, may be considered preferable when applications of regression methods are not possible, or when there is a need for analyses of easier implementation and of most objective interpretation. This fact is clearly observed, for instance, in the methodologies of Kang (2002), which feature a single value as a stability measure. Two environments are considered more similar if they produce more similar rankings of the tested genotypes. The similarity between two environments, that means the "distance" between these two environments, can be quantitatively expressed by Spearman's rank correlation coefficient between the rankings of the genotypes in these two environments.

IX. MULTIVARIATE METHODOLOGIES

With the advent of more sophisticated computational resources and computers with greater processing capacity, other methodologies, such as those based on multivariate analysis, became more accessible and are preferably used to the extent that most statistical packages were made available. One of the bases for conducting adaptability and stability analyses via multivariate models is the principal component analysis (PCA), which has its essence the application of the SVD (Singular Value Decomposition) method, which in turn, performs the linear decomposition of variables contained in a data array in an iterative manner, in order to summarize the information contained in a smaller number of explanatory vectors (Castelo et al., 2016). Multivariate means involving multiple dependent variables resulting in one outcome. Multivariate statistics are increasingly popular techniques used for analyzing complicated data sets. They provide analysis of many individual variables, which are correlated with one another to varying degrees. Multivariate statistics are an extension of univariate and bivariate statistics. Multivariate analysis (MVA) is a Statistical procedure for analysis of data involving more than two type of measurement or observation. It may also mean solving problems where more than two dependent variables are analyzed simultaneously with other variables. Multivariate analysis consists of a collection of methods that can be used when several measurements are made on each individual or object in one or more samples. Many statistical techniques focus on just one or two variables. Multivariate analysis (MVA) techniques allow more than two variables to be analyzed at once. The ultimate goal of these analyses is either explanation or prediction, i.e., more than just establishing an association. Choice of an appropriate procedure to be used in multivariable analysis depends on whether the dependent and independent variables are continuous, dichotomous, nominal, and ordinal or a combination of these.

Among the most common Multivariate methodologies in adaptability genetic studies, the following models outstand: AMMI (Additive Main Effect and Multiplicative Interaction) and GGE Biplot (Genotype plus Genotype by Environment) (Kempton, 1984; Zobel et al., 1988; Crossa, 1990; Yan et al., 2000). The GGE biplot, proposed by Yan et al. (2000) is the method based on the same principle that has been increasingly used in recent years in which, general terms, is similar to the AMMI model, with the key difference that, in the multiplicative component for the decomposition via SVD, only the effect on the environment is excluded, consequently considering the effects of genotypes and of the interaction together. Therefore, a model that considers the effect of the interaction as multiplicative besides capitalizing the G x E interaction more efficiently Zobel et al., (1988) and Kempton, (1984) stated, advantages such as quantification of each genotype and environment to the sum of squares of the interaction, and provide an easy interpretation of results by biplot graphs.

Both the AMMI methodology and GGE Biplot have the additional advantages of generating information on the genotypes with broad adaptability (combination of phenotypic mean and stability information on the same graph). These also important to aiding delineation of agronomic areas via identification of mega-environments (group of environments with similar G × E interaction standard, and consequently with little change in the ranking of the genotypes evaluated), which may indicate the most representative environments of each site and genotypes with specific adaptation to each region.

9.1. *Additive Main Effect and Multiplication of Interactions (AMMI) Model*

The AMMI (Additive Main Effects and Multifactorial Interactions) model combines the analysis of variance

for the main effects of genotype and the environment with the analysis of the principal component of the interaction with the genotype environment, providing a model replication, is applied to analyze the interaction effect of model additive ANOVA (Kaya et al., 2002). The AMMI model first applies the addition analysis of variance (ANOVA) model to the double entry data, and then applies the principal component analysis (PCA) model to the residuals of the additive model, that is, with interactive (Gauch, 2013). It has been shown to be useful in understanding the complex interactions between genotype and environment. The results can be graphed in a very informative biplotplot showing both primary and interactive effects on genotype and environment.

AMMI can partition the data into a sample-rich model and remove noisy residuals to achieve accuracy (Hunen, 1996). The AMMI model was developed by Zobel et al. (1988) and the amplitude of the G × E interaction was estimated according to the response of each variable (here referred to as the environment) in a rather original approach, by combining in a single model between ANOVA and principal component analysis (PCA). The idea is to treat the effect of the G × E interaction as a doubling component (more biologically realistic) and the other effects (genotype and environment) as purely additive effect components (Castelo et al., 2016). The AMMI method uses the multivariable SVD technique to reduce the information contained in an n × m data array (genotype and environment, respectively) into cumulative vectors, systematically (in order of importance). The largest part of the variation contained in the data and thus in the G × E interaction. Since its revelation, this method has been widely used for studies of the adaptability of a single important crops such as wheat (Kempton, 198; Zobel et al., 1988). $Y_{ij} = \mu + G_i + E_j + \sum_{n=1}^{n} \lambda_n \alpha_{in} y_{jn} + e_{ijk}$.

Where, $\boldsymbol{\lambda_k}$ is the eigenvalue associated with the k^{th} principal component; r_{ik} is the i^{th} element of the eigenvector for λ_k associated with genotypes, S_{jk} is the j^{th} element of the eigenvector for associated with λ_k environments, Y_{ij} is the yield of genotype g in environment e; μ is the grand mean; g, is the genotype mean deviations (the genotype means minus the grand mean); ej is the environment mean deviations; m is the number of PCA axes retained in the model and εij is the residual.

An important feature of this method is the ability to obtain graphs of principal components retained in AMMI model analysis and scores plots of PC axes as a function of average yield. The genotype and environment scores can be plotted on the same graph and used to visually determine stability and similarity between genotypes and environments. Therefore, it is useful to perform ecological partitioning of genotypes, through cluster analysis to determine genotype-environment relationships when two or more major components are retained (Ferreira et al. associates, 2006). If the experiment is repeated, the error term εij is the difference between the mean Yij and the unique observation for repetition r. can be added. The least squares fit to the equilibrium data was obtained by adjusting the additive first by analysis of normal variance (ANOVA) and then analysis of the interaction (i.e. non-additive residual) by PCA (Left, 2013). In the AMMI model, multiplier terms are combined to explain the change of the quadratic interaction. Such models are based on the decay to single values and to vectors of the residual matrix of the related linear model.

Two fundamental problems that confuse both agronomists and plant breeders are interaction and noise; therefore, agricultural scientists must look for effective statistical tools to mitigate these challenges. AMMI solves both of these problems. For agricultural problems of genotype-environment interaction, there are two basic alternatives, one targeting the genotype and the other targeting the environment. One option is to search

for genotypes that are high yielding, broad-adapted, and win-win in the growing area of interest. Another option, especially relevant when the first one fails, is to subdivide the cropland into several relatively homogenous macro-environments (with few interactions in each macro-environment) and then select and recommend varieties for each medium (Huhn, 1996). When it comes to noise, there are four basic options; better experiments, more repetitions, experimental design analysis and treatment design analysis, so AMMI can achieve better accuracy and provide free copies in addition to options above.

Gauch et al. (2008) concluded that the fundamental reason why AMMI is appropriate for agricultural research is that the ANOVA portion of AMMI can separate the major G and E effects and the GE interaction effects, which makes researchers research encounters very different problems and opportunities. AMMI is suitable for interdisciplinary research groups including crop and soil experts; Agronomists mainly focus on genotype and genotype by interactions with the environment and soil scientists focus on environment and interactions. As a result, AMMI offers a better chance than other graphically rendered responsive and large environments. The reward of effective statistical analysis of agricultural trials is faster improvements in yield, disease resistance, nutritional quality, and other important traits.

The AMMI method is used for three main purposes:-

A) Model diagnosis : - AMMI is more appropriate in the initial statistical analysis of yield trials, because it provides an analytical tool for diagnosing other models as sub cases when these are better for a particular data set (Tazu, 2011).

B) To clarify genotype - environment interactions: AMMI summarizes patterns and relationships of genotype and environments (Kempton, 1984; Zobel et al., 1988; Crossa et al., 1990).

C) To improve the accuracy of yield estimates that is equivalent to increasing the number of replicates by a factor of two to five (Zobel et al., 1988; Crossa et al., 1990). Such gains may be used to reduce costs by reducing the number of replications, to include more treatments in the experiment, or to improve efficiency in selecting the best genotypes.

9.2. *Limitation of AMMI*

The AMMI model has some disadvantages. If the number of components retained in the model is large (**m** is grater or equals to 3), it is difficult to describe the behavior of the GE interaction effects due to the impossibility of obtaining graphs in more than three dimensions. It is possible to plot all pairs of components but, in this case, each component accounts only for a small portion of the total GE variation. Also, the environmental response pattern cannot be estimated directly from the AMMI model. Hence, the AMMI model is mainly useful to identify the most stable and responsive genotypes, visually, in two or at most three dimensions. As the environmental genotype response pattern is almost always required by the plant breeders, this must be identified through one of the methods discussed previously (Ferreira et al., 2006).

9.3. *Genotype Plus Genotype by environment (GGE) Biplot Methods*

9.3.1. *Basic Concepts of biplot*

As Hunt (2002) stated, the biplot concept was first proposed by Gabriel (1971). Any two-input array or matrix X containing n rows and m columns can be thought of as the product of two matrices A, with n rows and r

columns, and B, with r rows and m columns. Therefore, the matrix X can always be decomposed into two component matrices A and B. If r equals 2 then the matrix X is said to be a second-order matrix. Each row of matrix A has two values that can be displayed as a point in a two-dimensional graph. Similarly, each column of matrix B has two values and can also be displayed as a point in a two-dimensional graph. When n rows of A and m columns of B are displayed in a single graph, the graph is called a "biplot". Thus, the binary plot of a second-order matrix contains n m points, which correspond to n × m values in the matrix itself, but still contains all the matrix information. The previous use of biplots in analysis of TEM data has been advocated by various authors, including Cooper and Delacy (1994) and Yan et al., (2007). They saybiplot has become a popular data visualization tool in many areas of scientific research, including psychology, medicine, business, sociology, ecology and agrosciences. The biplot tool has become increasingly popular among plant breeders and agricultural researchers since its use in crop evaluations and major environmental investigations (Yan et al., 2000).

X. Approximation of Any Two-Way Table using a Rank-Two Matrix

A biplot is obviously an elegant display of a rank-two matrix. In reality, however, it is rare that a two-way data set is exactly a rank-two matrix. Nevertheless, if a two-way data set, such as the yield data of a number of genotypes tested in a number of environments, can be approximated by a rank-two matrix, the latter can then be displayed in a biplot (Gabriel, 1971). The process of decomposing matrix X into its component matrices A and B is called 'singular value decomposition' (SVD), the result of which is r principal components (r equals the smaller of n and m). If the first two principal components (PC1 and PC2) explain a large proportion of the total variation of X, X is said to be sufficiently approximated by a rank-two matrix and can be approximately displayed in a biplot.

The output interpretation of multivariate statistics the biplot abscissa and ordinate shows the trait main effect and first principal component (PC1) term, respectively. The horizontal and vertical lines that divide the graph into four quadrants indicate the interaction score of zero and trait grand mean, respectively. Displacement along the vertical axis indicates the interaction difference between genotypes and environments. Similarly, displacement along the horizontal axis indicates the difference in genotype and environment main effect. The genotypes with PC1 scores close to zero indicate general adaptation across the environments, whereas with larger PC1 scores indicate specific adaptation of genotypes to environments which have the same PC1 scores and sign. The relative magnitude and direction of genotypes along the abscissa and ordinary axis in biplot explain the response pattern of genotypes across the environments. The genotype with PC1 score close to zero and high trait mean is considered to be stable. The environment with PC1 scores close to zero indicates smaller variation in interaction and relative ranking of genotypes are stable at these locations. This biplot is also known as AMMI1 as it considers one PC into account. It is commonly used for genotypic evaluation (Dia et al., 2016).

10.1. *Biplot (PC1 vs. PC2)*

Biplot is clearly an elegant display of second-rate matrices. In practice, however, it is rare that a double-entry dataset is exactly a second-order matrix. However, if a double-entry dataset, such as yield data from several genotypes tested in several environments, can be approximated by a second-order matrix, then the data set the

latter data can be displayed in binary histograms (Gabriel, 1971). The process of decomposing a matrix X into its component matrices A and B is called "single value decay (SVD), the result of which is r principal components (r equals the smaller of n).and m). If the first two principal components (PC1 and PC2) explain a large part of the total variation of X, then X is said to be approximated sufficiently by a second-order matrix and can be approximated in a binary histogram. .In the output interpretation of multivariate statistics, the abscissa and the biplothierarchy indicate the main effect of the characteristic and the first principal component (PC1) term, respectively. The horizontal and vertical lines dividing the histogram into four quadrants indicate an interaction score of 0 and the overall feature mean, respectively. Moving along the vertical axis represents differences in genotype-environment interactions.

Similarly, movement along the horizontal axis indicates the difference between genotype and the main environmental effect. Genotypes with a PC1 score close to zero showed a general adaptation across environments, while a larger PC1 score showed a specific adaptation of genotypes to environments with the same PC1 score and marker. The relative magnitude and direction of genotypes along the horizontal and normal axes in the two plots explain the response patterns of genotypes in environments. Genotypes with a PC1 score close to zero and a high trait mean are considered stable. Media with a PC1 score close to zero showed smaller interaction variability and the relative rank of genotypes was stable at these positions. This Biplot is also known as AMMI1 because it takes PC into account. It is commonly used for genotyping (Dia et al., 2016).

10.2. *Concepts of Genotype Plus Genotype by Environment (GGE)*

The concept of GGE originates from analysis of MET of crop cultivars. The yield of a genotype (or any other measure of genotype performance) in an environment is a mixed effect of genotype main effect (G), environment main effect (E) and GE. In normal MET, E accounts for 80% and G and GE each account for about 10% of the total variation (Hunt, 2002). For the purpose of cultivar evaluation, however, only G and GE are relevant (Gauch and Zobel, 1996). Furthermore, both G and GE must be considered in cultivar evaluation: hence the term ‘GGE’ (Yan et al., 2000). Simultaneous examination of G and GE is, thus, an important principle in cultivar evaluation. The GGE model applies the SVD to the data, subtracting the environment effects, because these biplots display both G and GE, which are the two sources of variation relevant to cultivar evaluation; as a result this model applies based on multiplicative linear-bilinear site regression.

10.3. *Models for Constructing GGE Biplot*

Biplot GGE shows the GGE portion of the MET dataset relative to other biplot types. Biplot GGE is important to display relevant information for crop evaluation and biplot GGE can be generated based on single value decomposition (SVD) through; Environmentally-centric data; Environment-centric data and in the environment the bias data is normalized and the environment-centric data and error data are normalized in the environment.

The steps in biplot analysis.

1) Centering the data, i.e. subtracting the respective environmental means from each of the cells.
2) Subjecting the environment-centered data to SVD, which results in singular values genotype and environment, scores for each of the n principal components, n being the number of environments. SVD is a

complex mathematical operation that decomposes a matrix into two component matrices using the least-squares method.

3) Partitioning the singular value into genotype and environment scores for each of the principal components. Theoretically, the singular value can be partitioned in any proportion, but symmetrical partitioning is preferred because it results in the same units for both the genotype scores and the environment scores and for all principal components.

4) Plotting the PC1 scores against the PC2 scores to generate a biplot. Biplots using other principal components are also possible. The plotting can be done using a spreadsheet, but the abscissa and ordinate must be drawn to scale.

5) Labeling the biplot with the genotype and environment names, this can be a very tedious job.

6) Added additional lines to facilitate biplot visualization and interpretation.

The purpose of scaling is to put variables or environments in a comparable scope, i.e. maxmin. Scaling is optional for genotype data (GED), but is necessary if the variables have different units. For (GED) of a given characteristics expressed in the same unit of measure in all environments. Scaling = "0" means the data has not been scaled or subdivided by anything. Other options for scaling data in a GGE biplot chart include scaling to the standard deviation inside the environment, scaling to the standard error inside the environment, and scaling to the medium. Using scaling = "0" will retain information about the differential standard deviation in different environments, which can be used as a measure of the ability to distinguish between environments. Using Scaling = "1" discards this information and assumes that all environments are equally important. Using Scaling = "2" can eliminate any inconsistencies between environments regarding their test failure while retaining information about the environments' discriminability. Copied data is required to use this option. Using Scaling = '3' eliminates unit and data range differences between variables while preserving the discriminability of environments (Yan et al., 2007).

Centering = "2", indicating that the data were centered on the environment (i.e. main effect E was removed from the data and the biplot shows only G GE). Other centering options in GGE charts include: 0, do not center; 1, middle large average, useful when the main effect of the row and the main effect of the column are concerned; and 3, double center. The choice of centering method is also characteristic for the research objective. Using Centering = "0" is useful for visualizing the original data and is effective for data sets with large mean values close to 0. The less than and greater sum of PC1 and PC2 in parts hundred indicates that the GGE histogram explains (G GE) the variations. In general, the higher this value, the more confidence the researcher has in biplot-based interpretations. However, if a smaller fraction of the total variation is explained, this does not necessarily mean that the biplot is useless, review the diagnostics section of the model instead. S.V.P indicates that single values are fully partitioned into the environment score prior to biplot construction to improve the biplot's suitability for visualizing relationships between environments. In contrast, SVP = "1" indicates that single values are fully partitioned into rows or genotype scores to improve biplot suitability for comparison of genotypes. These two SVP options are also useful for visualizing the genotype's response to the environment (e.g. which model wins where) (Yan et al., 2007).

Overall, the use of dichotomous analysis of genotype (G) plus genotype-for-environment (G GE) interactions

by plant breeders and other agricultural researchers There has been a significant increase in the last 5 years for multi-environment experimental analysis of data (Yan et al., 2007). The GGE plot is even superior to the AMMI plot in large environmental analysis and genotyping because it explains more GE and has biplot internal product characterization. Power Discrimination vs. The representative view of the GGE biplot is effective in evaluating test environments, which is not possible in AMMI analysis.

The recently developed GGEbiplot method (Yan et al., 2000) provides a more elegant and useful way of displaying MET data. It effectively solves both the problem of environmental discrimination and the problem of genotype selection for a given environment based on average yield and stability. It also allows for environmental as well as genotyping assessment. Furthermore, it facilitates the interpretation of GE as a genotypic factor by the interaction of environmental factors (Hunt, 2002).

10.4. *Singular Value Decomposition for Environment Centered Data*

$Y_{ij} - Y = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon ij$ Where; Y_{ij} is the mean yield of genotype i in environment j Y is the mean yield across all genotypes in environment j λ_1 and λ_2 are the singular values for the first and second principal components, PC1 and PC2, respectively. ξi_1 and ξi_2 are the PC1 and PC2 scores, respectively, for genotype i.ηj_1 and ηj_2 are the PC1 and PC2 scores, respectively, for environment j ε_{ij} is the residual of the model associated with genotype i in environment j.

10.5. *Visualization of Multi-Environment Trial data*

In the belief that a picture is worth a thousand words, many attempts have been made to present MET data graphically. The general scheme for graphically displaying MET data such as this is to plot the mean yield of each genotype against a measure of stability, which can be any of the parameters listed in Lin et al (1986). In summary, the following application of GGE biplotis mentioned:

1) Visualizing the performance of different genotypes in a given environment.
2) Visualizing the relative adaptation of a given genotype in different environments.
3) Visual comparison of two genotypes in different environments.
4) Visual identification of the best genotype(s) in each environment.
5) Visualizing groups of environments.
6) Visualizing the mean performance and stability of genotypes.
7) Visualizing the discriminating ability and representativeness of environments.
8) What which won where Polygon View.

10.6. *Strength of the GGE-Biplot Approach*

The GGE biplot method graphically displays the main effect of genotype and the interaction with the genotyping environment of METs, which are the only two parts of yield variation relevant to genotyping and identification. Environment assuming that the GGE of the MET is sufficiently approximated by the first two principal components, all the individual genotype relationships within the MET will be visualized using a GGE plot. Such a biplot graphically solves three out of four uses of MET (i) data analysis by investigating possible

differences of the large environment with the target environment; (ii) selection of superior genotypes for individual megaen environments; and (iii) choose a better test environment.

10.7. *Constraints of GG-E Biplot Approach*

All methods have their own limitations. The limitations of the GGE biplot lie in four aspects. First, it requires balanced data; second, it may explain only a fraction of the total GGE; third, it lacks a measure of uncertainty; fourth, although elegant, two-slot GGE analysis is rather tedious to perform with conventional tools. Now that the GGE biplot software is available, the fourth limitation is no longer an issue. Once the data is prepared, all functions are just one click away. Although quite common, unbalanced MET data is not really a problem with the GGE biplot approach; they are a matter of test design and implementation, creating problems for all kinds of analysis. The GGE biplot software offers two options for this problem. It allows generating a subset of balances, which can be used in GGEbiplot analysis; alternatively, the missing cells are automatically replaced with the average output of the respective environments.

In either case, the imbalance means that some of the information contained in the data cannot be used effectively. Therefore, the design and implementation of the test should be improved to avoid missed cells as soon as possible. Biplot GGE can only explain a small proportion of GGE when the main effect of genotype is significantly smaller than that of GE and when GE pattern is complex, in such cases GGE biplot including PC1 and PC2 can insufficient to explain the GGE, although the most important model of the MET has been shown.

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