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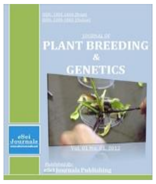
Available Online at eSci Journals
Journal of Plant Breeding and Genetics
ISSN: 2305-297X (Online), 2308-121X (Print)
http://www.escijournals.net/JPBG



AMMI AND GGE BIPLOT ANALYSIS OF BREAD WHEAT GENOTYPES IN THE NORTHERN PART OF ETHIOPIA

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ABSTRACT

The genotype environment interaction manipulates the selection criteria in a multipurpose crop like wheat. Ten bread wheat genotypes were evaluated at five wheat growing locations of Tigray region in the year 2011. Yield data was analyzed using the additive main effect and multiplication interaction model (AMMI) and GGE biplot. The AMMI analysis of variance for grain yield detected significant effects for genotype, location and genotype by location interaction. Location effect was responsible for the greatest part of the variation, followed by genotype and genotype by location interaction effects. Based on AMMI stability value, G4, G10, G8 and G9 were the most stable genotypes, while G1, G2, and G3 were the most responsive genotypes. The GGE biplot also showed G1, G2, G3, and G4 have long vectors and located far away from the biplot origin and hence are considered to have larger contribution to GEI (specifically adapted genotypes). G10 however is widely adapted genotype. The 'which won where' feature of the GGE biplot identified G4 as the winning genotype at Samre, Hagereselam, and Atsbi, while G1 winning at Quiha and Wukro. The GGE biplot also identified two bread wheat mega-environments. This indicates that analysis of multi-location trail data using GGE and AMMI model is important for determining visual comparisons, adaptability/stability focusing on overall performance to identify superior genotypes.

Keywords: GEI, GGE, AMMI, adaptability, bread wheat, Tigray.

INTRODUCTION

Wheat is one of the major cereal crops principally grown in the highlands of Ethiopia, basically in the south east, central and North West parts. Considerable amount is also produced in the northern and southern regions (CSA, 2011). Around 1.7 million ha of land at national level was covered by bread wheat and 3 million tons were produced in 2010 (FAO STAT, 2012).

Wheat is the most important cereal crop in the mid and high land areas of the Tigray region, its productivity remained unsatisfactory because of lack of improved varieties (early maturing, drought tolerant, and high yielding genotypes), poor soil fertility, and moisture stress. Some of the improved varieties tested in the region were found to be adaptable to the agro ecology of the region and are still under cultivation, but majority of these have showed lower yield performance. Even the performance of the improved varieties being cultivated in the region is low and this could be due to the genotype by environment interaction.

According to Yan and Kang (2003), it is known that mean grain yield across environments are sufficient indicator of genotypic performance only in the absence of genotype by environment interaction. Most of the time, GEI complicates breeding, testing and selection of superior genotypes. It is important for wheat breeders to identify specific genotypes adapted or stable to different environment(s), thereby achieving quick genetic gain through screening of genotypes for high adaptation and stability under varying environmental conditions prior to their release as cultivars.

A variety of statistical procedures are in fact available to analyze and determine the results of multi-location trials and GEI data. However, two multivariate analysis such as AMMI and GGE biplot analysis has been performed in this study. Crossa (1990) pointed out that

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the Additive main effect and multiplicative interaction (AMMI) model proved to be a powerful tool in diagnosing GEI patterns.AMMI analysis can also be used to determine stability of the genotypes across locations using the PCA (principal component axis) scores and ASV (AMMI stability value). Moreover the GGE (genotype plus genotype by environment interaction) analysis is an effective method which is based on principal component analysis (PCA) to fully explore multi-environment trials (METs). GGE analysis partitions G + GE into principal components through singular value decomposition of environmentally centered yield data (Yan, 2001). The objective of this study was to analyze multi-location trail data of wheat using multivariate analysis to draw varietal recommendation.

MATERIALS AND METHODS

Experimental design and methods: The experiment was performed under rain fed condition in 2011cropping season at five wheat growing locationso in Tigray region, Northern Ethiopia. Ten genotypes (Mekelle-01, Mekelle-02, FRET1, Mekelle-03, HAR-2501, HAR-1868, Picaflor, Jeferson, M20ESWYT-46 and Shehan) were evaluated in a Randomized complete block design with three replications. HAR-2501 and HAR-1868 were standard checks which are currently grown by farmers of the region and these two varieties were released at national level by Holleta Agricultural Research Center. Shehan on the other hand, is an early maturing local variety which is susceptible to rust. The plot area was eight rows of 1.5 meters long and 20 cm spacing and the seeds were sown using hand drill. Sowing dates ranged from 28 June to 7 July, 2011 depending on the onset of the growing season. The seeding rate was 150 kg/ha and the plots were equally fertilized with Urea and DAP fertilizers at the rate of 50 and 100 kg/ha, respectively. All agronomic managements were implemented equally as per the recommendation. Finally, grain yield data was taken from the central six rows and was considered in to analysis.

Statistical analysis: Statistical computations and estimation were carried out using Gen Stat 12th (Gen Stat, 2009) statistical software. Before data analysis, homogeneity of residual variance was determined by Bartlet's test (Steel and Torrie, 1980) and the data collected was homogenous. In addition, normality test was also computed, and the data had confirmed that it came from normal distribution. Then, data for grain yield were pooled to perform the analysis of variance across **locations. Since** the pooled analysis of variance considers only the main effects, the additive main effect and multiplicative interaction model (AMMI) was computed. Beginning with the ordinary ANOVA procedure for two way analysis of variance, the AMMI analysis first separates additive variance from the multiplicative variance (interaction), and then applies PCA to the interaction, i.e., to the residual portion of the ANOVA model to extract a new set of coordinate axes which accounts more effectively for the interaction patterns (Gauch and Zobel, 1987). Moreover, AMMI analysis was also used to determine stability of the genotypes across locations using the PCA (principal component axis) scores and ASV (AMMI stability value). ASV was also calculated for each genotype according to the relative contribution of IPCA1 to IPCA2 to the interaction sum of square. Genotypes having least ASV were considered as widely adapted genotype. Similarly, IPCA2 score near zero revealed more stable, while large values indicated more responsive and less stable genotypes.

To graphically visualize the relationship between testers and entries, determine the 'which won where' portion, and to identify mega environment, a GGE biplot (Yan, 2001) analysis was also undertaken using GGE biplot in the Meta analysis of Gen Stat 12th edition (GenStat, 2009). Thuse GGE biplot in determining stability revealed that genotypes located near the biplot origin are considered as widely adapted genotypes, while genotypes located far as specifically adapted.

RESULT AND DISCUSSION

Additive main effect and multiplication interaction (AMMI)analysis: Genotype, location and genotype by location interactions were estimated by the additive main effect and multiplicative interaction (AMMI) model (Table 1). Variance analysis of AMMI model for grain yield (Qt/ha) detected significant effects for genotype, location and genotype by location interaction. The presence of the genotype by location interaction was indicated by changes in relative rankings of genotypes over various locations. The location effect was responsible for the greatest part of the variation, followed by genotype and genotype by location interaction effects. Similar findings were also obtained by Tarakanovas and Ruzgas (2006) on the additive main effect and multiplicative interaction analysis studies of wheat varieties. Results from the present AMMI analysis of variance of the ten genotypes also revealed that only mean square of the first interaction principal component axis (IPCA1) was found to be highly significant (P<0.001). But, the second and third IPCAs captured in non-significant portion of the variability. Addis (2003) also confirmed a significant effect only for the first IPCA score on his genotype by environment interaction study of bread wheat genotypes under dry land condition of Tigray region. According to Crossa et al. (1990) AMMI with two, three or four IPCA axes is the best predictive model. In the present study, the AMMI analysis further revealed that the first three interaction PCs accounted for a total of 97.43% of the interaction sum of square, with 77.78% of the corresponding degrees of freedom (Table 1). The first principal component axis (PCA1) of the interaction captured 68.08% of the interaction sum of square in 33.3% of the interaction degrees of freedom. Similarly, the second principal component axis explained further 17.69% of the GEI sum of square. The first and second IPCA altogether explained 85.77% of the variability in grain yield of the ten genotypes tested at five locations. While, the IPC3 accounted for 11.66% of the genotype by location sum of square. According to Zobel et al. (1988) the first two interaction principal component axis best explains the interaction sum of squares. In the present study, the 11.66% of the interaction sum of square, which was contributed by the IPCA3 is considered as noise.

Furthermore, the interaction principal component axis (IPCA) scores of genotype in the AMMI analysis indicated stability of the genotypes across locations. The closer the IPCA2 scores to zero, the more stable the genotypes across their tested environments. Hence, Picaflor was the most stable genotype, followed by FRET1 and M20ESWYT-46. Jeferson and Mekelle-03 were the most unstable genotypes (Table 2). Moreover, locations Quiha and Wukro had shown highest IPCA1 scores and hence contributed largely to GEI. These testing locations were high yielding sites.

AMMI stability value (ASV) was also computed to determine stability of the genotypes (Table 2). The ASV is the distance from the coordinate point to the origin in a two-dimensional of IPCA1 scores against IPCA2 scores in the AMMI model (Purchase et al., 2000).

Table 1: AMMI analysis of variance for grain yield tested at five locations

Source of variation	d.f.	SS	MS	Explained %
Total	149	10357	69.5	
Genotypes	09	1107	123.0***	10.7
Location	04	6461	615.1***	62.4
Block	10	523	52.3***	-
Interactions	36	1012	28.1***	9.80
IPCA1	12	689	57.4***	68.08
IPCA2	10	179	17.9^{Ns}	17.69
IPCA3	08	118	14.8 ^{Ns}	11.66
Residuals	06	26	4.3	-
Error	90	1255	13.9	-

*p<0.5, **p<0.01, ***p<0.001, Ns non-significant, d.f=degrees of freedom, SS=sum of square, MS=mean square.

Table 2: The first three IPCA scores and ASV for the genotypes.

Genotype	PCA1	IPCA2	IPCA3	ASV
FRET1 (G3)	1.73	0.43	0.12	0.6
Shina (G6)	0.68	-0.91	0.75	2.5
Hawi (G5)	-0.78	0.70	0.65	3.1
Jeferson (G9)	0.13	-1.65	-0.62	1.2
Mekelle-03 (G4)	1.76	1.55	-0.21	0.6
M20ESWYT-46 (G10)	0.08	-0.48	1.36	0.6
Mekelle-01 (G1)	-2.12	0.59	0.04	8.2
Mekelle-02 (G2)	-1.75	0.26	0.00	6.8
Picaflor (G8)	-0.27	0.09	-1.65	1.1
Shehan (G7)	0.53	-0.60	-0.44	1.9

IPCA=interaction principal component axis scores, ASV=AMMI stability value

In ASV method, a genotype with least ASV score revealed the most stable. Accordingly, genotypes Mekelle-03, M20ESWYT-46, Picaflor and Jeferson had general adaptation, while genotypes G1, G2, and G5 were the most unstable. This was in agreement with Farshadfar (2008) who has used ASV as one method of evaluating grain yield stability of bread wheat varieties. Similar reports were also observed in Fereny (2007) who has studied adaptability and stability pattern of spring wheat using ASV and other stability parameters.

In general, analysis using this AMMI model had been exploited in the variety evaluation of barley (Abay and Bjornstad, 2009), wheat (Hintsa et al, 2011; Addis, 2003; Mohamed, 2009; Korkut et al., 2007, Farshdfar, 2008), teff (Haile, 2009), and sorghum (Adugna, 2008).

The large yield variation due to location, which is irrelevant to cultivar evaluation and mega-environment investigation (Yan et al., 2000), justified the selection of a GGE biplot as the appropriate method for analyzing the MET data. Moreover, detailed stability analysis of the tested genotypes based on their IPCA scores using the GGE biplot of analysis is presented in Fig 1 and 2.

GGE biplot analysis: The polygon of substitution lines in Fig.1 is formed by connecting vertex genotypes, by connecting straight lines and rest of genotypes fall inside the polygon. The vertex genotypes were G1, G4, G7 and G5. These genotypes are the best or poorest genotypes in some or all environments because they are farthest from the origin of biplot except G5 (Yan and Kang, 2003). According to Yan et al. (2001), a single year trial may indeed have limited value because of the year-to-year variation. Nevertheless, the authors believed that biplot analysis of single year multi-location trial data is worthwhile. Yan (2001) explained the GGE biplot analysis as a multivariate analytical technique that graphically displays a two way table and allows visualizing the relation among entries, testers and their interactions. In the present investigation, the GGE biplot graphic analysis of the ten bread wheat varieties tested at five locations revealed that the first two principal components explained 88.97% of the total variance (Fig 1). This GGE biplot is used to facilitate visual analysis of the genotype by location data. Accordingly, statistically stable genotypes and locations were located near to the bi plot origin, with scores practically null for the two interaction axis (IPCA1 and IPCA2). The genotype, which lie near the origin and practically stable was G10, and had wide adaptability; and G8 is located a little bit farther from the origin hence had medium stability across the five locations.

On the other hand, genotypes G1, G2, G3, G4, and G7 were located far away from the origin, which were more responsive to environment change and are considered as specifically adapted genotypes. The genotype which was located near the origin was less responsive than the Corner genotype. In addition, the lines connecting the genotypes to the biplot origin measure genotype differences from the grand mean, and genotypes with long vectors were assigned as either the best or the poorest performers in the environment. Similarly, G10 located near the biplot origin showed average performance. G1, G2, G3, and G4 have long vectors and located quite far away from the biplot origin and had larger contribution to genotype by location interaction.

Yan et al., (2000) stated that in the graphic analysis the first principal component (IPCA1) represents cultivar productivity, and the second principal component (IPCA2) cultivar stability.

Hence, the GGE biplot showed that the ideal genotype must have a high IPCA1 value (high productivity) and an IPCA2 value next to zero (more stable). Thus based on the graphic interpretation, the present study showed that genotype G4 had the largest PCA1 score, and hence had the highest average grain yield. The IPCA2 value of this genotype, however, was the largest indicating its specific adaptation. In contrast, G10 yielded poorly at all sites but was relatively stable, as indicated by its small PCA1 scores (low yielding) and relatively small PCA2 scores (stable). Genotypes that had PCA1 scores >0 were identified as higher yielding and those that had PCA1 scores <0 were identified as lower yielding. Accordingly, the average yield of G5, G6 and G7 were below average and highly unstable (large absolute PCA2 scores). In contrast, genotypes G1, G2, G3, G4, and G8 had positive PCA1 scores and were identified as high yielder genotypes. Fig 2 showed the relationship among genotypes in biplot analysis hence; the biplot revealed that G3 and G4 were similar because the angle between them was smaller. In contrast, genotype G1 and G6 were dissimilar as their angle was larger.

In addition, the positions of the genotypes in opposing quadrants on the Cartesian plan also showed their dissimilar genetic performance, as observed for G1 and G6, G1 and G7, G2 and G6, G2 and G7, G3 and G5, G4 and genotype G5. Moreover, the relationship among testers was also graphically depicted in the GGE biplot (Fig 2). The cosines of the angle between the testers normally estimated the correlation coefficient between them. Hence the pair of testers, which were positively correlated had an angle between their vectors less than 90^o (QU and WU, QU and AT, WU and HA, AT and HA, AT and SM, HA and SM); while the angle between vectors of tester QU and SM was approximately 90^0, and were not correlated (Fig 2).

With respect to the contribution of testing locations to the GEI, location Atsbi (AT) had least contribution as it lied closest to the origin, but locations Wukro (WU) and Hagreselam (HA) were made the highest contribution. The biplot in this trail also indicated that genotype G3 and G4 were performed above average in locations SM and HA while G1, G2 and G8 in QU, AT and WU. Meanwhile, discriminating ability was an important measure of a test environment. Another equally important measure of a test environment was its representativeness of the target environment. An ideal environment should be highly differentiating of the genotypes and at the same time representative of the target environment. Hence in the current experiment, locations SM (Samre) and WU (Wukro) were most discriminating of the entries as indicated by the longer distance between their markers and the origin. However, due to their relatively large PCA2 score, genotypic differences observed at both locations did not exactly reflect the genotypes in average yield over all sites. On the other hand, location AT (Atsbi) was not actually the most discriminating as distance of its vector was the smallest, but varietal difference at this site was highly consistent with those averaged over all sites because it had almost zero IPCA2 scores and lowest IPCA1. These results were also confirmed to the observations made by Dehghani et al. (2006); Tesfaye et al. (2007); Abay and Bjornstad (2009) on their studies of wheat and barley.

To explicitly display the 'which-won-where' pattern and sensitivity degree between the variety and environment, polygon view of a GGE biplot based on the IPCA1 and IPCA2 values was displayed in Fig 2. The perpendicular lines in the biplot have divided the biplot in to 5 sectors in which each location fell in either of the sectors. Yan and Kang (2003) explained that the polygon view of a biplot was the best way to visualize the interaction patterns between genotypes and environments and to effectively interpret a biplot. In this study, this 'which won where' feature of the biplot identified wining genotypes; G4 for instance was the winning/corner genotype in locations SM, HA, and AT. Similarly, G1 (Mekelle-01) was the vertex/winning genotype in location QU and WU. According to the findings of Yan and Tinker (2006), the vertex genotypes were the most responsive genotypes, as they have the longest distance from the origin in their direction. On the other hand, the result also showed some genotypes which fall in sectors where there were no locations at all; these genotypes are poorly adapted to five of the testing locations (G5, G6, G7, and G9).

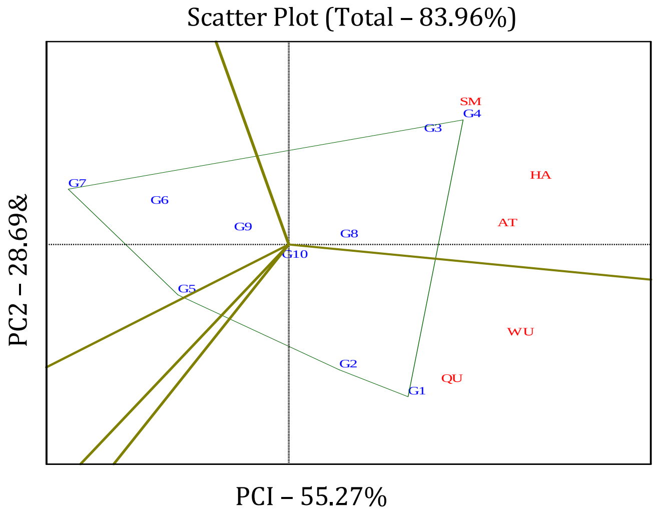

Figure 1: The 'which-won-where feature of the biplot. (Where, G = names of genotypes; the names of locations are abbreviated as SM Samre; HA Hagereselam; AT Atsbi; WU Wukro; and QU Quiha)

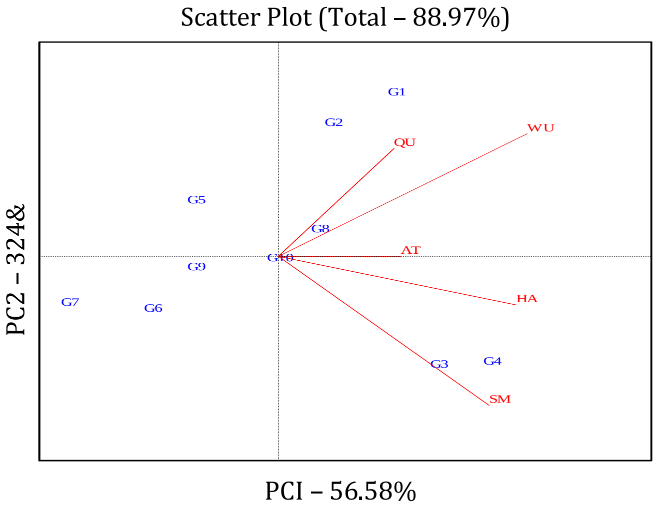

Figure 2: The biplot showing the relation among testers and mega environments

Yan *et al*. (2000) defined mega environments as a cluster of locations or environments that constantly share the same best variety. Hence, the result of this experiment identified two bread wheat mega-environments. The first mega-environment contained low yielding locations of HA, SA and AT with winning genotypes G3 and G4; the second mega-environment on the other hand, contained locations QU and WU. These results are also in agreement with Dehghani et al. (2006).

CONCLUSION

The presence of the genotype by location interaction for grain yield was indicated by the differential ranking of genotypes over the various locations. From this study it can be concluded that the significant GEI in grain yield among the genotypes revealed differential response of the genotypes across the testing sites which are exposed to variations in climate and edaphic factors. It is therefore, difficult to identify one superior genotype for all the locations which were included in the trial. This indicates that particular genotypes tended to rank differently in grain yields at different locations due to the presence of either genetic diversity or variation in locations. Thus testing newly developed genotypes under several environments and analysis using GGE and AMMI is important for evaluating adaptability/stability of performance and range of adaptation.

Therefore, based on the overall mean grain yield and stability of this multi-location trial, varieties Mekelle-01 and Mekell-02 could be scaled out to farmers in Wukro, Enderta and areas that share similar characteristics. Likewise, genotypes Mekelle-03 and FRET1 could be recommended for release to locations Hagere-selam, Samre and similar areas of the region and the country. Genotypes M20ESWYT-46 and Picaflor fortunately, could be grown in all testing locations.

ACKNOWLEDGEMENT

Thanks are due, to Local seed business project (LSB), Mekelle university, Mekelle for funding this research. Authors are also grateful to Mekelle agricultural research centre researchers and field assistants for their overall support and encouragements.

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