

Stability and Performance Assessment in 18 Short-Duration Rice Genotypes under Rain Fed Lowland Production Conditions of Ethiopia

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Abstract

In order to identify high yielding and stable short-duration lowland rice genotypes, field experiment was conducted with 18 rice genotypes for three consecutive years (2013-2015) at five locations in a randomized complete block design of three replications. Combined analysis of variance showed highly significant differences for the genotype and environments. The genotype by environment interaction (GEI) was also highly significant indicating differential response of genotypes to environments. The partitioning of total sum of squares exhibited that the GEI effect was a predominant source of variation (34.44%), followed by the environment and genotype effects of 24.3% and 19.04%, respectively. The GEI effect was nearly two times higher than that of the genotype effect, suggesting the presence of different environment groups. In the AMMI analysis, the first six interaction principal component axes (IPCA1 to IPCA6) were highly significant and together explained 92.18% of interaction sum of squares. AMMI stability value (ASV) discriminated genotypes G17, G16 and G8 as the stable genotypes. But, based on the yield stability index (YSI), the most stable genotypes with high grain yield were genotypes G16 and G11. AMMI1 and GGE biplots also recommended G16 and G11 as stable and high yielding genotypes, whereas G2 as unstable but high yielding. Thus, genotypes G16 and G11 could be released for wider adaptation while genotype G2 for specific adaptation.

Keywords: Lowland rice, AMMI, GGE, AMMI stability value, yield stability index.

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1. Introduction

Rice is the world's second most important cereal crop next to wheat in terms of total production and after maize in terms of area coverage and productivity (FAOSTAT, 2020). The crop is grown worldwide over an area of 163.24 Mha with a total production of around 740.95 Mt and world average productivity of 4.66 t ha⁻¹ (FAOSTAT, 2020). Globally, human consumption accounts for 85% of total production for rice, compared with 72% for wheat and 19% for maize and rice crop also provides 21% of global human per capita energy and 15% of per capita protein (Macleod *et al.*, 2002). Rice has also become a commodity of strategic significance and the fastest growing food source in Africa. Its adoption as a principal staple food is increasing and is grown and consumed in more than 43 African countries (AfricaRice, 2017), and yet domestic production never meet local rice demand leading to huge annual import. In Ethiopia, rice is an increasingly important food, feed and cash crop and, it is also source of employment for the youth and women as well as other actors involved along the rice value chain. Despite its economic and food security importance, productivity of the crop is constrained by several factors such as terminal moisture stress, cold stress, low soil fertility, blast and sheath rot, among other things. Terminal moisture stress is predominantly a common problem in lowland rain fed rice cultivation. High yielding rice varieties with short growing duration are required to sustain rain fed lowland rice production in Ethiopia. To this end, introduction and screening of different rice genotype through multi-environment evaluation has been practiced under rice variety improvement program.

Multi-environment trials are conducted to evaluate yield stability performance of plant materials in diverse environmental conditions (Yan *et al.*, 2000; Yan and Rajcan, 2002). Genotypes grown in different environments often show significant fluctuations of performance for yield and yield related traits. These changes are influenced by the different environmental conditions such as variations in moisture, soil nutrients, temperature and relative humidity, and this is referred to as genotype-by-environment (GE) interaction (Kang, 2002). The GE interaction reduces the association between phenotypic and genotypic values and leads to bias in the estimates of gene effects and combining ability for various characters that are sensitive to environmental fluctuations less amenable to selection (Farshadfar *et al.*, 2000; Kang, 2002). Hence, GE interaction must be either exploited by selecting best genotype for each specific environment or avoided by selecting widely adapted and stable genotype across a wide range of environments (Eisemann *et al.*, 1990; Kang, 2002).

Although different methods have been reported by scholars to understand pattern of GE interaction in multi-

environment data, the two most often used statistical models are additive main effects and multiplicative interaction (AMMI) as reported by Gauch and Zobel (1988) and Zobel *et al.* (1988), and genotype plus GE interaction (GGE) based on Yan *et al.* (2000). The AMMI analysis combines analysis of variance for genotype and environment main effects with principal components analysis of the G x E interaction into a unified approach (Gauch, 1988; Zobel *et al.*, 1988) while the GGE biplot as a data visualization tool is able to graphically demonstrate GE interaction patterns. GGE biplot is an effective tool to rank genotypes based on mean yield and stability and to identify mega-environments with corresponding winner genotypes as well as to evaluate test environments. Therefore, the objective of the current study was to identify high yielding short-duration lowland rice genotypes with wider or specific adaptation by applying AMMI and GGE statistical tools.

2. Materials and Methods

2.1 Plant materials, experimental design and trial management

In this study, including one check (*Ediget*), a total of 18 lowland rice genotypes were used and evaluated for grain yield and yield related traits (Table 1). The experiment was laid out using a randomized complete block design (RCBD) of three replications. Seeds of each genotype were hand drilled at the rate of 60 kg ha^{-1} in a plot size of 6m 2 and with a spacing of 20cm between rows. Each experimental plot comprised six rows of the gross plot, with only four harvestable rows. Fertilizers (UREA and DAP) were applied as per to local recommendations. The DAP was applied all at planting while UREA was applied in three splits-at sowing, tillering, and panicle initiation. Other crop management practices were applied to the entire experimental area uniformly.

2.2 Experimental sites

This experiment was executed at Woreta, Pawe, Assosa, Mai-Tsebri, and Jimma research stations from 2013 to 2015 during the main cropping seasons under rain fed lowland conditions. As presented in Table 2, experimental sites are different in terms of rainfall amount and distribution, elevation, and temperature. The location-year combination produced eleven environments including E1: Woreta 2013, E2: Maitsebri 2013, E3: Jimma 2013, E4: Woreta 2014, E5: Jimma 2014, E6: Maitsebri 2014, E7: Pawe 2014, E8: Woreta 2015, E9: Pawe2015, E10: Jimma 2015, and E11: Assosa 2015.

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

No.	Genotypes	Code
1	IR74052-184-3-3	G1
2	YUNJING 23	G2
3	WAB502-8-5-1	G3
4	PSBRC44	G4
5	WAB376-B-10-H3	G5
6	IR 83222-F11-167	G6
7	IR 83222-F11-18	G7
8	IR 83222-F11-200	G8
9	IR 83222-F11-209	G9
10	IR 83222-F11-66	G10
11	IR76999-52-1-3-2	G11
12	IR 83249-F9-29	G12
13	STEJAREE 45	G13
14	CHOMRONG	G14
15	WAB880-1-38-20-17-P1-HB	G15
16	WAB880-1-32-1-2-P1-HB	G16
17	IRAT112	G17
18	EDIGET (check)	G18

Table 2. Description of the test locations in Ethiopia over three years

Location	Coordinates		Elevation ^a (masl)	Rain fall ^b (mm)	Temperature (°C) ^c	
	Latitude	longitude			Min.	Max.
Woreta	11° 58' N	37° 41' E	1810	1300	11.5	27.9
Jimma	7° 46' N	36° 00' E	1753	1561	11.2	25.9
Maitsebri	11° 08' N	38° 08' E	1350	1296	15.0	36.0
Pawe	11° 19' 15" N	36° 24' 30" E	1091	1457	17.2	32.8
Assosa	10° 03' N	34° 59' E	1590	1050	14.0	29.0

^a masl: meter above sea level, ^b mm: millimeter, ^c Min: minimum and Max: maximum

2.3 Data collection and statistical analysis

Data were collected for days to heading (DTH), days to maturity (DTM), panicle length (PL), plant height (PH), number of filled grains per panicle (FSP), fertility rate (FR), grain yield (Gy), thousand seed weight (TSW) and disease data such as leaf blast (LB) and brown spot (BS) were collected based on 0-9 scale following IRRI standard evaluation system (IRRI, 1996); where 0: immune, 1: highly resistant, 2: resistant, 3 and 4: moderately resistant, 5 and 6: moderately susceptible, 7: susceptible, and 8 and 9: highly susceptible. Grain yield harvested from each plot was converted into kg ha⁻¹ at 14% standard grain moisture content. Data 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, and stability of rice genotypes (Zobel *et al.*, 1988) using GenStat (16th edition) statistical package. Moreover, GGE analysis, according to Yan *et al.* (2000), was employed to visualize grain yield stability and performance, and identify specifically adapted genotypes among 18 rice genotypes at eleven environments. 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:

$$ASV = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1Score)^2 + (IPCA2Score)^2}$$

Where, ASV= AMMI stability value; SS= sum of square; IPCA1 and IPCA2= the first and the second interaction principal component axes, respectively. 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 (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. YSI incorporates both mean yield and stability in a single criterion (Tumuhimbise *et al.*, 2014; Bose *et al.*, 2014) and low values of YSI show desirable genotypes with high mean grain yield and stability.

3. Results and discussions

3.1 Variation in traits

The combined analysis of variance over locations and years of all traits, and the AMMI analysis of variance for grain yield are presented in Table 3 and Table 4, respectively. Means squares of genotype (G), location (L), and year (Y) showed highly significant variation for all traits considered except for filled grains per panicle in the case of year effect (Table 3). Two-way interactions of all combinations and the three-way interactions (G x L x Y) (except for fertile tillers) showed significant variation for all traits revealing the inconsistency performance of genotypes for different traits across locations and over the years. Similar results were reported by Hasan *et al.* (2014), Ogunbayo *et al.* (2014) and Bose *et al.* (2014) for rice genotypes performance across sites and over seasons. The result in AMMI analysis of variance for grain yield revealed that environment (E), genotype (G) and genotype by environment (GE) interaction were highly significant (P<0.001). In multi-environment trial data, the largest variation in grain yield is attributed to E, followed by GE interaction and then by G (Gauch, 2006; Yan and Kang, 2003).

Table 3. Mean squares of grain yield and yield related traits in 18 lowland rice genotypes at five locations for three years

Source of variation	Degree of freedom	Traits ^a								
		Gy	DTH	DTM	PL	PH	FTP	FSP	FR	TSW
Genotype (G)	17	13071394.2***	2290***	544***	59.1***	7325.1***	17.9***	3049.4***	366.1***	346.1***
Year (Y)	2	4992248.8**	3778***	13767***	45.4***	1452.3***	740.9***	474.9ns	1786.0***	127.1***
Location (L)	4	24775165.1***	2297***	13540***	179.9***	2374.9***	544.9***	5510.1***	6526.4***	252.5***
G*Y	34	1881240.2***	44***	61**	4.2**	187.5**	4.9*	593.2***	93.2***	9.9*
G*L	68	3016525.5***	29***	66**	5.3***	118.3**	4.9**	416.6***	91.5***	8.5*
Y*L	4	43630073.7***	899***	5006**	83.3***	2853.5**	358.2***	9993.6***	590.9***	181.1***
G*Y*L	68	1953553.4***	33***	26**	3.3*	71.5**	3.7ns	665.9***	76.1***	9.5**
Error	394	657018	14.7	10.8	2.3	34.4	3.2	198	25.3	6.2

^aGy: grain yield (kg ha⁻¹), DTH: days to heading, DTM: days to maturity, PL: panicle length (cm), PH: plant height (cm), FSP: number of filled grains per panicle (no), FR: fertility rate (%) and TSW: thousand seed weight (g).

Table 4. AMMI analysis of variance for grain yield in 18 lowland rice genotypes at eleven environments

Source of Variation	Degree of freedom	Sum of squares (SS)	Mean Square (MS)	%total SS	%treatment SS	%GxE SS
Total	593	1167179964	1968263			
Treatments	197	907769374	4607966***			
Genotypes (G)	17	222217166	13071598***	19.04	24.48	
Environments (E)	10	283600326	28360033***	24.30	31.24	
Block	22	26612553	1209661**			
G x E	170	401951882	2364423***	34.44	44.28	
IPCA 1	26	112365614	4321754***			27.95
IPCA 2	24	90592511	3774688***			22.54
IPCA 3	22	67005829	3045720***			16.67
IPCA 4	20	36963500	1848175***			9.20
IPCA 5	18	33681278	1871182***			8.38
IPCA 6	16	29918616	1869913***			7.44
Residuals	18	7971605	442867			1.98
Error	374	232798038	622455	19.95		

DF: degree of freedom, SS: sum of squares, MS: mean squares

In this study, however, grain yield was largely influenced by GE interaction effect (34.4 %), followed by E (24.3%) and G (~19 %) effects which is in agreement with the findings Cantila *et al.* (2020) who reported that GE interaction, E, and G explained 52.3%, 26.8%, and 15.5% of the total variation. Treatment sum of square was also largely explained by GE interaction (44.3%), followed by E (~31.2%) and G (~24.5%) (Table 4). The variation attributed to GE interaction was nearly twice that of the genotype effect.

As reported by Yan and Kang (2003), the large GE interaction effect relative to genotype implies that environments might be divided into mega-environments to which genotypes responded differently. In this study it was also observed that the first six highly significant IPCAs (IPCA1 to IPCA6) together explained 92.2% of the total GE interaction effect, with each accounting for 28, 22.5, 16.7, 9.2, 8.4 and 7.4% of GE interaction, respectively (Table 4). However, Cantila *et al.* (2020) reported that the first four highly significant IPCAs explained 35.8%, 26.9%, 16.9% and 13.4% of GE interaction sum of squares while Tadesse *et al.* (2017) reported that the first three significant IPCAs explained 35.6, 27.1 and 18.8% of the total GE interaction sum of squares, respectively.

3.2 Mean performance of rice genotypes

The mean values of growth and yield traits of 16 lowland rice genotypes (days to 50% heading, days to 85% maturity, panicle length, plant height, filled grains per panicle, fertility rate, thousand seed weight, and grain yield) combined across eleven environments are presented in Table 5. In days to 50% heading and days to 85% maturity, nearly 44% of the genotypes had days to heading and days to maturity higher than the grand mean. The least days to heading was observed in three genotypes; G8 (72 days), G14 (71 days) and G16 (72 days) which was slightly lower than the standard check, G18 (73 days), while only one genotype (G14) was earlier than the standard check in terms of days to maturity. In the case of panicle length, genotypes G1, G3, G4, G5, G11, G14, G15 and G16 exhibited the longest panicle length and slightly longer than the standard check and about 50% of genotypes showed the tallest plant height, measuring 90 to 114 cm which was higher than the grand mean, but G9, G7, G3, and G11 were significantly shorter than the standard check, measuring 71 to 74.6 cm. The total number of filled grains per panicle was the highest in G10, followed by G12, G17, G4, G16, G2 and G18 which was higher than the grand mean and they also had high grain fertility rate. Thousand seed weight was the highest in G16 (32.8 g) and G18 (32.8g), followed by G13 (31.4g), G15 (31.3g), G14 (30.4g) and G17 (30.2g) with overall mean of 28.02g. Mean grain yield of genotypes also ranged from the lowest of 3439.1kg ha^{-1} for G13 to the highest of 5812.3kg ha^{-1} for G16 with grand mean of 4561 kg ha^{-1} . Only three genotypes (G2, G11 and G16) significantly outperformed the standard check (G18) with mean grain yield of 5409.8, 5423.1 and 5812.3kg ha^{-1} , respectively (Table 5). These high yielding genotypes also showed better resistance to major rice diseases (panicle blast and brown spot) compared to the other genotypes.

As presented in Table 6, genotypes responded differently across eleven environments. The mean grain yield across genotypes in terms of environments ranged from 3741 kg ha^{-1} at E1 to 5828 kg ha^{-1} at E4, with grand mean of 4561 kg ha^{-1} . E2, E4 and E11 were high yielding environments, followed by E8 and E9 while E1 was the lowest yielding environment (Table 6). This low performance of genotypes at E1 might be attributed to the poor environmental conditions, mainly of moisture stress and the condition became better in the following years. As reported by Tilahun *et al.* (2013) and Lakew *et al.* (2021) Fogera plains (Woreta, Dera and Libokemkem) are characterized by moisture stress (late-on set and early off-set of rainfall) which often negatively impacted yield performance of lowland rice. Short growth duration rice varieties are preferred by farmers in these areas which

help escape moisture stress and encourage double cropping thereby increasing productivity of their fields. Genotypes G7, G12 and G16 performed the best at the lowest yielding environment (E1), whereas G2, G11, and G14 had the highest mean grain yield at the most favorable environment (E4). Except for genotypes G6, G8, G9, G13, G17, and G18, each of the other genotypes were identified as one of the three high yielding genotypes at least in one of the environments. Genotype G16 performed the best for mean grain yield at seven environments (E1, E5, E6, E7, E8, E9, and E10) and it was one of the highest yielding genotypes in both poor and favorable environments (Table 6). The other four high yielding genotypes include G11 which performed best in five environments (E3, E4, E5, E7, and E11), G3 in four environments (E2 and E6, E8 and E10), and (G1, G2 and G5) each in three environments (E2 and E6, E7), (E3, E4, and E11), and (E2, E8, and E10), respectively (Table 6). The switch in ranking of genotypes across different environments demonstrated that the GE interaction effect was a crossover type (Yan and Hunt, 2001; Kang, 2002) in which the genotype selected for high yield under one environmental condition may not always be superior under another environmental condition.

Table 5. Mean performances of 18 lowland rice genotypes for grain yield and yield related traits at five locations over three years

Genotype	DTH (days)	DTM (days)	PL (cm)	PH (cm)	FGP (no)	FR (%)	TSW (g)	Gy (kg ha ⁻¹)	LB (scale)	BS (scale)
G1	91	122	20.0	75.6	87.3	83.0	22.7	4198.0	2.0	1.3
G2	79	117	18.0	82.8	96.1	94.5	30.7	5409.8	0.9	1.1
G3	85	119	21.4	112.6	90.5	85.4	29.0	4940.8	4.2	3.1
G4	96	125	20.6	90.0	102.5	89.2	23.7	4849.4	1.4	1.5
G5	86	119	21.6	111.5	88.1	86.0	30.3	4827.5	4.4	2.9
G6	82	118	18.0	68.3	89.4	90.8	23.7	3644.9	1.8	2.3
G7	87	120	17.7	72.0	83.1	91.4	25.1	4362.2	1.5	1.5
G8	72	115	17.5	73.1	87.8	92.3	23.8	3842.7	1.8	1.6
G9	76	116	17.2	71.5	84.1	81.8	23.7	3814.4	1.4	1.6
G10	89	121	19.0	99.0	106.4	91.5	25.5	4552.4	1.2	1.5
G11	94	124	20.3	74.6	93.1	92.8	29.6	5423.1	1.1	1.0
G12	74	115	19.3	79.1	104.7	94.0	28.3	4766.1	1.2	1.7
G13	74	115	18.4	89.0	72.7	93.0	31.4	3439.1	1.4	1.4
G14	71	110	20.4	114.4	78.8	94.0	30.4	4508.3	1.2	1.4
G15	74	116	20.5	96.5	96.6	89.0	31.3	4458.3	1.7	1.8
G16	72	115	19.6	90.0	101.1	94.0	32.8	5812.3	1.0	0.2
G17	74	114	19.3	90.1	103.0	91.6	30.2	4626.6	1.1	1.2
G18	73	112	18.8	99.3	96.8	95.1	32.8	4621.6	0.9	1.3
Mean	80	117	19.30	88.29	92.34	90.52	28.02	4560.98	1.68	1.58
CV (%)	4.76	2.80	7.94	6.64	15.33	5.54	9.10	17.77	53.00	33.70
LSD (5%)	1.85	1.59	0.74	2.84	6.81	2.43	1.20	392.31	0.44	0.27

DTH: days to heading, DTM: days to maturity, PL: panicle length, PH: plant height, FGP: number of filled grains per panicle, FR: fertility rate, TSW: thousand seed weight, Gy: grain yield, LB: leaf blast and BS: brown spot.

Table 6. Mean grain yield (kg ha⁻¹) of 18 lowland rice genotypes across even environments during (2013-2015) main cropping season

Genotype	Environments ^a											Mean
	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	
G1	2352	<u>6150</u>	2982	3437	3449	<u>4950</u>	<u>5179</u>	4003	5622	2889	5165	4198
G2	4494	5263	<u>7064</u>	<u>7747</u>	4021	4163	4008	5436	5157	4327	<u>7828</u>	5410
G3	3225	<u>7115</u>	2570	5247	5116	<u>4821</u>	3923	<u>5529</u>	4802	<u>5879</u>	6123	4941
G4	2406	5025	<u>6245</u>	5483	<u>5913</u>	3071	4896	4455	5940	5321	4590	4849
G5	2800	<u>7350</u>	2731	6751	4863	4396	3559	<u>5519</u>	4439	<u>5814</u>	4880	4827
G6	3726	5352	2569	5743	2405	3771	2477	3907	3839	2338	3968	3645
G7	<u>4836</u>	5255	3275	5869	2968	4092	3117	4764	4757	3088	5965	4362
G8	4042	5127	3135	4870	3953	3808	3200	3706	3622	2713	4094	3843
G9	3756	4477	2438	5192	3928	4142	2436	4870	4009	2379	4331	3814
G10	2468	4020	4460	5053	4388	4592	3691	4869	<u>6015</u>	3972	<u>6550</u>	4552
G11	3639	5927	<u>5589</u>	<u>6778</u>	<u>6955</u>	4533	<u>4892</u>	5453	5680	2716	<u>7493</u>	5423
G12	<u>5475</u>	5722	5367	6628	4428	4492	3300	4757	4129	2221	5909	4766
G13	2836	4165	2572	5258	3138	3283	2687	4488	2794	3101	3509	3439
G14	2961	5377	5479	<u>7085</u>	4338	4258	4311	4889	2809	3528	4558	4508

Genotype	Environments ^a											Mean
	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	
G15	3845	4510	2347	6099	5075	3958	3871	4533	6055	3280	5468	4458
G16	6155	5567	5575	5875	5756	5675	5774	5819	6174	5647	5918	5812
G17	3973	4995	3284	5869	5063	3917	4340	4588	5288	3634	5944	4627
G18	4340	4123	4825	5928	4520	4033	3882	4584	4120	4721	5761	4622
Mean	3741	5307	4028	5828	4460	4220	3863	4787	4736	3754	5447	4561
CV (%)	29.93	16.95	19.99	14.43	19.86	14.15	11.51	14.22	15.67	21.35	12.48	17.77
LSD (0.05)	1857.	1492.	1336.	1395.	1469.	991.0	737.9	1129.	1231.	1329.	1128.	392.3
	9	7	2	6	3	2	4	1	8	6	9	1

^aE1: Woreta 2013, E2: Maitebri 2013, E3: Jimma 2013, E4: Woreta 2014, E5: Jimma 2014, E6: Maitsebri 2014, E7: Pawe 2014, E8: Woreta 2015, E9: Pawe2015, E10: Jimma 2015, E11: Assosa 2015

3.3 AMMI stability value (ASV) and yield stability index (YSI)

Ranking of 18 lowland rice genotypes based on mean grain yield, IPCA 1 score, ASV, and YSI is presented in Table 7. In terms of mean grain yield, genotype G16 ranked first followed by G11, G2, and G3 with 5812, 5423, 5410 and 4941 kg ha⁻¹, respectively. The IPCA1 scores also demonstrated that G16 was the most stable genotype, followed by G10, G8, and G6, whereas the other high yielding genotypes (G11, G2, and G3) were unstable as they had high IPCA1 scores. ASV stability measure as proposed by Purchase et al. (2000) also stated that genotypes with the least ASV or have the smallest distance from the origin in the biplot are considered as the most stable genotypes, whereas those which have the highest ASV are considered as unstable. Accordingly, G17 was the most stable genotype for grain yield, followed by G16, G8, G13 and G15, as they had the least ASV while G2 was the most unstable genotype, followed by G4, G3, and G5 (Table 7).

Table 7. Ranking of 18 short-duration lowland rice genotypes based on, IPCA1 scores, AMMI stability value (ASV), and yield stability index (YSI) mean grain yield (Gm, kgha⁻¹) at eleven environments.

Genotype	IPCA1	Rank	ASV	Rank	YSI	Rank	Gm	Rank
G1	25.947	14	35.170	13	27	17	4198	14
G2	-37.508	18	46.600	18	21	10	5410	3
G3	36.539	17	45.321	16	20	8	4941	4
G4	-3.854	7	46.195	17	22	13	4849	5
G5	32.104	16	40.512	15	21	11	4827	6
G6	2.52	4	26.441	12	29	18	3645	17
G7	-3.728	6	22.465	9	22	14	4362	13
G8	2.028	3	11.744	3	18	6	3843	15
G9	4.175	9	17.927	7	23	16	3814	16
G10	-1.952	2	24.324	10	20	9	4552	10
G11	-16.511	12	25.915	11	13	3	5423	2
G12	-27.159	15	40.082	14	21	12	4766	7
G13	3.559	5	12.171	4	22	15	3439	18
G14	-17.596	13	21.885	8	19	7	4508	11
G15	9.958	10	12.415	5	17	5	4458	12
G16	0.39	1	6.375	2	3	1	5812	1
G17	3.976	8	6.190	1	9	2	4627	8
G18	-12.889	11	16.733	6	15	4	4622	9

The YSI estimate which combined mean yield and ASV rankings elucidated that G16 was the most stable genotype followed by G17, G11, and G18, because they had the least YSI. On the other hand, G1, G6 and G9 were the most unstable genotypes as they showed the highest YSI. Genotype G16 was the best genotype as it ranked first in mean yield, IPCA1 score YSI and, second in ASV. However, genotypes G11 and G2 which ranked second and third in mean yield showed inconsistency in stability ranking and, thus both were unstable. Inconsistency in the ranking of genotypes based on different approaches demonstrated the importance of considering both mean yield and stability performance to guide selection of genotypes in the breeding program (Farshadfar *et al.*, 2011).

3.4 AMMI and GGE biplots

AMMI biplots, AMMI1 (IPCA1 vs mean yield) and AMMI2 (IPCA1 vs IPCA2) were applied to further illustrate the effect of each genotype, environment and the interaction in the multi-environment data as presented in Figure 1 and Figure 2, respectively. In AMMI1 biplot, genotypes or environments laid on the same vertical line had similar mean yields and those laid on the same horizontal lines had similar interaction patterns (Crossa *et al.*, 1990). In addition, a genotype or an environment plotted on the right side of the central vertical axis had

higher yield than those of left hand side and, if a genotype or an environment has IPCA1 score of nearly zero, it has less interaction effect (Zobel *et al.*, 1988). Accordingly, genotypes G2, G3, G4, G5, G10, G11, G12, G16, G17, and G18 exhibited above average in mean yield. Of the three best yielding genotypes (G16, G2, and G11), G16 had the lowest IPCA1 score suggesting its wider adaptation and can be cultivated across tested environments while G2 and G11 had relatively large IPCA1 scores and thus unstable; that is, they had specific adaptations. In contrast, genotypes G1, G6, G8, G9, and G13 performed below average in mean yield with lower IPCA1 scores except for G1 which had larger IPCA1 score and then highly interactive (Figure 1).

With regard to environments, the highest yielding environment was E4, followed by E11 and E2, all with large IPCA1 scores indicating their strong contribution to the interaction effect. In contrast, E1, E3, E6 and E7 were low yielding with large IPCA1 scores except for E6 and E7 that had relatively smaller IPCA1 scores. On the other hand, E5, E8 and E9 were average yielding environments and closer to the biplot origin suggesting their smaller contribution to the interaction (Figure 1).

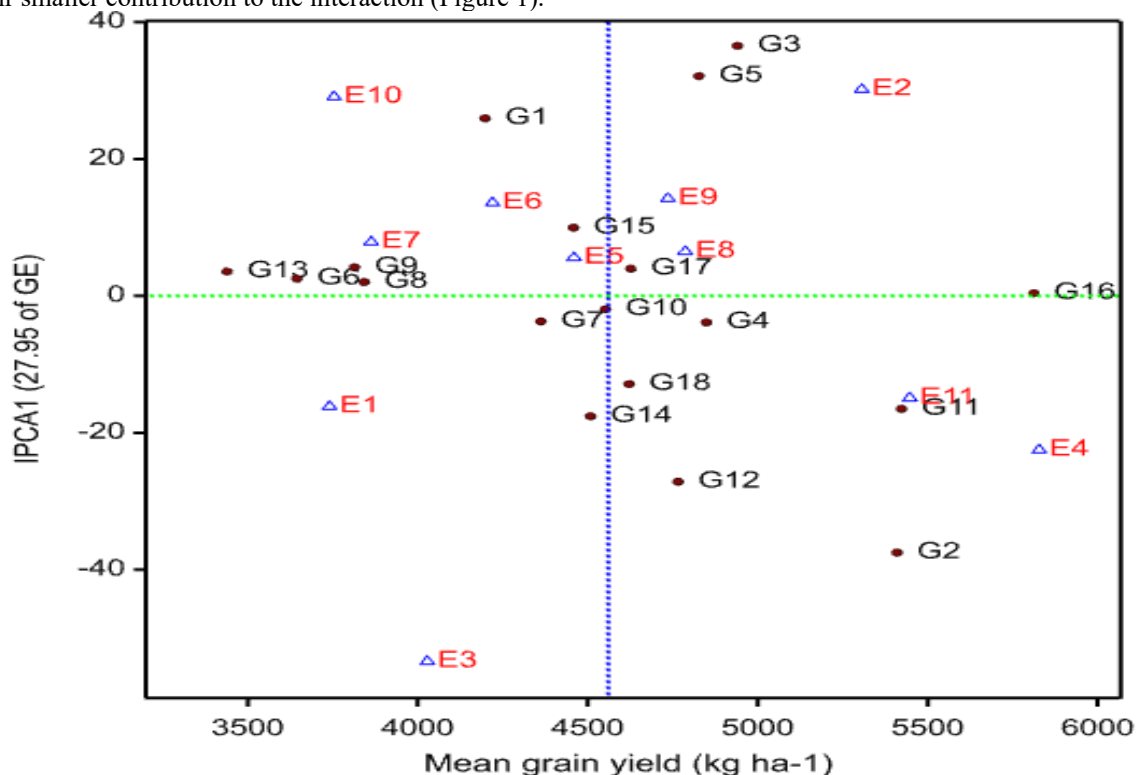


Figure 1. AMMI1 biplot showing the IPCA1 vs mean yields of 18 lowland rice genotypes at eleven environments. E1: Woreta 2013, E2: Maitebri 2013, E3: Jimma 2013, E4: Woreta 2014, E5: Jimma 2014, E6: Maitsebri 2014, E7: Pawe 2014, E8: Woreta 2015, E9: Pawe2015, E10: Jimma 2015, E11: Assosa 2015. Genotypes codes are presented in Table 1.

In AMMI2 biplot, environments positioned far from the biplot origin had large contribution to the GE interaction and if they are closer to the origin, they contributed for the stability of genotypes. Similarly, genotypes close to the biplot origin are stable while those distant are unstable and genotypes and environments positioned close to each other in the biplot have positive associations (Silivera *et al.*, 2012). Accordingly, significant GE interaction was attributed to E1, E2 and E3 as they were away from the biplot origin. In contrast, E6, E8 and E11 contributed the lowest to the GE interaction and thus most stable while the other environments (E4, E5, E7, E9 and E10) were intermediate (Figure 2). Genotypes G15, G16, and G18 were close to the biplot origin which suggested that they were relatively stable, G16 being the most stable and this was also in accordance with Figure 1. Located far away the biplot origin, genotypes G1, G2, G3, G5, and G12 were the most unstable and associated to different environments (Figure 2).

GGE biplot analysis is also a data visualizing tool used for, among other things, evaluating cultivars based on average yield and stability performance, identifying best cultivar in each environment and grouping environments based on cultivars performance (Yan, 2001; Yan *et al.*, 2007). In this study, the GGE biplots in Figures 3 and 4 each explained 59.11% of the total variation in grain yield of 18 rice genotypes, with the first and second principal component (PC1 and PC2) contributing 41.78% and 17.33% of the variations, respectively. Figure 3 demonstrates the ranking of 18 rice genotypes based on both mean grain yield and stability performance. Genotypes in the direction of the arrow or on the positive side of the vertical solid line are high yielding while those on negative side are with low mean yield (Yan, 2001). Moreover, genotypes with short vectors, regardless

of their directions, are more stable whereas with longer vectors are unstable (Yan and Tinker, 2006). In the present study, the best performing genotypes in terms of mean yield were G16, G11, G2 and G4 while poor performing genotypes were G13, G6, G9, G8, G7 and G1 as illustrated in Figure 3. With regard to stability of genotypes as dictated by the length of genotype vectors in either direction, G16, G13, G9 and G8 could be considered as the most stable genotypes. However, the latter three genotypes were poor in terms of mean yield performance. Genotypes G11 and G2 were also the highest in mean yield, G11 being relatively stable while G2 was unstable. Thus, genotype G16 followed by G11 was the highest yielding genotypes and consequently, G16 is the most ideal genotype for rain fed lowland rice cultivation in all environments due to high mean yield and high yield stability while G11 can be recommended for specific environments.

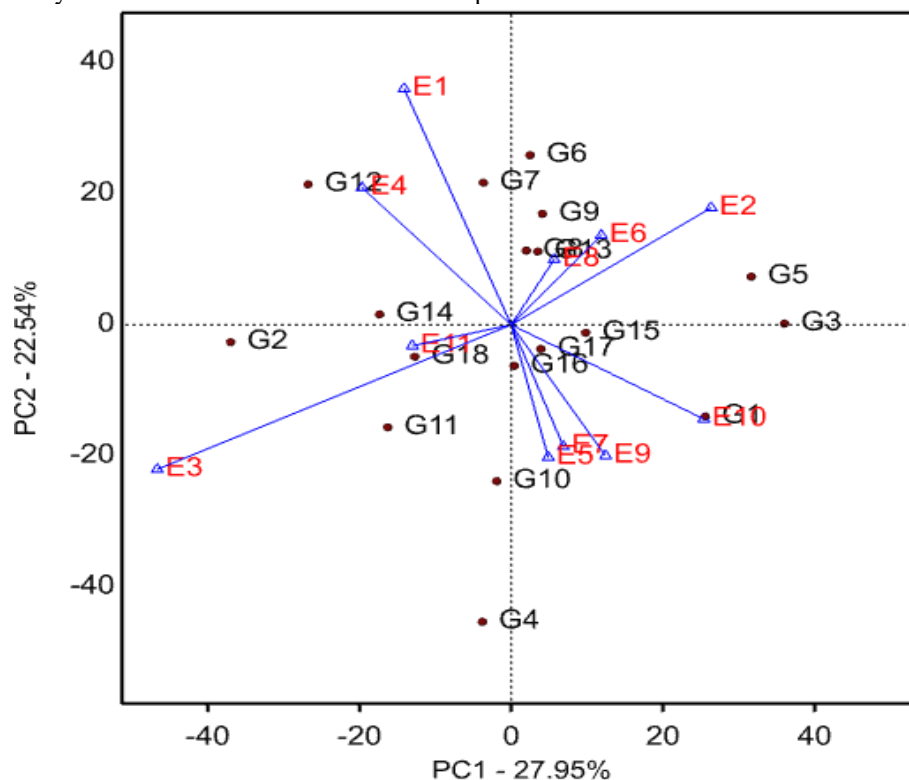


Figure 2. AMMI2 biplot showing the first two principal axes of interaction (IPCA1 vs IPCA2) for grain yield of 18 lowland rice genotypes at eleven environments. E1: Woreta 2013, E2: Maitebri 2013, E3: Jimma 2013, E4: Woreta 2014, E5: Jimma 2014, E6: Maitsebri 2014, E7: Pawe 2014, E8: Woreta 2015, E9: Pawe2015, E10: Jimma 2015, E11: Assosa 2015. Genotypes codes are presented in Table 1.

Another most attractive feature of a GGE biplot is its ability to show the ‘which-won-where’ pattern in a genotype-by-environment dataset, as it graphically demonstrates relationships of genotypes to different environments (Yan and Tinker, 2006). Genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments. Accordingly, genotypes G16, G11, G4, and G10 were better in the environments E9, E8, E7, and E5, whereas the genotypes G2, G12, G14, and G18 were better in the environments E1, E3, E4, and E11 (Figure 4).

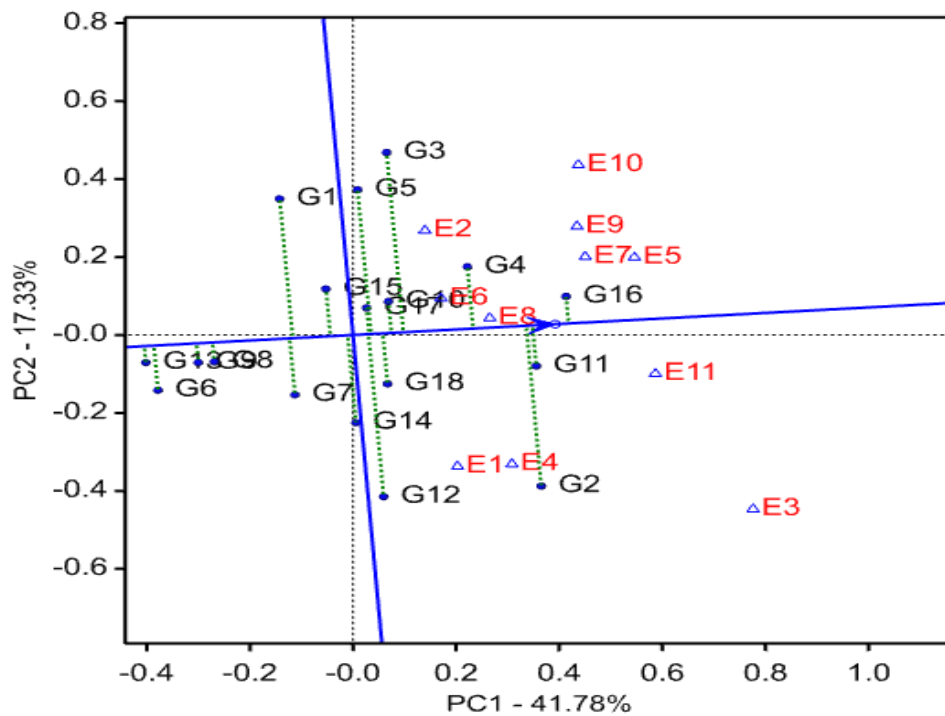


Figure 3. GGE biplot showing ranking of 18 genotypes based on stability and mean performance at 11 environments. E1: Woreta 2013, E2: Maitebri 2013, E3: Jimma 2013, E4: Woreta 2014, E5: Jimma 2014, E6: Maitsebri 2014, E7: Pawe 2014, E8: Woreta 2015, E9: Pawe2015, E10: Jimma 2015, E11: Assosa 2015. Genotypes codes are presented in Table 1.

Genotypes G3, and G5 also performed better in environments E2 and E10 while G1, G6, G7, G8, G9, G13 and G15 did not perform well in any of the environments. This biplot suggested the presence of three mega-environments where genotypes G2, G3 and G16 as winner genotypes at each group of environments, whereas genotypes G1, G6, G13 though identified as vertex genotypes but they were not associated to any environments indicating as they were not best at least in one environment (Figure 4).

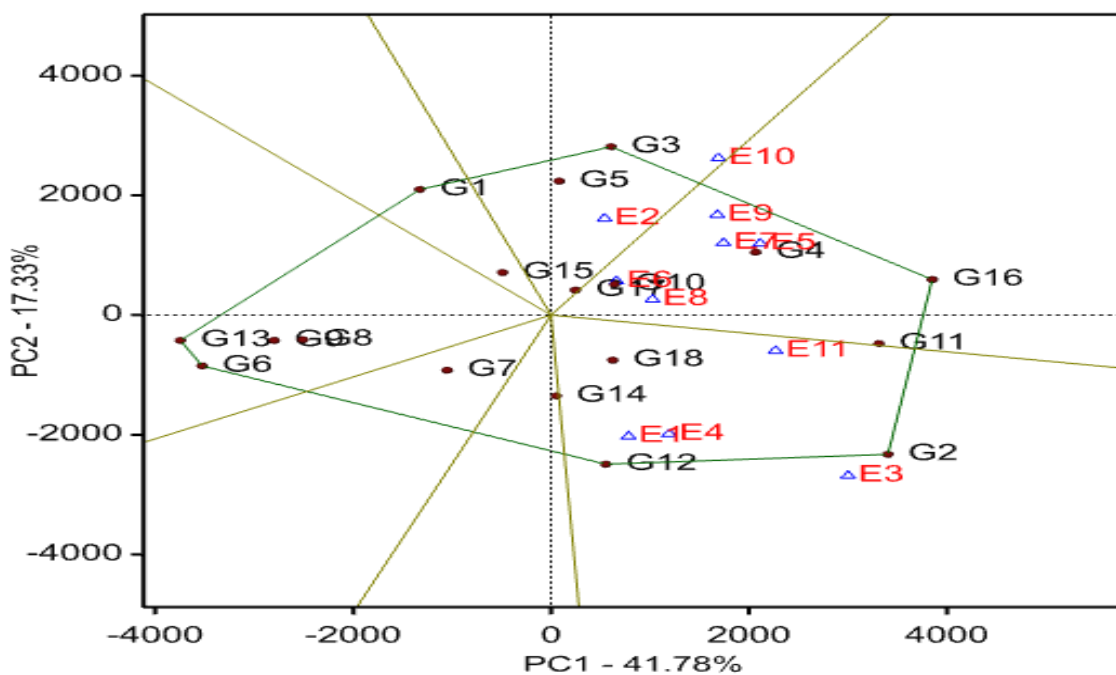


Figure 4. GGE biplot showing winner genotypes at specific environments. E1: Woreta 2013, E2: Maitebri 2013, E3: Jimma 2013, E4: Woreta 2014, E5: Jimma 2014, E6: Maitsebri 2014, E7: Pawe 2014, E8: Woreta 2015, E9: Pawe2015, E10: Jimma 2015, E11: Assosa 2015. Genotypes codes are presented in Table 1.

Conclusion and recommendation

The study of genotype x environment (GE) interaction is critical for appropriate genotype evaluation in multi-environment trials. Genotypes that showed both high mean yield performance and stability across a wide range of environmental conditions are desirable for rice production. However, the presence of GE interaction makes difficult which genotypes to select. In the current study, results indicated that the yield performance of rice genotypes was significantly influenced by GE interaction effects which contributed nearly two times higher than genotype effects. The GGE biplots and AMMI were also used to compare the performance of different genotypes across test environments. Genotypes G16, G11 and G2 were identified as the top three high yielding genotypes. Genotype, G16 was the highest yielding and most stable genotype, followed by G11 as shown by AMMI stability value, yield stability index, and GGE ranking biplot, while the remaining tested genotypes showed inconsistent performances across environments. Thus, considering the grain yield performance and stability of genotypes, G16 and G11 could be recommended for wider adaptation while G2 for specific adaptation.

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