Genotype by Environment Interaction and Grain Yield Stability Analysis for Finger Millet (*Eleusine coracana* (L.) Gaertn) Genotypes from Western Oromia

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Abstract

Crop yield is a complex trait influenced by a number of component characters along with the environment directly or indirectly. Genotype performance depends on its genetic potential and the environment where it is grown. Genotypes by environment (GxE) interactions are generally considered to be among the major factors limiting response to selection and the efficiency of breeding programs. Ten advanced finger millet genotypes and one standard check were evaluated at Bako and Gute research center for three years (2013-2015) and at Bilo Boshe for one year (2014) with objectives of identifying high yielding and stable genotypes. Analysis using additive main effect and multiplicative interaction (AMMI) model revealed highly significant ($P \leq 0.01$) variations among environments, genotype and GxE interaction. This implied that the tested genotypes respond differently over environments as the test environments are highly variable. Only the first IPCA-I was significant ($p \leq 0.01$) and contributed 41.57% of the total genotype by environment interaction. It is found that genotypes 214995 and BKFM0063 are high yielding and IPCA value closer to zero, an indicator of stable yield performance across years and location. Analysis using Eberhart and Russell regression model showed that genotypes 214995, BKFM0063 and BKFM0052 were the most stable candidates with better grain yield of 2.99, 2.70 and 2.53 ton ha^{-1}, regression coefficients of 0.9879, 1.22 and 0.9459 and reasonably acceptable deviation from regression 0.0321, -0.01135 and 0.0607, respectively, further confirming that these genotypes are stable and widely adaptable. Genotype and genotype by environment interaction biplot (GGE) also portrayed the stability of Acc. 214995. Overall, the AMMI, Regression and GGE Biplot revealed similar results and both 214995 and BKFM0063 genotypes were proposed for possible release. Finally, 214995 was released and recommended for the test environments and similar agro-ecologies of western Ethiopia based on farmers preferences, stable yield performance and disease tolerance across locations.

Keywords: AMMI, Finger millet, IPCA, G X E interaction, Stability

Introduction

Finger millet (*Eleusine coracana* L.) Gaertn) is an allotetraploid (2n = 4× = 36) annual cereal crop that includes two distinct subspecies: subsp. *coracana* (cultivated finger millet) and subsp. *Africana* (wild finger millet) (Hilu, 1994). It is an important food crop cultivated widely in arid and semi-arid regions of the world, especially in East Africa, India and in other Asian countries (Rudin *et al*, 2004). Finger millet is potentially a climate-resilient and nutritious crop with highly nutritive and antioxidant properties (Kumar *et al*, 2017) and very importantly, finger millet grain is gluten-free, rich in calcium, fiber, iron and, has excellent malting qualities (Chandrashekar, 2010 and Pradhan *et al*, 2010). In Ethiopia also, finger millet is an important staple food crop widely grown.

The productivity of this crop is limited by shortage of stable and high yielding finger millet varieties. The performance of a genotype is dependent on its genetic potential, the environment, and the interaction between the genotype and the environment. The consequences of the phenotypic variation depend largely on the environment and this variation is further complicated by the fact that not all genotypes react in similar ways to change in environment and no two environments are exactly the same (Yan and Hunt, 2001).

Genotypes x environment interactions are said to be exist when the responses of two genotypes to different levels of environmental factors fail to be respond similarly (Allard and Bradshaw, 1964). A pooled analysis of variance able to calculate the interactions and describe the main effects but is not explanatory to describe the interaction effect (Asnake *et al*., 2013). An appropriate analytical model such as additive main effects and multiplicative interaction (AMMI) can treat both the additive main effect and multiplicative interaction component employing the analysis of variance (ANOVA) and Interaction Principal Components (IPCA) (Gauch and Zobel, 1996). Furthermore, AMMI and GGE biplot analysis are considered as an effective graphical tool to diagnose genotype by environment interaction patterns (Gauch and Zobel, 1996; Yuksel *et al.*, 2002). Grain yield performance is not the only parameter for selection as a genotype with the highest grain and would not necessarily mean stable and adaptable across location and years. The regression model suggested by Eberhart and Russell (1966) allows for the computation of a complete analysis of variance with individual stability regression coefficient (bi) estimates and deviation from regression line (s^2di). The model considers a stable variety as the one with a high mean yield, bi = 1 and $s^2di = 0$. The Eberhart and Russell (1996) model and AMMI stability analysis could be the preferable tools to identify stable, high yielding and adaptable genotype (s) for varied or specific environments. The plant breeders need to identify adaptable and stable high yielding genotypes with other desirable traits under varying environmental conditions prior to release as a variety (Showemimo *et al.,* 2000; Mustapha *et al.,* 2001). Therefore, the objectives of this study were (i) to examine the influence of genotype x environment interaction on yield of genotypes, (ii) to assess the yield stability of promising genotypes (ii) and to identify high yielding genotypes.

Materials and Methods

Experimental materials, experimental sites and procedures

Eleven brown seeded finger millet genotypes including standard check (Gute) were tested at Bako and Gute for three cropping seasons (2013-2015) and at Bilo Boshe for one season (2014). The genotypes were planted in a randomized completely block design (RCBD) with three replications in which each plot comprises of five rows having 5 m length. The spacing between rows and plants were 40 cm and 10 cm, respectively. Seed rate of 15 kg ha^{-1} and fertilizer rate of 110 kg ha^{-1} DAP and 65 kg ha^{-1} Urea were used. Urea was applied in split form; half at planting and the rest half at 35 days after emergence. Management practices were done as per recommendations. The middle three rows were harvested and grain yield analysis was carried out.

Data analysis

Grain yield analysis was carried out using regression (Eberhart and Russell, 1966) and AMMI models in Agrobase software (Agrobase, 2000). Additive main effect and multiplicative interaction (AMMI) model

AMMI model equation: $Yger = \mu+\alpha g+\beta e+\sum n\lambda n\gamma gn\delta en+ \varepsilon ger+\rho ge$; Where:

Yger is the observed yield of genotype (g) in environment (e) for replication (r); *Additive parameters:* μ is the grand mean; αg is the deviation of genotype g from the grand mean, βe is the deviation of the environment e; *Multiplicative parameters:* λn is the singular value for IPCA, γgn is the genotype eigenvector for axis n, and δen is the environment eigenvector; εger is error term and ρge is PCA residual.

Eberhart and Russell Regression Model

$Yij = \mu i +biIj +S^2dij$; where Yij is the mean performance of the ith variety (I = 1, 2, 3…, n) in the jth environment; μi is the mean of the ith variety overall the environments; bi is the regression coefficient which measures the response of ith variety to varying environments; S^2dij is the deviation from regression of ith variety in the jth environment and Ij is the environmental index of the jth environment.

Genotype and Genotype by Environment Interaction (GGE) biplot

Different methods haven been used to determine genotype by environment interaction and stability analysis to identify superior genotypes with wide adaptation or sensitive for different environments. The genotypes and genotype by environment (GGE) biplot analysis is the most common currently utilized (Yan &Tinker 2005; Yan et al. 2007). GGE biplot analysis was carried out using the method suggested by Yan (2001) for multi environment data:

$Yij - \mu j = \lambda_1 \alpha_{i1} \gamma_{j1} + \lambda_2 \alpha_{i2} \gamma_{j2} + \varepsilon ij$: Where Yij is mean of genotype i in environment j; μj is mean value of environment j; k is the number of principal components retained in the model; λ_1 and λ_2 the singular value of PC1 and PC2, respectively; α_{i1} and α_{i2} are the PC1 and PC2 scores, respectively, for genotype i; γ_{j1} and γ_{j2} 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.

Table 1.List of study genotypes and the test environments with their codes

No	Genotype	Genotype code	No	Environments	Environment code
1	214995	a	1	Bilo- Boshe 2014	A
2	BKFM0058	b	2	Bako 2013	B
3	BKFM0052	c	3	Bako 2014	C
4	203547	d	4	Bako 2015	D
5	229727	e	5	Gute 2013	E
6	BKFM0063	f	6	Gute 2014	F
7	203356	g	7	Gute 2015	G
8	203351	h			
9	BRCFM-8-04	i			
10	Anno-1	j			
11	Gute	k			

Result and Discussions

Analysis of Variance

The mean grain yield of the eleven tested genotypes ranged from 2.12 ton ha^{-1} (acc. 203356) to 2.99 ton ha^{-1} (acc. 214995) with a grand mean of 2.54 ton ha^{-1} (Table 2). The mean grain yield across seven environment ranges from 1.67 ton ha^{-1} at Bilo Boshe in 2014 to 3.45 ton ha^{-1} at Bako location in 2015 main cropping seasons (Table 2). Not only the genotypes and locations, but also variations in seasons or environmental conditions during different seasons significantly influence the grain yield performance. Similarly, Birhanu *et al.,* (2015) reported genotypes, environments and genotype by environment interaction, indicating the high environmental variations and differential response of genotypes to the variable environments. Similar results were reported by Girma *et al*, (2011) for field pea and Dagnachew *et al*, (2014) for Triticale.

Table 2: Mean seed yield (ton ha^{-1}) of 11 finger millet genotypes tested in seven environments.

Genotype	Mean grain yield (ton ha^{-1})							
		Bako			Gute		B/Boshe	
	2013	2014	2015	2013	2014	20	2014	Mean
214995	3.85	3.18	3.69	3.04	3.08	1.78	2.31	2.99
BKFM0058	2.79	2.00	4.04	1.72	3.26	2.04	1.74	2.51
BKFM0052	3.18	1.93	4.05	2.32	3.10	1.89	1.25	2.53
203547	3.79	2.64	3.29	2.33	2.93	1.75	1.33	2.58
229727	3.58	2.45	2.99	2.60	2.92	2.53	2.60	2.81
BKFM0063	3.67	2.24	4.14	2.20	2.98	1.54	2.17	2.70
203356	2.73	2.04	2.50	1.99	2.48	1.87	1.25	2.12
203351	3.09	2.31	2.93	3.10	2.86	1.98	1.85	2.59
BRCFM-8-04	3.19	2.29	3.23	1.79	2.79	1.93	1.22	2.35
Anno-1	2.64	2.01	3.73	2.15	2.16	1.67	1.43	2.26
Gute	2.56	2.78	3.32	2.62	2.93	1.69	1.26	2.45
Mean	3.19	2.35	3.45	2.35	2.86	1.88	1.67	2.54
CV (%)	10.8	9.3	21.0	19.9	11.2	19.7	15.2	
F- Value	**	**	Ns	*	**	Ns	**	

CV=*coefficient of variation,* ** highly significant, * significant

Stability analysis

AMMI Analysis

The combined analysis of variance revealed highly significant ($P \leq 0.01$) variations among environments, genotypes, and Principal Component Analysis (IPCA-1) and significant difference ($P \leq 0.05$) for genotype x environment interactions but non-significant differences for the remaining IPCAs (Table 3). This indicated that, the genotypes responded differently over environments or finger millet genotypes responses were affected by an environment and the test environments are highly variable. In this study, highly significant and considerable percentage of GxE interaction (41.57%) is explained by IPCA-I. The second and third IPCA contributed 18.74% and 17.23% G x E interaction, respectively.

Table 3. AMMI analysis of variance for seed yield of finger millet genotypes tested in seven environments in western Ethiopia in 2013- 2015

Source	DF	SS	MS	% G x E Explained	% cumulative interaction
Environments	6	85.960	14.327**		
Genotypes	10	12.716	1.272**		
Genotype x Envt. Interactions	60	25.320	0.422*		
IPCA I	15	10.525	0.702**	41.57	41.57
IPCA II	13	4.744	0.365ns	18.74	60.30
IPCA III	11	4.364	0.397ns	17.23	77.54
Residuals	140	40.622	0.290		

*Grand mean = 2.536; $R^2 = 0.7631$; Coefficient of variation (CV %) = 21.24; *, ** = Significant at $P < 0.05$ and $P < 0.01$ levels, respectively.*

Therefore, we preferred the first IPCA used to describe genotype by environment interaction and placement on the biplots. Accordingly, the AMMI analysis result revealed that 214995, BKFM0052 and BKFM0063 attained IPCA values relatively close to zero and hence are better stable and widely adaptable genotypes across location and gave relatively higher grain yield.

IPCA value for Gute variety (standard check) was relatively close to zero showing that the variety is stable but gave lower yield below the average. Whereas, 229727, 203547 and 203351 genotypes were high yielder, gave above the mean but scored IPCA value deviating from zero. This indicated that these genotypes are not stable and adaptable for specific environment (Table 4). Asnake *et al.* (2013) and (Yuksel *et al.* 2002) reported results in agreement with the present study. Relatively higher mean grain yield was recorded from Bako site during 2013 and 2015. Similarly, BKFM0052 gave the highest grain yield at Bako location during the 2015 cropping season than it did at other locations and years (Table. 4 and Fig 1). Bilo Boshe is among the extremely low yielding environments (Fig 1).

Generally, AMMI model revealed that genotypes 214995 and BKFM0063 showed stable performance across years and locations, gave better average grain yield and thus potential candidates for variety verification.

Table 4: Mean grain yield (GY) (ton ha-1 and IPCA1 scores of genotypes

No	Genotype name	IPCA1 score	Stability rank	GY(ton ha^{-1})	Yield rank
1	214995	0.2907	5	2.99	1
2	BKFM0058	-0.2778	4	2.51	7
3	BKFM0052	0.1325	3	2.53	6
4	203547	-0.6707	11	2.58	5
5	229727	0.5373	9	2.81	2
6	BKFM0063	0.1182	2	2.70	3
7	203356	-0.5340	8	2.12	11
8	203351	-0.4410	7	2.59	4
9	BRCFM-8-04	0.3773	6	2.35	9
10	Anno-1	0.5577	10	2.26	10
11	Gute	-0.0903	1	2.45	8

Environment

No.	Location name	IPCA 1 score	GY (ton ha^{-1})	Yield rank
1	Bilo Boshe 2014	0.2196	1.67	6
2	Bako 2013	0.0977	3.19	2
3	Bako2014	0.3564	2.35	4
4	Bako2015	-1.1329	3.45	1
5	Gute 2013	0.5743	2.35	4
6	Gute2014	-0.2422	2.86	3
7	Gute2015	0.1271	1.88	5

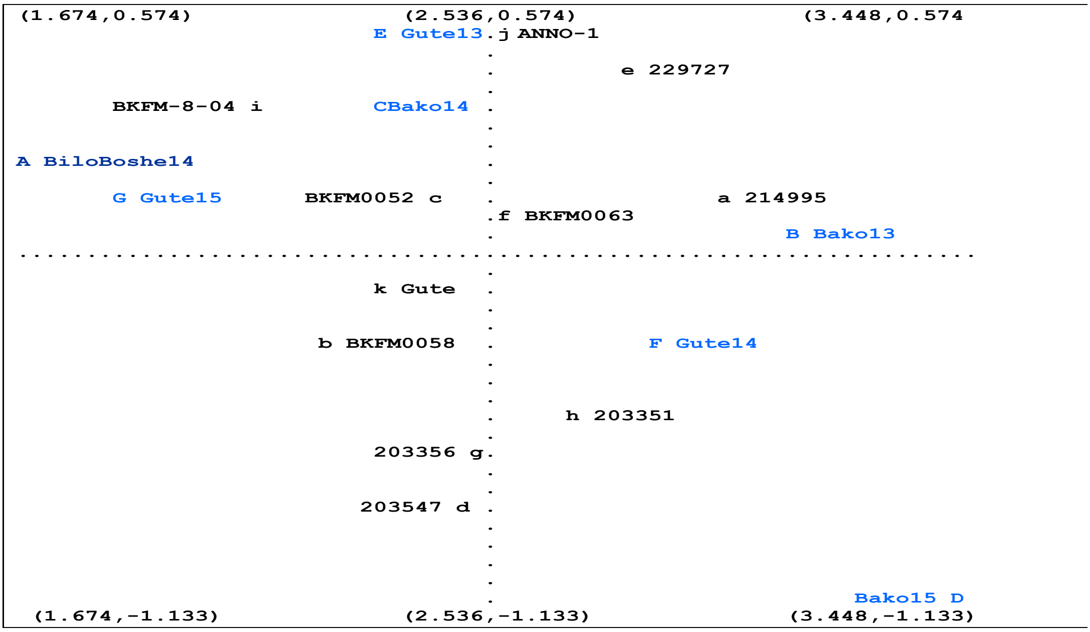

Fig 1. AMMI Biplot showing genotypes grain yield stability and preferential adaptation environment

Analysis Based on Eberhart and Russell Model

Mean square due to genotypes were highly significant ($P \leq 0.01$) and interaction of genotype x environment (linear) were significant ($P \leq 0.05$) (Table 5). The significances of genotypes x environments (linear) showed difference in yield performance among the genotypes under different environments. In agreement to the present study, Dagnachew *et al.* (2014) reported significant genotype by environment interaction for finger miller varieties tested across four locations for two seasons in Ethiopia. Sujay Rakshit *et al.* (2012) reported significant differences for genotypes and genotype x environment (linear) in sorghum. Chaudhary *et al.* (1994) also reported significant differences for genotypes and genotype x environment (linear) in field pea.

Table 5: Analysis of variance using Eberhart and Russel's Model for grain yield of 11 finger millet genotypes tested in seven environments in western Ethiopia.

Source of variation	DF	SS	Mean square
Genotypes	10	4.239	0.424**
Environment + Genotype x Environment	66	37.093	0.562
Environment in linear	1	28.653	
Genotype x Environment (linear)	10	2.276	0.228*
Pooled deviation	55	6.164	0.112
Residual	154	15.838	0.103

Grand mean = 2.536; R^2 = 0.8338; Coefficient of variation (CV, %) = 21.90;
**, ** = Significant at P < 0.05 and P < 0.01 levels, respectively.*

The mean grain yield performance, regression coefficient (b_i) and squared deviation (s^2di) from the regression values are presented in Table 6. According to Ebrehart and Russell (1996) model, genotypes with high mean yield and regression coefficient (bi) equal to unity and deviation from regression (s^2di) approach to zero is stable and widely adapted. Thus, pipeline accession 214995, BKFM0063 and BKFM0052 were the most stable candidates with better grain yield (2.99, 2.70 and 2.53 ton ha^{-1}), regression coefficients approaching one (0.9879, 1.22 and 0.9459) and reasonably acceptable deviation from regression that approaches to zero (0.0321, -0.01135 and 0.0607), respectively, implying that those genotypes are stable and widely adaptable than the other genotypes (Table 6). Kebede *et al.*, (2016) also reported similar result for finger millets. An ideal genotype has the highest average grain yield, a regression coefficient (bi) value of approximately one and a mean square deviation from regression (s^2di) value close to zero. These results are consistent with those reported by Farshadfar (2008).

The regression coefficients were relatively far from unity for Acc. 203547, Acc. 229727, Acc. 203356, Acc. 203351 and BRCFM-8-04 (Table 6). This indicated that the above five genotypes are less stable and characterized by specific adaptability. The result obtained using Eberhart and Russell (1966) model is in agreement with AMMI model. Acc. 229727 gave the highest grain yield (2.81 ton ha^{-1}) but the regression coefficient (bi) much lower than unity indicating specific adaptability (Table 5). Similarly, Gute variety (standard check) gave lower grain yield below the average, regression coefficients (bi) closer to one and squared deviations from regression (s^2di) also closer to zero and hence are poorly adapted to all environments (Table 5). Dogan *et al.* (2011) reported results on triticale varieties that are in agreement with the present study.

Table 6: Regression coefficient (bi) and squared deviation from linearity of regression (s2di) by the test genotypes revealed using Eberhart and Russell model.

Genotypes	Regression coefficient (bi)	Squared deviations from	Grain yield (tons ha-1)
214995	0.9879	0.0321	2.99
BKFM0058	1.0460	0.0125	2.51
BKFM0052	0.9459	0.0607	2.53
203547	1.1639	0.1244	2.58
229727	0.4471	-0.0233	2.81
BKFM0063	1.2289	-0.0113	2.70
203356	1.4084	-0.0342	2.12
203351	1.3174	0.0292	2.59
BRCFM-8-04	0.6978	-0.0574	2.35
Anno-1	0.6600	0.0095	2.26
Gute	1.0966	-0.0407	2.45

*Standard error of beta = 0.2074; t = Tons; ha = Hectare; *, ** = Significant at P < 0.05 and P < 0.0 levels, respectively.*

Stability Analysis Using GGE Biplot Techniques

The biplot analysis showed that a total variation of 67.87% was explained by the first two principal components (41.69 and 26.18% by PC1 and PC2, respectively) (Fig. 2). Genotype 214995 fall in the first concentric circle, closer to IPCA stability horizontal line and away from the mean vertical line. This indicated that the genotype is the best stable and high yielder than the remaining tested genotypes and followed by BKFM0063. The standard check, Gute variety also showed stable performance but inferior in grain yield and even blow the average. Genotypes Acc. 229727 and Acc. 203351 produced high average yield but unstable across years and environments (Fig 2). Birhanu *et al.* (2015) also reported similar results in stability analysis of finger millet genotypes in moisture stressed areas of northern Ethiopia.

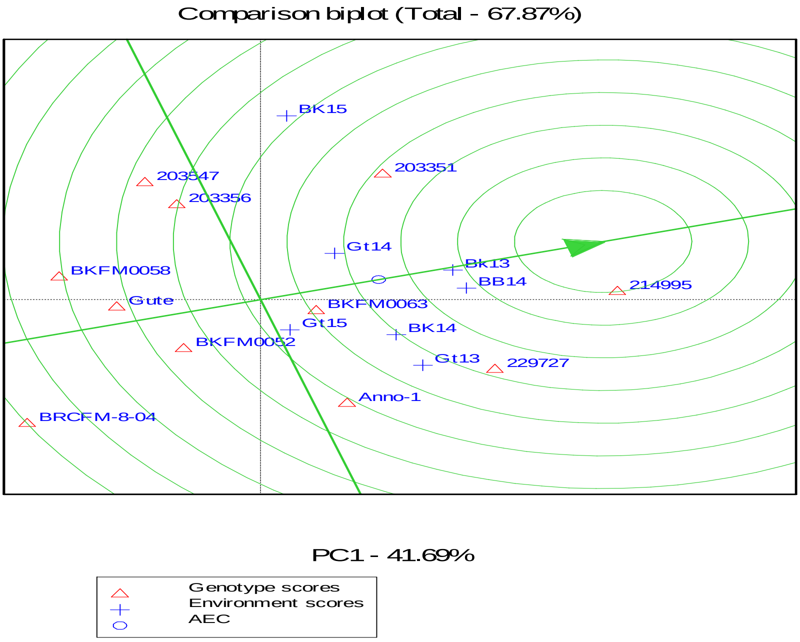

Fig 2. GGE biplot analysis showing the stability of genotypes and test environments.

The GGE biplot presented in Figure 3 indicated the best performing genotype (s) for specific environment and the group of environments. The rays of the biplot divided the plot in to six sections. The environments appeared in three of them, revealing three mega environments. According to Yan *et al.* (2007), when different environments fell in to different sectors, it shows that they had different high yielding cultivars for those sectors and also the presence of a cross over interaction. The vertex families for each quadrant represented the genotypes with the highest yield in the specific environment. The highest yielding genotype in Billo Boshe in 2014 was Acc. 214995. Whereas, genotypes Anno-1, Acc. 203351 and 229727 showed specific adaptation at Gute in 2015, Bako in 2015 and Gute in 2013, respectively. BARCFM-8-04 was low yielding with specific adaptation at Gute in 2015 (Fig 3). Similar results were reported by Yan & Tnker (2005).

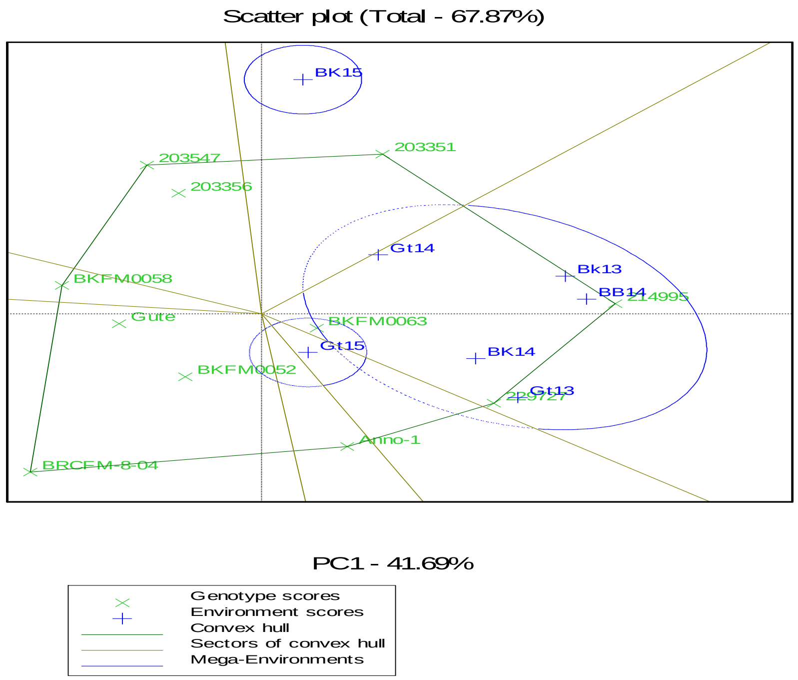

Fig. 3. GGE biplot showing the relationship among environments and the specific ideal niches of the tested genotypes.

Generally, GGE biplot analysis, AMMI and Eberhart and Russell model revealed that genotype Acc. 214995 was a stable and high yielding (2.99 ton ha^{-1}) variety with 21.99% yield advantage over the best standard check Gute (2.54 ton ha-1). Besides, the candidate variety were resistant to blast disease, purple flower color which is the typical character for the presence of resistant gene to blast disease and presence of dominant gene. Therefore, the candidate variety was verified across locations both on farmers field and on station in 2016, evaluated by the national variety release committee with active participation of farmers and finally the variety was officially released in April 2017 and recommended for production in the test environments are areas with similar agro ecology.

Conclusions

The ANOVA showed that the effects of environments, genotypes and genotype x environment interaction (GxE) were important in trait expression and performance of genotypes. The investigated stability analysis models (AMMI, Regression model and GGE biplot) enabled to classify genotypes and environments for their stability. Those stability models identified Acc. 214995 as relatively stable accompanied by high grain yield performance. All the models indicated the standard check Gute was stable and with low grain yield. Besides, BKFM0063 and

BKFM0052 were also relatively stable and better yielding genotypes and thus were verified for possible release. However, only Acc. 214995 was officially released based on farmers' preferences, and multi-location stability and grain yield performance. GGE biplots gave more visual interpretation than just selecting the best performing genotypes and it also allowed visualization of cross over genotype by environment interaction through the polygon view. The Regression, AMMI and GGE biplot analysis result revealed almost similar selections of superior, stable genotypes and classification of environments.

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