Journal of Natural Sciences Research
ISSN 2224-3186 (Paper) ISSN 2225-0921 (Online)
Vol.15, No.2, 2024

Evaluation of Maize Varieties through Data Analysis of Multi-Environment Trials: Application of Multiplicative Mixed Models

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Abstract

Ethiopia is a significant maize producer in Africa Over the last two decades, Ethiopia's maize sector has undergone significant transformation. Farmers in Ethiopia require a consistent supply of new and improved varieties to meet their ever-changing production and marketing challenges. Breeders can no longer function without multi-environment trials (MET) analysis for varietal evaluation. To accurately select superior varieties that contribute to agricultural productivity, efficient statistical methods for maize variety evaluation must be used. The goal of this study was to identify better maize varieties based on yield performance by analyzing data from multi-environment trials using multiplicative mixed models. In this study, 32 maize varieties, including four checks, were sown across seven major maize growing areas in Ethiopia using RCB design, with three replications during the main cropping season in 2020. The results revealed that under the linear mixed model, the factor analytic models were found to be an efficient method for maize MET data analysis. The investigated FA models exhibit improved data fitting, resulting in a significant improvement in heritability. SXM1910008 and 3XM1920126 showed good yield performance over correlated locations, including Ambo, Bako, Hawasa, and Wondogenet, and were therefore identified as potentially useful stable genotypes with a wide range of adaptability. This is because the improved analysis technique we used here showed that correlated locations were the basis for genotype selection. Through the use of more effective statistical models, the analysis of data from multi-environment trials can offer a more robust framework to evaluate maize varieties with increased confidence in choosing superior varieties across a range of environments. Therefore, expanding the use of this effective analysis technique is essential for improving the choice of superior varieties in maize breeding program.

Keywords: factor analytic model, MET analysis; BLUP, mixed model, maize

DOI: 10.7176/JNSR/15-2-01

Publication date: May 31st 2024

1. Introduction

Maize is the second most widely produced crop in the world. In Africa (SSA) maize area coverage has increased by about 66% from 2007 to 2020. Maize grain yields have doubled from around 1.6 t/ha in 1990 to 4 t/ha in recent years, which are the highest level in sub-Saharan Africa after South Africa (FAOSTAT, 2020). In most SSA countries, maize covers >50% of the land area allocated for cereal production (Masuka *et al*., 2017). Maize is therefore an important cereal for the economic wellbeing and food security of hundreds of millions of households in SSA (Fisher *et al*., 2015). Maize accounts for 45% of the total calories and 43% of the total protein derived from cereals in eastern and southern Africa (Shiferaw *et al*., 2011). Despite its importance in the region, maize yields in SSA are still the lowest compared with other regions of the world (Masuka *et al*., 2017).

In Ethiopia, maize ranks first in total production (>10.5milion tons) and grain yield (4.18 t/ha), and second in area coverage (> 2.5 million hectares) among all the cereals (CSA, 2021). Ethiopia is a significant maize producer in Africa. The maize sector in Ethiopia has experienced a significant transformation over the past two decades. Important factors for the increased productivity include Increased availability and use of modern inputs (e.g. improved hybrid seeds and inorganic fertilizers), better extension services and increasing demand (Tesdeke Abate *et al*., 2015). Despite the recent progress, maize national average grain yield in Ethiopia is still very low relative to the potential of the crop and world's average due to lack of well-adapted and improved cultivars (Legesse *et al.,* 2020). The national average yield of maize is higher than Africa's average (2.21 t/ ha), the figure

is lower than the world's average yield (5.80 t/ha) (FAO, 2020).

Maize is widely adapted across diverse environmental conditions, being cultivated from moisture stress areas to high rainfall areas and from lowlands to the highlands of Ethiopia (Kebede Mulatu *et al*., 1993). Maize is grown in a wide range of environments, and maize varieties differ for their range of environmental adaptation, primarily conditioned by their flowering time, tolerance to abiotic stresses, and disease resistance (Mercer and Perales, 2019).

Ethiopia is a country of great climate variation (EMA, 1988), leading to high level of genotypes by environments interactions (GxE). As a result, the grain yield of different maize varieties may vary from environment to environment. The impact of environmental factors on different genotypes may vary implying that the productivity of plant may also vary from one environment to the next; because they will not necessarily express their genetic potential in the same way when environmental conditions varied. Stability of performance is also of special importance in Ethiopia and similar countries where environmental conditions vary considerably and means of modifying the environment are far from adequate. In addition, low cultivar turnover and genotype environment (GE) interaction predominantly contribute to low yield in small-scale farming systems (Demiselew et al., 2016, Legese *et.al* 2018). Analysis of multi-environment trials (MET) becomes indispensable for breeders for varietal evaluation. Each cultivar reacts specifically to changing climatic and soil conditions; some of them exhibit high GE interaction, while in others it is low. Based on classical statistical method of analysis, the estimation of G x E interaction and yield stability analysis of Ethiopian maize has been addressed by other workers (Wende, 2003; Gezahegn et al., 2008; Mosisa and Habtamu, 2008; Solomon et al., 2008).

Numerous GxE studies have been conducted on the Ethiopian maize genotypes to strengthen understanding of the environmental and genetic factors causing the interaction as well as an assessment of their importance in the relevant G x E system could have a large impact on plant breeding and a number of maize hybrid genotype were developed and tested to different locations by different research centers, but most of them failed to adapt due to the dynamics of the growing environment and climate change effects in the area (Wende, 2003; Gezahegn et al., 2008; Mosisa and Habtamu, 2008; Solomon et al., 2008; Muluken, 2009; Mohammed, 2020). Therefore the new hybrids should be tested in multi-location for their wide adaptation and MET analysis using efficient statistical methods must be employed for the evaluation of maize varieties to accurately select superior varieties that contribute to agricultural productivity.

Analysis of variance (ANOVA), which is computed using ordinary linear models (LMs) that use ordinary least square (OLS) methods of estimation for unknown parameters, is a traditional approach frequently used for the analysis of multi-environment trial (MET) data sets. This approach includes an ANOVA table for source of variation testing with overall f-test, post hoc multiple comparison testing with mostly list significance difference (LSD), and Duncan testing for observed means. Multivariate analysis techniques like AMMI (additive main effects and multiplicative interaction) and GGE (genotype plus genotype by environment interaction) are used to conduct additional analysis to learn more about the genotype by environment interaction (GEI) component (Rodrigues, 2018; Yan and Tinker, 2006). One significant flaw with this approach is that it couldn't handle error variance heterogeneity across trials, spatial variation within trials, unbalanced data, and missing values, as many authors (Gogel et al. 2018; Smith et al. 2005) pointed out.

By adding fixed and random terms to the model for systematic variability and relaxing the distributional assumptions surrounding the residual error, the linear mixed model (LMM), an extended linear model, can take into account confounded factors in the experimental units (Kelly et al. 2007; Smith et al. 2005). According to Yang (2010), the LMM is a potent and powerful statistical model that allows for the computation of BLUPs (best linear unbiased predictions) for random effects as well as unbiased estimates of the variance component using REML (restricted maximum likelihood estimation) for random terms (Yang, 2010). LMMs can be used for both balanced and unbalanced field trial data, as well as for extended analysis with factor analytic models (Smith et al. 2018). By shrinking the estimates of genotype effects closer to their true value, MET data analysis under LMM with random genotype could increase the precision for genotype ranking. Through FA models, the covariance structure of GE effects has been further improved.

Bako national maize research program routinely develops and evaluates new maize hybrids adapted to the mid-altitude sub humid and transitional highland maize agro-ecology of Ethiopia. Although maize has many advantages, some of the challenges include biotic and abiotic stress, which confronts the breeder when developing improved varieties. Thus, this study was planned to evaluate the performance of promising maize varieties that might suit the local and regional market through data analysis of MET using more efficient statistical methods.

2. Materials and Methods

2.1 Description of study area

The experiment was conducted at seven locations representing major maize-growing agro-ecologies of Ethiopia. These locations vary in altitude, temperature, total annual rainfall and soil types (Table 1) and the locations represent the main maize-producing agro-ecologies of the country ranging from mid-altitude sub-humid to transitional high land sub-humid.

Table 1. Description of the study locations

Location	Altitude (m.a,s.l)	Soil type	Rainfall (mm)	Geographical position		Temperature	
				Latitude	Longitude	Maximum	Minimum
Bako	1650	Nitisol	1598	9° 06’	37°09’	29	12.78
Asosa	1547	Nitisol	1276.2	100° 02'	340° 31’	33	21
Jimma	1753	Nitosol	1561	7 0° 46’	360° 00’	23	18
Pawe	1120	Nitisol	1250	110°19’	36° 24’	32.6	16.5
Wondo Genet	1780	Alluvial	1128	7° 19’	38° 38’	26	11
Ambo	2175	Vertisol	1265.7	8° 57’	37° 51’	25.6	11.7
Hawasa	1650	sandy loam	959	7° 03’	38° 30’	26.9	12.4

Source: Ethiopian institute of agricultural research (2019)

2.2 Planting materials

Twenty maize hybrids with four commercial cheacks (BH546 BH 547 BH661 and Limu) were evaluated in the multi-location trial (Table 2). These hybrids were developed or adapted by the National Maize Research Program of the Ethiopian Institute of Agricultural Research (EIAR) based at Bako Agricultural Research Center (BARC).

2.3 Experimental design and trial management

The trial was conducted during the 2020 main cropping season in Randomized complete block design (RCBD) with three replications. Each hybrid was planted in a two-row plot of 5 m long with spacing of 0.75 m between rows and 0.25 m between plants within a row. Two seeds were sown per hill for each genotype and later thinned to one plant at three to four leaf stages to get the generally recommended total plant population of 53,000 plants per hectare. Planting was done immediately after the onset of the main rainy season after an adequate soil moisture level to ensure good germination and seedling development. The NPS fertilizer at the rate of 150 kg /ha was applied once at planting time at all locations as per the recommendation (MoA, 2018), while 200 kg/ha Urea at Ambo and Pawe and 250 kg/ ha Urea at Hawasa,Bako, Wendo Genet Jima and Asosa was applied in split, half at thinning and the remaining half at knee height

2.4 Linear mixed model

Consider a MET dataset collected from t trials (environments can be used instead) in which m varieties are grown (all varieties may not be grown in all trials). The j^{th} trial, $j = 1…t$, consists of n_j plots arranged in a rectangular array with c_j columns by r_j rows ($n_j = c_j r_j$). Let $\boldsymbol{y}_j$ be the (n_j x 1) data vector for trial j, ordered as rows within columns, and let $y = (y'_1, y'_2, ..., y'_t)'$ be the (n x 1) data vector combined across the t trials, where $n = \sum_{j=1}^{t} n_j$. The linear mixed model for y can be then written as

$$y = X\alpha + Z_g\gamma_g + Z_p\gamma_p + \varepsilon \quad (1)$$

where α is vector of fixed effects (including terms for the grand mean, the environment's main effects, global spatial trends at each trial, and other trial-specific fixed effects) with an associated design matrix X (assumed to be full column rank), γ_g is the mt x 1 vector of random genetic (or variety by trial) effects with associated

design matrix Z_g, γ_p is a vector of non-genetic (or peripheral) random effects (including terms associated with the blocking structure at each trial, and other trial-specific random effects), with associated design matrix Z_p, and ε is the n x 1 vector of residual errors across all trials.

The random effects from the linear mixed model (equation 1) are assumed to follow a Normal distribution with mean zero vector and variance-covariance matrix, that is

$$E\begin{pmatrix}\gamma_g\\ \gamma_p\\ \varepsilon\end{pmatrix}=\begin{pmatrix}0\\0\\0\end{pmatrix}, \quad \text{var}\begin{pmatrix}\gamma_g\\ \gamma_p\\ \varepsilon\end{pmatrix}=\begin{bmatrix}G_g & 0 & 0\\ 0 & G_p & 0\\ 0 & 0 & R\end{bmatrix}$$

where G_g is variance matrix for genetic effects, G_p is the variance matrix of non-genetic (or peripheral) random effects and R is the variance matrix of the random error effects. In the analysis of MET data using a linear mixed model, the vector for residual effects ε can be partitioned into residual effects within each individual trial. That is, $\varepsilon = (\varepsilon_1'....\varepsilon_t')'$ where ε_j is the $n_j \times 1$ vector of residual effects for the j[th] trial. This can be modeled with be modeled to an IID variance structure of the form $R_j = \sigma_j^2 I_{n_j}$.

2.5 Model for Genetic Effects (γ_g)

Smith *et al.* (2001) presented an alternative parsimonious model for γ_g using a factor analytic (FA) model approach to provide a variance structure for the genetic variance matrix G_g. This model can adequately represent the nature of heterogeneous variances and covariance found to occur in most MET data. Thus, the γ_g can be modeled with multiplicative terms. That is

$$\begin{aligned}\gamma_g &= (\lambda_1 \otimes I_m) f_1 + ... + (\lambda_k \otimes I_m) f_k + \zeta \\ &= (\Lambda \otimes I_m) f + \zeta\end{aligned} \tag{2}$$

where λ_r is the $t \times 1$ vector of loadings, f_r is the $m \times 1$ vector of factor scores ($r = 1...k$), ζ is the $mt \times 1$ vector of residuals, Λ is the $t \times k$ matrix of loadings $\{\lambda_1 \ldots \lambda_k\}$ and f is the $mk \times 1$ vector of factor scores $(f_1' f_1'...f_k')'$. The random effects f and ζ are assumed to follow a Normal distribution with zero mean vector and variance-covariance matrix

$$\begin{bmatrix}G_f \otimes I_m & 0\\ 0 & \Psi \otimes I_m\end{bmatrix}$$

where Ψ is a diagonal matrix of specific variances represents the residual variance not explained by the factor model, that is $\Psi = diag(\Psi_1 \ldots \Psi_t)$. The factor scores are commonly assumed to be independent and scaled to have unit variance, so that $G_f = I_k$.

The genetic effects γ_g can be considered as a two dimensional (genotype by environment) array of random effects, and can be assumed to have a separable variance structure for the ($mt \times mt$) variance matrix G_g which can be written as

$$G_g = \mathrm{G_e} \otimes G_v$$

where G_e is the $t \times t$ genetic variance matrix representing the variances at each trial and covariances between trials, and G_v is the $m \times m$ symmetric positive definite matrix represents variances of environment effects at each genotype and the covariances of environment effects between genotypes. It is typically assumed that the varieties are independent and that $G_v = I_m$. However, if the pedigree information of the varieties is available, other forms of G_v can be applicable (see Oakey *et al*. 2006; 2007). Based on equation 2 the variance of genetic effects would be

$$\begin{aligned}\text{var}(\gamma_g) &= (\Lambda\Lambda' + \Psi) \otimes I_m \\ &= \mathrm{G_e} \otimes I_m\end{aligned}$$

Thus, the FA model approach results in the following form for G_e

$$G_e = \Lambda\Lambda' + \Psi$$

In the model, the variance parametric in these variance matrices are directly estimated using REML estimation method.

2.6 Model for Non-genetic Effects (γ_p)

The random non-genetic effects γ_p can be considered as sub- vectors $\gamma_{pj}^{(b_j \times 1)}$ for each trial, where b_j is the number of random terms for trial j. These random terms are based on terms for blocking structure (replicate blocks or other terms). In the analysis of MET data, the sub-vectors of γ_p are typically assumed to be mutually independent, with variance matrix G_{pj} for trial j, with the block diagonal form given below. Thus, there is a variance matrix for the set of none-genetic effects at each trial, That is,

$$G_p = \oplus^t{}_j G_{pj} = \begin{bmatrix} G_{p1} & 0 & \cdots & 0 \\ 0 & G_{p2} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & G_{pt} \end{bmatrix}$$

The most common form for the variance matrix of these extraneous effects is a simple variance component structure, where $G_{pj} = \sigma_j^2 I_{bj}$

2.7 Estimation, testing and software

In a linear mixed model, the significance of fixed effects may be assessed using the Wald test. The distribution of the traditional Wald statistic is asymptotically chi-squared. Many people view this test as anti-conservative (Butler et al., 2009). A F approximation was introduced by Kenward and Roger (1997) along with an adjusted Wald statistic that performed well in a variety of situations. To estimate the variance parameters from the linear mixed model using REML, ASReml was used in the R environment (Butler et al., 2009). ASReml implements the Average Information (AI) algorithm (Gilmour et al., 1995)).

The variance-covariance parameters in G_g , G_p and R, as well as the fixed and random effects, α , γ_g and γ_p, are all estimated during the estimation process for the linear mixed model. This involves two interconnected processes, where the fixed and random effects are estimated using best linear unbiased estimation (BLUE) and best linear unbiased prediction (BLUP), respectively, and the variance parameters of the model are estimated using residual maximum likelihood (REML, Patterson & Thompson 1971). To determine whether random effects in the linear mixed model are significant, use the Residual Maximum Likelihood Ratio Test (REMLRT). The fit of two nested models with same fixed effects can only be compared using the REMLRT.

3. Results and Discussion

3.1 GxE analysis

The FA model was considered for GxE analysis while keeping the single stage-wise analysis on individual plot yield data. The adequacy of the FA model with two factors was formally assessed as it is fitted within a mixed model framework based on the percentage of GxE variance explained by the factor components (Cullis et al., 2010). Table 2 presents the results from the factor analysis. It includes the total percentage of (GxE) variance explained by the model's factor components for each trial as well as for all trials. Except for the two trials Jimma and Asosa, the FA models fit almost all trials well, and the genetic variance was well explained by the two factor components. Nearly 70 percent of the GxE variance was explained by the two multiplicative terms of the factor analytic models, with the first multiplicative term accounting for 53 percent of that variance. Because it shows inadequate fit for the dataset, the FA model for more than two factors was not taken into consideration. The FA models do not adequately explain Assosa and Jimma, which can occur because these trials lack correlation with the other trials or are unique in comparison to the others.

Table 2. Results from fitting FA model.

	Factor1	Factor2	All
Ambo	99.5	0.5	100
Asosa	22.69	1.47	24.15
Bako	73.48	1.05	74.53
Hawasa	80.24	19.76	100
Jimma	18.88	4.98	23.86
Pawe	0.02	70.33	70.35
Wondogenet	61.55	2.17	63.72
%var FA-1= 53.51,		% var FA-2=70.19	

%varFA-1= percentage of GxE variance explained from fitting FA model with a single factor; %varFA-1=prrcentage of GxE variance explaned from fitting FA model with two factors.

Using a dendogram for cluster analysis, factor analysis also yields another significant result. The dendrogram in Figure 1 (a) was used in the cluster analysis to group the trials based on their genetic similarity. The dendrogram suggests that there may be three clusters of trials, with the first cluster having a maximum of four trials based on Cullis et al.(2010)'s suggestion regarding the dissimilarity cut-off (roughly about 0.6) at which clusters are formed. This demonstrates that the genotype ranking is different for the trials found in different clusters, but nearly identical for all trials found within these formed clusters. Genotype selection, therefore, was performed index, provided that the formed clusters are reasonably for each of the clusters.

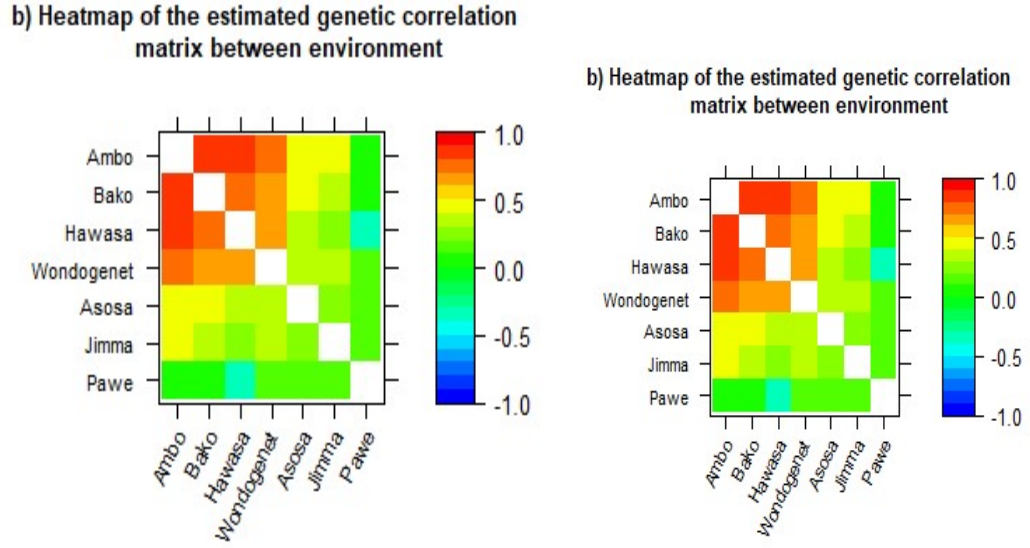

Figure 1. Dendrogram of the dissimilarity matrix (a) and heatmap representation of the genetic correlation matrix (b).

Aside from the dendrogram, other typical factor analysis summaries include a heatmap of the genetic correlations between all trials. This is depicted in Figure 1 (b), which portrays the correlation patterns between trials. The heatmap shows that the majority of the trials are highly correlated, with only a few having a weak correlation. This indicates that genotype selection can be performed by averaging genotype means across nearly all trials in the first cluster with the red color. There are also trials with a negative genetic correlation, such as

one between Pawe and Hawasa (Table 5), implying that there may have been a reversal in genotype rankings among these negatively correlated trials. The bi-plot in Figure 3 also demonstrated the concept of variety performance and stability across environments, as well as the discriminating power of each trial. Trials with a long arm from the center of the bi-plot indicates a high genetic variance compared to the others, and have a relatively high discriminating power for genotypes. Thus, Pawe, Hawasa and Bako had high genetic variance compared to the others. Therefore, based on the dendrogram and heatmap in Figure 1, and the bi-plot (Figure 2) and the genetic correlation as well from Table 5, we looked at three clusters of trials (C1, C2, and C3), with Ambo, Bako, Hawasa, Wendogenet and Assosa in C1, Jimma in C2, and Pawe in C3. In this paper, we used an average of BLUPs as a selection index to choose superior and stable varieties by ranking average BLUPs within clusters, with the first cluster (C1) being used for selection because it contains relatively more correlated trials.

Table 3. Genetic correlation between environments

	Ambo	Asosa	Bako	Hawasa	Jimma	Pawe	Wondogenet
Ambo	1						
Asosa	0.48	1					
Bako	0.86	0.42	1				
Hawasa	0.86	0.37	0.72	1			
Jimma	0.45	0.23	0.40	0.3	1		
Pawe	0.08	0.11	0.10	-0.4	0.19	1	
Wondogenet	0.79	0.39	0.69	0.6	0.37	0.14	1

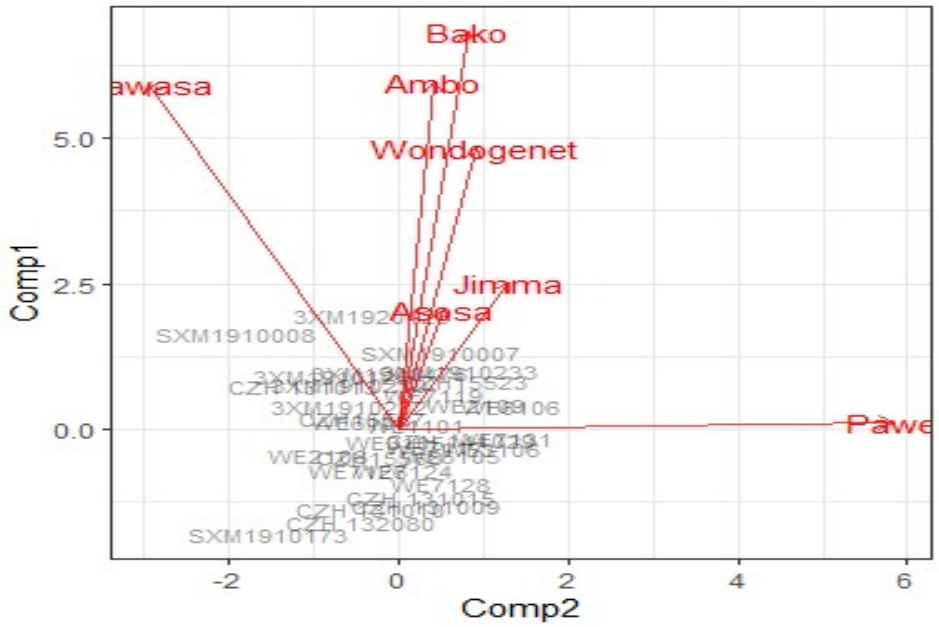

Figure 2. Bi-plot analysis

3.2 Variance components

The REML estimation produces unbiased and efficient estimates for variance component parameters at each trial. Table 4 shows the genetic variance, error variance, and heritability from the final fitted FA model for each trial. Variance component parameter estimates range from 0.52 to 1.78 for genetic variance, 0.56 to 3.33 for error variance, and 62.05 to 90.92 for heritability. Bako had more genetic variation. This indicates that the genotype discrimination power at these testing sites was relatively high. This could be attributed to Bako's significantly

higher rainfall amounts and distribution during that growing season. This also highlights the importance of meteorological data from a specific cropping season in recommending the best genotype for a specific cropping season, as well as its broader application across the country's many agro-ecologies.

Table 4. Variance component results MET analysis using FA models

	Genetic variance	Error variance	Heritability
Ambo	1.00	0.56	90.92
Asosa	0.52	0.68	73.32
Bako	1.77	3.33	77.26
Hawasa	1.22	1.40	84.75
Jimma	0.94	2.28	62.05
Pawe	1.35	1.55	75.29
Wondogenet	1.05	0.59	86.99

Plant breeders frequently compute narrow-sense heritability (h^2) or broad-sense heritability (H^2) on a genotype-mean basis to quantify and ultimately compare the precision of METs. The latter is the portion of phenotypic variability that can be attributed to the total genotype variability, which includes additive, dominance, and epistatic variability. Plant breeders frequently measure the precision of a single field trial or a series of field trials using heritability (Piepho and Möhring, 2007).

The preferred models for plant breeding field trial data analysis are linear models. However, when their underlying assumptions are broken, models that use the classical regression type frequently perform poorly and frequently produce biased parameter estimates. This frequently occurs when the data is unbalanced, lacking, and tainted with outliers. Due to these issues, estimates of the heritability and prediction power of genetic and non-genetic effects are inaccurate.

Robust statistical techniques offer a theoretically sound and intuitively appealing framework for getting around some of the limitations of traditional analysis, most notably its limitation in the analysis of incomplete and correlated MET data. Having a precise and accurate understanding of heritability is essential for the plant breeding program to be successful. Learning more about the genetic components that contribute to significant character variations is of primary interest to plant breeders. Accordingly, from the standpoint of plant breeding programs, it is essential to estimate various genetic variances and make judgments about their inheritance based on estimates of various genetic parameters obtained by using reliable statistical techniques like FA mixed mode statistics. Thus, the heritability of yield at each trial is shown in Figure 3 using randomized complete block (RCB) analysis and FA analysis. It shows that using FA analysis improves heritability. In general, analyzing MET data with FA model improves genotype evolution precision and accuracy by appropriately exploiting the information stored in the MET dataset (Smith and Cullis, 2018; Cullis et al. 2010).

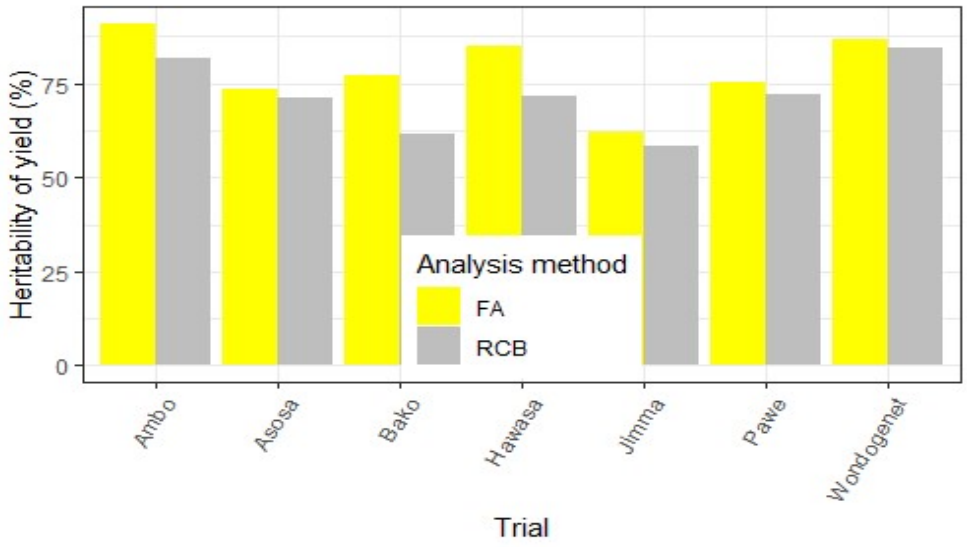

Figure 3. Improvements in heritability through the applications of FA models

3.3 BLUPs for genotypes across trials

A standard method for estimating random effects in a mixed model is best linear unbiased prediction (BLUP). BLUPs do have the property of minimum mean square error of prediction, and they can form a more accurate estimation of the underlying effects. Genotype effects are mostly fitted as random terms in a plant breeding context where accuracy of genotype ranking is important for selection of superior genotypes. This is more required in the early stages of genotype trials conducted with a large number of entries. The performance of genotypes can be ranked based on the values of BLUPs averaged across correlated environments of the 1st cluster (C1), excluding Jimma and Pawe since they are in different clusters. Table 7 shows that more than 31% (10) of the 32 genotypes had average grain yields of better than 6.5 t/ha. However, the predicted mean grain yield indicated two genotypes with a higher mean yield across trials of the first cluster (C1): one is SXM1910008, and the other is the check ,3XM1920126 (Table 5). BLUP analysis also revealed that these two genotypes did poorly at Asosa, Jimma, and Pawe, implying that these sites were not found to be ideal for selecting maize genotypes for this study. According to the enhanced method of analysis we used here, cluster one (Cl) would be the basis for genotype selection, and thus the genotypes SXM1910008 and 3XM1920126 had good yield performance over correlated trials, Ambo, Bako, Hawasa, and wondogenet, and can potentially be used as stable genotypes with broad adaptability.

Table 5. BLUPs for genotype means across clasturs of correlated enviroments (C1)

Genotype	Ambo	Bako	Hawasa	Wondogenet	Asosa	Jimma	Pawe	Average at C1
SXM1910008	8.91	10.91	**6.29**	**5.70**	6.97	7.40	4.53	**7.95**
BH661	**9.33**	**11.43**	5.78	5.44	6.91	7.68	6.34	7.78
SXM1910007	8.76	11.32	4.78	5.38	6.67	8.03	7.35	7.56
Limu	8.46	10.44	4.35	5.49	6.83	6.37	8.22	7.19
3XM1900476	8.38	10.51	4.72	4.53	6.49	7.27	6.93	7.04
3XM1910230	8.12	9.97	4.75	5.00	6.77	7.66	6.38	6.96
BH546	8.27	10.50	5.01	3.52	6.51	7.08	6.14	6.82
CZH 131013	8.06	9.52	4.99	4.42	6.54	7.11	5.83	6.75
CZH15523	8.27	10.33	4.12	4.21	**7.53**	7.94	7.58	6.73
WE7119	8.04	9.99	4.11	4.48	6.30	7.41	7.81	6.66
BH547	7.75	10.17	4.37	3.66	7.38	6.98	5.74	6.49
WE6106	7.87	9.35	3.43	5.10	7.31	7.24	**8.55**	6.44
WE2109	7.89	9.93	3.69	4.20	5.72	7.22	8.10	6.43
WE6103	7.49	9.25	4.05	4.86	6.15	7.98	5.98	6.42
CZH15587	7.55	9.67	4.10	3.42	6.04	6.62	6.29	6.19
WE1101	7.50	9.12	3.68	4.27	6.75	6.31	7.56	6.14
Grand Total	7.41	9.31	3.71	4.00	6.38	7.04	6.90	6.11
WE3105	7.19	9.26	3.51	4.45	5.80	7.63	6.93	6.10
WE7117	7.13	8.94	3.20	4.55	5.63	6.75	6.99	5.96
WE7131	7.32	9.59	2.93	3.93	7.15	**8.23**	8.24	5.94
WE3106	7.15	9.65	2.85	3.91	7.18	7.83	7.89	5.89
CZH 141029	7.28	8.83	3.17	4.13	6.38	7.12	8.00	5.85
WE2108	6.88	8.99	3.73	3.24	5.85	7.43	5.52	5.71
CZH15568	6.92	9.09	3.36	3.20	5.60	6.49	7.08	5.64
WE6105	6.99	8.45	2.95	3.80	6.37	7.88	7.80	5.55
WE7126	6.66	8.72	3.25	3.21	6.50	6.01	6.14	5.46
WE7124	6.71	8.61	2.99	3.44	5.90	6.04	7.27	5.44
WE7128	6.49	8.66	2.53	3.22	5.72	6.27	7.53	5.23
CZH 131015	6.26	7.45	2.42	3.46	6.00	6.61	7.17	4.90
CZH 131009	6.12	8.00	2.25	2.62	5.71	6.56	7.27	4.75
CZH 131010	6.00	7.48	2.50	2.87	5.40	6.38	6.38	4.71
CZH 132080	5.77	7.60	2.33	1.94	5.79	6.27	6.23	4.41
SXM1910173	5.50	6.20	2.68	2.21	6.30	5.41	5.00	4.15

4. Conclusion

Farmers in Ethiopia require a steady supply of new and improved varieties to help them meet their constantly changing production and marketing challenges. Breeders no longer can function without the analysis of multi-environment trials (MET) for varietal evaluation. Each cultivar responds differently to shifting climatic and soil

conditions; some show high GE interaction while others show low GE interaction.

Because MET data is not always balanced and/or complete, ANOVA-based techniques may not be appropriate for analyzing it. The linear mixed model provides a strong framework for dealing with imbalanced and/or incomplete data while also relaxing the ANOVA distributional assumptions surrounding the residual error. For this study, the linear mixed model with the FA models was found to be an efficient method of data analysis. The multiplicative mixed model analysis significantly improves the MET data analysis results, as demonstrated by the evidence of heritability measure. The analysis has improved because the GE effects are now modeled using FA models. The investigated FA models exhibit improved data fitting, resulting in a significant improvement in heritability.

SXM1910008 and 3XM1920126 were found to be potentially useful as stable genotypes with a wide range of adaptability because they demonstrated good yield performance over correlated locations, including Ambo, Bako, Hawasa, and wondogenet. This is due to the fact that the enhanced method of analysis we employed here revealed that correlated locations served as the base for genotype selection.

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