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# Multi environment and spatial analysis of early maturing sorghum [*Sorghum bicolor* (L.) Moench] genotypes in dry lowland areas of Ethiopia

**Amare Seyoum[1], Amare Nega[1], Kedanemaryam Wagaw[1], Taye Tadesse[2], Diriba Tadesse[2], Alemu Tirfessa[1], Habte Nida[3], Adane Gebreyohannes[1], Sewmehone Siraw[1], Tsegaye Gebremariam[4], Chalachew Endalamaw[1], Hailemariam Solomon[1], Tamirat Bejiga[1], Tokuma Legesse[1], David Jordan[5], Emma Mace[5], Daniel Nadew[1], Ligaba Ayele[1] and Meron Bogale[1]**

[1]Ethiopian Institute of Agricultural Research (EIAR), Melkassa Agriculture Research Center, P. O. Box 436, Adama, Ethiopia.
[2]Ethiopian Institute of Agricultural Research (EIAR), Head Quarter, P. O. Box 2003 Addis Ababa, Ethiopia.
[3]Purdue University, 610 Purdue Mall, West Lafayette, IN 47907, United States.
[4]Tigray Agricultural Research Institute (TARI), P. O. Box 492, Mekelle, Ethiopia.
[5]Queensland Alliance for Agriculture and Food Innovation, Hermitage Research Facility 604 Yangan Rd Warwick QLD 4370, Australia.

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**In Ethiopia, drought usually occur due to delay in onset, dry spell after sowing, drought during critical crop stage (flowering and grain filling stage) and too early cessation of rainfall. These situations can be addressed by developing improved sorghum varieties which are resistance to drought. Developments of sorghum varieties resistant to drought and producing better grain yield while addressing the plant biomass requirement is one of the strategies in the sorghum breeding program in dry lowland environment. A total of 90 early maturing sorghum genotypes were evaluated along with two standard check varieties to estimate the grain yield, plant height, days to flowering, days to maturity and overall agronomic aspects and stability of performance across the test environments. The trial was conducted using Randomized Complete Block Design (RCBD) in row and column arrangement. Linear mixed model has been used to predict and identify stable and superior varieties across the test environment. Correlations of the trials range from positive +1 to -1 where positive correlation is an indication of similarity among the testing environments while negative correlation is an indication of non-similarity among testing environments. Moreover, using the biplot it was observed that the stability and correlation among testing site where the angle between the two lines measure the strength of correlation. Improvement in heritability has been obtained due to spatial variation using advanced statistical analysis methods without any additional cost. Three genotypes exhibited better yield advantage, higher plant biomass and overall plant aspect including drought tolerance. In addition, these genotypes were preferred by farmers in their overall agronomic desirability (drought tolerance, earliness, head exertion and compactness, grain size and shape and threshability. Also, the national variety releasing committed has evaluated the variety verification trial both on station and farmers' field condition in 2018/2019 and they decided the release of the candidate variety 14MWLSDT7114 (2005MI5060/E-36-1) for commercial production in dry lowland environment.**

**Key words:** Genotype, heritability, mixed model, Spatial analysis, GEI, correlated environment.

## INTRODUCTION

Sorghum is the second most widely cultivated cereal in sub-Saharan Africa following maize (FAO, 2012). Over 23 million hectares of land in the continent is allocated for sorghum production annually with the total annual grain volume of about 26 million tones. It is believed to have originated in Ethiopia as evidenced by the early history of domestication of the sorghum crop there. Ethiopia is the third largest producer of sorghum in Africa after Nigeria and Sudan. Sorghum is the most important cereal crop worldwide used for food, feed, production of alcoholic beverages, and biofuel. Sorghum is primarily grown as a food grain crop in Ethiopia and preferred next to Teff for its *injera* (leaven bread) making quality. However, the biomass produced from sorghum is equally important for sorghum growing farmers in Ethiopia in order to address the feed demand (Amare et al., 2019).

It is the third most important cereal crop area coverage, which share 18% of the area covered by cereals and 14.6% of the area covered by grain crops. The total production of sorghum is 5.1 million tons produced from 1.9 million ha of land and with the national average productivity of 2.71 tons per hectare (CSA, 2018). The overall production and productivity of sorghum have showed an increasing trend over the past decade. A small improvement in productivity of sorghum has the potential to transform rural livelihoods and also boost the national economy. Most of the sorghum acreages in Africa including Ethiopia are located in areas that are prone to high temperature and frequent drought stress. Drought stress caused by low and erratic rainfall and exasperated by high temperature common in most sorghum growing regions of the world, is the most important abiotic factor limiting sorghum productivity.

In Ethiopia, drought is usually occurring due to delay in onset, dry spell after sowing, drought during critical crop stage (flowering and grain filling stage) and too early cessation of rain. These situations can be overcome by developing improved sorghum varieties which are tolerant to drought. Since the inception of sorghum research in Ethiopia concerted, efforts have been made to realize a strong research program that could be able to develop varieties with high drought tolerance, widely adapted, high yielding, early maturing and striga resistance with multiple resistance traits to address major biotic and abiotic factors.

However, until recently the breeding program relied on exotic germplasm which had a high harvest index compared to local landraces that led to a low adoption rate because of a number of factors such as poor grain market, farmers' interest in multi-purpose and high biomass cultivars. Hence, the notion of client-oriented breeding to increase adoption of improved technologies and enhancing genetic gain through breeding is timely agenda for sorghum breeders. Taking these into account modification of the breeding program is undergoing to increase efficiency and bring sustainable impact on the research and development endeavors.

Development and deployment of high yielding, early maturing, drought tolerant and striga resistant varieties with improved nutrition has been the major strategies for the national sorghum breeding program in Ethiopia. The recent breeding pipelines will produce varieties that are more acceptable for farmers due to higher grain yield, good grain quality and acceptable biomass production while providing much greater stability of performance than currently cultivated landraces and improved varieties. Ethiopian sorghum is a great source of novel genes and valuable traits for improving the sorghum crop worldwide.

Exploitation of genetic diversity is the most important strategies for plant breeding, and this must be inferred by field performance expression of the phenotype. The consequences of the phenotypic variation depend largely on the environment. This variation is further complicated by the fact that not all genotypes react similar ways to the change in environment. Genotype by environment interactions (GEI) happens when two or more genotypes perform differently in more than two environments. The different response of genotypes across the testing environment is considered as a hindrance in identifying, selecting and recommending of crops (Taye et al., 2016). Use of appropriate design and analysis model could be very vital either to identify high performing genotypes for target environments or stable genotypes across a given set of environments. The stage of plant development in which drought stress is most severe determines the associated yield reduction in the crop. Yield reduction is the most severe among the stress damages when the plant sink capacity is being set, and pollination is disrupted and embryos are aborted (Westgate and Boyer, 1985). Breeding for drought tolerance requires careful selection of the target environment; the choice of selection environment is important to achieve high genetic gain from selection (Cooper et al., 2006).

Different statistical methods for the analysis of multi-environment trial (MET) data have been used for crop improvement programs. The aim of crop improvement is most often to select either high performing genotypes for target environments or stable genotypes across a given set of environments. MET is usually analyzed using a two-stage approach, in which variety means are first estimated separately for each trial and then combined to

*Corresponding author. E-mail: seyoumamare99@gmail.com.

form the data for an overall analysis. The latter methods include mixed effect models (Talbot, 1984) and the fixed effects additive main effects and multiplicative interactions (AMMI) model (Welham et al., 2010). The two-stage approach is an approximation of the combined analysis of the raw plot data from all trials. If there is error variance heterogeneity between trials and spatial variation or unequal replication within trials, the approximation may be poor in estimation by classical ANOVA. Smith et al. (2001a) presented a weighted mixed model for the second-stage analysis that aimed at accommodating these sources of error variation, thereby reducing efficiency losses. The superior approach, however, is the spatial MET analysis of Kelly et al. (2007), in which individual plot data are analyzed and a separate spatial covariance structure and error variance allowed for each trial. Therefore, the objective of this study was to know and quantify the magnitude of genotype by environment interaction (GEI), heritability and identify high yielding, early maturing, with high biomass and stable sorghum variety for commercial release.

## MATERIALS AND METHODS

A total of 90 sorghum genotypes including two standard checks Melkam and Dekeba which developed by pedigree breeding method were used in this study to evaluate their performance. The experiment was conducted at six locations which represented the dry lowland sorghum growing agro-ecology, namely: Miesso, Kobo, Shiraro, Humera, Erer and Mehoni Agricultural Research Centers in 2014, 2015 and 2016 main cropping seasons (Table 1).

### Description of genotypes evaluated in this variety trial

The genotypes were developed via pedigree breeding method at Melkassa Agricultural Research Center. The genotypes involved in this variety trial were developed through crossing and have pedigree selection have been done up to F5 and F6 generations based on grain yield component traits and plant height. Multi environment evaluation has been conducted from 2014 to 2016 targeting the dry lowland environments of Ethiopia. Based on grain yield performance, plant height and flowering time, three candidate varieties were proposed to be verified and released for growers (Table 2).

### Experimental design and field managements

Randomized Complete Block Design (RCBD) was used to laid out these variety trial with two replications in a row column arrangement to minimize the special variability (trends) in estimating the genetic value. Each plot contained two rows of 5 m length separated by 0.75 m. At all locations sowing was done in between last week of June to first week of July when enough rain was received. Plantation was done manually by drilling along the farrow, and population was adjusted by thinning considering 0.20 m as spacing between plants. DAP fertilizer was applied at planting time with the rate of 100 kg $ha^{-1}$ and urea was side dressed when the plant reached at knee height at 50 kg $ha^{-1}$ basis. Days to 50% flowering, plant height (cm), grain yield per plot (GY), days to 90% physiological maturity (DTM), plant aspect (PAS) data were collected and analyzed to identify stable and superior varieties compared with the standard check variety.

### Statistical analysis

Mixed effect models have been well developed over the past three decades, first with applications to animal breeding (Henderson, 1984) and then to other disciplines. Data analyses based on mixed models are readily done with the use of modern statistical software. Mixed-effects model contains experimental factors of both fixed and random-effect types, with appropriately different interpretations and analysis for the two types. So, the data was subjected to Linear Mixed Model (LMM) analysis to estimate the prediction (BLUPs) and Heritability based on different methods (RCBD, Spatial and Spatial + MET).

The estimation of variance components in mixed model assume Gaussian random terms by restricting maximum likelihood (REML); where REML procedure maximizes the joint likelihood of all error contrasts rather than of all contrasts as in ordinary maximum likelihood. In the original description of REML, Patterson and Thompson (1971) suggest that the score equation for the variance components may be solved iteratively using the Fisher scoring (FS) algorithm. For many applications, this strategy presents computational difficulties due to the large size of the matrices to be inverted and multiplied. Thompson (1977) presented an overview of the methodology with particular reference to animal breeding applications and showed how some of the computational burdens of the FS algorithm may be overcome.

### Spatial mixed model for MET trials

The experiment laid was down in a rectangular array of $j^{th}$ trials j= 1. . . p, consists of $N_j$, plots with $r_j$, rows and $c_j$ columns ($N_j = r_j \times c_j$) (Smith et al., 2001b). The vector of data $y_j^{(NjX1)}$ is ordered correspondingly as rows with in column. The model for the combined vector of data across environment (trials) $y^{(nx1)}$= {$y_j$}, n = $\sum_{j=1}^{p} N_j$ is given by:

$$y = X\tau + Zu + e \quad (1)$$

where $\tau^{(tx1)}$ and $u^{(bx1)}$ are vector of fixed and random effect respectively. $X^{(nxt)}$ and $U^{(bx1)}$ are the associated design matrices with the former assumed to be of full column ranks. The vector of residuals is given by e. Therefore, the distribution of the vector of data y is Gaussian with mean X$\tau$ and variance matrix H= $ZGZ' + R$.

Error e term also consists of a vector of sub error {$e_j$}, where $e_j^{(Njx1)}$ is vector of plot errors for $j^{th}$ trial and decomposed into a spatially dependent process $\xi_j$ and an independent white noise process $\eta_j$. The error variance matrix for trial j is given by $R_j = \sigma_j^2 \sum_j(\alpha j) + \sigma_{\eta j}{}^2 I_{Nj}$ , where $\Sigma_j$ is a spatial correlation matric that is a function of $\alpha_j$ with associated variance $\sigma_j{}^2$. The parameter $\sigma_{\eta j}{}^2$ is variance of the white noise process. The assumption is that spatial process for $\xi_j$ is second order stationary so that the correlation between plots depends only on the distance between them. It also further assumed that the two dimensional process is separable so one can write $\Sigma_j = \Sigma_{cj} \otimes \Sigma_{rj}$, where $\Sigma_{cj}$ and $\Sigma_{rj}$ are the correlation matrices for column and rows respectively. However, many researches (Gilmour et al., 1997) show that separable autoregressive process of order one which is denoted by AR1xAR1 most of often provide an adequate variance structure for local spatial trend. In addition, errors from different trials are assumed to be independent.

The random effect u consists of sub vectors $\{u_i\}$ , where $u_i^{(bix1)}$ is the vector of effect for the $i^{th}$ random term, i=1. . .q. the matrix Z is

**Table 1.** Description of testing locations.

| Site | Longitude | Latitude | Altitude in m.a.s.l | Soil type | Rain fall in mm | Minimum T°C | Maximum T°C |
|---|---|---|---|---|---|---|---|
| Miesso | 39°21'E | 8°30'N | 1470 | Vertisol | 571 | 16 | 31 |
| Shiraro | 39°9'E | 14°6'N | 1179 | Vertisol | 615 | 20.4 | 34 |
| Kobo | 39°38'E | 12°09'N | 1513 | Vertisol | 678 | 14.8 | 32 |
| Mehoni (Fachagama) | 39°70'E | 12°70'N | 1578 | Clay | 539 | 12.81 | 23.24 |
| Humera | $40^0$9'E | $9^0$16'N | 750 | Vertisol and fluvic soil | 590 | 26.7 | 40.8 |
| Erer | $42^0$15'E | $9^0$10'N | 1297 | Vertisol | 778 | 17 | 37 |

**Source:** National Metrology data of 2016/17 cropping season, m.a.s.l=meters above sea level, T°=Temperature.

**Table 2.** List of genotypes evaluated in this variety trial.

| Genotype | Pedigree | Background |
|---|---|---|
| 14MWLSDT7026 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7029 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7031 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7033 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7034 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7035 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7036 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7040 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7042 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7060 | Macia/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7073 | SDSL2690-2/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7074 | SDSL2690-2/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7098 | MR812/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7100 | MR812/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7114 | 2005MI5060/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7115 | ICSR24010/B_35 | Crossed lines at Melkassa |
| 14MWLSDT7129 | ICSR24010/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7138 | WSV387/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7145 | WSV387/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7157 | WSV387/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7176 | WSV387/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7177 | WSV387/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7191 | WSV387/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7193 | WSV387/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7196 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7201 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7207 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7209 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7234 | Macia/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7238 | Macia/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7241 | Macia/E-36-1 | Crossed lines at Melkassa |

**Table 2.** Contd.

| | | |
|---|---|---|
| 14MWLSDT7251 | Macia/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7253 | Macia/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7278 | Macia/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7279 | Macia/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7308 | Teshale/B-35 | Crossed lines at Melkassa |
| 14MWLSDT7310 | Teshale/B-35 | Crossed lines at Melkassa |
| 14MWLSDT7311 | Teshale/B-35 | Crossed lines at Melkassa |
| 14MWLSDT7322 | SDSL2690-2/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7324 | SDSL2690-2/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7325 | SDSL2690-2/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7329 | SDSL2690-2/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7332 | SDSL2690-2/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7354 | MR812/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7356 | MR812/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7362 | 2005MI5060/B-35 | Crossed lines at Melkassa |
| 14MWLSDT7364 | 2005MI5060/B-35 | Crossed lines at Melkassa |
| 14MWLSDT7388 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7395 | MR812/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7400 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7401 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7402 | WSV387/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7405 | Macia/76T1#23 | Crossed lines at Melkassa |
| 14MWLSDT7410 | ICSR24010/B-35 | Crossed lines at Melkassa |
| 14MWLSDT7413 | WSV387/E-36-1 | Crossed lines at Melkassa |
| 14MWLSDT7425 | MR812/B-35 | Crossed lines at Melkassa |
| Dekeba | ICSR24004 | Standard Check |
| Melkam | WSV387 | Standard Check |

partitioned conformably as [Z1 . . .Zq]. It assumed that the sub vector of u is mutually independent. Variance matrix $G_i$ for the $i^{th}$ random term has many possible forms including the standard variance component structure $G_i = \sigma_i^2 I_{bi}$. Let $u_g$ be the mpx1 vector of genetic effect for m varieties for each p environments ordered as varieties with in environments. It represents two-dimensional (varieties by environment) array of effect, namely $U_g^{(mxp)}$, where $u_g = vec(U_g)$. It is assumed that the associated variance structure has a separable form with $var(u_g) = G_e \otimes G_v$, where $G_e$ and $G_v$ are the symmetric *p x p* and *m x m* component matrices for environment and varieties, respectively. When $G_v = I_m$, just for simplicity, therefore $var(u_g) = G_e \otimes I_m$, and the matrix $G_e = \{\sigma_{jj'}\}$ is the so called genetic variance matrix. The diagonal elements are genetic variance for individual environments and the off –diagonal elements are genetic covariance between pairs of environments. The spatial mixed model for the above model 1 of MET data can then be written as:

$$y = X_\tau + Z_u + e = \quad X_\tau + Z_0 u_0 + Z_a\, u_a + e, \qquad (2)$$

the fixed effect $\tau$ includes environmental main effects and trial specific effects for extraneous field variation (Gilmour et al., 1997), $u_g$ is variety effects at each environment with associated design matrix $Z_g^{(nxmp)}$ and $u_0$ comprise and additional random effect with design matrix $Z_0$, and variance matrix $G_0$.

In breeding program, there are many possible forms of genetic variance matrix structures. In mixed model of MET data, the standard structure is given by $G_e = \sigma_v^2 J_p + \sigma_{ve}^2 I_p$, where $\sigma_v^2$ and $\sigma_{ve}^2$ are the variance components for variety main effects and *V x E* interactions respectively, where as $J_p$ is a *p x p* matric of one. This implies that all environments have the same genetic variance and all pair of environments have the same genetic covariance. Due to inefficient estimation or unstable even for moderately large values of *p.* Smith et al. (2001b) proposes an alternative variance structure model which is called factor analysis that is analogous of AMMI of Gauch (1988, 1992). This model captures the nature of heterogeneous variances and covariance that occur in most MET data. The factor analytic (FA) model is a regression-type model (*y=ax+b*), which can be fitted to an increasing number of dimensions k.

**Table 3.** Summary of early maturing variety trials.

| Trials | Row | Column | genotype | Mean grain yield (t ha$^{-1}$) | Genetic variance | Error variance |
|---|---|---|---|---|---|---|
| KB14PYTLSL | 14 | 40 | 433 | 3.17 | 2.87 | 0.34 |
| MS14PYTLSL | 14 | 40 | 433 | 2 | 0.32 | 0.181 |
| HM15SG2N02 | 30 | 6 | 90 | 1.27 | 1.69 | 0.346 |
| MS15SG2N02 | 30 | 6 | 90 | 1.48 | 0.44 | 0.131 |
| SH15SG2N02 | 30 | 6 | 90 | 2.46 | 1.09 | 0.361 |
| MH16SG2N02 | 30 | 6 | 90 | 2.46 | 0.98 | 1.133 |
| MS16SG2N02 | 30 | 6 | 90 | 2.56 | 0.28 | 0.232 |
| SH16SG2N02 | 30 | 6 | 90 | 2.19 | 0.61 | 0.628 |
| ER15SG2N02 | 30 | 6 | 90 | 1.13 | 0.15 | 0.029 |

Therefore, the model with variety main effects and k-factor analytic model for genotypes by environment interaction (GEI) is special case of (k+1) factor analytic model for variety effects at each environment. The concurrence of genotypes and populations between testing site was used to allow the trial series to be analyzed as a single MET as of each trial consisting similar hybrids, which is the current best practice method to analyze field trials for plant breeding programs.

## RESULTS AND DISCUSSION

Based on the linear mixed model analysis stable and superior varieties across the test environment has been predicted and identified (Tables 3 to 6 and Figures 1 to 4). Three genotypes exhibited better yield advantage, higher plant biomass and overall plant aspects including drought tolerance. Hence, the variety 14MWLSDT7114 (2005MI5060/E-36-1) had 21.2%, the variety 14MWLSDT7196 (WSV387/76T1#23) had 17.7% and 14MWLSDT7329 (SDSL2690-2/76T1#23) had 27.2% superiority in plant height. Mean grain yield performance of genotype 14MWLSDT7114 displayed 12.2%, genotype 14MWLSDT7196 and genotype 14MWLSDT7329 varieties had also 13.7 and 20.2% grain yield advantage compared to the standard check variety Dekeba and Melkam (Table 4). In addition to the grain yield advantage in comparison with the recently nationally released standard check variety, these three genotypes also showed stable grain yield performance across years and environments (Figure 3).

In this study three genotypes showed stable grain yield performance across years and across environments. In addition, these genotypes were preferred by farmers by their overall agronomic desirability (drought tolerance, earliness, head exertion and compactness, grain size and shape, threshability). The national variety releasing committed has been evaluated the variety verification trial (VVT) both on stations and farmers' field conditions in 2018/2019 and finally verified the release of 14MWLSDT7114 (2005MI5060/E-36-1) variety for production. The results of the summary statistics (Table 3) indicate that Kobo is the most yielder for overall genotypes in terms of grain yield and other yield parameters. In another way, Erer is less yielder when compared with all other environments in terms of yield trait.

Figure 1 indicates how early maturing sorghum lines are correlated over the environments. Correlation among the trials ranged from positive +1 to -1 where positive correlation is an indication of similarity among the testing environments while negative correlation indicates dissimilarity among testing environments. This implicates the selection for promising materials. When the correlations among environments are positive, the selection for the best material based on a given environment is similar to the selection for the best materials in the other environments, for example, KB14PYTLSL, MS15SG2N02, MS16SG2N02 and SH16SG2N02. On the other hand, when environments are negatively correlated, there is a rank change among the genotypes so that the best material selected based on a given environment shows less performance in other environments like SH16SG2N02, HM15SG2N02 and BB15SG2N02.

One can briefly observe the stability and correlation among testing sites in Figure 2 where the angle between the two lines measures the strength of correlation. Less angle between the two lines indicates existence of correlation most often if less than 90' but if the angle is just around 90' it indicates the independency among the environments. Furthermore, when the angle between the two lines is more than 90', this indicates the negative correlation between the two environments. The distance of the line from the center measures the stability of the line. Less distance from the center indicate stability while far distance from the center indicates instability of the environment. Similarly, the length of the arrows indicates that the discrimination of the trials. So, MS16SG2N02 is the most discriminating trials fallowed by KB14PYTSL and SH16SG2N02.

**Table 4.** Predictions of genotypes using linear mixed model for grain yield (t $ha^{-1}$).

| Genotype | ER15SG2N02 | HR15SG2N02 | KB14PYTLSL | MH16SG2N02 | MS14PYTLSL | MS15SG2N02 | MS16SG2N02 | SH15SG2N02 | SH16SG2N02 | Mean |
|---|---|---|---|---|---|---|---|---|---|---|
| 14MWLSDT7026 | 1.32 | 1.71 | 3.98 | 3.49 | 2.54 | 1.85 | 2.99 | 2.45 | 3.33 | 2.63 |
| 14MWLSDT7029 | 1.19 | 1.45 | 3.61 | 3.23 | 2.24 | 1.64 | 2.83 | 2.56 | 2.18 | 2.33 |
| 14MWLSDT7031 | 1.15 | 1.49 | 3.85 | 3.64 | 1.99 | 1.84 | 2.96 | 3.40 | 2.92 | 2.58 |
| 14MWLSDT7033 | 1.14 | 1.38 | 3.42 | 2.89 | 2.16 | 1.53 | 2.61 | 2.62 | 2.35 | 2.23 |
| 14MWLSDT7034 | 1.27 | 2.36 | 3.89 | 4.06 | 2.39 | 1.81 | 2.99 | 2.75 | 2.19 | 2.64 |
| 14MWLSDT7035 | 1.24 | 1.34 | 3.79 | 3.72 | 2.32 | 1.75 | 2.73 | 2.73 | 3.03 | 2.52 |
| 14MWLSDT7036 | 1.29 | 1.66 | 4.04 | 4.07 | 2.39 | 1.91 | 3.07 | 2.81 | 2.80 | 2.67 |
| 14MWLSDT7040 | 1.18 | 1.27 | 3.46 | 2.96 | 2.26 | 1.54 | 2.63 | 2.29 | 2.25 | 2.20 |
| 14MWLSDT7042 | 1.22 | 1.32 | 3.60 | 3.09 | 2.37 | 1.62 | 2.76 | 2.31 | 3.12 | 2.38 |
| 14MWLSDT7060 | 1.09 | 1.30 | 3.36 | 2.15 | 1.99 | 1.51 | 2.86 | 2.62 | 2.13 | 2.11 |
| 14MWLSDT7073 | 1.06 | 1.07 | 2.97 | 3.31 | 2.07 | 1.24 | 2.12 | 2.19 | 1.49 | 1.95 |
| 14MWLSDT7074 | 1.18 | 1.46 | 3.47 | 2.31 | 2.26 | 1.54 | 2.72 | 2.48 | 2.48 | 2.21 |
| 14MWLSDT7098 | 1.30 | 1.39 | 3.50 | 1.81 | 2.71 | 1.50 | 2.45 | 1.87 | 2.54 | 2.12 |
| 14MWLSDT7100 | 1.20 | 1.64 | 3.77 | 2.67 | 2.19 | 1.76 | 2.82 | 2.93 | 2.83 | 2.42 |
| 14MWLSDT7114 | 0.93 | 1.22 | 3.28 | 2.11 | 1.46 | 1.53 | 2.73 | 3.19 | 3.31 | 2.20 |
| 14MWLSDT7115 | 1.19 | 1.24 | 3.32 | 1.66 | 2.37 | 1.43 | 2.57 | 2.15 | 2.44 | 2.04 |
| 14MWLSDT7129 | 1.09 | 0.83 | 2.64 | 1.63 | 2.33 | 0.98 | 1.85 | 1.49 | 1.16 | 1.56 |
| 14MWLSDT7138 | 1.20 | 1.40 | 3.60 | 2.48 | 2.30 | 1.63 | 2.92 | 2.74 | 1.94 | 2.24 |
| 14MWLSDT7145 | 1.32 | 1.27 | 3.42 | 1.99 | 2.81 | 1.44 | 2.43 | 1.67 | 1.93 | 2.03 |
| 14MWLSDT7157 | 1.17 | 1.31 | 3.27 | 1.23 | 2.35 | 1.40 | 2.58 | 2.25 | 1.71 | 1.92 |
| 14MWLSDT7176 | 1.32 | 1.40 | 3.82 | 3.70 | 2.63 | 1.73 | 2.58 | 2.42 | 2.68 | 2.48 |
| 14MWLSDT7177 | 1.15 | 1.39 | 3.43 | 2.53 | 2.18 | 1.53 | 2.66 | 2.42 | 1.76 | 2.12 |
| 14MWLSDT7191 | 0.95 | 0.76 | 2.54 | 2.67 | 1.88 | 0.98 | 1.85 | 2.06 | 1.88 | 1.73 |
| 14MWLSDT7193 | 1.05 | 1.23 | 3.35 | 2.84 | 1.86 | 1.52 | 2.59 | 2.99 | 2.42 | 2.21 |
| 14MWLSDT7196 | 1.31 | 1.80 | 4.02 | 2.69 | 2.47 | 1.88 | 3.09 | 2.64 | 3.45 | 2.59 |
| 14MWLSDT7201 | 1.16 | 1.49 | 3.68 | 2.72 | 2.09 | 1.71 | 3.18 | 2.91 | 2.19 | 2.35 |
| 14MWLSDT7207 | 1.25 | 1.55 | 3.99 | 4.16 | 2.27 | 1.89 | 2.99 | 3.07 | 3.10 | 2.70 |
| 14MWLSDT7209 | 1.14 | 1.17 | 3.12 | 1.91 | 2.29 | 1.31 | 2.38 | 2.06 | 1.30 | 1.85 |
| 14MWLSDT7234 | 1.30 | 1.41 | 3.95 | 3.48 | 2.47 | 1.84 | 3.15 | 2.71 | 2.75 | 2.56 |
| 14MWLSDT7238 | 1.16 | 1.35 | 3.34 | 2.45 | 2.27 | 1.46 | 2.56 | 2.30 | 1.83 | 2.08 |
| 14MWLSDT7241 | 0.93 | 0.77 | 2.70 | 1.73 | 1.72 | 1.10 | 2.36 | 2.41 | 1.02 | 1.64 |
| 14MWLSDT7251 | 1.19 | 1.17 | 3.28 | 1.86 | 2.39 | 1.40 | 2.37 | 2.20 | 1.94 | 1.98 |
| 14MWLSDT7253 | 1.20 | 0.95 | 2.85 | 1.57 | 2.63 | 1.08 | 2.04 | 1.37 | 1.61 | 1.70 |
| 14MWLSDT7278 | 1.18 | 1.40 | 3.50 | 2.19 | 2.26 | 1.57 | 2.59 | 2.61 | 2.26 | 2.17 |
| 14MWLSDT7279 | 1.23 | 1.58 | 3.58 | 3.51 | 2.42 | 1.59 | 2.70 | 2.17 | 2.43 | 2.36 |
| 14MWLSDT7308 | 1.00 | 1.06 | 3.23 | 3.59 | 1.73 | 1.45 | 2.72 | 2.87 | 2.46 | 2.24 |
| 14MWLSDT7310 | 1.24 | 1.20 | 3.43 | 1.76 | 2.53 | 1.48 | 2.57 | 1.90 | 2.64 | 2.08 |
| 14MWLSDT7311 | 1.07 | 1.06 | 3.19 | 2.39 | 2.02 | 1.39 | 2.32 | 2.70 | 2.70 | 2.09 |
| 14MWLSDT7322 | 1.01 | 1.10 | 3.18 | 1.71 | 1.80 | 1.41 | 2.75 | 2.89 | 1.64 | 1.95 |
| 14MWLSDT7324 | 1.28 | 1.51 | 3.79 | 2.74 | 2.49 | 1.73 | 2.85 | 2.45 | 2.26 | 2.35 |

**Table 4.** Contd.

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 14MWLSDT7325 | 1.12 | 1.14 | 3.23 | 1.77 | 2.16 | 1.40 | 2.55 | 2.35 | 1.92 | 1.96 |
| 14MWLSDT7329 | 1.46 | 1.89 | 4.40 | 5.17 | 2.85 | 2.09 | 3.32 | 2.65 | 3.64 | 3.05 |
| 14MWLSDT7332 | 1.26 | 1.63 | 3.99 | 4.96 | 2.33 | 1.88 | 3.01 | 3.01 | 2.87 | 2.77 |
| 14MWLSDT7354 | 1.15 | 1.42 | 3.53 | 2.95 | 2.14 | 1.60 | 2.71 | 2.69 | 2.67 | 2.32 |
| 14MWLSDT7356 | 1.31 | 1.54 | 3.79 | 4.00 | 2.58 | 1.71 | 2.78 | 2.21 | 3.09 | 2.56 |
| 14MWLSDT7362 | 1.29 | 1.25 | 3.44 | 1.50 | 2.68 | 1.47 | 2.69 | 1.94 | 1.94 | 2.02 |
| 14MWLSDT7364 | 1.25 | 1.51 | 3.81 | 2.22 | 2.37 | 1.76 | 2.93 | 2.71 | 3.41 | 2.44 |
| 14MWLSDT7388 | 1.22 | 1.40 | 3.64 | 3.74 | 2.32 | 1.65 | 2.77 | 2.58 | 1.65 | 2.33 |
| 14MWLSDT7395 | 1.20 | 1.46 | 3.72 | 2.05 | 2.24 | 1.71 | 2.80 | 2.90 | 3.07 | 2.35 |
| 14MWLSDT7400 | 1.24 | 1.42 | 3.64 | 3.76 | 2.42 | 1.64 | 2.74 | 2.27 | 2.57 | 2.41 |
| 14MWLSDT7401 | 1.28 | 1.67 | 3.92 | 4.42 | 2.43 | 1.83 | 2.80 | 2.73 | 2.31 | 2.60 |
| 14MWLSDT7402 | 0.92 | 0.69 | 2.53 | 1.53 | 1.78 | 0.98 | 1.92 | 2.24 | 1.50 | 1.57 |
| 14MWLSDT7405 | 1.10 | 1.29 | 3.38 | 2.16 | 2.02 | 1.51 | 2.74 | 2.77 | 2.09 | 2.12 |
| 14MWLSDT7410 | 1.20 | 1.41 | 3.57 | 2.38 | 2.28 | 1.61 | 2.91 | 2.54 | 2.46 | 2.26 |
| 14MWLSDT7413 | 1.36 | 1.51 | 4.04 | 2.63 | 2.67 | 1.87 | 3.08 | 2.48 | 2.91 | 2.51 |
| 14MWLSDT7425 | 1.14 | 1.21 | 3.28 | 1.81 | 2.20 | 1.42 | 2.51 | 2.26 | 2.29 | 2.01 |
| Dekeba | 1.29 | 1.33 | 3.51 | 3.16 | 2.66 | 1.52 | 2.53 | 1.90 | 2.16 | 2.23 |
| Melkam | 1.34 | 1.59 | 3.59 | 2.51 | 2.80 | 1.55 | 2.55 | 1.95 | 1.94 | 2.20 |
| Mean | 1.19 | 1.36 | 3.50 | 2.75 | 2.29 | 1.56 | 2.68 | 2.46 | 2.36 | 2.24 |

ER15SG2N02= Erer 2015 NVT, HR15SG2N02=Humera 2015 NVT, KB14PYTLSL=Kobo 2014 PYT, MH16SG2N02=Mehoni 2016 NVT, MS14PYTLSL=Miesso 2014 PYT, MS15SG2N02=Miesso 2015 NVT, MS16SG2N02=Miesso 2016 NVT, SH15SG2N02=Shiraro 2015 NVT, SH16SG2N02= Shiraro 2016 NVT.

**Table 5.** Genetic correlation among trials using early maturing sorghum varieties.

| Trials | KB14PYTLSL | MS14PYTLSL | HM15SG2N02 | MS15SG2N02 | SH15SG2N02 | MH16SG2N02 | MS16SG2N02 | SH16SG2N02 | ER15SG2N02 |
|---|---|---|---|---|---|---|---|---|---|
| KB14PYTLSL | 1 | 0.544 | 0.639 | 0.991 | 0.442 | 0.622 | 0.817 | 0.729 | 0.818 |
| MS14PYTLSL | 0.544 | 1 | 0.365 | 0.428 | -0.387 | 0.284 | 0.231 | 0.32 | 0.928 |
| HM15SG2N02 | 0.639 | 0.365 | 1 | 0.63 | 0.266 | 0.396 | 0.516 | 0.464 | 0.535 |
| MS15SG2N02 | 0.991 | 0.428 | 0.63 | 1 | 0.537 | 0.625 | 0.843 | 0.735 | 0.734 |
| SH15SG2N02 | 0.442 | -0.387 | 0.266 | 0.537 | 1 | 0.323 | 0.55 | 0.39 | -0.068 |
| MH16SG2N02 | 0.622 | 0.284 | 0.396 | 0.625 | 0.323 | 1 | 0.524 | 0.459 | 0.472 |
| MS16SG2N02 | 0.817 | 0.231 | 0.516 | 0.843 | 0.55 | 0.524 | 1 | 0.619 | 0.522 |
| SH16SG2N02 | 0.729 | 0.32 | 0.464 | 0.735 | 0.39 | 0.459 | 0.619 | 1 | 0.544 |
| BB15SG2N02 | 0.818 | 0.928 | 0.535 | 0.734 | -0.068 | 0.472 | 0.522 | 0.544 | 1 |

ER15SG2N02= Erer 2015 NVT, HR15SG2N02=Humera 2015 NVT, KB14PYTLSL=Kobo 2014 PYT, MH16SG2N02=Mehoni 2016 NVT, MS14PYTLSL=Miesso 2014 PYT, MS15SG2N02=Miesso 2015 NVT, MS16SG2N02=Miesso 2016 NVT, SH15SG2N02=Shiraro 2015 NVT, SH16SG2N02= Shiraro 2016 NVT.

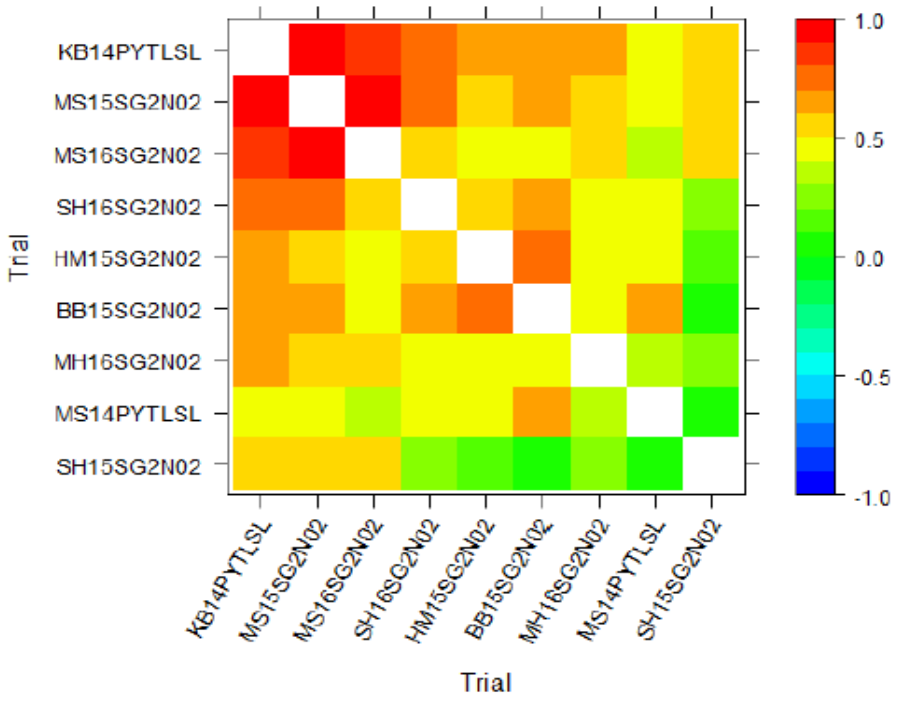


**Figure 1.** Genetic correlations amongst in early maturing sorghum testing environments.

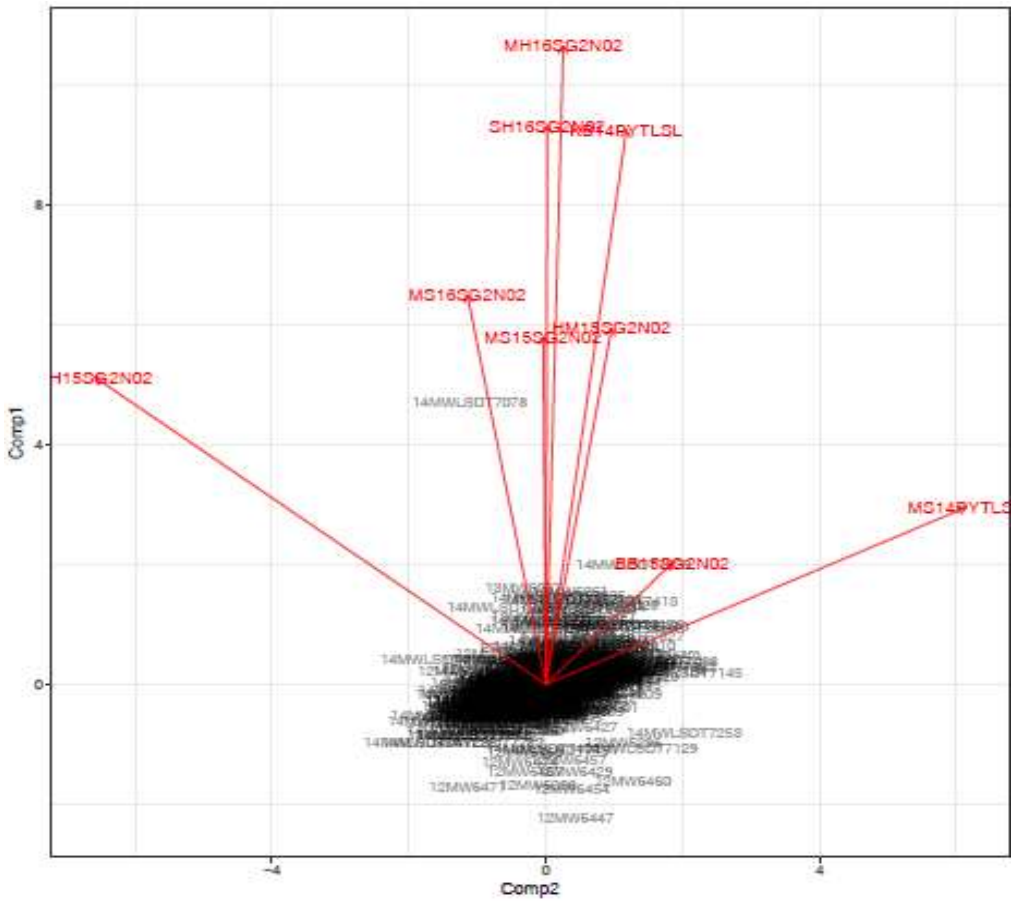


**Figure 2.** Correlation among testing environments using the angle between two lines.

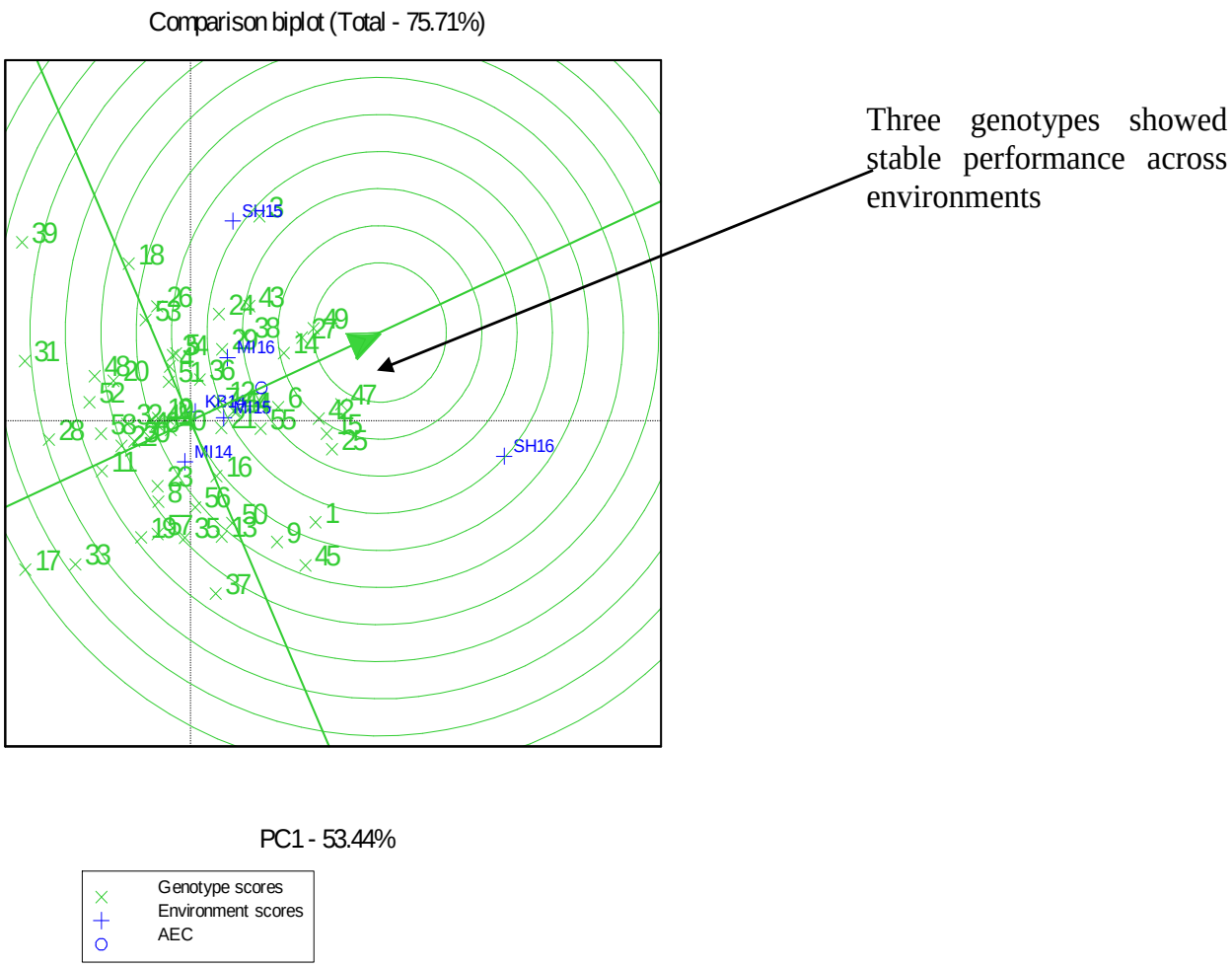


**Figure 3.** Comparison of grain yield performance among genotypes.

The comparison biplot was used to identify three superior and stable genotypes across the testing environments. Heritability is one objective in plant breeding; where high heritability indicates possible selection for targeted traits in breeding Hence, using advanced statistical models, we can increase the genetic gain. Figure 4 indicates improvements in heritability by the advanced statistical methods (Table 4).

## Conclusion

Three genotypes exhibited better yield advantage, higher plant biomass and overall plant traits including drought tolerance. The genotypes; 14MWLSDT7114 (2005MI5060/E-36-1) had 21.2%, 14MWLSDT7196 (WSV387/76T1#23) had 17.7% and 14MWLSDT7329 (SDSL2690-2/76T1#23) had 27.2% superiority in plant height. Mean grain yield performance of genotype 14MWLSDT7114 displayed 12.2%, genotype 14MWLSDT7196 and genotype 14MWLSDT7329 had also showed 13.7 and 20.2% grain yield advantage compared to the standard check variety Dekeba and Melkam. Correlation of the trial's ranges from positive + 0.928 to - 0.387 where positive correlation indicates the strength of their correlation (similarity) among the testing environments while negative correlation indicates dissimilarity among testing environments. One can briefly observe the stability and correlation among testing sites as shown in Figure 2 where the angle between the two line measures the strength of correlation and the length of the arrow showed us discriminability of the testing environments. Figure 3 indicates improvements in heritability by using advanced statistical methods (RCBD, Spatial, Spatial + MET).

From this study three genotypes were showed stable grain yield performance across years and across environments. In addition, these genotypes were preferred by farmers in their overall agronomic desirability (drought tolerance, earliness, head exertion and compactness, grain size, shape and threshability). The national variety releasing committed has been evaluated

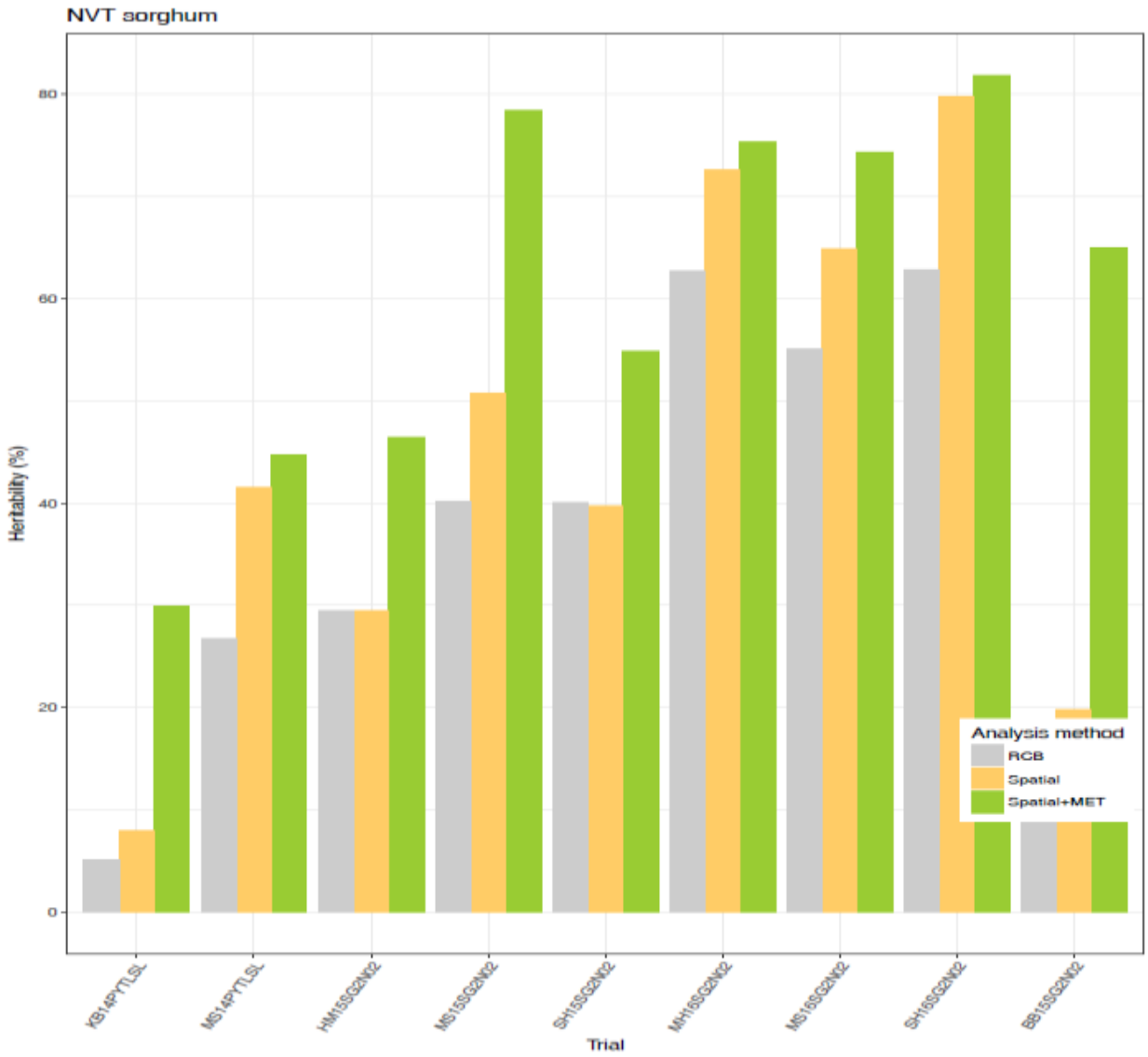


**Figure 4.** Improvements in heritability through applications of different statistical models.

**Table 6.** Predictions of top genotypes using linear mixed model for plant height (cm).

| S/N | Genotype | KB14 | MS14 | MS15 | MS16 | SH15 | SH16 | Mean |
|---|---|---|---|---|---|---|---|---|
| 1 | 14MWLSDT7026 | 195 | 195 | 161 | 169 | 213 | 222 | 192 |
| 2 | 14MWLSDT7029 | 224 | 182 | 170 | 189 | 224 | 218 | 201 |
| 3 | 14MWLSDT7031 | 190 | 187 | 167 | 182 | 242 | 217 | 198 |
| 4 | 14MWLSDT7033 | 175 | 191 | 167 | 184 | 218 | 222 | 193 |
| 5 | 14MWLSDT7034 | 187 | 192 | 159 | 184 | 239 | 215 | 196 |
| 6 | 14MWLSDT7035 | 182 | 184 | 174 | 186 | 260 | 228 | 202 |
| 7 | 14MWLSDT7036 | 191 | 187 | 166 | 193 | 229 | 235 | 200 |
| 8 | 14MWLSDT7040 | 194 | 189 | 164 | 191 | 236 | 212 | 198 |
| 9 | 14MWLSDT7042 | 191 | 199 | 171 | 195 | 241 | 227 | 204 |
| 10 | 14MWLSDT7060 | 178 | 179 | 151 | 153 | 203 | 188 | 175 |
| 11 | 14MWLSDT7073 | 198 | 176 | 160 | 166 | 234 | 217 | 192 |
| 12 | 14MWLSDT7074 | 179 | 173 | 149 | 165 | 224 | 206 | 183 |

**Table 6.** Contd.

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 13 | 14MWLSDT7098 | 218 | 216 | 161 | 183 | 238 | 208 | 204 |
| 14 | 14MWLSDT7100 | 247 | 203 | 174 | 186 | 251 | 234 | 216 |
| 15 | 14MWLSDT7114 | 187 | 193 | 149 | 166 | 224 | 209 | 188 |
| 16 | 14MWLSDT7115 | 189 | 192 | 152 | 175 | 252 | 220 | 197 |
| 17 | 14MWLSDT7129 | 183 | 206 | 168 | 189 | 239 | 211 | 199 |
| 18 | 14MWLSDT7138 | 198 | 194 | 172 | 177 | 239 | 216 | 199 |
| 19 | 14MWLSDT7145 | 194 | 194 | 165 | 190 | 239 | 243 | 204 |
| 20 | 14MWLSDT7157 | 221 | 198 | 161 | 174 | 235 | 234 | 204 |
| 21 | 14MWLSDT7176 | 181 | 160 | 214 | 162 | 246 | 212 | 196 |
| 22 | 14MWLSDT7177 | 195 | 168 | 200 | 164 | 198 | 198 | 187 |
| 23 | 14MWLSDT7191 | 171 | 183 | 159 | 168 | 223 | 198 | 184 |
| 24 | 14MWLSDT7193 | 186 | 182 | 147 | 155 | 210 | 196 | 179 |
| 25 | 14MWLSDT7196 | 184 | 172 | 158 | 155 | 226 | 194 | 181 |
| 26 | 14MWLSDT7201 | 192 | 181 | 154 | 188 | 246 | 213 | 196 |
| 27 | 14MWLSDT7207 | 197 | 178 | 166 | 175 | 240 | 228 | 197 |
| 28 | 14MWLSDT7209 | 188 | 182 | 164 | 179 | 224 | 220 | 193 |
| 29 | 14MWLSDT7234 | 190 | 183 | 169 | 173 | 233 | 180 | 188 |
| 30 | 14MWLSDT7238 | 51 | 183 | 166 | 180 | 228 | 228 | 173 |
| 31 | 14MWLSDT7241 | 198 | 176 | 156 | 182 | 238 | 215 | 194 |
| 32 | 14MWLSDT7251 | 204 | 182 | 178 | 181 | 255 | 237 | 206 |
| 33 | 14MWLSDT7253 | 174 | 195 | 166 | 182 | 237 | 226 | 197 |
| 34 | 14MWLSDT7278 | 197 | 181 | 155 | 161 | 214 | 204 | 185 |
| 35 | 14MWLSDT7279 | 201 | 195 | 169 | 177 | 277 | 210 | 205 |
| 36 | 14MWLSDT7308 | 275 | 199 | 179 | 205 | 278 | 272 | 235 |
| 37 | 14MWLSDT7310 | 221 | 220 | 191 | 200 | 256 | 235 | 220 |
| 38 | 14MWLSDT7311 | 219 | 198 | 166 | 214 | 279 | 253 | 222 |
| 39 | 14MWLSDT7322 | 231 | 184 | 175 | 196 | 292 | 245 | 221 |
| 40 | 14MWLSDT7324 | 234 | 223 | 192 | 215 | 277 | 259 | 233 |
| 41 | 14MWLSDT7325 | 215 | 192 | 182 | 195 | 279 | 246 | 218 |
| 42 | 14MWLSDT7329 | 197 | 183 | 163 | 169 | 257 | 209 | 196 |
| 43 | 14MWLSDT7332 | 179 | 167 | 147 | 158 | 212 | 196 | 176 |
| 44 | 14MWLSDT7354 | 173 | 154 | 153 | 163 | 190 | 192 | 171 |
| 45 | 14MWLSDT7356 | 173 | 180 | 155 | 159 | 212 | 199 | 180 |
| 46 | 14MWLSDT7362 | 192 | 175 | 157 | 173 | 218 | 214 | 188 |
| 47 | 14MWLSDT7364 | 196 | 191 | 167 | 174 | 250 | 230 | 202 |
| 48 | 14MWLSDT7388 | 196 | 182 | 163 | 167 | 223 | 214 | 191 |
| 49 | 14MWLSDT7395 | 176 | 164 | 157 | 161 | 216 | 206 | 180 |
| 50 | 14MWLSDT7400 | 200 | 179 | 164 | 170 | 221 | 208 | 190 |
| 51 | 14MWLSDT7401 | 184 | 182 | 161 | 170 | 228 | 220 | 191 |
| 52 | 14MWLSDT7402 | 256 | 219 | 175 | 181 | 290 | 276 | 233 |
| 53 | 14MWLSDT7405 | 194 | 182 | 165 | 189 | 236 | 204 | 195 |
| 54 | 14MWLSDT7410 | 203 | 205 | 170 | 181 | 236 | 217 | 202 |
| 55 | 14MWLSDT7413 | 190 | 184 | 164 | 154 | 232 | 203 | 188 |
| 56 | 14MWLSDT7425 | 188 | 182 | 156 | 190 | 244 | 225 | 198 |
| 57 | Dekeba | 135 | 149 | 136 | 141 | 186 | 177 | 154 |
| 58 | Melkam | 163 | 171 | 153 | 145 | 182 | 181 | 166 |
| | Mean | 193 | 186 | 165 | 177 | 236 | 218 | 196 |

KB14= Kobo 2014, MS14= Miesso 2014, MS15= Miesso 2015, MS16= Miesso 2016, SH15= Shiraro 2015, SH16= Shiraro 2016.

the VVT both on stations and farmers' field conditions in 2018/2019 and finally verified the release of the variety

14MWLSDT7114 (2005MI5060/E-36-1) for commercial production.

## CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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