Net Journal of Agricultural Science
Vol. 1(1), pp. 10-16, March 2013
Full Length Research Paper

Genotype by environment interaction and grain yield stability analysis of rice (*Oryza sativa* L.) genotypes evaluated in north western Ethiopia

Sewagegne Tariku[1]*, Taddesse Lakew[1], Mulugeta Bitew[2] and Mitiku Asfaw[1]

[1]Adet Agricultural Research Center, P.O. Box 8, Bahir Dar, Ethiopia.
[2]Pawe Agricultural Research Center, P.O. Box 2003, Addis Ababa, Ethiopia.

Accepted 21 February, 2013

ABSTRACT

Sixteen rainfed lowland rice genotypes were evaluated at three locations of eight environments in north western Ethiopia from 2006 to 2008 to identify stable and high yielding genotypes for possible release. The experiment was conducted using Randomized Complete Block Design with three replications. Combined analysis of variance showed highly significant differences among genotypes, environments and genotype by environment interactions for grain yield. The additive main effects and multiplicative interaction (AMMI) analysis of variance indicated that the genotype-by-environment interaction sum of squares was about 3.5 times larger than that for genotypes, which determined substantial differences in genotypic response across environments. The presence of genotype-by-environment interaction was clearly demonstrated by the AMMI model, when the interaction was partitioned among the first four interaction principal component axis (IPCA) which cumulatively captured 91.13% of the total GEI. The stability study indicated that among the tested genotypes, no variety was found to be stable; however, genotypes such as GEN13, GEN12, GEN10 and GEN9 showed high yield potential in favorable environments. In this study, environments (testing locations) fell into three sections, where most of the tested genotypes showed specificity. However, some of the genotypes were not found to be best to any of the environments. As a breeding strategy on rice in the country, it is suggested to execute national variety trial at a number of locations to cluster the testing locations into homogenous groups. This can bring a difference in the rice sector of the country. Among the tested genotypes, the highest grain yield was obtained from genotypes GEN13, GEN12 and GEN9 (4.07, 3.96 and 3.69 t ha-1, respectively) across environments. Out of the tested genotypes, three genotypes were selected and verified, of which genotype “GEN9” has been officially released with the vernacular name “EDGET” meaning development, for large scale production.

Keywords: Additive main effects and multiplicative interaction, rice, stability, genotype-by-environment interaction.

*Corresponding author. E-mail: sewagegne2000@yahoo.com. Tel: (+251) 9 11 82 66 43.

INTRODUCTION

Among the target commodities that have received due attention in promotion of agricultural production, rice is considered as the “millennium crop” expected to contribute in ensuring food security in Ethiopia (MoARD, 2010). Though introduced recently, the importance of rice is being well recognized both by the Government and different stakeholders as the crop is treated as one of the major national research projects, the trend of area coverage and total production is on the increase, the number of small scale farmers and private investors involving in production and processing and the request for improved rice varieties is increasing.

Variety development is one of the major research focuses of the national rice research project in the country

for sustainable production. The general rice breeding scheme includes evaluating a number of genotypes at various stages and testing selected ones at several locations. The multi-location testing, however, usually results in genotype-by-environment interactions that often complicate the interpretation of results obtained and reduce efficiency in selecting the best genotypes (Annicchiarico and Perenzin, 1994). This interaction is the result of changes in cultivar's relative performance across environments, due to differential responses of the genotypes to various edaphic, climatic and biotic factors (Dixon and Nukenine, 1997).

Information on genotype × environment interaction leads to successful evaluation of stable genotype, which could be used for general cultivation. Yield is a complex quantitative character and is greatly influenced by environmental fluctuations; hence, the selection for superior genotypes based on yield per se at a single location in a year may not be very effective (Shrestha et al., 2012). Thus, evaluation of genotypes for stability of performance under varying environmental conditions for yield has become an essential part of any breeding program.

Several methods have been proposed to analyze genotype × environment interaction and phenotypic stability. These methods can be divided into two major groups: univariate and multivariate stability statistics (Lin et al., 1986). A combined analysis of variance can quantify the interactions and describe the main effects. However, it is uninformative for explaining genotype × environment interaction. Among multivariate methods, the additive main effect and multiplicative interaction analysis (AMMI) has been extensively applied in the statistical analysis of multi-environment cultivar trials (Kempton, 1984; Crossa, 1990; Gauch and Zobel, 1997).

The AMMI model is a hybrid that involves both additive and multiplicative components of the two-way data structure. AMMI biplot analysis is considered to be an effective tool to diagnose GEI patterns graphically. In AMMI, the additive portion is separated from interaction by analysis of variance (ANOVA). Then the Principal Component Analysis (PCA), which provides a multiplicative model, is applied to analyze the interaction effect from the additive ANOVA model. The biplot display of PCA scores plotted against each other provides visual inspection and interpretation of genotype × environment interaction components. Integrating biplot display and genotypic stability statistics enables genotypes to be grouped based on similarity of performance across diverse environments (Thillainathan and Femandez, 2001).

This method has been shown to be effective because it captures a large portion of the genotype × environment interaction sum of squares, it clearly separates main and interaction effects that present agricultural researchers with different kinds of opportunities and the model provides agronomically meaningful interpretation of the data (Ebdon and Gauch, 2002). The results of AMMI analysis are useful in supporting breeding program decisions such as specific and broad adaptation and selection of environment (Gauch and Zobel, 1997). Therefore, the objectives of this study were to assess the extent of genotype × environment interaction for grain yield, to evaluate rice genotypes for their yield performance and stability and to select and release genotypes with high grain yield and other desirable traits either for specific and/or wide area production depending on their differential responses to environments.

MATERIALS AND METHODS

Fourteen rainfed lowland rice genotypes which were promoted from preliminary variety trial to national variety trial plus two checks (Table 1) were evaluated in North Western part of Ethiopia from 2006 to 2008 at three locations of eight environments including, Woreta (ENV1, ENV2 and ENV3), Addis Zemen (ENV4 and ENV5) and Pawe (ENV6, ENV7 and ENV8). The locations where the experiment was conducted were different in soil type, altitude, temperature (Table 2) and in total rainfall received per annum and its distribution (Table 3). Randomized Complete Block Design (RCBD) with three replications was used. Each plot had six rows of 5 m length and spaced 0.2 m apart. Fertilizer was applied at the rate of 69/23 kg ha^{-1} of N/P_2O_5 in the form of urea and DAP, respectively. Total DAP was applied at planting while urea was applied one third at planting, one third at tillering and the remaining one third at panicle initiation. A dry seed rate of 60 kg ha^{-1} was used and seeds were sown using drilling method of planting in a row. Plantings were done in the main cropping season (rainy season) following the optimal dates in each respective location. All relevant agronomic practices were applied when deemed necessary.

Data on grain yield and some other traits were collected. However, this paper mainly focuses on grain yield data (t ha^{-1} at 14% moisture level and estimated on the basis of four central harvestable rows). Analysis of variance was done for each environment. Bartlett's test was used to assess homogeneity of error variances prior to combine analysis over environments. The grain yield data for 16 genotypes in 8 environments were subjected to combine and AMMI analysis of variance using Crop Stat version 6.1, statistical software (CropStat, 2007). In the analysis, each combination of a single location and year was considered as an environment. AMMI uses ordinary ANOVA to analyze the main effects (additive part) and Principal Component Analysis (PCA) to analyze the non-additive residual left over by the ANOVA (Gauch, 1993). The interaction is the genotype PCA score multiplied by that of the environment. When a genotype and environment have the same sign on their respective first PCA axis, their interaction is positive, if different, their interaction is negative. An AMMI plot is a graph where aspects of both genotypes and environments are plotted on the same axis so that interrelationship can be visualized. It provides a pictorial view of the transformed G × E interaction (Kempton, 1984) for any interpretation. In a biplot where IPCA1 is on the vertical axis and mean yield on the horizontal, genotypes that appear almost on a perpendicular line had similar means and those that fall almost on a horizontal line had similar interaction patterns. Genotypes or environments with large IPCA1 scores, either positive or negative had large interactions, whereas genotypes with IPCA1 score of zero or nearly zero had smaller interactions (Crossa et al., 1990). The biplot of the first two IPCA axis demonstrates the relative magnitude of the GEI for specific genotypes and environments. The further away from the axis center genotype or environment is, the larger the genotype × environment

Table 1. List of testing lowland rice genotypes and their mean performance for grain yield and some other agronomic traits in eight environments from 2006 to 2008.

Genotype	Geno type code	Days to maturity	Plant Height (cm)	% filled spikelets/ panicle	Disease score (0-9)		Grain color	Thousand grain weight (g)	Grain yield (t ha^{-1})
					LB	PB			
TOX3449-117-3-3-3	GEN1	143.0^{ab}	92.1^{bcde}	89.3^{cd}	1.3	1.5	White	29.6^{bc}	2.81^{f}
TOX4339-WAT-44-3-3-1-2-1	GEN2	141.6^{bc}	89.0^{def}	88.7^{cde}	1.5	1.6	White	27.7^{de}	1.96^{g}
HOO4-7-1-B5	GEN3	141.4^{bc}	97.6^{b}	85.4^{de}	1.5	1.9	Red	27.0^{ef}	3.06^{def}
HO13-5-3-B4	GEN4	143.0^{ab}	89.6^{def}	90.2^{bc}	1.6	2.0	Red	30.5^{b}	2.83^{f}
SIK273-388-2-1-2	GEN5	139.1^{c}	87.3^{ef}	91.4^{bc}	1.8	1.4	White	27.6^{de}	3.34^{abcd}
SIK295-291-4-2	GEN6	145.0^{a}	85.7^{f}	84.3^{de}	1.2	1.3	White	29.0^{cd}	3.42^{bcde}
FOFIFA3737	GEN7	130.0^{ef}	94.0^{bcd}	92.4^{abc}	1.5	1.4	White	30.9^{b}	3.03^{def}
FOFIFA3730	GEN8	130.5^{e}	88.5^{def}	93.1^{abc}	1.6	1.3	White	30.4^{b}	3.01^{ef}
WAB189-B-B-B-8-HB	GEN9	127.7^{f}	87.8^{ef}	96.8^{a}	1.0	1.o	White	32.3^{a}	3.69^{abc}
IAC164 (Check)	GEN10	135.9^{d}	90.5^{cdef}	92.1^{abc}	2.0	2.4	Red	23.8^{g}	3.63^{abc}
TGR42	GEN11	132.0^{e}	94.1^{bcd}	89.2^{cd}	1.8	2.0	Red	28.2^{cde}	3.09^{def}
AD03	GEN12	133.1^{e}	96.1^{bc}	93.7^{abc}	2	2.5	Red	27.8^{de}	3.96^{ab}
AURAT17	GEN13	132.1^{e}	105.0^{a}	92.1^{abc}	1.5	1.5	Red	28.3^{cde}	4.07^{a}
AURAT05	GEN14	131.6^{e}	103.4^{a}	93.5^{abc}	2.1	2.5	Red	28.1^{de}	3.55^{abcd}
AURAT7	GEN15	131.6^{e}	97.5^{b}	92.4^{abc}	1.8	2.4	Red	27.7^{de}	3.40^{abcd}
XJIGNA (Check)	GEN16	130.9^{e}	96.3^{bc}	94.3^{ab}	2.0	2.0	White	25.8^{f}	3.29^{cdef}
MEAN		135.5	93.4	91.2	1.6	1.9		28.4	3.26
CV (%)		3.5	10.1	6.3				8.4	25.6
F-test (5%, 1%):									
Genotype (Gen)		*,**	*,**	*,**				*,**	*,**
Environment (Env)		*,**	*,**	*,**				NS	*,**
Gen × Env		*,**	*,**	*,**				*	*,**

*, ** = significant at <0.05 and <0.01 probability levels; NS = non significant; LB = Leaf blast, PB = Panicle blast.

Table 2. Description of experimental locations.

Agroecological character	Locations		
	Woreta	Pawe	Addis Zemen
Latitude	11° 58′ N	11° 9′ N	11° 92′ N
Longitude	37° 41′ E	36°3′E	37° 7′ E
Altitude (masl)	1810	1050	1780
Annual rainfall (mm)	1300	1457	1032
Mean maximum temperature (°C)	27.9	32.75	29.96
Mean minimum temperature (°C)	11.5	17.17	11.31
Soil type	Vertisol	Cambisol	Fluvisol

interaction.

RESULTS AND DISCUSSION

Analysis of variance

Bartlett's test indicated homogenous error variance for the trait yield in each of eight environments and allowed to proceed further for pooled analysis across environment. The combined analysis of variance is presented in Table 4. Genotype (G), environment (E) and genotype × environment interaction (GEI) were significant ($P \leq 0.01$) for grain yield. Such statistical interaction resulted from the changes in the relative ranking of the genotypes from one environment to another. The significant genotype × environment interaction effects demonstrated that genotypes responded differently to the

Table 3. Annual rainfall received and its monthly distribution in the experimental locations.

Location	Annual rainfall (mm)*	Distribution by month											
		Jan	Feb	Mar	Apr	May	June	July	Aug	Sept	Oct	Nov	Dec
Woreta	1300	0	0	0	0	0	110	580	440	120	50	0	0
Addis Zemen	1032	0	0	0	0	0	87	455	350	105	35	0	0
Pawe	1457	0	0	0	0	57	170	600	450	130	50	0	0

***** Mean of 10 years

Table 4. Combined analysis of variance of grain yield for 16 lowland rice genotypes evaluated at eight environments in 2006 to 2008.

Source	DF	SS	MS	Explained SS (%)
Total	383	888.278		
Replications	2	0.147		
Environments (E)	7	302.819	43.259**	34.09
Genotypes (G)	15	93.441	6.229**	10.52
G*E	105	309.091	2.943**	34.78
Error	254	182.850	0.719	

** Significant at P ≤ 0.01 probability level; DF = degree of freedom; SS = sum of square; MS =mean square.

Table 5. Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield of 16 lowland rice genotypes across 8 environments.

Source	DF	SS	MS	Explained SS (%)
Genotype(G)	15	30.94	2.06**	12.79
Environment(E)	7	101.63	14.52**	42.02
G × E	105	109.28	1.04**	45.19
IPCA1	21	42.64	2.03**	39.01
IPCA2	19	31.99	1.68**	29.27
IPCA3	17	15.99	0.94**	14.62
IPCA4	15	9.43	0.63*	8.63
G × E residual	33	9.23		8.44
Total	127	241.85		

*, ** Significant at P ≤ 0.05 and P ≤ 0.01 probability level, respectively.

variation in environmental conditions of location which indicated the necessity of testing rice varieties at multiple locations. This also shows the difficulties encountered by breeders in selecting new varieties for release. The factors explained (%) show that rice grain yield was affected by environment (34.09%), genotype (10.52%) and their interaction (34.78%). The mean grain yield of the 16 genotypes ranged from 1.96 to 4.07 t ha^{-1}. And, the highest grain yield was obtained from genotypes GEN13, GEN12 and GEN9 (Table 1).

AMMI analysis

The AMMI analysis of variance for lowland rice grain yield (t ha^{-1}) of 16 genotypes tested in eight environments showed that 42.02% of the total sum of squares was attributed to environmental effects, only 12.9% to genotypic effects and 45.19% to genotype × environment interaction effects (Table 5). The environments were diverse and caused the greatest variation in grain yield. The genotype × environment interaction sum of squares was about 3.5 times larger than that for genotypes, which determined substantial differences in genotypic response across environments.

The presence of GEI was clearly demonstrated by the AMMI model, when the interaction was partitioned among the first four interaction principal component axis (IPCA) as they were significant P = 0.01 in a postdictive assessment. The IPCA1 explained 39.01% of the interaction

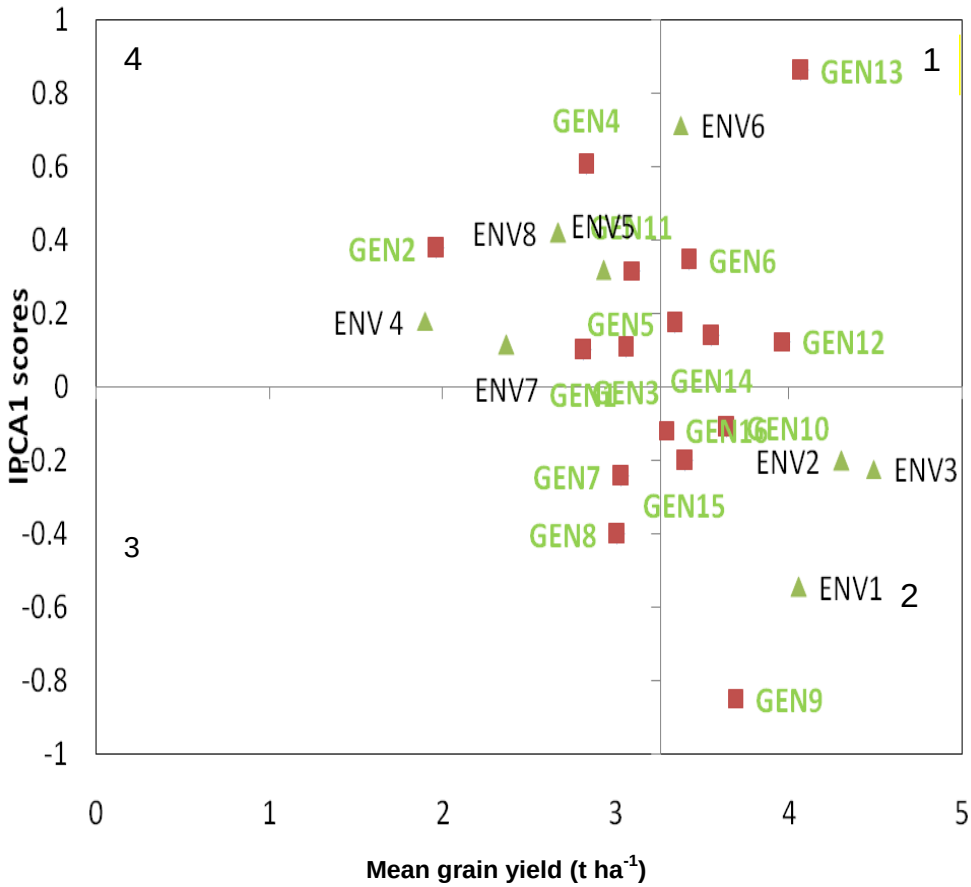

Figure 1. AMMI biplot of 16 rice genotypes and eight environments for grain yield (t ha^{-1}) using genotypic and environmental scores.

sum of squares in 21% of the interaction degree of freedom (DF). Similarly, the second, third and fourth principal component axis (IPCA 2-4) explained a further 29.27, 14.62 and 8.63% of the GEI sum of square, respectively (Table 5). They cumulatively captured 91.13% of the total GEI using 72 DF. This implied that the interaction of the 16 rice genotypes with eight environments was predicted by the first four components of genotypes and environments, which is in agreement with the recommendation of Sivapalan et al. (2000). However, this contradicted the findings of Gauch and Zobel (1996) which recommended that the most accurate model for AMMI can be predicted using the first two IPCAs. These results indicate that the number of terms to be included in an AMMI model cannot be specified a prior without first trying AMMI predictive assessment (Kaya et al., 2002). In general, factors like type of crop, diversity of the germplasm and range of environmental conditions will affect the degree of complexity of the best predictive model (Crossa et al., 1990).

The AMMI analysis provided a biplot (Figure 1) of main effects and the first principal component scores of interaction (IPCA1) of both genotypes and environments. The differences among genotypes in terms of direction and magnitude along the X-axis (yield) and Y-axis (IPCA1 scores) are important. In the biplot display, genotypes or environments that appear almost on a perpendicular line of a graph had similar mean yields and those that fall almost on a horizontal line had similar interactions (Crossa et al., 1990). Thus, the relative variability due to environments was greater than that due to genotypic differences. Genotypes or environments on the right side of the midpoint of the perpendicular line have higher yields than those on the left side. As a result, genotypes including GEN13, GEN12, GEN9, GEN10, GEN14 and GEN6 were generally high yielding (4.07, 3.96, 3.69, 3.64, 3.55 and 3.42 t/ha, respectively) (Figure 1). In contrast, GEN2, GEN1 and GEN4 were generally low yielding genotypes. Environments ENV1, ENV2 and ENV3 and to some extent ENV6 were always on the right hand side of the midpoint of the main effect axis, seemed to be favorable environments, while ENV4 and ENV5 were generally less favorable environments.

Genotypes or environments with large negative or positive IPCA scores have high interactions, while those with IPCA1 scores near zero (close to horizontal line) have little interaction across environments and vice versa for environments (Crossa et al., 1990) and are considered

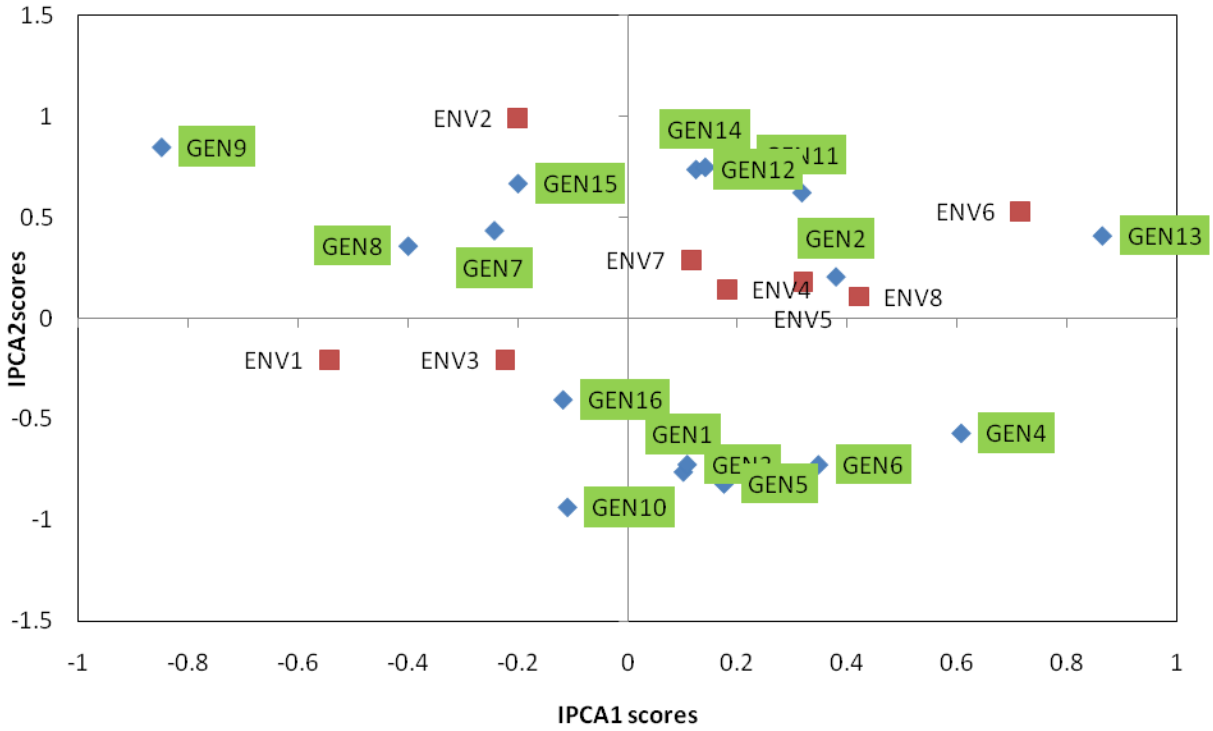

Figure 2. Biplot of the second interaction principal component axis (IPCA2) against the first interaction principal component axis (IPCA1) scores for grain yield of 16 lowland rice genotypes in eight environments.

more stable than those further away from the line. In the biplot, genotypes GEN13, GEN12, GEN10 and GEN9 were vertically distant apart; however, they did not fall close to the horizontal line. This implies that these genotypes lack stability but had high yield potential in favorable environments.

Since, IPCA2 scores were also important (29.27% of G × E SS) in explaining genotype × environment interaction, the ballot of the first two IPCAs was also used to demonstrate the relative magnitude of the GEI for specific genotypes and environments (Figure 2). The IPCA scores of genotypes in the AMMI analysis is an indication of stability or adaptation over environments (Gauch and Zobel, 1996). The greater the IPCA scores, the more specifically adapted is a genotype to certain environments (Sanni et al., 2009). The more the IPCA scores approximate to zero, the more stable or adapted the genotype is over all the environments sampled. The biplot of the first two IPCA does not show the best adapted genotype and/or genotypes to most environments. However, GEN13 and GEN12 were well adapted to high yielding environment of ENV6 while GEN9 and GEN15 were well adapted to high yielding environment of ENV2. The varieties used as check (GEN10 and GEN16) were found to be well adapted to the high yielding environments of ENV1 and ENV3.

In Figure 2, the environments fell into three sections: the best genotypes with respect to ENV1, ENV2 and ENV3 were GEN10, GEN16, GEN9, GEN7, GEN8 and GEN15. Genotypes, GEN14, GEN12, GEN1, GEN2, and GEN13 were best for ENV4, ENV5, ENV6, ENV7 and ENV8. On the other hand, genotypes GEN4, GEN1, GEN3, GEN5 and GEN6 were not found to be fit to any of the testing locations. Considering the environments tested in this study, no single location had both IPCA 1 and IPCA2 scores close to zero line. This indicates that all the environments had potential for large GEI.

Conclusion

The AMMI statistical model has shown that the largest proportion of the total variation in grain yield was attributed to environments in this trial. As a result, almost all of the evaluated genotypes were affected by the genotype × environment interaction effects, so that no genotype had superior performance in all environments. Most of the genotypes showed environment specificity. In this study, the AMMI model classified the testing environments into three sections. Accordingly, six of the tested genotypes were found to be best for environments ENV1, ENV2 and ENV3; while the other six genotypes were found best for environments ENV4, ENV5, ENV6, ENV7 and ENV8. However, four of the tested genotypes were not found best to any of the testing environments. As a breeding strategy, it is be better to execute national variety trials at a number of locations in different regions of the country. So that it would be possible to cluster the

testing locations into homogenous groups to be used for breeding for specific adaptation and/or for broad adaptation. Among the tested genotypes included in this study, three genotypes were selected and promoted to verification based on their performance for grain yield and other agronomic traits including earliness, medium to tall height, high spikelet fertility percentage, white seed color, big seed size, better disease reaction and farmers' preferences. Of which, genotype, GEN9 has been officially released by the national variety release committee with the vernacular name "EDGET'' meaning development for large scale production.

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