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Research paper

Stability analysis of lowland rice genotypes in rain-fed environments of Northwest Ethiopia

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Seventeen medium-maturing lowland rice genotypes along with a check variety were raised in a randomized complete block design of three replications and assessed for yield stability and performance under rain fed lowland conditions at Woreta, Pawe, Maitsebri, Jimma and Assosa. AMMI analysis of variance indicated that environments, genotypes and their interaction accounted for 43.06%, 12.03% and 22.04% of the total sum of squares (SS) for grain yield, respectively. The first four interaction principal component axes were significant and together explained 85.8% of interactions SS. Averaged over environments, genotype G16 had the highest yield of 6.56 t ha^{-1} , G2 (6.32 t ha^{-1}), G6 (5.49 t ha^{-1}) and G7 (5.49 t ha^{-}). Genotypes G5, G6, G7, G14 and G16 had lower AMMI stability value and yield stability index. In AMMI 1 and AMMI 2 biplots G6, G7 and G16 were found to be high yielding and stable while G2 was less stable but high yielding. Thus, genotypes G2, G6 and G16 were considered as candidate varieties and verified, out of which G16 was approved for release by the name 'Abay'. Genotypes G2, G6, and G7can be used as potential parent materials in rice breeding program.

Key words: *lowland rice, GE interaction, AMMI analysis, grain yield*

INTRODUCTION

Rice (*Oryza sativa* L.) is an economically and culturally important crop supporting more than half the world's population (Barker *et al.*, 1985). Its consumption is growing faster than any other food crops in Africa and it is also a cash crop providing employment in more than 40 African countries (AfricaRice, 2017). In Ethiopia, rice is one of the most important strategic food security crops and it becomes the source of income and employment along the value chain. The crop is predominantly cultivated by small scale farmers. Currently, private investors also showed great interest in rice business probably due to policy changes and huge local as well as international market opportunity. A rapid shift in food habit for rice consumption has sharply increased the demand for the grain in most regions of the country. Rice is used as food in a variety of forms, including *injera* a flat and thin bread, bread, local drinks (*tella* and *areki*), porridge, *kinche,* cakes, and as table rice. In addition, by-products such as husk used for fuel, charcoal making and soil amendment; rice bran for beef fattening and poultry feed; and rice straw as major source of animal feed. In the last ten years (2011 to 2020) only, rice cultivation in Ethiopia has significantly increased in area, total production and productivity by 178.3%, 202.7% and 26%, respectively(CSA, 2011; CSA, 2020). Increases were recorded in all rice producing regions of the country but the lions share comes from Amhara region which contributed about 63% of annual production (CSA, 2020). Currently, total annual production and productivity have reached about 268,223 thousand tons and 3.15 t ha^{-1}, respectively, covering 85,288.87ha of land cultivated by 230,496 rice farmers (CSA, 2020). Current production systems comprise predominantly of rainfed lowlands and uplands, with minor contribution from irrigated rice. Despite an increase in area expansion and domestic production of rice, it is not yet able to address local demands and thus, rice import tended to rise drastically. Every year, the government invests huge amount of foreign currency to import milled rice (Addis *et al.*, 2018).

On the other hand, the rapid area expansion and the presence of untapped highly suitable land for rice cultivation; about 5million ha for rain fed and 3 million ha for irrigated rice (MoARD, 2010) shades a light of hope that the coming years will be brighter than the previous. Because of the expansion of the crop in diverse environmental conditions, relative performance of the rice varieties exhibited variation as they are evaluated at different sites over years. The variations in the performance of varieties are attributed to the effects of genotype by environment (GE) interaction (Falconer and Mackay, 1996). This type of interaction reduces selection efficiency and the accuracy of new variety recommendation (Crossa and Cornelius, 1997). Several statistical methods are used to minimize the effect of the GE interaction on the selection of cultivars and the prediction of the phenotypic response to diverse environments. The additive main effect and multiplicative interaction (AMMI) method which integrates analysis of variance (ANOVA) and principal component analysis (PCA) into a unified approach is one of the most important statistical tools to analyze multi-environment trials (Zobel *et al.*, 1988; Crossa *et al.*, 1990; Gauch and Zobel, 1996). AMMI analysis of variance enables us study the main effects of genotypes and environments and, a principal component analysis for the residual multiplicative interaction among genotypes and environments. Furthermore, AMMI quantifies the contribution of each genotype and environment to the sum of squares, and provides an easy graphical interpretation of the results by the biplot technique to concurrently classify genotypes and environments (Zobel *et al.*, 1988). Therefore, with this technique, one can readily identify productive cultivars with wide or narrow adaptability, as well as identify mega-environments in which to conduct field trials (Gauch and Zobel, 1996; Ferreira *et al.*, 2006). The objective of this study was to study stability and performance of medium maturing lowland rice genotypes in diverse environments based on the AMMI method.

MATERIALS AND METHODS

This experiment was conducted at Woreta, Pawe, Maitsebri, Assosa, and Jimma from 2013 to 2015. Including one check (Gumara), a total of 18 lowland medium maturing rice genotypes (Table 1) were evaluated for grain yield. At each location, the experiment was laid out using a randomized complete block design of three replications. Seeds of each genotype were hand drilled at the rate of 60 kg ha^{-1} in a plot size of 7.5m^2, with a spacing of 20cm between rows. Each experimental plot was with six rows of 5m long each. Fertilizers (Urea and DAP) were applied as per to local recommendations. DAP was applied all at planting while Urea was used in three splits. Other crop management and protection practices were applied to the entire experimental area uniformly when necessary. Two border rows were excluded in data collection and grain yield per plot data were collected by harvesting the entire central four rows and estimated based on adjustment at 14% moisture level and converted to ton ha^{-1}.

The grain yield data for eighteen rice genotypes at twelve environments were subjected to analysis of variance using the General Linear Model (PROC GLM) of the SAS Procedure version 9.0 of the SAS software (SAS 2002) to determine significant variation among genotypes and environments and their interaction. Mean performance of different traits were separated using Least Significant Difference (LSD) method at 0.05 level of probability. Additive main effects and multiplicative interaction (AMMI) model was applied to assess the effect of genotype by environment interaction, adaptability and stability of rice genotypes using GenStat 16th version statistical package (GenStat, 2013). In this study, AMMI stability value (ASV) was estimated for each genotype according to the relative contributions of the principal component axis scores (IPCA1 and IPCA2) to the interaction sum of squares according to Purchase *et al.* (2000) as described below:

$$\mathrm{ASV}=\sqrt{\left[\frac{\mathrm{SSIPCA1}}{\mathrm{SSIPCA2}}\,(\mathrm{IPCA1Score})\right]2+(\mathrm{IPCA2Score})2}$$

Where, ASV= AMMI stability value; SS= sum of square; IPCA1 and IPCA2= the first and the second interaction principal component axes, respectively.

Table 1. Description of 18 rice genotypes evaluated at twelve environments over three years

No.	Genotypes	Code	Source
1	WAS 161-B-6-B-B-1-B (NERICA-L-38)	G1	Africa Rice
2	WAB 326-B-B-7-H1	G2	Africa Rice
3	IR 83372-B-B-115-4	G3	IRRI
4	IR 83377-B-B-93-3	G4	IRRI
5	IR 83383-B-B-141-2	G5	IRRI
6	IR 83372-B-B-115-3	G6	IRRI
7	IR 83383-B-B-141-1	G7	IRRI
8	IR80420-B-22-2	G8	IRRI
9	IR80463-B-39-3	G9	IRRI
10	IR 72768-8-1-1	G10	IRRI
11	IR 75518-18-1-2-B	G11	IRRI
12	IR 75518-84-1-1-B	G12	IRRI
13	YUNLU N0.33	G13	IRRI
14	IR 81047-B-106-2-4	G14	IRRI
15	WAS 161-B-6-B-1 (NERICA-L-36)	G15	Africa Rice
16	ARCCU16Bar-21-5-12-3-1-2-1	G16	Africa Rice
17	ARCCU16Bar-13-2-16-2-1-1	G17	Africa Rice
18	GUMARA (check)	G18	Ethiopia

The larger the IPCA score is, either negative or positive, the more adapted a genotype is to a certain environment. Smaller ASV scores indicate a more stable genotype across environments (Purchase *et al.*, 2000; Farshadfar *et al.*, 2011). Yield stability index (YSI) was also estimated using the sum of the ranking based on yield and ranking based on the AMMI stability value i.e YSI= RASV+RY, where RASV is the rank of the genotypes based on the AMMI stability value; RY is the rank of the genotypes based on yield across environments (Tumuhimbise *et al*., 2014) and low values of YSI show desirable genotypes with high mean grain yield and stability.

RESULTS AND DISCUSSION

Variation and mean performance

The combined analysis of variance revealed significant variation among genotypes, environments and genotype by environment (GE) interaction for mean grain yield of 18 lowland rice genotypes (Table 3). The relative contribution of environment, genotype, and GE interaction indicated that environment was the most important source of variation for grain yield performance. Environment explained 43.05% of total sum of square (SS) of grain yield while GE interaction accounted for 22.05% and the least was by the genotype (12.03%) (Table 3). This large yield variation explained by environments indicated that the environments were diverse and the major part of variation in grain yield could be attributed to environmental changes. Similarly, Zemede and Mekbib (2021) reported highly significant variations among genotypes, environments and their interactions on grain yield and the largest variation was accounted by environments (60.6%), followed by GEI (20.6%) and then genotypes (18.2%). In contrary to our report, Bose *et al.* (2014) and Akter *et al.* (2014) found out that larger portion of variation in grain yield was attributed to the genotypes, followed by GE interaction and the least to the environments. In the other hand, Sharifi *et al.* (2017) reported that 41% of the total sum of squares was explained by GE interaction effects, environmental effects (29%), and genotype effects (30%) using nine promising rice genotypes. Similarly, Huang *et al.* (2021) reported that the highest variation in grain yield of rice genotypes was attributed to GE interaction (37.1%), followed by genotype (35.6%) and environments (16.5%). They further explained that the significances variation by GE interaction effect revealed that the genotypes had variable performance in the tested environments, i.e., a change in the average rank of the genotypes was observed among the environments which suggested running a more refined analysis to understand the magnitude and pattern of GE interaction.

Table 4 presented the mean grain yield performance of 18 lowland rice genotype including one improved lowland rice variety as a check (Gumara) evaluated at Woreta, Maitsebri, Jimma, Pawe and Assosa from 2013 to 2015 during the main cropping seasons (May to November). The mean grain yield of rice genotypes averaged over environments indicated that G16 and G17 had the highest (6.56 t ha^{-1}) and the lowest (4.21 t ha^{-1}) mean grain yield, respectively, with grand mean yield of 5.07 t ha^{-1} (Table 4). Across all environments, mean grain yield performance of G18 (check variety) was 4.64 t ha^{-1}. Except for G12 (4.41 t ha^{-1}) and G17 (4.21 t ha^{-1}), mean grain yield of all genotypes across environments was higher than the check variety (Table 4). However, only two genotypes, G2 (6.32 t ha^{-1}) and G16 (6.56 tha^{-1}) were significantly higher than the check variety in terms of mean grain yield, with grain yield advantage of 41.4% and 36.2%, respectively. Although not significant, two other genotypes, G6 (5.49t ha^{-1}) and G7 (5.49t ha^{-1}) also gave appreciably higher mean yield over the check variety with yield advantage of 18.3% (Table 4). Considering the environment, the mean yield of environments across genotypes ranged from 3.03 t ha^{-1} at E1 to 7.45 t ha at E8. Furthermore, E8 and E9 were the highest yielding environments with mean yield of 7.45 t ha^{-1} and 6.26 t ha^{-1},

Table 2. Description of the test locations in North West Ethiopia

Location	Latitude	longitude	Elevation (m a.s.l)	Rain fall (mm)	Mean temperature (°C)	
					Min	Max
Woreta	11° 58' N	37° 41' E	1810	1300	11.5	27.9
Pawe	11° 19′ 15″N	36° 24′ 30″E	1091	1457	17.2	32.8
Maitsebri	11° 08′ N	38° 08′ E	1350	1296	15.0	36
Jimma	7° 46' N	36° 00' E	1753	1561	9.0	28
Assosa	10° 03’N	34° 59’E	1590	1132	14.4	28.9

a.s.l: above sea level, mm: millimeter.

Table 3. Combined ANOVA for grain yield (t ha^{-1}) of 18 lowland rice genotypes at twelve environments from 2013 to 2015 main cropping season

Source of variation	DF	SS	MS	F value	%TSS
Genotype (G)	17	219.403842	12.9061084	13.33***	12.03
Environment (E)	11	784.955224	71.3595658	73.68***	43.05
G x E	187	402.101332	2.1502745	2.22***	22.05
Error	430	416.479377	0.968557		
Total	647	1823.1892			

DF: degree of freedom, SS: sum of square, MS: mean square, %TSS: total sum of square explained in percentage respectively, whereas E1and E10 were found to be the lowest yielding environments, with mean yield of 3.03t ha^{-1} and 3.80 t ha^{-1}, respectively (Table 4). Genotype G16 performed the best in mean yield at ten of the twelve of environments; E1, E2, E4, E5, E6, E7, E9, E10, E11and E12. Similarly, other better performing genotypes include G6 at E3, E4 and E11; G7 at E3, E9 and E12, and G8 at E1, E3 and E8, each ranked among the top three at three of the twelve environments (Table 4).

Table 4. Mean grain yield of 18 medium maturing lowland rice genotypes at 12 environments

Genotype	Environments^a												
	E1	**E2**	**E3**	**E4**	**E5**	**E6**	**E7**	**E8**	**E9**	**E10**	**E11**	**E12**	**Mean**
G1	2.73	4.89	4.59	5.92	3.90	5.69	6.14	6.51	6.80	2.57	4.12	5.02	4.91
G2	5.86	6.32	6.15	6.42	6.19	6.14	6.40	6.17	6.99	5.49	6.40	7.35	6.32
G3	2.30	5.44	6.17	2.04	4.59	5.24	2.45	7.88	5.71	4.08	4.60	4.21	4.56
G4	3.31	6.88	5.52	4.93	5.22	6.16	4.38	7.14	6.59	3.09	2.49	3.95	4.97
G5	2.39	5.32	5.76	5.26	4.67	6.12	4.76	7.50	6.21	3.66	4.53	4.92	5.09
G6	2.32	6.22	6.39	6.73	3.91	5.31	5.83	8.41	5.84	3.86	5.27	5.74	5.49
G7	2.29	5.78	6.27	6.21	4.03	5.69	4.88	8.40	7.67	3.95	4.33	6.38	5.49
G8	4.53	6.45	6.24	3.77	4.21	6.04	3.18	8.61	6.65	4.01	4.45	4.56	5.22
G9	2.63	6.93	5.16	3.50	4.31	6.41	3.33	8.81	7.16	3.60	4.06	5.00	5.08
G10	2.20	5.12	4.95	4.93	3.59	6.05	5.86	5.33	6.70	4.01	3.84	5.93	4.88
G11	2.59	5.05	5.03	4.95	4.73	6.60	3.97	7.39	6.45	3.35	3.31	4.49	4.83
G12	2.81	4.26	5.99	3.77	4.14	5.60	2.34	7.37	4.58	3.84	4.48	3.78	4.41
G13	2.64	5.78	4.79	5.66	4.12	4.30	5.66	7.38	6.24	3.80	4.05	4.14	4.88
G14	2.51	5.33	4.91	5.30	4.20	5.41	4.63	8.16	7.21	3.60	4.20	3.92	4.95
G15	2.14	4.92	4.54	5.80	4.04	5.24	5.53	6.27	6.30	2.80	3.27	5.44	4.69
G16	5.57	6.67	6.22	7.40	6.15	6.29	6.42	8.47	7.20	5.23	6.39	6.66	6.56
G17	3.14	4.04	4.20	4.58	4.76	4.82	3.83	5.70	4.98	2.95	3.99	3.57	4.21
G18	2.51	4.66	4.81	6.51	4.28	3.61	3.64	8.62	3.31	4.43	5.20	4.07	4.64
Mean	**3.03**	**5.56**	**5.43**	**5.20**	**4.50**	**5.60**	**4.62**	**7.45**	**6.26**	**3.80**	**4.39**	**4.95**	**5.07**
CV (%)	**36.41**	**12.52**	**17.87**	**25.24**	**14.06**	**9.90**	**18.33**	**18.47**	**13.19**	**21.04**	**24.70**	**21.10**	**19.40**
LSD (5%)	**1.83**	**1.16**	**1.61**	**2.18**	**1.05**	**0.92**	**1.41**	**2.28**	**1.37**	**1.32**	**1.80**	**1.73**	**1.56**

^{a}E1: Woreta 2013, E2: Maitsebri 2013, E3: Woreta 2014, E4: Jimma 2014, E5: Maitsebri 2014, E6: Pawe 2014, E7: Assosa 2014, E8: Woreta 2015, E9: Pawe 2015, E10: Maitseberi 2015, E11: Jimma 2015, E12: Assosa 2015. Underlined figures indicate the top three high yielding genotypes at each environment.

Table 5. AMMI analysis of variance for grain yield in 18 lowland rice genotypes

Source	DF	SS	MS	%TSS	%G x ESS
Total	647	1823.2	2.818		
Treatments	215	1406.5	6.542**	77.14	
Genotypes	17	219.4	12.906**	12.03	
Environments	11	785	71.36**	43.06	
Interactions	187	402.1	2.15**	22.04	
IPCA 1	27	151.2	5.6**		37.60
IPCA 2	25	94.1	3.765**		23.40
IPCA 3	23	66.1	2.874**		16.44
IPCA 4	21	33.6	1.599*		8.36
IPCA 5	19	18.7	0.985ns		4.65
IPCA 6	17	11.7	0.688ns		2.91
Residuals	27	9.7	0.36		2.41
Error	408	383.2	0.939	21.02	

DF: degree of freedom, SS: sum of square, MS: mean square, ns: not significant, TSS: total sum square, G x ESS: genotype by

Moreover, G2 gave the best mean yield at six of twelve environments; E1, E5, E7, E10, E11and E12 (Table 4). Even the check variety (G18) was found to be one of top three high yielding genotypes at three environments namely E4, E8 and E10. However, genotypes including G3, G5, G10, G12, G13, G15 and G17 could not rank among the top three genotypes in any of the environments. Results demonstrated that there was a rank change of genotypes in mean yield across environments which could be attributed to the seasonal variability. For instance, the mean grain yield across 18 genotypes at Woreta was the least in 2013(3.03 t ha^{-1}) but the highest in 2015 (7.45 t ha^{-1}). Fogera (Woreta) area often experience terminal moisture stress which affected rice grain yield in 2013 but the conditions in 2014 and 2015 cropping seasons was relatively favorable. This change of ranks in mean yield of genotypes indicated the presence of cross over GE interaction across environments which need further investigation to understand the patterns of GE interactions (Sharifi *et al*., 2017; Huang *et al*., 2021; Akbarzai *et al*., 2021; Ohunakin, 2021).

AMMI analysis of variance

To clarify the patterns of GE interaction, the AMMI analysis of variance was applied for mean grain yield of rice genotypes.

The analysis revealed that variances due to genotypes, environments, and GE interactions were significant (P<0.01). The results also showed that the main effects of genotype and environment accounted for 12.03% and 43.06% of the total sum of square, respectively, and the GE interaction effect accounted for 22.04% of the total sum of squares for grain yield (Table 5). The large sum of squares for the environments indicates that the environments were diverse and much of the variation for grain of genotypes was attributed to the environment which is in agreement with the findings of Lakew *et al*. (2017), Akbarzai *et al*. (2021) and Ohunakin (2021). Unlike our result, Bose *et al*. (2014) and Akter *et al*. (2014) reported that significant variation in grain yield was attributed to the genotypes, followed by GE interaction and the least to the environments. In this study, the total of sum of square explained by the GE interaction was much smaller than that of the environment but larger than that explained by the genotype main effect revealing that contribution of the environments to the interaction was greater and genotypes responded differentially across diverse environmental conditions. This phenomenon most frequently affects progress in breeding as it limits the association between the phenotype and genotypic values of genotypes under investigation (Yan, 2002). The GE interaction as clearly demonstrated by the AMMI model, was further partitioned among the first four significant interaction principal component axes (IPCA1 to IPCA4) and together explained 85.80% of the total GE interaction sum of squares (Table 5). Moreover, though not significant, the fifth and sixth interaction principal component axes (IPCA5 and IPCA6) together further explained 7.56% of GE interaction sum of squares. The IPCA1 alone explained 37.60% of the GE interaction sum of squares. Similarly, the second, third and fourth principal component axes (IPCA2 to IPCA4) explained 23.40%, 16.44% and 8.36% of the GE interaction sum of squares, respectively (Table 5). As it was clearly demonstrated, the interaction of the 18 lowland rice genotypes with twelve environments was predicted by the first four significant components of genotypes and environments, which is in agreement with the reports of Sivapalan *et al*. (2000) and Huang *et al*. (2021) but in contrary to the findings of Gauch and Zobel (1996) which recommended that the most accurate model for AMMI can be predicted using the first two IPCAs.

AMMI stability analysis

The IPCA1 scores and other stability parameters values along with mean grain yield of 18 rice genotype are presented in Table 6. As explained by (Bose *et al*., 2014; Akter *et al*., 2015; Shafiri *et al*., 2017; Lingaiah *et al*.,2020; Huang *et al*., 2021), genotypes with smaller IPCA1 scores are assumed to be more stable than those with larger scores. Accordingly, G5 was the most stable genotype, followed by G7, G11, G14, G17 and G18 as they had smaller IPCA1 score and ranked as the first six more stable genotypes indicating that these genotypes have stable performance over twelve environments while G1, G3, G8, G9 and G10 were the most unstable genotypes. AMMI stability value (ASV) also showed that G5 had the lowest score and thus most stable genotype which is in agreement with the explanations of Purchase *et al*. (2000) who proposed that a genotype with the least ASV score is the most stable. However, mean grain yield performances of stable genotypes were lower than the three high yielding genotypes (G2, G6 and G16) (Table 6). As reported by Mohammadi et al. (2007) and Mohammadi and Amri (2008), stable genotypes don't necessary give higher yield, and hence genotype selection should consider both high mean yield and stability. In this regard, yield stability index (YSI) which combines ranks based on mean yield and ASV should be considered to determine the stability of the genotypes with high mean grain yield (Tumuhimbise *et al*., 2014). Accordingly, G4, G5, G7, G14 and G16 had the lowest YSI values compared to the other genotypes and thus considered as stable and high yielding genotypes. Therefore, G6, G7, and G16 were the stable and high yielder genotypes across the testing environments (Table 6).

Table 6. Ranking of 18 lowland rice genotypes based on mean grain yield and AMMI stability parameters

Genotype	Gm	Rank	IPCAg[1]	Rank	ASV	Rank	YSI	Rank
G1	4.908	10	-0.8423	15	1.4055	13	23	13
G2	6.324	2	-0.6682	11	1.1225	10	12	6
G3	4.559	16	1.2651	18	2.0328	18	34	18
G4	4.971	8	0.2313	7	0.7897	8	16	7
G5	5.093	6	0.0025	1	0.066	1	7	2
G6	5.486	4	-0.3537	8	0.6895	7	11	4
G7	5.489	3	-0.1404	4	0.3801	3	6	1
G8	5.225	5	1.0129	17	1.6333	16	21	10
G9	5.075	7	0.9132	16	1.6106	15	22	11
G10	4.876	12	-0.7592	12	1.3629	12	24	14
G11	4.826	13	0.1643	5	0.505	5	18	9
G12	4.413	17	0.8270	14	1.4261	14	31	16
G13	4.88	11	-0.4070	10	0.6658	6	17	8
G14	4.948	9	0.0680	3	0.2265	2	11	5
G15	4.691	14	-0.7972	13	1.3312	11	25	15
G16	6.556	1	-0.3980	9	0.8051	9	10	3
G17	4.213	18	-0.1738	6	0.4175	4	22	12
G18	4.638	15	0.0555	2	1.6788	17	32	17

Gm: genotype mean for grain yield, IPCAg[1]: the first multiplicative interaction principal component axis for genotypes, ASV: AMMI stability value and YSI: Yield stability index

AMMI biplot analysis

Yield data from multi-environment trials (MET), are usually quite large, and it is difficult to grasp the general pattern of the data without some kind of graphical presentation (Yan, 2000). The biplot technique as first reported by Gabriel (1971) provides a powerful solution to this problem. Biplot analysis is the most powerful interpretive tool for AMMI model (Mahalingam *et al*., 2006; Akter *et al*., 2014). B iplots are graphs where both genotypes and environments are plotted on the same axis so that the inter-relationships can be visualized. There are two basic AMMI biplots, the AMMI 1 biplot where the main effects (genotype mean and environment mean) and IPCA1 scores for both genotypes and environments are plotted against each other, whereas in the second biplot (AMMI 2 biplot) scores for IPCA1 is plotted against scores of IPCA2.

AMMI 1 biplot

As illustrated in Figure 1, AMMI 1 biplot showed the main effects of eighteen rice genotypes and twelve environments (the x-coordinate) plotted against the interaction effects (the y-coordinate). In the biplot, genotypes that group together have similar adaptation while environments which group together influences the genotypes in the same manner (Gauch *et al*., 1996). Genotypes G2, G6, G7, G8, and G16 had above average yield and these genotypes adapted to favorable environments, while genotypes G1, G3, G10, G11, G12, G13, G15, and G17 adapted to poor environments with grain yields of below the average (Figure 1). Four genotypes G4, G5, G9, and G14 exhibited intermediate mean yield, relatively similar to the check variety (G18), but they varied in stability. Mean grain yield values of either genotypes or environments closer to the origin of the interaction effect axis (IPCA1) provide a smaller contribution to the interaction than those that are further away. This result demonstrated that genotypes G4, G5, G7, G11, G14, and G18 showed greater stability. However, their average grain yields were among the lowest, and, therefore, these genotypes could not be recommended. On the other hand, the genotypes G1, G3, G8, G9 and G10 were the most unstable, with averages close to the overall average (Figure 1). Among tested genotypes, G16 and G2 had the highest mean yield and it appears that G16 was more stable than G2.

The genotypes G6 and G7 were also the next high yielding (> 5.5 t ha^{-1}) and both were relatively stable (Figure 1). Hence, genotype G2 was identified as specially adapted genotype while G6, G7 and G16 showed relatively wider adaptation across mentioned environments, with G16 being the leading in mean grain yield and stability. According to AMMI 1 biplot, twelve environments exhibited wider variation in main effects performance and in their patterns of interaction (IPCA1). Environments E8 and E9 were the most favorable while E1 and E10 were least favorable environments. On the other hand, majority of the environments were intermediate in performance but different in their contribution to the overall interaction effect (Figure 1).

With regard to the interaction, some of the environments showed close to zero IPCA1 score indicating their small contribution to the interaction effect (E1, E5, E9, E10 and E11) where all the genotypes performed well in these environments. Environments E2, E3, E6, and E12 exhibited an intermediate contribution to the overall interaction effect while a high contribution to the interaction effect was attributed to E4, E7, E8, and E12 (Figure 1). Bose *et al*. (2014), Akter *et al*. (2015), Shafiri *et al*. (2017), Lingaiah *et al*. (2020) and Huang *et al*. (2021) also reported similar pattern of interactions in different rice genotypes.

AMMI 2 biplot

The AMMI 2 biplot was produced using genotype and environmental scores of the first two interaction principal component axis (PC1 and PC2) to determine the interaction pattern of the 18 lowland rice genotypes tested in 12 environments (Figure 2). AMMI 2 biplot clearly demonstrates "which- won-where" pattern and also reveals the sensitivity degree of genotypes to different environments (Li *et al*., 2006). Purchase (1997) explained that the genotypes positioned close to the biplot origin are more stable and thus showed wider adaptation than those which are far from the center of the biplot.

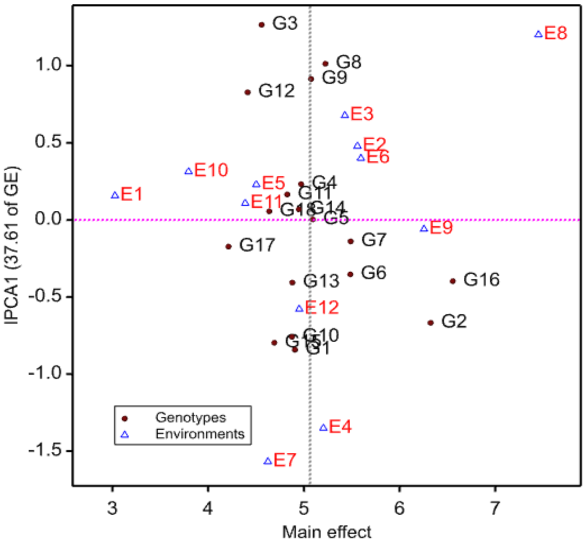

Figure 1. AMMI1 biplot of the first interaction principal component axis against main effects for 18 medium maturing lowland rice genotypes at 12 environments. E1: Woreta 2013, E2: Maitsebri 2013, E3: Woreta 2014, E4: Jimma 2014, E5: Maitsebri 2014, E6: Pawe 2014, E7: Assosa 2014, E8: Woreta 2015, E9: Pawe 2015, E10: Maitseberi 2015, E11: Jimma 2015, E12: Assosa 2015.

Moreover, the genotypes occurring close together on the biplot will tend to have similar yields in all environments, while genotypes far apart may either differ in mean yield or show a different pattern of response over the environments (Akter *et al*., 2014). In the present study, genotypes G5, G6, G13, G14, G16 and G17 were relatively close to the biplot origin and thus, they are more stable genotypes showing wider adaptation over the studied environments, whereas genotypes G2, G11, and G14 showed moderately stable performance.

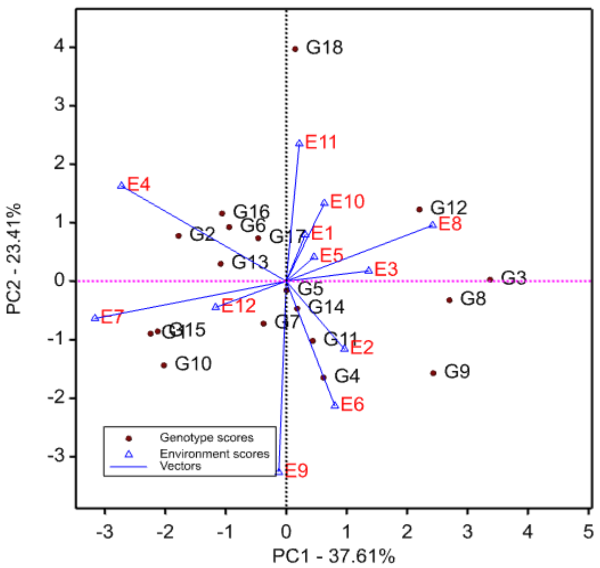

Figure 2. AMMI2 biplot of the first and the second interaction principal component axes for 18 medium maturing lowland rice genotypes at 12 environments in grain yield. E1: Woreta 2013, E2: Maitsebri 2013, E3: Woreta 2014, E4: Jimma 2014, E5: Maitsebri 2014, E6: Pawe 2014, E7: Assosa 2014, E8: Woreta 2015, E9: Pawe 2015, E10: Maitseberi 2015, E11: Jimma 2015, E12: Assosa 2015.

On the other hand, genotypes G1, G4, G8, G9, G10, G12, G15, and G18 were positioned away from the biplot origin indicating their higher interaction to the environments and hence, these genotypes exhibited narrow adaption (Figure 2). The check variety (G18) had a specific adaptation to environments E10 and E11, whereas genotype G12 was adapted to environment E8; genotypes G3 and G8 to environment E3; genotypes G4, G9 and G11 to environments E2 and E6; genotype G2 to environment E4; genotypes G1, G10 and G15 to environment E7. Other associations between genotypes and environments can be seen in Figure 2. Among environments, it appears that environments E1, E2, E3, E5 and E12 were the largest contributors to the phenotypic stability of tested rice genotypes as they were relatively close to the biplot origin. On the other hand, environments E4, E6, E7, E8, E9 and E11 largely contributed to the overall G × E interaction, because they were positioned far from the biplot origin in AMMI 2 graph (Figure 2).

CONCLUSION

Selecting high yielding and stable genotypes is a frequent challenge to breeders as grain yield is one of the quantitative traits most influenced by environmental factors. AMMI statistical model is a great tool to identify stable and high yielding rice genotypes for specific as well as for diverse environments. In the present study, analysis of variance for the AMMI model of grain yield indicated that genotypes, environments, GE interaction and AMMI components were significant. AMMI analysis revealed that the largest proportion of the total variation in grain yield was attributed to testing environments, followed by GE interaction. The mean grain yield of genotypes averaged over environments indicated that G16 had the highest mean yield of 6.56 t ha^{-1} and G17 showed the lowest mean yield of 4.21 t ha^{-1}. Genotype G2 ranked second in mean grain yield (6.32 t ha^{-1}) but tended to be unstable. Genotypes G6 and G7 were the 3rd high yielding and more stable than G2 and G16. Theses high yielding genotypes were also resistant to leaf and panicle blast diseases. The genotypes G4, G5, G6, G7, G11, 14, G16 and G17 were not as such affected by the G x E interaction and thus would perform well across a wide range of environments. It is concluded that among genotypes tested, G2, G6 and G16 were the leading in mean grain yield with yield advantage of 36.2%, 18.3% and 41.4% over the check, G18 (4.64 t ha^{-1}), respectively. Therefore, G2, G6 and G16 were identified as candidate varieties and endorsed for verification for possible release. Subsequently, considering farmers' feedback and evaluation by national variety release technical committee, G16 was recommended for cultivation by the name 'Abay' as improved lowland rice variety in areas of Northwest Ethiopia that require medium maturing lowland rice varieties. The other high yielding and diseases resistant genotypes G2, G5, G6, and G7 can be parental materials in rice breeding programs aiming for high yielding and other traits of interest.

AUTHOR CONTRIBUTIONS

This work was carried out in collaboration between authors. Author Taddesse Lakew planned the project, conducted experiment, collected data and performed statistical analysis and drafted the manuscript. Authors Abebaw, Assaye, Atsedemariam, Mulugeta and Hailemariam conducted experiment and collected data.

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COMPETING INTERESTS

The authors declare that they have no competing interest

ETHICS APPROVAL

Not applicable

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