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STUDYING GXE INTERACTION UNDER DIFFERENT MANAGEMENT SYSTEM AND YIELD LEVEL USING LINEAR-BILINEAR MODELS: THE CASE OF CIMMYT INTERMEDIATE TO LATE HYBRIDS TRAILS IN EASTERN AFRICA

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A B S T R A C T

CIMMYT, with national programs, conducts selection of stress-tolerant genotypes under managed stress conditions; this investigation is expected to add information to the existing knowledge. Data sets used in this study comes from Intermediate to Late Hybrid Trails (ILHT) conducted in five Eastern and Central Africa (ECA) countries from 2008 to 2011. Trials, ranging from 18 in 2009 to 29 in 2010 were used. Trials are categorized into four management systems and two yield levels. Variance Components, broad sense heritability (H), Site Regression (SREG), Genotypic Regression (GREG), Completely Multiplicative Model (COMM) and Factor Analytic (FA) models were fitted. Results are discussed and compared with those stated in literature. We argue that it is preferable to first fit the fixed effect models before proceeding to the mixed effect model, as the former shows the level of complexity of the GE component and number of Axis required to explain it. The fixed effect model, SREG2, is preferable for trails targeting to compare hybrids with checks. From the GGE biplots it was noted that the first two PC did not account for sufficient percentage of variation for all years which witnessed complexity in the GE component for this data. Nevertheless, since PC1 accounted for large percentage of variation than PC2, the plot still gives some idea of which hybrids are favored and where. Most importantly, location of genotypes along PC1 can serve for judging yielding potential of the genotypes to guide in selection decision. Equivalence between Finlay – Wilkinson and GREG was established. The few environmental covariables obtained for 2009 was used to fit Partial Least Square (PLS) regression. The result indicated complexity in the GE component, as PLS latent factors accounted for small percentage of variation. It was recommended to use information from SREG2, GREG2 and FA(1) models in order to identify stable genotype.

Keywords: AMMI, Biplot, Factor Analytic Model, GREG, Mixed effect model, SREG, Stability.

INTRODUCTION

Maize grain yield is reported as being considerably reduced under drought and low-N conditions (Bänziger et al., 2006). Developing hybrids effectively requires a genotype testing network that cover the target region adequately, achieves a high level of precision and repeatability in estimating genotypic means. National programs with support of CIMMYT lines serve a large number of farmers over a wide area and are exposed to both technical and financial constraints. It is thus important to stick to appropriate subdivision of a breeding target region and to setup strategy for selection of lines for such situations. CIMMYT GMP conducts selection of stress-tolerant genotypes indirectly under managed stress conditions, however the selection efficiency of this approach is not known and provision of additional information will help to understand the scenario better. Trails in Africa are conducted in two sub-regions, Eastern and Southern Africa; within each sub-region in different countries, at different locations and over years. However, in large and heterogeneous target regions such as Africa genotypes are expected to respond differently to variation in environmental factors such as temperature, soil fertility, and precipitation. Africa is divided into various agro-ecology and is highly exposed to both optimal and stress conditions. The presence of GE in plant breeding

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experiments is considered either as inconsistent responses of some genotypes to such environments due to genotypic rank change or as changes in the absolute differences between genotypes without rank change. In certain situations genotypic rank changes can be observed which may even lead to what is known as Cross over Interaction (COI) (Frankham et al., 2007; Lynch and Walsh, 1998, Cooper et al., 1996). This phenomenon, referred to as COI, introduces a degree of uncertainty into the measurement of overall genotype performance and thus complicates selection for broad adaptation (Basford and Cooper, 1998). A strategy to reduce or avoid GE interactions is to explore local adaptation by subdividing the plant breeding program. But, this may not always be a solution. It is rather important to understand the cause of GE in plant breeding and work towards disaggregating the GE, and adjusting parameters for the occurrence of GE because subdivision of a target region into more homogenous sub-regions will not always increase selection efficiency (Atlin et al., 2001, and Baker, R.J, 1988a).

Several models are commonly used for describing the mean response of genotypes over environments and for studying and interpreting GE in agricultural experiments: linear models, bilinear models, and linear-bilinear models. The objective of this study is therefore to understand the pattern of variability and GE interaction under various management systems and yield levels to identify links between models that are used to disaggregate and interpret the GE interaction component.

MATERIALS AND METHODS

Number of trial sites used for the study varies from year to year (Table 1). Number of locations and trails in a given year may not always match, because more than one trail is planted in same location. Five Eastern and Central African countries: Ethiopian, Kenya, Tanzania, DR Congo and Uganda, were included in the Regional trail set. Locations are also associated with the different types of stress management systems. For example, Chirendzi (in 2009) and Kiboko (in 2008 and 2010) are considered 'Managed Drought' (MD), characterized by low yield. Similarly, Asfsf-Arusha (2008) and Bako (throughout) were used as 'Managed Low N' (MLN). Majority of locations are however considered 'Optimal'. Trails were set in four management systems: managed-stress, random stress and optimal conditions. Managed stress is set as managed drought and managed low N (Table 1). Some observations made on the pattern of occurrence of management type and trails are: 1) Maseno (trail 6), and Busia (trail 17) in Kenya are the only sites that were used as sole 'Random Drought' site in 2008 and Maseno was never repeated in subsequent years; 2) Elgon Downs (trail 3) were considered 'Random Drought' in 2009, but the same location were considered 'Optimal' in 2010 (trail 18) and 2011 (trail 15); 3) Kakamega (trial 14) and Muguge (trial 16), both in Kenya are, considered 'Random Drought' in 2009, but the former was considered 'Optimal' in subsequent years (trail 32 in 2009; trails 22, 26 and 34 in 2010; and trail 31 in 2011). In general, two trails for 2008, three in 2009, and one trail in 2011 are the only trails considered 'Random Drought'. There was no trail site for 'Random Drought' in 2010. Therefore, estimated parameters such as Least Square Means (LSM), Variance Components and H may not be precise for these management types due to low number of observations.

A trail mean were computed within year and trails classified as being 'high' or 'low' yielder based on yield cut-off point of 3 t/h. Atlin et al. (2001) proposed this classification to serve as a basis for selection of target environments in breeding. Trail codes are consistent across locations within a given year but vary from year to year. About 51% of trails in 2008 are classified as low yielders, which is high compared to other years. Proportions of trails classified as high yielding are 67%, 66% and 60% for 2009, 2010 and 2011 respectively. Thus there is sufficient number of trails to fit a model for yield level by year (Table1).

Models which accounted for variations in trails, year, genotypes, and their interactions were fitted as:

$$YLD = \mu + Y + L(Y) + R(LY) + B(RLY) + G + GY + GL(Y) + \varepsilon$$

Where Y=year, L=location, R=replication, B=incomplete block, G=genotype

Different Trails may have been given the same code in different years, therefore trails are considered as nested within year in the specification of the models. This model fitted to all data provides overall variance components for Trail, Year, Genotype, their interactions and the error term. It thus shows the overall pattern of occurrence of variability, before trails are split into groups (by management type and yield level). The second approach was fitting the above model for Yield Levels (P) and Management Types (M). It is understood that trails under different management conditions depict different characteristics and estimating variance components, H and BLUPs by management type is commonly practiced among breeders.

Table 1. Number of trails for a combination of year, management type and yield level. Note that trails are given different codes per year. Therefore trail codes from two or more years may or may not coincide.

	Year			
	2008	2009	2010	2011
Trials by Management Types				
Managed Drought	3	3	3	2
Managed Low N	2	1	2	1
Optimal	18	11	24	21
Random drought	2	3	-	1
Trails with H < 0.15	4	2	4	6
Trials by yield group				
Low yield (< 3 t/ha)	12	6	10	10
High Yield (> 3 t/ha)	13	12	19	15
Total number of trials	25	18	29	25

The yield level and management types would not be incorporated in the same model simultaneously since it over-fit the data.

However, in models (1) and (2), 'Management Type' and 'Yield Level' were included respectively to estimate overall contributions of each of them. This helps to determine whether there is sufficient variability among the management types (and yield levels) in order to consider them as legitimate groups where breeders may have to consider them as separate selection environment.

$$YLD = \mu + M + Y(M) + L(YM) + R(LYM) + B(RLYM) + G + GM + GY(M) + GL(YM) + \varepsilon \text{.....(.1)}$$

$$YLD = \mu + P + Y(P) + L(YP) + R(LYP) + B(RLYP) + G + GP + GY(P) + GL(YP) + \varepsilon \text{.....(..2)}$$

Where M=Management type, Y=year, L=location, R=replication, B=block, P=yield level

Because of changes in the coverage of management type and yield level each year, interaction of year with these terms does not make sense. Therefore, year is considered to be nested within management type or within yield level. Similarly, since locations fall under the different management types, or yield level, location is considered to be nested under a combination of Y and M or Y and P. Nevertheless, these models may be over-parameterized since they are additional factors imposed on the already designed experiment. The number of locations that fall under drought or low N conditions is very few compared to the optimal situation and this might introduce some bias in their comparison. Breeders are thus advised to plan setting experiments under this management situation to generate more replication. In the fixed model scenario, however, contrast can be set to test differences between these groups. Therefore, it is advisable to use model (1) and (2) and fit for each management type and yield level.

Normally about 20-30% of the lines are expected to be carried over from one year to the next to form a basis for evaluation of new entries in a given year. However, 16 lines were included in the trials for three consecutive years (2008 - 2010). Nevertheless, no line appeared consistently over the four year period (2008-2011). In addition, among lines tested in 2010, only four were repeated in 2011.

Several statistical models and methods of analysis were developed for analysis of Multi-Environment Trials (MET) data over the years and a good review is presented in Smith et al. (2005). Crossa et al. (2009) described both fixed and mixed versions of most of these models and presented examples on their use. These models are originated from principles of Williams (1952) which has later been extended by Gollob (1968) and Mandel (1969, 1971) and they are all interrelated. Crossa et al. (2002) called these models families of linear-bilinear models and showed how families of these models are related.

The General Linear-Bilinear Model (Yan et al., 2007 and Burguen˜ o et al., 2008) in matrix have the following form:

$Y = \sum_{h=1}^{m} \beta h X hij + \sum_{k=1}^{t} \lambda k\, \alpha ik \gamma jk + \varepsilon ij$ ----------(3)

Where, $\boldsymbol{X}$ is known constant, $\boldsymbol{\beta h}$ is the vector of regression coefficients for the linear term.

One form of fixed linear-bilinear models, a special case of (3), for non-replicated data may be stated as:

$Y = \mu + E + G + \sum_{k=1}^{t} \lambda k\, \alpha ik \gamma jk + \varepsilon ij$ ----------(4)

where E is environmental and G varietal main effects, λ is the singular value of the k^{th} multiplicative component,

αik are kth left singular vector for ith genotype representing genotype sensitivity to hypothetical environmental factors represented by the kth right singular vector with elements of γjk . According to Gauch (1988) and Gauch et al (2001), this model is known as AMMI.

Three important variants of model (3) were also discussed in literature (example, Crossa et al., (2010). They are i) Site Regression (SREG), also known as GGE biplot, where Site main effect is separately estimated but Genotype main effect and GE interaction is combined; ii) Genotype Regression (GREG), where genotype main effect is separately estimated and environment main effect and GE is combined; iii) Completely Multiplicative Model (COMM), where no main effect is estimated separately. Cornelius and Seyedsadr (1997) expressed the above models in matrix form. Each of these models may be fitted as a fixed effect or mixed effects. Burgueno et al. (2008) and Crossa et al. (2010) discussed and described the two possibilities with their advantage and disadvantages.

In the SREG model, the bilinear term fits the main effects of genotypes (G) plus the GE interaction, a composition of which is subjected to singular value decomposition and is different from what is being fitted in the AMMI (Crossa et al, 2009). In addition, SREG2 can be perceived as consisting of a set of multiple regression equations for each environment on genotypic regressor variables.

A mixed-model analogue of AMMI and/or SREG has been developed using the Factor Analytic (FA) model for approximating the variance-covariance GE structure (Piepho 1998; Smith et al. 2002, 2005; Piepho and Mohring 2005; Cornelius et a, 1999). Crossa et al. (2006) and Burguen˜ o et al. (2008) described implementation of these models. Burgueno et al. (2008) described the equivalence between $SREG_2$ and FA(2) for finding subsets of genotypes and environments without crossover interaction (COI). We envisage that similar development can also lead to the equivalence of $GREG_1$ and Finlay-Wilkinson models with FA(1). Since Finlay and Wilkinson (1963) are equivalent to $SREG_1$with the role of genotype and environment interchanged (Yan and Tinker, 2005, 2006), it is straight forward to establish the fact that the fixed effect model $GREG_1$ is equivalent to stability analysis models of the Finlay-Wilkinson (1963) and the Eberhart - Russell (1966), with some re-parameterization. Following Burguen˜ o et al. (2008), in this re-parameterization, the first multiplicative term, αi1γj1 is considered as the genotype regressions with coefficients αi1 on environmental indicesγj1. The λk parameter can be absorbed into αi1 or γj1, such that $\alpha * \mathrm{i}1 = \lambda[\mathrm{f}]\,\mathrm{k}\ \alpha\mathrm{i}1$ and $\gamma * \mathrm{j}1 = \lambda(1-\mathrm{f})\mathrm{k}\ \gamma\mathrm{j}1$., where f lies between 0 and 1. Although the Mixed model approach (FA models) are flexible and have several benefits (Crossa et al, 2010), often a maximum of FA(2) is fitted and the Eigen values are absorbed in the random variables. But the fixed effect approach provides a measure of how much each component contributed to the variation in the GE (or GGE) and helps decide how far the GE (or GGE) component is complex. We therefore argue that the fixed effect models are first fitted and observations made before proceeding to the FA models.

Furthermore, Burguen˜ o et al. (2008) showed the equivalence between the FA(2) and SREG2 as a set of multiple regressions. They also argued that the interpretation of the loadings and scores of the FA(2) is the same as that obtained by the $SREG_2$. Under factor rotation of the FA(2) to a principal component solution, Burguen˜ o et al. (2008) showed that the directions and projections of the vectors of FA(2) and $SREG_2$ in the biplot are the same. Therefore, the same principle can be used to justify equivalence of $GREG_1$ and FA(1), which is easier to demonstrate as we are dealing with one component only. In a situation where FA(1) is applied to 'E+GE', the score of the first factor measures genotypic sensitivity to latent environmental variable. The difference between the fixed and mixed model approach is therefore that, the former is based on observed environmental variable, which is average of all genotypes per site, while the later uses latent (unobservable) environmental variable. Proportion of variation GREG1 is accounted for is an indicator of how much of the 'E+GE' variation can be explained by a linear term. It is therefore important to first fit GREG1 and observe PC1 before proceeding to fit the FA(1) model for stability analysis.

Incorporating external environmental covariables helps to explain genotype by environmental interaction (GE). Multivariate Partial Least Square (PLS) Regression model is one such useful type of models (Vargas et al., 1999; Crossa et al., 2010). It generalizes and combines features from principal component analysis (PCA) and multiple regression. Following Crossa et al., when genotypic response over environment (Y) is modeled using environmental covariables, the jxh matrix Z of H (h=1, 2 ,3…., H)

environmental covariables can be stated in bilinear form as follows:

$Z = t1p'1 + t2p'2 + \cdots . + tmp'm + Em = TP' + E$----(5)

where the T matrix contains the tj jx1 vectors which are latent environmental covariables (known as Z-score, indexed by environments), and the P matrix contains the p1....ph hx1 Z-loading vectors (indexed by environmental covariables) and E has the residual. Similarly, the response variable matrix Y in bilinear of the form:

$Y = t1q'1 + t2q'2 + \cdots . + tmq'm + Fm = TQ' + F$ ---(6)

Where the Q matrix contains the q1....qh lx1 vector called Y-loading (indexed by genotype) and F has residual. The relationship between Z and Y is transmitted through the latent variableT. The PLS performs simultaneous but separate principal component analysis of Z andY.

Interpretation of AMMI2 and SREG2 are similar. The interpretation is based on genotypic and environmental vectors drawn from the origin (0, 0) to the end points of the location of scores (Gower and Hand, 1996). They explained that an angle of less than 90° or larger than 270° between the two vectors is an indicator of positive genotype positive response at that environment, a negative response if the angle is between 90° and 270°. Phenotypic correlation of environments or genotypes can also be approximated using cosine of the angle between the two, an angle of zero, 90° (or –90°) and 180° indicating a correlation of +1, 0, and –1, respectively.

In this paper, we fit different models and explore their relationship in the analysis and interpretation of MET data. Practical importance of some of the models emphasized and selectively fitted to the data.

RESULTS AND DISCUSSION

Variance Components after excluding local checks and locations for which H<=0.15 were obtained for the various classifications (Tables 2-6). Different checks are used in different sites, and are known locally only and cannot be included in the model. The Variance Component (VC) and H are generated for two time periods, 2008-2010 and 2008-2011 (Tables 3-5). That is because 16 entries appeared in all the three years and thought that it would be reasonable to compare the two time periods. In addition, the VC and H are estimated for management and yield level. Management and yield level were also combined to produce categories with reasonably large number of sites so that convergence is attained during model fitting using REML.

Table 2. Variance Components and H of Grain yield for a model that includes management type or Yield level, for 2008-2010 Eastern and Central Africa ILHT regional trails. Keys are: T=management or yield level, Y=year, L=location, R=replication, B=block, G=genotype, H=broad sense heritability. In the source of variation column, T stands for either management type or yield level factors. For example, variance component (T) for management type is 1.38, while for Yield level it is 5.54.

Source of variation	Management Type	Yield level
T	1.38	5.54
Y(T)	0.17	0.06
L(YT)	3.38	1.64
R(TYL)	0.18	0.18
B(TYLR)	0.13	0.13
G	0.10	0.11
GT	0.00	0.01
GY(T)	0.08	0.08
GL(YT)	0.21	0.20
Residual	0.81	0.81
H	0.72	0.75

In assessing H we found that, 48%, 50%, 34% and 44% of the trails in 2008, 2009, 2010 and 2011 respectively recorded H > 0.50. Trails in 2009 generally recorded better performance as 78% of them have H>0.40, compared to the remaining years where this percentage is 45 for 2010 and 48 for 2008 and 2011. Trails in 2010 recorded relatively low H probably due to their large size (as number of trails is the maximum in 2010). Five sites in 2008 (15, 24, 25, 34 and 40), three in 2009 (9, 12, 35) and two sites in 2010 (22, 26) has recorded highest H (> 0.70). All these sites are optimal sites.

Except for 'MLN, >3 t/ha' and 'RD, >3 t/ha' trail categories, GxE variance component (L*G(Y)) is higher than Genotypic Variance in all other categories, indicating the fact that genetic variability is masked by higher GxE interaction. From Statistical marginality condition, interpretation of the main effects may not be feasible if the interaction term is significant. Therefore, it is important to account for GxE term when estimating parameters. Most of these categories are associated with low yield situation and indicates potential for selection under stressed circumstances.

Variance Component for Management types (Tables 3 & 4) is high indicating presence of considerable variation in this category which provides an opportunity of breeding for the different management system. The details of parameter estimates are given in Table 3 for 2008-2010 and in Table 4 for 2008-2011 data sets.

Table3. Variance Components, after excluding local checks and locations with H<=0.15, by management for Grain Yield, 2008-2010 Eastern and Central Africa ILHT regional Trail.

	Optimal	Managed low N	Managed Drought	Random Drought
Y	0.20	0.00	0.4133	2.5768
L(Y)	3.93	1.00	1.0967	0.3763
R(YL)	0.14	0.29	0.3870	0.1059
B(YLR)	0.09	0.14	0.2926	0.3141
G	0.11	0.00	0.1146	0.0274
YG	0.13	0.08	0.0435	0.00
GL(Y)	0.23	0.13	0.0786	0.2028
Residual	0.93	0.27	0.5127	0.4872
H	0.70	0.0	0.841	0.812

Table 4. Variance Components, after excluding local checks and locations with H<=0.15, by management for Grain Yield, 2008-2011 Eastern and Central Africa Regional variety trail.

	Optimal	Managed low N	Managed Drought	Random Drought
Y	0.03	0.00	0.00	0.86
L(Y)	3.52	0.78	0.41	0.61
R(YL)	0.12	0.23	0.28	0.10
B(YLR)	0.12	0.17	0.26	0.30
G	0.15	0.00	0.11	0.02
YG	0.13	0.12	0.001	0.00
GL(Y)	0.28	0.10	0.10	0.17
Residual	0.86	0.39	0.45	0.45
Trail	36	6	7	6
H	0.80	0.00	0.90	0.47

For combined analysis of 2008-2010 and 2008-2011 data, H for 'Managed Drought' remained high indicating possibility of selection for stressed environment (Table 3 & 4). For the 2008-2011 data H for 'Random Drought' is reduced to 0.47. There is only one such trail in 2011 and may have contributed in reversing the result. On the other hand, H for 'Optimal' and 'Managed Drought' has substantially increased. This may be due to the fact that majority of the hybrids in the 2011 trail are new entries and exhibited better heritability (Table 4). For Yield level categories, there is considerable improvement in H for the data of 2008-2011 over that of 2008-2010. Particularly, H for 'Low yield' category increased from 0.53 to 0.72 (Tables 5). From analysis of the 2008-2010 data by management and year combination, H showed considerable reduction for all categories. 'Managed Drought' in 2010 has the lowest H (0.02) which indicates that the previous high H for analysis of all years must have been contributed from 2008 and 2009 data sets.

To avoid low number of sites for 'Managed Drought' management types were re-categorized with yield level as 'Managed Drought + MLN', 'Random Drought', 'Optimal > 3 t/ha' and 'Optimal < 3 t/ha'. 'Managed Drought' and 'Low N' are merged to increase replications. Variance components and H for these categories are given in Table 6. It is now evident that high yielding trails in the 'Optimal' category are repeatable, as those in low yielding category registered H of about 0.08. The 'Managed Drought + MLN' category, although slightly reduced, still have high H but this is purely attributed to 'Managed Drought' trails alone. Therefore, it is better to isolate 'Random Drought' and 'Managed Low N' in future analysis as they are not repeatable possibly for reasons of low number of trails.

Results from phenotypic and genotypic correlations (Table not presented for brevity) shows that 'Managed Low N' in 2009 is relatively poorly associated with all other categories. Particularly it has the lowest correlation (r=0.43) with 'Optimal' in 2008. In contrary, 'Managed Low N' in 2008 has relatively stronger association with the other categories. There is very strong correlation between 'Optimal' and 'Managed Drought' regardless of year of experiment. 'Managed Low N' in 2008 has strong correlation with 'Managed

Drought' regardless of trail year showing validity of combining the two to overcome shortage of replication. 'Random Drought' seems to correlate better with 'Managed Drought' than 'optimal'. The genetic correlation identified the relatively low correlation between 'Managed Low N' and 'Optimal' in 2010 only.

Table 5. Variance Components and H for High and Low yield levels after locations with H<=0.15 are removed (Grain Yield), for Eastern and Central Africa ILHT regional variety trail for two time periods, 2008 – 2010, and 2008-2011.

	2008 - 2010		2008 - 2011	
Source of variation	High	Low	High	Low
Y	0.11	0.04	0.02	0.06
L(Y)	2.50	0.25	2.16	0.32
R(YL)	0.20	0.14	0.16	0.12
B(YLR)	0.10	0.18	0.13	0.19
G	0.17	0.02	0.22	0.03
GY	0.14	0.04	0.15	0.03
GL(Y)	0.24	0.13	0.29	0.13
Residual	1.11	0.36	1.00	0.35
H	0.76	0.53	0.84	0.72

BLUPs for 2008-2011 trail data by Yield level are computed (but not presented for brevity). The result shows that predicted yield for 'high' category is in the order of 5 to 6 t/ha. But two hybrids from 2011 trail, HYTECH11 and HYTECH20, recorded lowest predicted mean. Predicted mean in the 'Low' yield category is in the order of 2 t/ha, but few hybrids such as CKH08008, CKH08002, and CKH08053 has lowest predicted mean and may not have sufficient potential for future candidacy.

As indicated earlier, this data has come from regional variety trails where hybrids are compared with checks and breeding gains are evaluated, therefore we felt that the fixed version of SREG is more appropriate (since we are not interested in prediction) to fit (Gauch 2006; Yang et al. 2009) despite current controversies as to whether Factor Analytic model or Fixed SREG is more appropriate.

Examination of ANOVA table shows that percentage contribution of environmental variation, out of overall variability in the yield, is generally large. This ranges from 40% in 2009 to 69% in 2008. These values are 57% and 67% respectively in 2010 and 2011. Contribution of Genotype variation is 2%, 2%, 3% and 3.7% in 2008, 2009, 2010 and 2011 respectively. Proportion of GE (out of all variability in yield) is 8%, 7%, 10% and 14% for 2008, 2009, 2010 and 2011 respectively. Yan, et al 2001, by analyzing Ontario Winter wheat found similar results, except that in their case genotype contribution ranged from 1.8% to 28.5%. About 48% of variation in yield in 2009 is designated as random error, while this value is only 12% in 2011. This shows that there is some systematic variation operating in the data which could not be accounted for in 2009 but the trials are well managed in 2011.

Table 6. Variance Components, after excluding local checks and locations with H<=0.15, by a combination of Management Type and Yield Level for Grain Yield, 2008-2011 Eastern Africa Regional variety trail. The columns are 'Optimal' management and yield > 3 t/ha, 'Optimal' management and yield < 3 t/ha, 'MD+LN' stands for a combination of Managed drought and managed Low N.

	Optimal > 3 t/ha	*Optimal< 3 t/ha*	MD + LN	Random Drought
Y	0.00	0.07	0.00	0.86
L(Y)	2.15	0.12	0.51	0.61
R(YL)	0.14	0.03	0.26	0.10
B(YLR)	0.13	0.08	0.22	0.30
G	0.21	0.00	0.06	0.02
YG	0.15	0.06	0.00	0.00
GL(Y)	0.30	0.11	0.16	0.17
Residual	1.01	0.25	0.44	0.45
Number of Trails	32	10	13	6
H	0.83	0.08	0.89	0.47

We argue that fitting SREG, (sometimes including GREG or COMM) is more important and statistically meaningful than AMMI. This is because in statistical marginality theory of effects, main effects cannot be interpreted independently if the interaction term is significant. In the analysis of MET data, the GE term is often highly significant with GE sum of square being much higher than that of G. Therefore, combining the G and GE effects and subjecting to SVD or FA model is appropriate. However, in a situation where the significance probability for the main effects (E and G) is much smaller than that for GE, then AMMI model might be more appropriate to fit. Consequently, the result shows that proportion of variation accountable by GGE (out of the total, E+G+GE, variation) increased from 12.7% in 2008 to 21% in 2011, 2009 and 2010 being about 8.9 % each (Figures 1-2). In other words, in 2008, 3.6% of the total variability (E+G+GE) is accounted for by PCA1 (and about 5.5% accounted for by the first two PCAs). In 2011 PCA1 accounted for about 9.9% (about 45% of G+GE variation) of the total variation, while 12.2% of the total variation is accounted for by the first two PCAs. Therefore, more component of the G+GE variation is explained by the new axis in 2011 than in 2008, hence the biplot is more informative for 2011 data. Based on arguments set out by Yang et al. 2001, the G+GE component in all the three years is important (as all contributed > 10% of E+G+GE variation), but the first two PCA did not account sufficiently for the G+GE variation in all years, the total contribution being 58% in 2011 followed by 50% in 2010 and 2009. Contribution of the first two PCA is low in 2008 (less than 50%) and may not be important in selection or delineation of mega-environment.

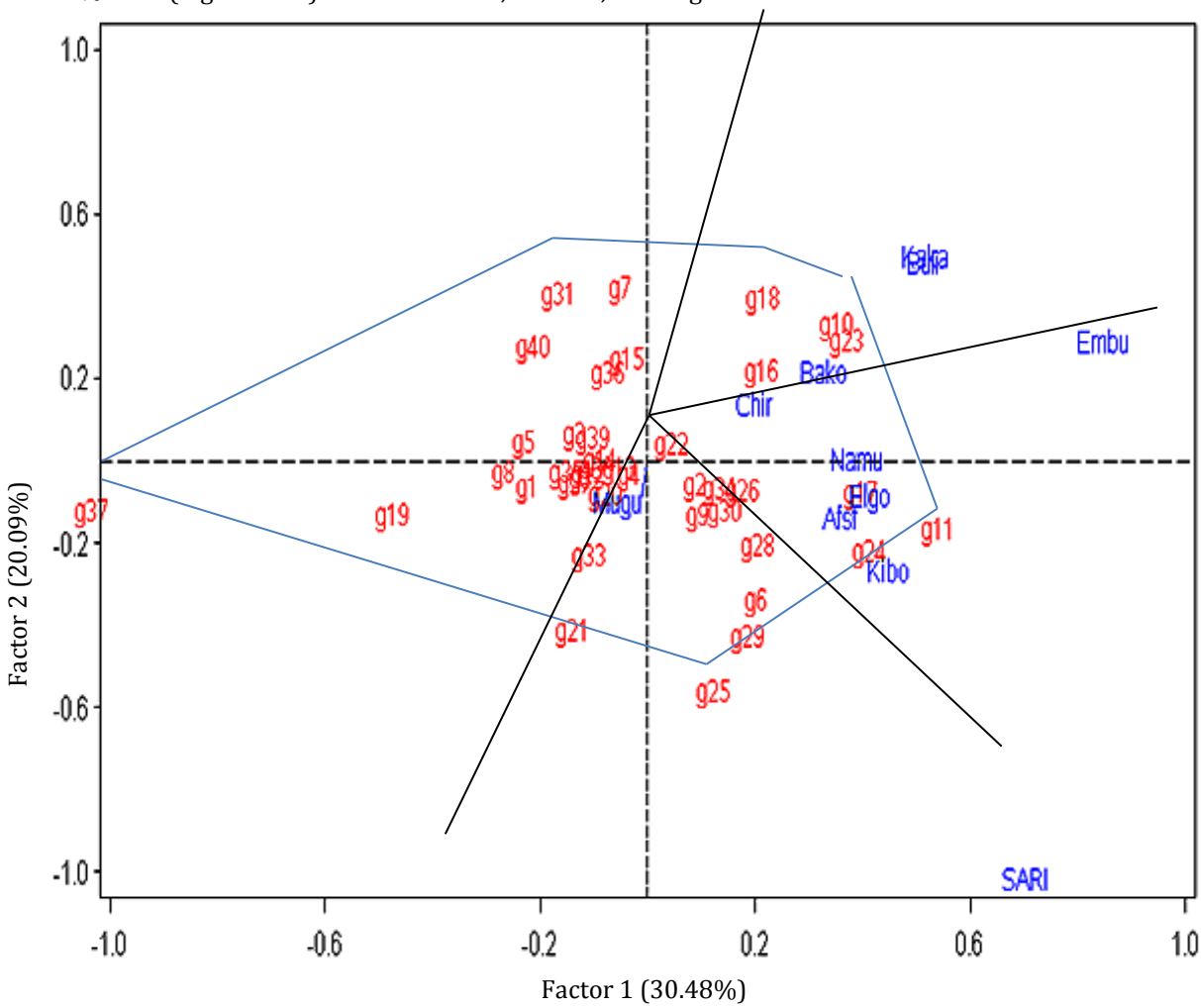

Figure 1. Site Regression (SREG2) Biplot of the first two PCA for ILHT Eastern Africa regional trial 2009 data. A polygon is imposed on the biplot by joining the outer genotypes (vertex genotypes) and drawing straight line from the origin perpendicular to the lines.

To be able to obtain > 65% contribution, one may have to consider up to 5 PCA axes, which is not useful for valid interpretation. But, a peculiar phenomenon in 2010 and 2011 is that the first PCA alone accounted for > 40% of variation in the G+GE, which may be useful to measure potential of the genotypes in these years. When this result is compared with AMMI2 model, the contribution of the axes considerably decreased, particularly, the 2010 data set showed huge reduction. This shows that the GE component is indeed complex and cannot easily be disaggregated and interpreted. However, since the first PCA is highly loaded for 2010 and 2011, some general remarks may be made. First it would be good to see consistency of the plot over the years.

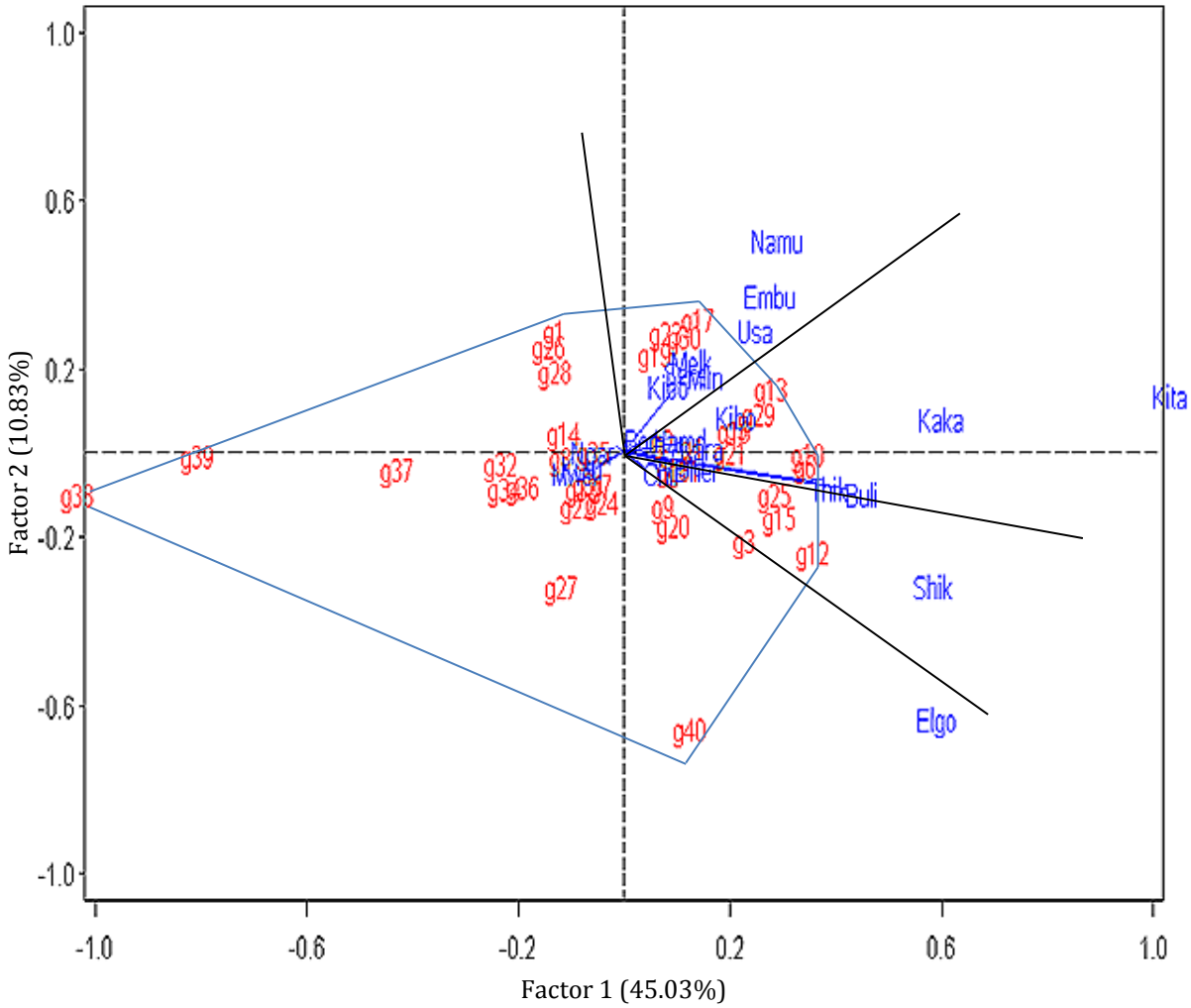

Figure 2. Site Regression (SREG2) Biplot of the first two PCA for ILHT Eastern Africa regional trial 2011 data. A polygon is imposed on the biplot by joining the outer genotypes (vertex genotypes) and drawing straight line from the origin perpendicular to the lines.

It is apparent that the environment has mostly positive on the first PCA, apart from changing position of the locations from year to year. By drawing an imaginary polygon that connects corner genotypes so that all other genotypes fell inside the polygon, and then drawing straight line from the origin of the biplot to each side of the polygon, it is possible to identify 'what - wins – where'(Yan et al, 2000, 2001). Results for 2009 and 2011 are presented in Figures.1 and 2 respectively. Consequently in 2009, the vertex genotypes particularly located on positive side of PCA1 are wining genotypes in a given environment. Genotype 10 is the wining genotypes at Kakamega. Genotype 11 wins at Embu which is close to its side of the line. Genotype 18 without a site in its sector is not the highest yielding in any environment. Genotype 25 is a winner in Kiboko although this site is not in its sector. Such inconsistencies may have occurred due to the fact that

the first two PCAs have not accounted for sufficient proportion of variation in 'G+GE'. Genotype G37, a check known as WH403 has very low PCA1 and is lowest yielder in most sites in this year and seem non-adaptable, while the other two checks (G38-WH505 and G39-H513) are located close to the origin, although may not be adaptable to any of the sites, which contradict the expectation that checks are varieties already adapted to the sites. G19 hybrid known as CKH08053 is also associated with low PCA1 and is low yielder throughout. This hybrid is located very close to G37 check and may perform similarly. On the other hand, G31 and G40 are low yielders at Kiboko, Asffs and SARI and are less adapted to these areas. But since the first two PCA are accountable for about 51% of the GGE variation, caution should be taken in interpreting the result. Bulinidi and Kakamega, the 'Random Drought' locations in 2008, are paired on the biplot and are associated with G10, G16 and G23, which shows that the locations still demonstrate some similarity even in different years.

Biplot for 2010 is different from other years in the sense that genotypes are distributed to the four quadrants proportionally. Genotypes G22, G24, G26, G15 are associated with small PCA1 and are low yielders which may not be adapted. The main interest here is to compare performance of the three checks, G39, G40 and G41, with the hybrids. The plot shows that all of them are located in different quadrants and seem to perform differently. For example, G39 which is low yielders is not well adapted to most of the environments, while G40 seem to be adapted to Elgton.

In 2011, the two checks, G38 and G39, are associated with low PCA1 and are very low yielders throughout. The reason for inclusion of these varieties in the trails should be examined. G37, another check variety is also low yielder and non-adaptable at any of these locations. The other three checks, G34 (H513), G35 (WH403) and G36 (WH505) which appeared in the regional trials consistently from 2008 to 2011, also have relatively small PCA here, like in 2009, but are close to the origin. All of them are also well adapted to two sites, Muguga and Maseno. The genotypes, G1, G26 and G28, which formed group on the plot, has small PCA1 and are lowest yielders at Elgton, Shik, Think, and Buli. Among the vertex Genotypes, those appearing isolated and stood clear from others, G12 and 40, are associated with sites where they won. Accordingly, G12 won in Shika (and thinka as well), while G40 won at Elgon. There is however no clear cut for a group of genotypes that appeared together around the vertex. This might be due to the fact that the Biplot did not have sufficient information since the variation accounted by GGE is not that large.

To establish equivalence between GREG1, Finlay Wilkinson regression (1963) and FA(1) models, we present results from the ILHT data set. Results from GREG2 shows that PCA1 contributed 91%, 84%, 87% and 87% of the 'E+GE' variations in 2008, 2009, 2010 and 2011 respectively. This result is in contrary with those obtained from SREG2, where PCA1 contributed in the range of 30% to 45%. Such differences might have occurred due to the fact that in GREG, 'E+GE', variation is highly dominated by variations in 'E', unlike variations in 'G' which is small. Therefore, PCA1 mainly captured variations in 'E' as the 'GE' component is relatively small. This indicates that the Finlay – Wilkinson regression type would explain stability of these hybrids. We however choose to fit Eberhart and Russell Stability model (1966) within the mixed effect model framework to obtain the stability parameters using Factor Analytic model (Piepho et al, 1997, 1998a). Eberhart and Russell in their fixed effect approach advocate that a genotype with regression slope approaching unity and deviation variance approaching zero is more stable. The Factor Analytic model computes genotypic sensitivity parameter to the Latent environmental index. In the traditional Eberhart and Russell approach, genotype means are regressed on environmental means to obtain stability parameters. This approach has however been criticized since environmental means are calculated from genotype performance and do not provide an independent information for judging stability of genotypes.

For stability study only 'Optimal' trials are included in the analysis since sites dedicated to ' Managed Drought', 'Random Drought' and 'Low N' trials are very few and that these stressed environments would be under represented and the results biased. Sites categorized as 'Optimal' are 20, 15 and 24 for 2008, 2009 and 2010 respectively. Often about 20% to 30% of the genotypes are carried to the following year, but all genotypes included in a given year appears in all sites. Therefore, stability is obtained on yearly basis for those genotypes included in a given year, but overall stability is obtained for genotypes used during 2008-2010 (Table 7). Heterogonous error variance approach is used in FA

model so that each genotype will have an associated deviation from the fitted model.

Results show that mostly different genotypes are stable in different year, except CKH08072, CKH08066, and CKH08004, which are stable in 2009 and 2010. Genotype CKH08051 which is among the first five high yielding genotypes in 2008 and 2010 is stable in 2008 but not in other years. Genotype CKH08017 is top yielder and stable (intermediate stability in 2009) in 2010, the required quality from genotype performance. The check variety, WH403, is high yielding in 2008 but unstable; it is stable in 2009 but exceptionally low yielder (very small PCA1 of SREG2), and has intermediate performance both in stability and yield in 2010. This shows that it is not possible to provide a clear-cut approach of selecting stable genotype; breeders must consider several criterions to select genotypes of interest based on their objectives. In general, to judge the relative stability of genotypes, it is better to look at 'Stability Coefficients', 'Stability Variance' or 'unexplained variation' and the genotype's relative position on the biplot of SREG2 for yield potential. For a genotype to be stable it therefore needs to have small stability coefficient, small unexplained variation and high or intermediate SREG2 PCA1 value (an indicator of high or intermediate yield level).

Table 7. Stability Parameters for ILHT 2008-2010 Eastern Africa Regional Trial Data set. This analysis is only for 16 Genotypes that are repeated over all the three years period.

Genotype Code	Stability coefficients	Unexplained variation	Least Square means	STD Error of the mean
CKH08004	1.507	0.297	3.577	0.253
CKH08017	1.373	0.434	3.881	0.241
CKH08036	1.850	0.497	4.048	0.313
CKH08039	1.877	0.400	4.592	0.313
CKH08041	1.555	0.427	3.724	0.267
CKH08047	1.947	0.510	4.205	0.328
CKH08048	2.115	0.613	4.625	0.357
CKH08049	2.380	0.820	4.508	0.403
CKH08051	2.020	0.827	4.829	0.350
CKH08066	1.469	0.316	3.757	0.249
CKH08072	1.372	0.674	3.809	0.253
CKH08073	1.794	0.407	4.027	0.301
CKH08075	1.516	0.295	3.886	0.255
CKH08078	1.471	0.430	3.815	0.255
CKH08079	1.645	0.360	3.804	0.277
H513	1.703	0.314	3.733	0.283
WH403	1.657	0.908	3.745	0.303
WH505	1.808	0.217	4.188	0.295

PLS model is fitted for ILHT 2009 only due to lack of availability of environmental covariables for other years. Very few environmental covariable were obtained for 2009 but analysis conducted to show the possible benefit that PLS biplot may provide and contrast that can be made with other biplots when sufficient number of environmental covariable exists. Results from PLS is shown using Figure 3. Three latent vectors of PLS may be obtained (as the covariables are only 3). The three latent vectors can explain only about 28% of variations in the GE component. The two latent vectors explained about 98% of the variation in the environmental covariable but explained about 18% of variation in the GE interaction component only, which is even smaller than what was explained by the SREG showing complexity of the GE component. This is related to the fact that very few environmental covariables are used, two of which are on temperature and highly related. But the good indication for importance of the method is that such very few environmental covariable could explain considerable portion of variation in the response variable. The result also shows that the minimum and maximum temperature values are highly associated as expected as they are very close in the plot. This indicates that the minimum and maximum temperature affects the genotype performance in the same way. The biplot did not completely manage to separate high and low yielding genotypes due to low percentage accountability of the latent factors. But, the biplot seems to somehow agree with SREG plot in commonly identifying some high and

low yielding genotypes. For example, both plots highlighted Genotypes 23, 16 and 22 as high yielding and Genotypes 37 and 8 as low yielding. As the rainfall covariable is located in the top right quadrant, it is associated with high yielding genotypes. More environmental covariables might be required to provide a better interpretation of the GE component as it is complex and could not be effectively disaggregated.

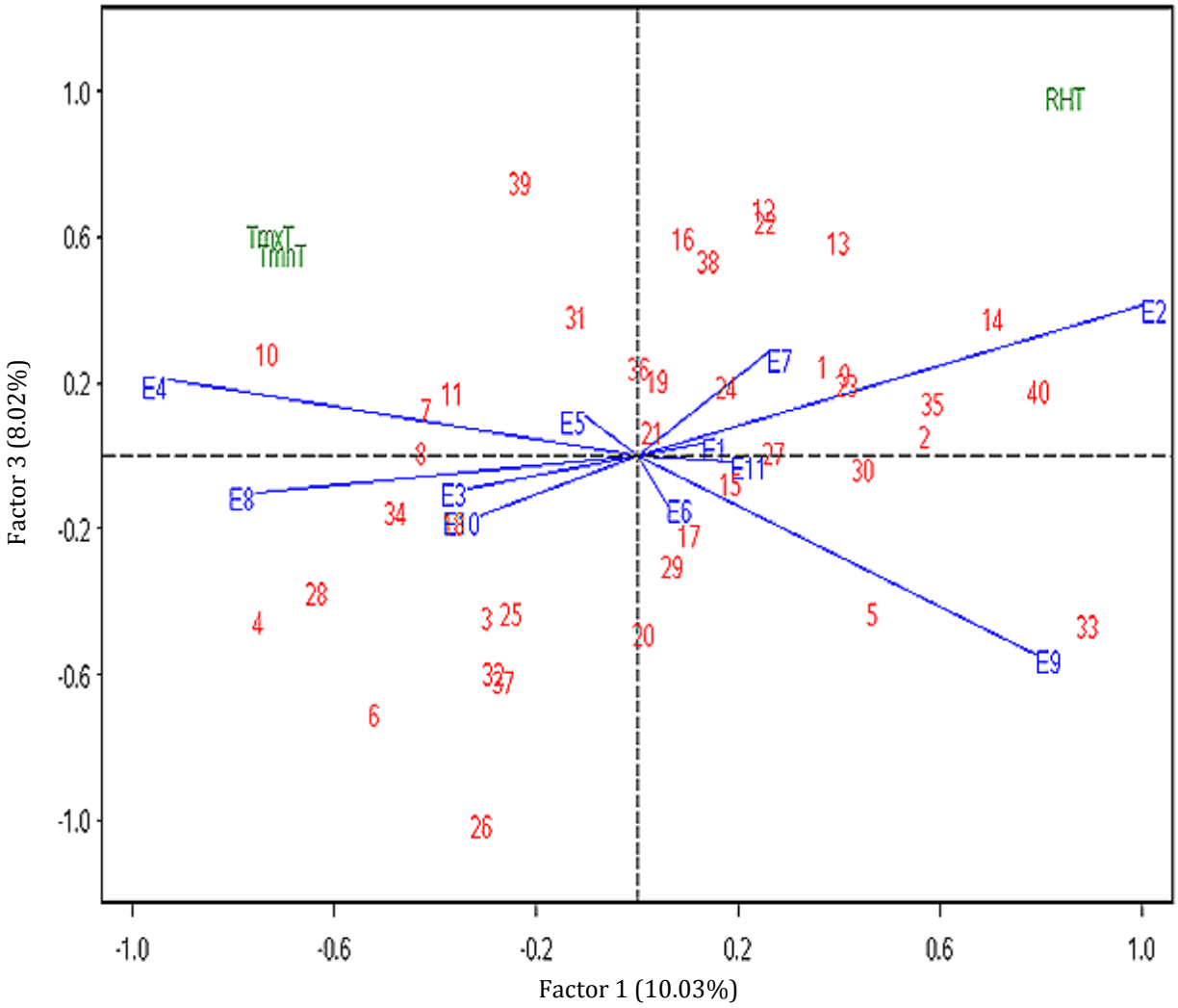

Figure 3. Biplot of the first and second PLS factors representing 11 locations (indexed as E1 to E11, locations in eastern and central Africa region where CIMMYT conduct trials in collaboration with national programs) as Z-Score, 40 genotypes (indexed by 1 to 40) as Y-loading supported by 3 environmental covariables (TmxT=maximum Temperature, TmnT=minimum temperature, RHT=average annual rainfall) as Z-Loading. Measurements for the environmental covariable are that of 2009.

REFERENCES

Atlin, G.N., R.J. Baker, K.B. Mcrae, And X. Lu. 2000. Selection response in subdivided target regions. Crop Sci. 40:7–13. (http://repository.cimmyt.org)

Baker, R.J. 1988a. Differential response to environmental stress. p.492–504. In B.S. Weir et al. (ed.) Proceedings of the Second International Conference on Quantitative Genetics. Sinauer, Sunderland, MA.

Baker, R.J. 1996. Recent research on genotype-environmental interaction. p. 235–239. In Proc. V Intl. Oat Conf. and VII Intl. Barley Genet. Sym., Vol. 1. Invited papers. Univ. Ext. Press, Univ. of Saskatchewan, SK, Canada.

Burgueño, J., J. Crossa, P.L. Cornelius, And R.-C. Yang. 2008. Using factor analytic models for joining environments and genotypes without crossover genotype × environment interaction. Crop Sci. 48:1291–1305.
(www.ca.uky.edu/pss/Cornelius,Paul(

Cornelius, P.L., And J. Crossa. 1999. Prediction assessment of shrinkage estimators of multiplicative models for multi-environment cultivar trials. Crop Sci. 39:998–1009. (www.ca.uky.edu/pss/Cornelius,Paul(

Cornelius, P.L., And M.S. Seyedsadr. 1997. Estimation of general linear-bilinear models for two-way tables. J. Statist. Comput. Simulation 58:287–322. (www.ca.uky.edu/pss/Cornelius,Paul(

Cornelius, P.L., M. Seyedsadr, And J. Crossa. 1992. Using the shifted multiplicative model to search for "separability" in crop cultivar trials. Theor. Appl. Genet. 84:161–172. (www.ca.uky.edu/pss/Cornelius,Paul(

Crossa, J., J. Burgueno, P.L. Cornelius, G. Mclaren, R. Trethowan,And A. Krishnamachari. 2006. Modeling genotype × environment interaction using additive genetic covariances of relatives for predicting breeding values of wheat genotypes. Crop Sci. 46:1722–1733. (www.ncbi.nlm.nih.gov › Journal List › Genetics › v.186(2); Oct 2010)

Crossa, J., P.L. Cornelius, K. Sayre, And J.I. Ortiz-Monasterio. 1995. A shifted multiplicative model fusion method for grouping environments without cultivar rank change. Crop Sci. 35:54–62. of cultivar effects for subdivided target regions. Crop Sci. 45:1151–1159.

Crossa, J., And P.L. Cornelius. 1997. Site regression and shifted multiplicative model clustering of cultivar trials sites under heterogeneity of error variances. Crop Sci. 37:406–415.

Crossa, J., P.L. Cornelius, And W. Yan. 2002. Biplots of linear-bilinear models for studying crossover genotype × environment interaction. Crop Sci. 42:619–633. (link.springer.com/article/10.1198%2F108571104X4423)

Crossa, J., R.-C. Yang, and P.L. Cornelius. 2004. Studying crossover genotype × environment interaction using linear-bilinear models and mixed models. J. Agric. Biol. Environ. Stat.9:362–380.

Eberhart, S.A., And W.A. Russell. 1966. Stability parameters for comparing varieties. Crop Sci. 6:36–40.

Finlay, K.W., And G.N. Wilkinson. 1963. The analysis of adaptation in a plant-breeding programme. Aust. J. Agric. Res. 14:742–754.

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

Gauch, H.G. 2006. Statistical analysis of yield trials by AMMI and GGE. Crop Sci. 46:1488–1500.

Gauch (ed.) Genotype-by-environment interaction. CRC Press, Boca Raton, FL. Cornelius, P.L., J. Crossa, M.S. Seyedsadr, G. Liu, and K. Viele.2001. Contributions to multiplicative model analysis of genotype-environment data. Statistical Consulting Section, American Statistical Association, Joint Statistical Meetings. 2001 Proceedings, American Statistical Association, Aug. 7, 2001 [CDROM]. Atlanta, GA.

Gauch, H.G., H.-P. Piepho, and P. Annicchiarico. 2008. Statistical analysis of yield trials by AMMI and GGE: Further considerations. Crop Sci. 48:866–889.

Girma Taye, Tesfaye Getachew & Geletu Begiga. 2000. AMMI adjustment for yield estimate and classification of genotypes and environments in Field pea (Pisum Sativum L.) Journal of Genetics and Breeding, vol. 54, 183-191

Girma Taye & Fufa Hundura. 2000. Use of AMMI for yield estimate and classification of genotypes and environments in Teff [Eragrostis tef]. Journal of tropical Forest resources. Vol. 15, no.2.

Gower, J.C., and D.J. Hand. 1996. Biplots. Chapman and Hall, London.

Piepho, H.P. 1998. Methods for comparing the yield stability of cropping systems—a review. J. Agron. Crop Sci. 180:193–213. (ftp://ftp.fao.org/ag/.../Rusinamhodzi11AgronomySust.Developm.pdf)

Piepho, H.P., and J. Mohring. 2005. Best linear unbiased prediction

Smith, A., B.R. Cullis, and R. Thompson. 2002. Exploring variety- environment data using random effects AMMI models with adjustment for spatial field trends: Part 1: Theory. In M.S. Kang (ed.) Quantitative genetics, genomics and plant breeding. CABI Publishing, Oxford, UK.

Smith, A.B., B.R. Cullis, and R. Thompson. 2005. The analysis of crop cultivar breeding and evaluation trials: An overview of current mixed model approaches. J. Agric. Sci. 143:1–14.

Yan, W., and N.A. Tinker. 2005. An integrated system of biplot analysis for displaying, interpreting, and exploring genotype by environment interactions. Crop Sci. 45:1004–1016.

Yan, W., and N.A. Tinker. 2006. Biplot analysis of multi-environment trial data: Principles and applications. Can. J. Plant Sci. 86:623–645.

Yan, W., L.A. Hunt, Q. Sheng, and Z. Szlavnics. 2000. Cultivar evaluation and mega-environment investigation based on GGE biplot. Crop Sci. 40:596–605.

Yan, W., P.L. Cornelius, J. Crossa, and L.A. Hunt. 2001. Two types of GGE biplots for analyzing multi-environment trial data. Crop Sci. 41:656–663.

Yan, W., M.S. Kang, B. Ma, S. Woods, and P.L. Cornelius. 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci. 47:643–655.

Yang, R.-C. 2007. Mixed model analysis of crossover genotype environment interactions. Crop Sci. 47:1051–1062.