GGE Biplot Analysis of Genotype X Environment Interaction of Cold Tolerant Green Super Rice Genotypes in Ethiopia

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ABSTRACT

The experiment was conducted in Fogera and Shire-Maitsebri from 2016-2018 main cropping seasons with the major objectives of high yielding, cold tolerant, disease resistance and early maturing GSR rice varieties for the high altitude of lowland production system. A total of 15 GSR genotypes including two checks were used in the study. The trial was laid out in randomized complete block design with three replications with plot size of 7.5 m^2. The combined analysis of variance revealed significant difference on grain yield, days to maturity, days to heading, panicle length, filled grain per panicle, plant height and thousand grains weight (P≤0.01). Three genotypes (G2, G6 and G4) showed significant difference than the standard checks on grain yield and gave grain yield advantage of 32.6 %, 27.9 % and 22.3 %, respectively. The genotype main effect plus genotype x environment interaction (GE) biplots were used to analyse and visualize pattern of the interaction component. The first two principal components (PC1 and PC2) of the GGE explained 79.34 % with PC1= 54.09 % and PC2=25.25 % of GGE sum of squares, respectively. Genotypes, G2 (Yungeng 31) and G6 (KB-2) combined both high stability performance and high mean grain yield across the test environments and characterized as an ideal genotypes and proposed for national variety release.

Key words: GSR, cold, stability, GGE bi-plot, rice

INTRODUCTION

Rice (Oryza sativa L.) which was originated from the tropics and subtropics is widely cultivated in diverse environments. The tremendous growth of human population worldwide has increased the demand for rice production, [1] requiring an improvement of 50% by the year 2025. [2] Due to its origin in tropical and subtropical regions, rice is more sensitive to cold stress than other cereals crop such as Wheat and Barley. Therefore, the production of rice is severely limited by cold stress in temperate areas. [3] Cold stress is the major factor affecting rice growth, productivity, its distribution worldwide. [4] Production of rice is affected primary due to its vulnerability to cold stress at seedling stage, as well as reproductive stage leading to spikelet sterility.

In Africa, rice also constantly increasing as staple food and there has been increasing demand in Africa in the past three decades from 1999-2018; [5] however, these demands have not been commensurate with the total production and most of African countries are net importer of milled rice, which costs 6.4 billion USD annually. [5] Although rice has recently introduced to Ethiopia, recognizing its importance as a food security crop and a source of income and employment opportunity. [6] The production, productivity and consumption of rice in Ethiopia is constantly increasing in the country. [7] Ethiopia's geography is noticeable by immense depressions and mountains. Consequently vast arable lands are located at high altitudes more than 2000 meter above sea level. Rice can grow in

wide agro climatic zones; however, low temperature stresses are serious challenges for rice farmers at high elevations in the tropics. Lack of cold tolerant rice varieties in the high lands of Ethiopia is the main constraints for the promotion of rice. Therefore, the main objectives of these studies was to evaluate the performance and stability of cold tolerant lowland greed super rice genotypes for their wider or specific recommendation in the North-West Ethiopia and similar agro ecologies.

MATERIALS AND METHODS

The experiment was conducted for 3 years (2016-2018) in two locations; Fogera and Shire- Maitsebri, The locations are where the trials conducted differ in soil type, annual rain fall, altitude and annual temperature based on the experiments nature (Table 1). A total of 15 genotypes

including two checks used (Table 2).The trial was laid out in randomized complete block design with three replications with a plot size of 7.5 m^2 (Six rows with 5 m long with 0.25 m row spacing). Seed rate of 60 kg/ha was used and direct seeding methods in a row was applied. Fertilizer (UREA and DAP) were applied based on each location recommendation. All DAP was applied at the time of sowing. For UREA, split application was applied; 1/3 at sowing, 1/3 at active tillering and the remaining 1/3 during panicle initiations. Other agronomic practices were applied according to each location recommendations. The data were subjected to the GLM procedure for analysis of variance using SAS software V.9.0. And Genotype x environment and stability analysis were done by using Genstat 18th edition software.

Table 1: Description of study environment for Lowland GSR experiment for cold tolerant

Location	Altitude (m)	Latitude	Longitude	Annual rain fall (mm)	Temperature ^{0}C (Mean)	
					Max	Min
Fogera/Woreta	1810	11^{0}58'N	37^{0}41' E	1300	27.9	11.5
Shire/Mai-tsebri	1350	13^{0}05' N	38^{0}08' E	1296	36.0	15.0
Gondar/Dembiya	NA	NA	NA	NA	NA	NA
Jimma	NA	NA	NA	NA	NA	NA

Table 2: List of genotypes used for national variety trial for cold

No.	Genotype	Seed Source	No.	Genotype	Seed Source
1	Yungeng 44	CASS/ China	9	P-37	CASS/ China
2	Yungeng 31	CASS/ China	10	P-38	CASS/ China
3	Yungeng 45	CASS/ China	11	P-39	CASS/ China
4	Yungeng 38	CASS/ China	12	Li Jing 9	CASS/ China
5	Fengdao 23	CASS/ China	13	Li jing 11	CASS/ China
6	KB-2	CASS/ China	14	Check1(Ediget)	Fogera/NRRTC
7	Songgeng9	CASS/ China	15	Check (KOMBOKA)	Fogera/NRRTC
8	P-28	CASS/ China			

RESULT AND DISCUSSION
Combined analysis of variance

The combined analysis of variance for grain yield of fifteen rice genotypes presented (Table 3). Genotype (G), environment (E) and genotype x environment interaction (GE) were highly significant (P<0.001) for grain yield. The combined analysis of variance for grain yield, days to maturity, days to heading, panicle length and filled grain per panicle, plant height and thousand grains weight showed significant difference (P≤0.01). The analysis of environment effect also revealed

significant difference (P≤0.01) for grain yield and other agronomic characters. The genotype x environment interaction effect was significant for all traits (P≤0.01). The three way interaction of genotypes x location x years were showed significant variation (P≤0.01) for yield and other agronomic characters (Table 4). The study revealed that genotypes responded differently to grain yield and other agronomic characters in different environments over years. This pointed out the advantage of executing multi location

trial to explore the response of genotypes for their specific or wider adaptability.

The significant interaction difference of the three way interaction of genotype x location x years revealed that the possibility of getting genotypes which can be adapted widely/or specifically. As indicated (table 3), the mean grain yield of the 15lowland green super rice genotypes ranged from 3108.4 kgha^{-1} (G13) to 4840.3 kg ha^{-1} (G2). Compared to the standard checks (G14 and G15), ten genotypes (G2, G6, G4, G1, G12, G5, G8, G9, G3 and G10) were statistically high yielder than the checks. However only

the three genotypes G2, G6and G4 showed significant difference than the standard checks on grain yield and other agronomic traits and gave grain yield advantage of 32.6 %, 27.9 % and 22.3 %, respectively. GGE-bi-plot analysis revealed that G2 and G6 are high yielding and most stable among tested genotypes in both environments (Figure 3). There is no grain sterility observed in both genotypes (G2 &G6) and have better panicle exertion which can fit the cold tolerant characteristics. Following this result these two genotypes (G2 and G6) are proposed for national variety release.

Table 3: Combined analysis of variance of grain yield for fifteen Green Super Rice genotypes evaluated at six environments

Source of variation	DF	SS	MS	F-value	P
Genotype (G)	14	58559939.4	4182852.8	5.18	<.0001
Environment (E)	5	652733497.1	130546699.4	161.58	<.0001
GE	70	151171026.0	2159586.1	2.67	<.0001
Error	175	141385695.0	807918		
Total	266	1018721298.0			

GE=Genotype x Environemnt interaction; DF= Degree of freedom; SS=Sum of Squares; MS=Means of Squares

Table 4: Mean grain yield and other yield related parameters of 15 lowland green super rice genotypes for cold tolerant at Fogera and Shire-Mai-Tsebri over three years (2016-2018)

Genotype	Genotype code	DTH	DTM	PL	PH	FTP	FGP	Phacc	Gykgha
Yungeng 44	G1	95.3	132.7	17.6	81.4	10.5	114.2	1.2	4233.1
Yungeng 31	G2	91.3	127.4	19.2	87.4	10.6	123.4	1.0	4840.3
Yungeng 45	G3	94.3	134.3	18.5	78.7	11.5	116.4	1.3	3830.6
Yungeng 38	G4	91.8	127.9	19.6	85.5	10.2	124.2	1.2	4464.7
Fengdao 23	G5	92.4	151.1	16.7	74.5	16.6	91.7	1.7	3981.7
KB-2	G6	90.4	127.2	17.4	78.2	11.0	104.3	1.2	4667.8
Songgeng9	G7	84.7	123.8	17.7	75.7	11.7	95.6	2.2	3272.8
P-28	G8	89.4	127.9	16.7	74.6	11.8	99.1	1.5	3898.7
P-37	G9	87.4	122.7	16.7	73.6	12.8	101.7	1.0	3863.8
P-38	G10	100.4	137.4	19.0	80.9	12.4	101.7	2.0	3734.3
P-39	G11	88.1	121.3	17.2	77.4	13.0	96.3	1.7	3309.2
Li Jing 9	G12	86.1	122.8	19.7	86.6	10.8	119.0	1.0	4079.5
Li jing 11	G13	103.6	138.8	16.9	63.0	12.7	89.3	3.0	3108.4
Check -Ediget	G14	89.1	120.2	18.8	85.1	10.9	96.1	1.3	3649.5
Check - Komboka	G15	104.6	116.6	16.8	60.4	13.4	104.3	1.7	3373.2
	Mean	92.6	128.9	17.9	77.5	12.0	105.1	1.5	3883.0
	CV (%)	5.7	14.3	7.2	5.9	22.9	10.8	34	23.1
	Genotype (G)	***	***	***	***	***	***	***	***
	Environment (E)	***	***	***	***	***	***		***
	Year (Y)	***	NS	***	***	***	***		***
	G*E	***	***	***	***	***	NS		***
	G*E*Y	***	***	***	***	***	***		***

Note: *, **, and *** refers to significant at 5%, 1% and 0.1% level, NS=non -significant, CV= coefficient of variation, G*E= genotype by environment, G*E*Y= genotype by environment by year, DH= days to 50% heading, DM= days to 85% maturity, FGP= filled grains/panicle, PH= plant height (cm), PL= panicle length (cm),Phacc=Phenotypic acceptabilityand Gykgha= grain yield (kg/ha)

Polygon view of GGE biplot analysis

The polygon (which-won-where) view of the GGE biplot is drawn by joining extreme genotypes and perpendicular lines (ray) passing from the polygon sides divides the biplot in to sectors (Fig. 1). According to [8] the GGE explains the genotype main effect (G) and the genotype x environment

interaction (GE), which are the two most important source of variation for genotype evaluation in multi environment trails. The polygon view of GGE biplot (Fig. 1) is the best way for the identification of winning genotypes with visualizing the interaction patterns between genotype and environments [9] in multi environment data

analysis. In this biplot, a polygon was formed by connecting the vertex genotypes with strait lines and the rest of the genotypes were placed within the polygon. The vertex genotypes were G2, G13, G14 and G5 having the largest distance from the origin. These vertex genotypes are the best or poorest in some or all environment [9] because they are farthest from the origin of the biplot. In Fig 1, there are four rays which divided the biplot in to four sections. The genotypes fell in to four sections but there were no environments fell in to section 4. The first section contains six genotypes (G2, G6, G4, G3, G5, G12 and G1) and the vertex genotypes for this section was G2, suggesting the high yielding genotype for these six environments following G6 and G4. The second section (vertex genotype of G13) contains three genotypes (G10, G15 and G13) were the poorest yielding genotypes. Similarly, the third section contains five genotypes (G8, G9, G7, G11 and G14), whereas there were no genotypes under the forth section. The partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 accounted for 54.09 % and 25.25 % of GGE sum of squares, respectively, explained 79.34 % of the total variation (Fig. 1)
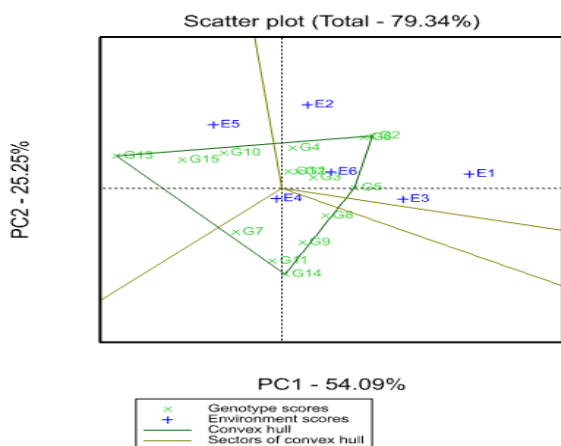

Figure 1: The polygon view of GGE biplot to the identification of winning genotypes and their related mega-environments (here, G= Genotypes, E=Environment)

Ranking of genotypes based on mean and stability performance

In GGE biplot analysis, the estimation of yield and stability of genotypes (Fig. 2) were done by using the average environment coordinate (AEC) methods. [10,11] The line passing through the biplot origin is called average environment (tester) coordinate (AEC), which is defined by the average PC1 (represent mean yield) and PC2 (stability) scores for all environments. [9] The line which passes through the origin and is perpendicular to the AEC, represents the stability of genotypes. Either direction away from the biplot origin, on the axis, indicates greater GE interaction and reduced stability. For selection, the ideal genotypes are those with high mean yield and high stability (closes to the origin and has the shorter vector from the AEC). G2 followed by G6 were the most stable and high mean yield whereas G13 was the least stable and as well as least mean yield. The genotypes on the right side of the line with no arrows had yield performance greater than the mean yield and those genotypes on the left side of this line had yield less than the mean yield. These results are in line with those obtained by. [12-15]
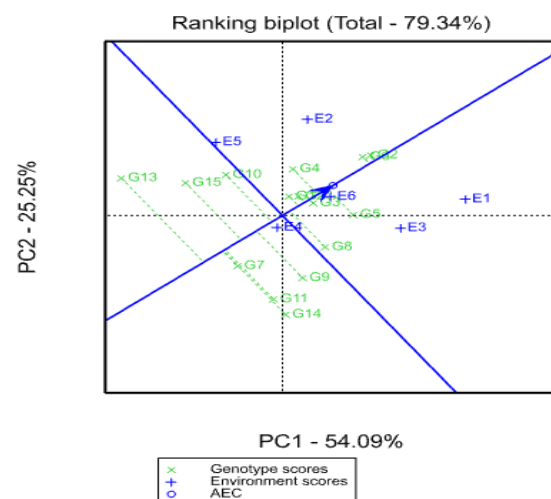

Figure 2 GGE biplot showing the ranking of genotypes for both yield and stability performance over environments

Evaluations of genotypes relative to ideal genotypes

The ideal genotypes are the one that have high mean yield (PC1) and less GE interaction or high stability (PC2) [16,17] The center of the concentric circles represented the position of ideal genotypes(Fig. 3),

which is defined by a projection onto the mean-environment axis that equals the longest vector of the genotypes that had above average mean yield and a zero projection onto the perpendicular line (zero variability across environments). A genotype is more desirable if it is close to ideal genotype. [18,19] Therefore G2 was closer to the ideal genotype followed by G6, G4, G3 and G12 being more desirable than other genotypes (Fig. 3). On the other hand, G 13, G15, G7, G14, G11, G9 were considered to be undesirable because they are placed far from the ideal genotypes. Identification of ideal genotypes through GGE biplot methods is a proper tool to identify most stable and high yielding genotypes.
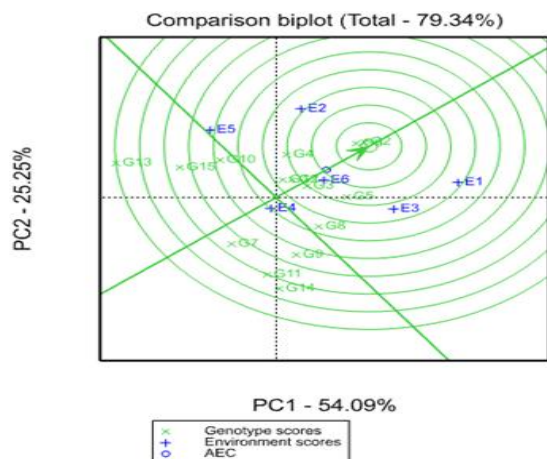
Figure 3.GGE biplot of ideal genotype and comparision of the genotypes with respect to the ideal genotype.

Evaluations of environments relative to ideal environments

Similar to ideal genotype, an ideal environment or location is defined and show by the small circle with an arrow pointing it (Fig 4). E6 is an ideal environment. E3 and E1 were the second and third desirable environments because both had high PC1 scores and Less PC2 scores. E5 and E2 are the most discriminating environments because of their low PC1 and high PC2 scores. The test environments should have large PC1 scores in order to discriminate genotypes in terms of the genotypic main effect and absolute small PC2 scores in

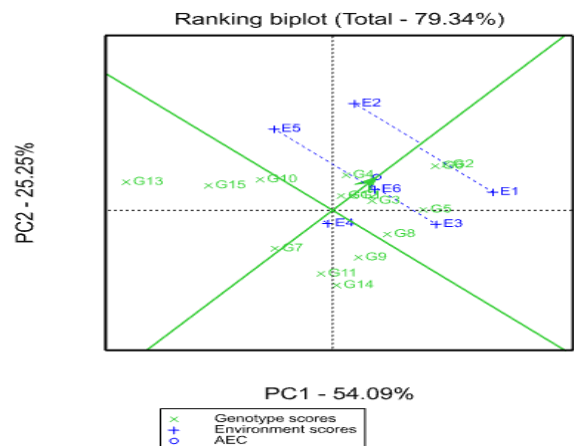order to be more representative of the overall locations. [20]

Figure 4 GGE biplot of ideal environments and comparison of the environments with the ideal environment.

CONCLUSION AND RECOMMENDATIONS

The present study revealed that significant differences among genotypes and environments for grain yield and related agronomic traits suggesting differential response of genotypes to varied environments. Mean grain yield and stability performance over environments of each genotype is explored by using AEC methods. These methods showed that G2 (Yungeng 31) followed by G6 (KB-2) had high mean grain yield as well as high stability out of the fifteen tested genotypes. These two genotypes are proposed for national variety release. The experiment revealed the importance of cold tolerance, high yield and diseases resistance in the evaluation of genotypes. Cold tolerance varieties allow rice producers to use high elevation areas for rice production. The proposed two varieties are crucial to boost production and productivity in high elevation of rainfed lowland rice production system of Ethiopia.

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REFERENCES

1. Khush, G. S. (2001), Green revolution: the way forward. *Nat. Rev*. 2: 815–22.
2. Liang, J, Lu Y, Xiao P, Sun M, Corke, H. and Bao, J. (2010), Genetic diversity and population structure of a diverse set of rice germplasm for association mapping. *Theor. Appl. Genet.* 121:475–87.
3. Africa Rice Center (Africa Rice). 2018. Continental Investment Plan for accelerating Rice Self-Sufficiency in Africa (CIPRiSSA). Abidjan, Cote dIvoire: 204pp.
4. Moraes de Freitas, GP., S. Basu, V. Ramegowda, E. B. Braga and A. Pereira (2016). Comparative analysis of gene expression in response to cold stress in diverse rice genotypes, Biochemical and Biophysical Research Communications, http://dx.doi.org/10.1016/j.bbrc.2016.02.004
5. Zhang, Q., Q. Chen, S. Wang, Y. Hong, and Z. Wang (2014). Rice and cold stress: methods for its evaluation and summary of cold tolerance-related quantitative trait loci. Rice, 7(1): 24.
6. Rice. Ethiopia's millennium crops. http://www.africarice.org/publications/ricetoday/Ethiopia%E2%80%99s%20millennium%20crop.pdf
7. CSA (2016). Central Statistical Agency. The Federal Democratic Republic of Ethiopia, Central Statistical Agency, Agricultural Sample Survey (2017), Report on Area and Production of Major Crops (Private Peasant Holdings, Meher Season), Statistical Bulletin, Addis Ababa, Ethiopia
8. Yan W, Kang MS, Ma B, Wood S, Cornelius PL. 2007. GGE biplot vs. AMMI analysis of genotype by environment data. Crop Sci.47:643-655
9. Yan, W and M S Kang. 2003. GGE biplot analysis: a graphical tool for breeders, Geneticists and Agronomists. 1st Edn., CRC Press LLC., BocaRaton, Florida, pp: 271.
10. Yan W. 2001. GGE biplot a window application for graphical analysis of multi-environment trial data and other types of two way data. Agron.J.93:1111-1118
11. Yan, W and L A Hunt. 2001. Interpretation ofgenotype × environment interaction forwinter wheat yield in Ontario. Crop Sci 41:19-25.
12. Naheif, E, M Mohammad. 2013. Genotype byenvironment interactions for grain yield in bread wheat *(TriticumaestivumL.)*. Global Sci. Res. J. 1(1): 045-052.
13. AnowaraAkter, JamilHasan, UmmaKulsum, H Rahman, M Khayum and R Islam. 2015. GGE Biplot Analysis for Yield Stability in Multi-environment Trials of Promising Hybrid Rice (Oryzasativa L.). Bangladesh Rice J.19(1):1-8
14. Atnaf M, Kidane S, Abadi S and Fisha Z. 2013. GGE biplots to analyse soybean multi-environment yield trial data in north Western Ethiopia. Journal of Plant Breeding and Crop science. Vol. 5(12),pp.245-254.
15. Jat, M.L., Jat, R.K., Singh, P., Jat, S.L., Sidhu, H.S., Jat, H.S., Bijarniya, D., Parihar, C.M. and Gupta, R. (2017) Predicting Yield and Stability Analysis of Wheat under Different Crop Management Systems across Agro-Ecosystems in India. American Journal of Plant Sciences, 8, 1977-2012. https://doi.org/10.4236/ajps.2017.88133
16. Fentaw A, MelkamuE and YeshitilaM. 2015. Genotype-Environment Interaction and Stability Analysis of Hybrid Maize Varieities in Northern West Ethiopia. International Journal of Plant Breeding and Genetics. Academic Journals Inc. DOI: 10.3923/ijpbg.
17. Gedif, M. and Yigzaw, D. (2014) Genotype by Environment Interaction Analysis for Tuber Yield of Potato (*SolanumtuberosumL.*) Using a GGE Biplot Method in Amhara Region, Ethiopia. *Agricultural Sciences*, 5, 239-249.http://dx.doi.org/10.4236/as.2014.54027
18. Kaya, Y, M Akcura and S Taner. 2006. GGEbiplot analysis of multi-environment yield trials in bread wheat. Turk. J. Agric. 30: 325-337
19. Mitrovic, B, D Stanisavljevi, S Treski, MStojakovic, M Ivanovic, G Bekabac and MRajkovic. 2012. Evaluation of experimental maize hybrids tested in multi-location trials using AMMI and GGE biplot analysis. Turkish J. Field Crops. 17(1): 35-40
20. Yan, W and I Rajcan. 2002. Biplot analysis of testsites and trait relations of soyabean in Ontario. Crop Sci. 42: 11-20.

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