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Grain Yield Stability and Adaptability of Finger Millet (Eleusine Coracana) Genotypes in Southern Ethiopia

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ABSTRACT

Multi-location study was conducted at locations namely Jinka, Kako and Alaba in two consecutive years (2011 and 2012 G.c) to identify high yielding, disease resistant/tolerant and stable performing finger millet genotype for potential areas of Southern region. The trails were arranged in a randomized complete block with three replications. Tadesse was used as standard check along collections screened (Six finger millet genotypes). The experimental plot size for was 5mX 7.5(37.m2). The spacing between rows was 45 cm and 15 cm between plants after thinning. The standard agronomic practices were applied equally according to local agro-ecological conditions. The grain yield in qt/ha with 14% moisture was measured. Additive Main effect and Multiplicative Interaction (AMMI), Genotype and Genotype by Environment interaction (GGE) biplot analysis model revealed that environment effects and genotype effects were highly significant implies environments are diverse and genotype were performing differently. According genotypes LR002, LR004 &LR005 showed stable and above mean performance across testing location and season. So this varieties should taken for verification trial with standard checks (recently released varieties) under locations were regional variety trials were conducted.

Keywords: *Finger millet, Jinka, Kako, yield stability, Multi-location trial, Genotype effect + Genotype by environment interaction effect (GGE)*

INTRODUCTION

Finger millet (*Eleusine coracana* (L.) Gaertn.) is one of the most important food cereals in the sub-Saharan Africa and south Asia. It is the most widely cultivated millet in the semi-arid tropical and subtropical regions of the world after pearl millet (*Pennisetum glaucum*) and foxtail millet (*Setaria italica*). It is also one of the critical plant genetic resources for the agriculture and food security of farmers inhabiting arid, infertile and marginal lands (Barbeau and Hilu, 1993).

In Ethiopia it occupies 4% of the total area allocated to cereals (nearly half a million hectares) each year and contributes about 4% to the total annual cereal grain production in the country. In the past decade, 2001-2010, finger millet production area in Ethiopia increased from 342,120 ha to 368,999 ha with an increase of 7.3%, and the productivity increased from 3,769,290 to 5,241,911 quintals with a proportion of 28%. (CSA, 2010). In southern region, especially Segan peoples and South omo zone the area coverage and production of the crop increased from year 2008 to 2013 (Wedajo Gebre,2015).

Ethiopian national sorghum research program increased its effort to identify additional high yielding varieties that can fit in a wide range of environments. Jinka Agricultural Research center and other national programs have resulted in considerable progress and identification of some improved finger millet varieties (Wedajo, 2015). Superior genotypes selected from different stages of screening were pulled together and evaluated at multiple locations representing different agro-ecologies. Therefore, this study was designed to conduct multi location trial for identifying high yielding, disease resistant and stable performing finger millet candidate for the target area.

MATERIALS AND METHODS

Field Trials

Multi-location field trials are conducted during 2011 at two locations and in three locations during 2012 in finger millet potential areas of Southern region: Halaba, Kako and Jinka.

Combination of years (2011, 2012) and locations (Halaba, Kako and Jinka) treated as five environments (Halaba 2011, Halaba 2012, Jinka 2012 , Kako 2011 and Kako 2012). The trails were arranged in a randomized complete block with three replications. Six finger millet genotypes which were screened at Jinka agricultural research center are chosen for the trials. Variety Tadesse was used as standard check along collections screened. The experimental plot size for each candidate was 5mX 7.5(37.m^2). The spacing between rows was 45 cm and 15 cm between plants after thinning. Seed of each candidate was planted in four rows, but only the two middle rows were harvested and measured. The standard agronomic practices were applied equally according to local agro-ecological conditions. The grain yield in qt/ha with 14% moisture was measured.

STATISTICAL ANALYSIS

Analysis of Variance (ANOVA)

A combined analysis of variance was performed for yield and other traits after checking for homogeneity of experimental error. In the combined analysis of variance, genotypes were assumed to be fixed while locations were considered as random variables (Gomez and Gomez, 1984). Combined analysis of variance over locations was carried out using the following statistical model.

$Y_{ijk}=\mu + G_i + E_j + GE_{ij} + B_{k(j)+} e_{ijk}$

Where; Y_{ijk} = observed value of genotype i in block k of environment (location) j,

μ = Grand mean of the experiment,

G_i = the effect of genotype i,

E_j =the effect of the j^{th} environment

GE_j = the interaction effect of genotype i with environment j,

$B_{k(j)}$ =the effect of block k in location (environment) j,

e_{ijk} =the error effect of genotype i in block k of environment j.

Mean separation was done using Duncan's multiple range tests. To compute the proportion of the total variance, estimation of variance components was performed by equating mean square to their expectations as shown in Table 3.

Table1. *Estimates of variance components and methods of determining variance component*

Source of variation	SS	DF	MS	Obtained	F-test		
					Required		
					5%	1%	Variance components
Total	SST	104	MS_T			-	-
Environment	SSL	4	MS_L	-	3.47	5.99	$\sigma^2E+g\sigma^2_{B(l)}+gr\sigma^2l$
Block(L)	$SS_{B(L)}$	10	$MSB_{(L)}$	$MS_L/MSB_{(L)}$	1.99	2.63	$\sigma^2E+g\sigma^2_{B(L)}$
Genotypes	SS_G	6	MS_G	$MSB_{(L)}/MS_E$	2.50	3.66	$\sigma^2E+r\sigma^2_{GxL}+rl\sigma^2g$
GxL	SS_{GxL}	24	MS_{GxL}	MS_G/MS_{GxL}	1.70	2.11	$\sigma^2_E+r\sigma^2_{GxL}$
Error	SS_E	60	MSE	MS_{GxL}/MS_E			σ^2_E

Where; L, G and B are the number of locations, genotypes and blocks, respectively. The σ^2_L, $\sigma^2_{B(L)}$, σ^2_G, σ^2_{GxL}, and σ^2_E, are variance components of environment blocks within environment, genotypes, genotype by environment interaction and error respectively.

GxL= Genotype by environment interaction, σ^2_E= variance component due to experimental error =MS_E, σ^2_{GxL} = the variance component due to genotype by environment interaction =MS_{GxL}-MS_E/r, σ^2_G = the variance component due to genotypes= MS_G -MS_{GxE}/rl, $\sigma^2_{B(L)}$ = variance component due to blocks with in environments =MS_B-MSE/g, σ^2_L = variance component due to location = MS_L-$MS_{B\ (E)}/rg$, σ^2T =total variance $=\sigma^2_l+\sigma^2_{B(l)}+\sigma^2_G+\sigma^2_{GxE}+\sigma^2E$, σ^2_k =variance due to one components (L, G.etc)

The proportion of variance accounted for each component was determined by dividing the variance component by the total variance component (σ^2_k/σ^2_T).

Stability Analysis

ANOVA only detects the existence of genotype by environment interaction (effects). Therefore,

significance of genotype by environment interaction mean square was further elaborated using various stability parameters. For this the means of genotypes over the replications were subjected to stability analysis using SAS (Hussien et al., 2000). AMMI model and biplot technique proposed by kempton (1984) were used for stability analysis.

Additive Main Effects and Multiplicative Interaction (AMMI) Model

Additive main effects and multiplicative interaction analysis (Zobel et al., 1988; Crossa, 1990) was also performed for grain yield using SAS (Hussien et al., 2000) software. It first fits additive effects for genotypes (G) and environment (E) by the usual additive analysis of variance (ANOVA) procedure to separate the additive effects of genotypes and environments, and then fits multiplicative effects for genotype by environment interaction by principal component analysis (PCA) to extract the pattern from the remaining genotype-environment interaction portion of the ANOVA. Essentially this means stripping out the additive effects of genotypes and environments from the two-way genotype – environment table, and then conducting a principal components analysis on the residuals. The resulting statistical model is therefore a hybrid of this two models, estimates (Zobel, 1990).

The AMMI model for the observed performance (Yij) of the i^{th} genotype in the j^{th} environment is:

$$Yij = \mu + gi + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij},$$

Where $\mu+g_i + e_j$ and e_{ij} are as described in the above equations, n is the number of principal component axes considered, λ_k is the singular value of the k^{th} axis in the principal component analysis, α_{ik} is the eigenvector of the i^{th} genotype for the k^{th} axis, γ_{jk} is the eigenvector of the j^{th} environment for the k^{th} axis, *eij* is the corresponding random error. The first axis represents that environmental variable which accounts for the largest amount of interaction, and which therefore discriminates most effectively between genotypes, and so on. The significance of the analysis was measured by appropriate F-test at various probability levels by comparing each principal components mean squares with the pooled within environment mean square. Those PCA axes, which were not significant, were pooled into residual term (eij).

To evaluate the test environments, which is not possible with the AMMI, the Genotype plus Genotype-environment (GGE) biplot analysis was carried out using the method suggested by Yan (2002) for multi-environment data. The GGE biplot is a biplot that displays the GGE part of MET data. The basic model for a GGE biplot is

$$Yij - \mu j = \lambda_1 \alpha_{i1} \gamma_{j1} + \lambda_2 \alpha_{i2} \gamma_{j2} + \varepsilon ij$$

Where Yij is mean of genotype i in environment j; μj is mean value of environment j; and λ_1 and λ_2 are the singular values for PC1 and PC2, respectively; αi1 and αi2 are the PC1 and PC2 scores, respectively, for genotype i; γj1 and γj2 are the PC1 and PC2 scores, respectively for environment *j*; and εij is the residual of the model associated with the genotype i in the environment *j*.

Result and Discussion

Analysis of variance was carried out to determine the effect of genotype, environment and their interaction on grain yield of finger millet genotypes (Table 2). Accordingly, except environment by genotype interaction, all sources of variances showed statistically significant differences. A large yield variation explained by environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield and environments played a significant role in the expression of traits being considered. Also difference between genotypes was significant; which indicates genotypes are genetically different. Non significant effect of genotype environment interaction implies consistent performance of finger millet genotypes across tested environment. In this experiment blocking was effective in reducing experimental error because difference between replication was highly significant.

Table2. *Combined analysis of variance for 7 varieties tested at five environments.*

Source of variation	DF	Type III SS	Mean Square
Environment	4	229476669.1	57369167.3***
Genotypes	6	5827890.6	971315.1*
Genotype xEnv.	24	10908130.8	454505.4*
Rep(environment)	10	79740309.7	7974031.0***

Table3. *The analysis of variance table for AMMI of grain yield for the 7 finger millet genotypes tested at five environments*

Source of variation	DF	SS	MS	% of total Explained	% of G×E Interaction SS
Total	104	351672943	3381471		
Environments	4	229476669	57369167**	65.2	
Genotype	6	5827891	971315*	1.65	
Genotype xEnv.	24	10908131	454505^{NS}	3.1	
IPCA 1	9	5617183	624131	1.6 1.6	
IPCA2	7	4042294	577471	1.15 2.75	
Residual	8	1248655	156082		

**, *, ^{NS} *=highly significant, significant and non-significant at P≤0.01, 0.5 level, respectively. Grand mean=2170.81, R-squared= 0.92, CV= 30 %*

The mean grain yield (kg/ha) ranged from 98.9 at Jarc2004 for LR003 to 5105 at Kako2003for LR005.

Kako2003 site gave highest grain yield (4313 kg/ha) followed by Alaba 2003 (3447 kg/ha) but Jarc 2004 gave lowest yield (295kg/ha). Based on mean grain yield genotype LR005 gave highest yield across testing locations followed by genotype LR004.

Similar resulted was obtained by Dagnachew et al. *(2014),* who reported significant differences among finger millet varieties for grain yield.

Table4. *The mean grain yield (kg/ha) obtained from seven genotypes across three environments*

Genotype designation	Environments					
	Alaba 03	Kako03	Alaba 04	Kako 04	Jinka04	Genotype mean
1 LR001	3412	4005	1216	1184	157.3	1995
2 LR002	3419	4960	1336	1674	351.7	**2348**
3 LR003	2843	4521	1314	1577	98.9	2071
4 LR004	3618	4634	1351	1513	379.6	2299
5 LR005	3886	5105	1567	1827	646.0	**2606**
6 LR006	2887	3328	1736	1390	187.8	1905
7 Taddesse	4064	3640	1090	818	245.8	1971
EM	3447	4313	1373	1426	295	
LSD	1227	1832.7	547.6	1262.6	157.2	2170.81
CV (%)	20.0	23.88	22.4	30	29.9	

EM= environment mean, LSD= least significant difference, CV (%) = coefficient variance

The GGE bi-plot (Figure 1), PC 1 and PC 2 explained 59.35 and 26.82%, respectively, of genotype by environment interaction.

Two groups of environments can distinguished; one group contains Jarc 2004, Kako 2003, kako2004, Alaba2004 environments. The three genotypes LR002, LR004 and LR005 were high yielding genotypes adapted under this distinguished, with winning genotype LRoo5 and, the second environment Alaba2003 was excluded since it doesn't belong to none of the distinguished groups.

The other vertex genotype LR006 and LR007 without any environment in their sectors were not the highest yielding genotypes in any of test environments rather they were poorest genotypes at all or some environments.

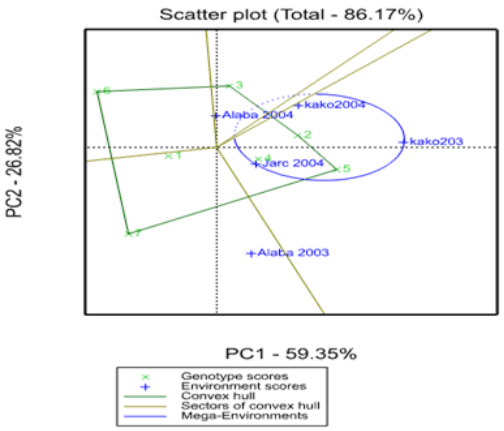

Figure1. *GGE biplot of seven finger millet genotypes for grain yield across five environments*

CONCLUSION AND RECOMMENDATION

Based on the result of multi location result three genotypes (LR002, LR004 and LR005) were

shown relatively stable and high yield performance across test environments. According genotypes LR002, LR004 and LR005showed stable and above mean performance across testing location and season. So this varieties should taken for verification trial with standard checks (recently released varieties) under locations were regional variety trials were conducted. And also the genotypes should be verified and released in target area and similar growing locations.

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