

Additive Main effect and Multiplicative Interaction Analysis of Grain Yield of advanced Bread Wheat (*Triticum aestivum* L) Genotype in Ethiopia

Gadisa Alemu^{1*}, Hussein Mohammed², Dawit Asnake¹, and Tesfahun Alemu¹

¹Kulumsa Agricultural Research Center, Assela, Ethiopia

²Hawassa University College of Agriculture, Hawassa, Ethiopia

*Corresponding author

Gadisa Alemu, National Wheat Research Program, Kulumsa Agricultural Research Center, Assela, P.O. Box 489, Ethiopia, E-mail: gadalemu@gmail.com

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Abstract

The present study was conducted to interpret Genotype main effect and GEI obtained by AMMI analysis and group the genotype having similar response pattern over all environments. Fifteen bread wheat genotypes were evaluated by RCBD using four replications at six locations in Ethiopia. The main effect differences among genotypes, environments, and the interaction effects were highly significant ($P \leq 0.001$) of the total variance of grain yield. Results of AMMI analysis of mean grain yield for the six locations showed significant differences ($P < 0.001$) among the genotypes, the environments and GEI. The environment had the greatest effect of the environmental sum of squares (35.28%) than the genotypes (33.46%) and GEI (31.45%) effect. The AMMI analysis for the IPCA1 captured 46.1% and the IPCA2 explained 28.6% the two IPC cumulatively captured 74.7% of the sum of square the GEI of bread wheat genotypes, when the IPCA1 was plotted against IPCA2. The genotype ETBW8075, ETBW8070 and ETBW9470 were unstable as they are located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The ETBW8078, ETBW8459, Hidase and ETBW8311 were genotype located near to the origin of the biplot which implying that it was stable bread wheat genotypes across environments. There is closer association between Lemu and ETBW8065 which indicate similar response of the genotypes to the environment. The best genotype with respect to location Kulumsa was ETBW9470, ETBW8075 was the best genotype for Dhera, ETBW8070 was the best genotype for Holeta while ETBW9466 was the best genotype for Arsi Robe. Arsi Robe and Kulumsa is the most favorable environment for all genotypes with nearly similar yield response for grain yield.

Keywords: Genotype, AMMI, GEI, IPCA

Introduction

Wheat is one of the most important cereal crops cultivated in the Ethiopia. It is an important and most widely cultivated food crop in the world and quantity produced is more than that of any other crop, feeding about 40% of the world population. This crop played a central role in combating hunger and improving the global food security. The grains of this plant provide about 20% of all calories and proteins consumed by people on the globe [1]. Wheat production in Ethiopia ranks fourth in area coverage surpassed only by teff, maize and sorghum and it is the third largest crop in total production [2].

Cultivars performance largely depends on their genetic makeup, environment and their interaction. Fluctuating response of genotypes across test environments is an usual phenomenon, known as GEI [3,4]. The main task in access to a stable wheat variety is to account for environmental effects and a definition of interaction. The improved wheat genotypes are evaluated in multi-environment trials to test their performance across different environments and to select the best genotypes in specific environments. It reduce the

selection efficiency in different breeding programs because in a GEI, measured traits are less predictable and cannot be interpreted using main effects (genotype or environment) and need more analysis [5]. GEI is also one of the most important reasons for the failure or decreased efficiency of breeding efforts to serve small resource poor farmers in different areas [6].

One of the multivariate techniques is the AMMI model. The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the $G \times E$ interaction. The additive main effect and multiplicative interaction (AMMI) method proposed by Gauch (1992) was a significant advance in the analysis and interpretation of $G \times E$ interaction [7]. AMMI biplot analysis is considered to be an effective tool to diagnose GEI patterns graphically. The model separates the additive variance from the multiplicative variance and then applies principal component analysis to the interaction portion to a new set of coordinate axes that explains in more detail the interaction pattern and the estimation accomplished using the least squares principle [8]. Purchase (1997) developed the AMMI Stability Value based on the AMMI model's principal components axis 1 and 2 respectively scores for each cultivar. The main objectives of the present study

are to interpret genotype main effect and GE interaction obtained by AMMI analysis and group the genotypes having similar response pattern over all environments [9].

Material and Methods

The experiment was conducted in the 2009/10 E.C. (2017-2018 G.C) main cropping season at six locations. The description of the testing locations is presented in Table 1. These locations represent the varying agro ecologies of the major wheat growing areas in central Ethiopia.

Table 1. Location and descriptions of weather condition for six locations

Location	Geographic position		Altitude	Soil pH	Soil type	Temperature(°C)		Rainfall (mm)
	Latitude	Longitude				Min	Max	
Kulumsa	08°01'10"N	39°09'11"E	2200	6	Luvisol	10.5	22.8	820
Asasa	07°07'09"N	39°11'50"E	2000	6.5	Gleysol	5.8	24	620
Dhera	08°19'10"N	39°19'13"E	1650	7	Andosol	14	27.8	680
Bekoji	07°32'37"N	39°15'21"E	2780	5	Nitosol	7.9	18.6	1020
Arsi Robe	07°53'02"N	39°37'40"E	2420	5.6	Vertisol	6	21.1	890
Holeta	NA	NA	2400	5	Nitosol	6.2	22.1	1044

The field experiment was laid out in RCBD with four replications. The experimental field plot was 6 rows of 2.5 m long with a 0.2 m inter-row spacing. Each plot was planted at a rate of 150 kg ha⁻¹. The fertilizer application and other crop management practices were done as per recommendations of each test locations. Weeds grown in the plots were removed manually starting from two weeks after sowing.

Table 2: The names, pedigree and selection history of the genotypes were evaluated in the experiment in 2017/18 cropping season at six locations

Name	Pedigree
Lemu	WAXWING*2/HEILO
ETBW8070	Line 1 Singh/ETBW4919
ETBW8078	Line 1 Singh/(Cham6/WW1402)
ETBW8084	Line 3 Singh/(Cham6/WW1402)
ETBW8311	ND643/2*WBLL1/3/KIRITATI//PRL/2*PASTOR/4/KIRITATI//PBW65/2*SERI.1B
ETBW8065	Line 1 Singh/ETBW4919
ETBW8427	SERI.1B//KAUZ/HEVO/3/AMAD/4/PYN/BAU//MILAN/5/ICARDA-SRRL-1
ETBW8459	CHIL-1//VEE'S'/SAKER'S'
ETBW9037	SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
ETBW9045	KINDE/4/CMH75A.66//H567.71/5*PVN/3/SERI
ETBW8075	Line 1 Singh/(Cham6/WW1402)
ETBW9464	MARCHOUCH*4/SAADA/3/2*FRET2/KUKUNA//FRET2*2/4/TRCH/SRTU//KACHU
ETBW9466	ATTILA/3*BCN//BAV92/3/TILHI/5/BAV92/3/PRL/SARA//TSI/VEE#5/4/CROC_1/AE.SQUARROSA(224)//2*OPATA*2/6/HUW234+LR34/PRINIA//UP2338*2/VIVITSI
ETBW9470	BAVIS#1/5/W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1
Hidasse	YANAC/3/PRL/SARA//TSI/VEE#5/4/CROC-1/AE.SQUARROSA(224)//OPATTA

Data collection

Data was collected on the following traits: days to heading, days to maturity, grain filling period, number of grains per spike, number of spikelet per spike, plant height, number of tiller per plant, spike length, biomass yield, harvest index, TKW, HLW and grain yield per plot.

Statistical Analysis

The grain yield data for fifteen bread wheat in six environments were used to combined analysis of variance (ANOVA) to determine the effects of environment, genotype and GEI. Before combine the data Bartlett's test was used to determine the homogeneity of variances

between environments to determine the validity of the combined ANOVA on the data and the data collected was homogenous. The AMMI analysis was performed using the model suggested by Crossa et al. (1990) as:

$$Y_{ij} = \mu + G_i + E_j + \sum_{n=1}^n \lambda_n \alpha_{in} y_{jn} + e_{ijk}$$

Where Y_{ij} is the yield of the i^{th} genotype in the j^{th} environment, μ is the grand mean, G_i is the mean of the i^{th} genotype minus the grand mean, E_j is the mean of the j^{th} environment minus the grand mean, λ_n is the square root of the Eigen value of the principal component analysis (PCA) axis α_{in} and y_{jn} are the principal component scores

for PCA axis n of the i^{th} genotype and j^{th} environment and e_{ijk} is the error term.

AMMI stability value (ASV): ASV as described by (Purchase (2000) was calculated as follows:

$$ASV = \sqrt{\frac{IPCA1_{sum\ of\ square}}{IPCA2_{sum\ of\ square}} (IPCA1_{score})^2 + (IPCA2_{score})^2}$$

Where $\frac{IPCA1_{sum\ of\ square}}{IPCA2_{sum\ of\ square}}$ is the weight given to the IPCA1-value by

dividing the IPCA1 sum of squares by the IPCA2 sum of squares [11].

Yield stability index: The yield stability index (YSI) was calculated as: $YSI = RASV + RY$

Where: RASV is the rank of the AMMI stability value and RY is the rank of the mean grain yield of genotypes (RY) across environments.

Result and Discussion

A combined analysis of variance for grain yield of the 15 bread wheat genotypes tested across 6 environments is presented in Table 3. The main effect differences among genotypes, environments, and the interaction effects were highly significant ($P \leq 0.001$) of the total variance of grain yield, environment main effect accounted for 35.28%, whereas genotype and $G \times E$ interaction effects accounted for 33.46% and 31.45% of the total variation, respectively (Table 3). The maximum environmental sum square indicated that there was a large difference between the testing location causing different genotypes to perform differently across the testing environments and the high percentage of the environment is an indication that the major factor that influence yield performance of bread wheat genotypes in Ethiopia is the environment. The result was in agreement with findings of Mohamed and Ahmed (2013) who found that bread wheat grain yield was significantly affected by environment. Melkamu et al. (2015) also reported that bread wheat grain yield was significantly affected by environment. Genotypes revealed highly significant ($p < 0.001$) differences for grain yield. This indicates that there was genetic difference among genotypes for this trait. This agrees with finding of Temesgen Bacha et al. (2015) who reported that genotype was highly significant difference for grain yield. Similarly Melkamu et al. (2015) reported that the bread wheat genotypes had a wider genetic variability for the entire traits. The genotypes showed inconsistent performances across the tested environments. The genotype ETBW9470 ranked first in three of the six environments (Arsi Robe, Asasa and Kulumsa). Similarly, two other best performing genotypes included ETBW8070 (Bekoji and Holeta) and ETBW9466 (Dhera) each ranking first in three of the environments. Genotype ETBW9470 showed the best yield of 6.56 t/ha in the highest-yielding Kulumsa, whereas ETBW9466 showed the best yield of 3.868 t/ha in the lowest-yielding environment Dhera (Table 4). In general, the ranking of genotypes changes from one environment to another and this is also an indication for the existence of $G \times E$ interaction due to variation among the testing locations.

The presence of significant $G \times E$ interaction showed the differential performance of bread wheat genotypes across environments and unstable performance of genotype across the different testing locations and complicates selection and recommendation of genotype in a specified environment. This means a particular

15 bread wheat genotype may not exhibit the same phenotypic performance under different environmental conditions or different genotypes may respond differently to a specific environment. That means, it is difficult to identify consistently superior genotypes across environments when $G \times E$ interaction is highly significant. In general, from the combined ANOVA (Table 3) superiority of genotypes across environments cannot be identified by considering their mean yield performance because $G \times E$ interaction is highly significant. Because of the interactions between genotypes and environments, yield of genotypes tested across vary and it is a problem for breeders to identify varieties that consistently give high yields in locations with diverse environmental conditions. This result is in agreement with the findings of Trakanovas and Ruzagas, (2006) and Temasgen Bacha et al. (2015) who reported that the GEI was highly significant reflecting the differential response of genotypes in various environments. Crossa (1990), elaborated that only qualitative or crossover interactions are relevant in agriculture, and appropriate statistical analyses are required for quantifying them. Furthermore, the traditional analysis of variance determines the values of each variance source and the significance of the contribution of each component, but it does not partition the interaction in to several components and thus other types of analyses should be performed. Hence, such multi-location trial data along with a highly significant $G \times E$ interaction requires measures of stability analysis techniques that will help to get more information on the $G \times E$ interaction as well as to assess the adaptation regions of the genotypes according to their favorable interaction.

Ammi Analysis

The results of AMM model for grain yield are presented in Table 3. As it can be seen from the table, the mean square of the three IPCA were highly significant ($p < 0.001$). AMMI multiplicative component further partitioned the GE interaction into five interaction principal component axes (IPCA). However, only the first three axes showed significant contribution to the GEI in the AMMI model. The remaining two principal components contributed insignificant portion of the variation.

Table 3: AMMI analysis of variance for grain yield of 15 bread wheat genotypes in six locations

Source of Variation	D.f	Sum Square	Mean square	Explained%
Genotype	14	206.3	14.74***	33.46
Rep(Env't)	18	19.03	1.05	
Environment	5	217.53	43.51***	35.28
Interactions	70	192.67	2.75***	31.45
IPCA1	18	88.9	4.94***	46.1
IPCA2	16	55.17	3.45***	28.6
IPCA3	14	29.82	2.13***	15.5
Error	267	98.46	0.43	
Total	359	733.99		
Grand mean=3.77		C.V=16.55		

*** very highly significant at $P < 0.001$

The AMMI biplot, which accounted for 74.7% of the $G \times E$ interaction, provides the interaction principal component scores of the 1st and 2nd IPCA with 34 degrees of freedom. The first PC axis (PC1) score explained 46.1 % of the variation in GEI, while the second PC axes accounted for 28.6% of the variability. Many researchers

witnessed that the best accurate AMMI model prediction can be made using the first two IPCA [16]. Therefore, the dataset obtained from the interaction of 15 genotypes tested at 6 environments was best predicted by the first two IPCAs. On the other hand, the IPCA scores of a genotype in the AMMI analysis are reported as indication of the stability of a genotype across environments [9,17]. Accordingly, the closer the IPCA scores are to zero (origin), the more stable the genotypes are across all their testing environments [9].

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for grain yield and yield components (Figure 1). The greater the IPCA scores (positive or negative) as it is a relative value, the more specifically adapted a genotype is to certain environments. The more IPCA scores approximate to zero, the more stable the genotype is across environments sampled [9,18]. AMMI2 analysis positioned the genotypes in different locations, indicating the interaction pattern of the genotypes. The AMMI analysis for the IPCA1 captured 46.1% and the IPCA2 explained 28.6% and the two IPCs cumulatively captured 74.7% of the sum of square the GEI of bread wheat genotypes. When the IPCA1 was plotted against IPCA2, Purchase (1997) pointed out that the closer the genotypes score to the center of the biplot the more stable is the genotype and the reverse is true [9]. When looking at the environments it is clear that there is a good variation in the different environments. Holeta (HL), Bekoji (BJ) and Dhera (DH) were the most discriminating environments as indicated by the long distance between their marker and the origin (Figure 1). However, due to their large IPCA2 score, genotypic differences observed at these environments may not exactly show the genotypes in average yield overall locations. Closer relationships were observed between Kulumsa (KU), Arsi Robe (AR) and Asasa (AS).

Genotypes with a smaller vector angle in between and have similar projection, designate their proximity in the grain yield. Those genotypes that are clustered closer to the centre tend to be stable and those plotted far apart are unstable in yield. According, genotype ETBW8075 (#11), ETBW8070 (#2) and ETBW9470 (#14) were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The ETBW8078 (#3), ETBW8459 (#8) and Hidase (#15) were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments. The rest of the bread wheat genotypes were unstable and were located distant from the origin. Genotype ETBW9066 (#13), ETBW8084 (#4), ETBW8459 (#8), and ETBW9470 (#14) are positively interact at Kulumsa and Arsi Robe. The genotype ETBW8070 (#2) positively interact at Bekoji and Holeta. This two location are highland wheat production locations. There is closer association between Lemu (#1) and ETBW8065 (#6) which indicate similar response of the genotypes to the environment. Projection of genotypes point to environmental vectors indicated specific interactions between genotype and environment. The genotype with highest positive interaction with location Kulumsa (KU) was ETBW9470 (#14); ETBW8075 (#11) interacted positively with Dhera (DH), while ETBW8070 (#2) had high interaction with Holeta (HL) while ETBW9466 (#13) was the best genotype for Arsi Robe (AR) (Figure 1).

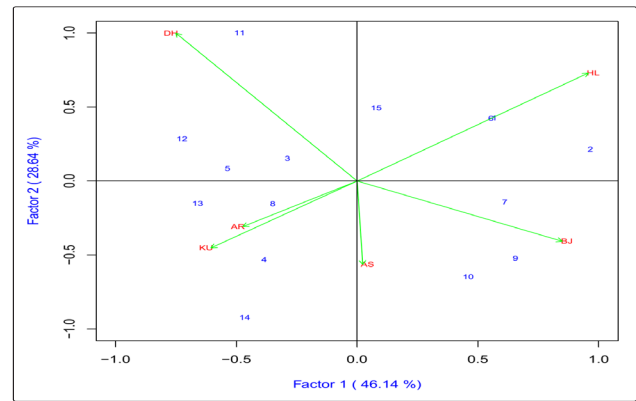


Figure 1: AMMI 2 Biplot of IPCA 1 against IPCA 2 for grain yield of 15 bread wheat genotypes tested across six locations

where 1=Lemu, 2=ETBW8070, 3=ETBW8078, 4=ETBW8084, 5=ETBW8311, 6=ETBW8065, 7=ETBW8427, 8=ETBW8459, 9=ETBW9037, 10=ETBW9045, 11=ETBW8075, 12=ETBW9464, 13=ETBW9466, 14=ETBW9470, 15=Hidase, (AR=Arsi Robe, AS=Asasa, BJ=Bekoji, DR=Dhera, HL=Holeta and KU=Kulumsa)

AMMI stability value (ASV)

The difference in stability measurement of the two principal components can be compensated by proportional difference between the IPCAs (1:2) then determined by Pythagoras theorem in effect of AMMI stability value. Purchase, (1997) noted that AMMI stability value (ASV) does not for quantitative stability measure by rather quantify and rank genotypes according to their yield stability [9]. The interaction principal component one (IPCA1) scores and the interaction principal component two in the AMMI model are indicators of stability. Considering the first interaction principal component (IPCA1) the genotypes ETBW9464, were the most stable genotype with IPCA1 value (-0.73) followed by ETBW9466, ETBW8311, ETBW8075 and ETBW9470 with IPCA1 value of (-0.66, -0.54, -0.49 and -0.47). When the second interaction principal component (IPCA2) was considered ETBW9470 was the most stable genotype with interaction principal component value (-0.93) followed by the genotype ETBW9045 with the IPCA2 value (-0.65). The two principal components have their own extremis, but calculating the AMMI stability value (ASV) is a balanced measure of stability [9]. The Genotypes with lower ASV values is considered more stable and genotypes with higher ASV are unstable. Based on ASV genotype ETBW8078 was the most stable with an ASV value of 0.49 followed by the genotype Hiddase, ETBW8459 with ASV value of 0.51 and 0.59 in grain yield respectively and the genotype ETBW8070, ETBW8075 and ETBW9470 were the most unstable with ASV value of 1.58, 1.28 and 1.19 in grain yield respectively (Table 4)

Yield stability index (YSI)

Stability is not the only parameter for selection, because the most stable genotypes would not necessarily give the best yield performance, hence there is a need for approaches that incorporate both mean yield and stability in a single index, that is why various authors introduced different selection criteria for simultaneous selection of yield and stability: rank-sum, modified rank-sum and

the statistics yield stability [19,20,21]. In this regard, ASV takes into account both IPCA1 and IPCA2 and justifies most of the variation in the GEI. The least YSI is considered as the most stable with high yield mean. It was applied to identify high yielding stable genotypes in cereal crops like maize and durum wheat [19,22]. By using these measures, suitable wheat genotype can be identified for varying existing environmental conditions. Based on YSI the most stable genotype with high grain yield is genotype Hidase (#15) with the value YSI (5) followed by ETBW8084 (#4), ETBW8427 (#7) and

ETBW9470 #14 and ETBW8078 (#3) with the value of YSI 10,12, 13 and 13, respectively and high yielding except ETBW8078 (#3) indicating that they were stable (widely adaptable) and high yielding. The genotype ETBW8075, ETBW9464 and ETBW8311 were unstable genotypes based on the value of yield stability index. Rank-sum (RS) introduced genotype ETBW8078 (RS=0.003) with low grain yield and followed by genotype ETBW9470 (RS=0.016) as the most stable genotypes with high grain yield. Both YSI and RS introduced genotype ETBW9470 as stable with high grain yield.

Table 4: Mean grain yield, ASV, YSI, RS, IPCA1 and IPCA2 of 15 bread wheat genotypes in six testing locations

SN	Genotype	GYLD	Rank	ASV	YSI	rASV	RS	IPCA1	IPCA2
1	Lemu	3.93	7	1.01	16	9	0.189	0.5728	0.4285
2	ETBW8070	4.6	2	1.58	17	15	0.336	0.9734	0.2157
3	ETBW8078	3.39	12	0.49	13	1	0.003	-0.2902	0.1529
4	ETBW8084	4.05	6	0.82	10	4	0.495	-0.3877	-0.5364
5	ETBW8311	3.11	14	0.87	19	5	0.018	-0.5407	0.0847
6	ETBW8065	3.91	9	0.99	16	7	0.031	0.5590	0.4268
7	ETBW8427	4.16	4	1.00	12	8	0.023	0.6165	-0.1452
8	ETBW8459	3.45	11	0.59	14	3	0.057	-0.3520	-0.1566
9	ETBW9037	4.11	5	1.19	16	11	0.174	0.6610	-0.5261
10	ETBW9045	3.9	10	0.99	16	6	0.059	0.4635	-0.6535
11	ETBW8075	1.53	15	1.28	29	14	0.265	-0.4901	1.0080
12	ETBW9464	3.35	13	1.21	26	13	0.355	-0.7313	0.2871
13	ETBW9466	3.91	8	1.08	18	10	0.128	-0.6653	-0.1524
14	ETBW9470	4.93	1	1.19	13	12	0.016	-0.4688	-0.9302
15	Hidase	4.29	3	0.51	5	2	0.104	0.0800	0.4969

Where; GYLD=mean grain yield, ASV=AMMI stability value, YSI=yield stability index, RS= Rank sum, IPCA=interaction principal component

Conclusion

The genotype x environment interaction (GEI) has been an important and challenging issue among plant breeders, geneticists, and agronomists engaged in performance testing. The GEI reduces association between phenotypic and genotypic values and leads to bias in the estimates of gene effects and combining ability for various character that are sensitive to environmental fluctuations. Such traits are less amenable to selection. Both yield and stability of performance should be considered simultaneously to reduce the effect of GEI and useful for selecting genotypes in a more precise and refined way. The genotype ETBW8075, ETBW8070 and ETBW9470 were unstable and ETBW8078, ETBW8459, Hidase and ETBW8311 were stable bread wheat genotypes across environments. The best genotype with respect to location Kulumsa was ETBW9470, ETBW8075 was the best genotype for Dhera, ETBW8070 was the best genotype for Holeta while ETBW9466 was the best genotype for Arsi Robe. Arsi Robe and Kulumsa is the most favorable environment for all genotypes with nearly similar yield response for grain yield.

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