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Genotype X Environment Interaction and Yield Stability of Bread Wheat Genotypes in South East Ethiopia

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Abstract: Twenty bread wheat genotypes and two checks were evaluated at six test locations of Central and South Eastern Ethiopia 2013/1014 during main growing season in a randomized complete block design using four replications. The objective of the study was to quantify the magnitude of genotype by environment interaction and yield stability of bread wheat genotypes. The additive main effect and multiplicative interaction effect model (AMMI) analysis revealed significant difference at (P=0.01) for genotype, location and genotype by location interaction for the response variable grain yield. Accordingly, the first and second IPCAs share 60.77 and 15.70% of the G x E SS captures 20.68 %.The AMMI model clearly indicate the genotype by environment interaction by partitioning into three significant component taking 89.70% of genotype by environment variation 20.68% of the variation in the genotype by environment interaction. According to the Stability analysis of the additive main effect and multiplicative interaction, biplot analysis ranking biplot the genotype Digelu and ETBW6738 were the most stable coupled with higher grain yield where as the genotypes Danda'a and ETBW6732 were unstable.in each tested location. Based on the AMMI, environments were highly variable both for main and interaction effects. Bokoji, Kulumsa, Sinana, Holeta and Asassa were favorable environments. Areka as low yielding (unfavorable) environments for majority of the traits. In general, the results of the analysis showed that bread wheat is highly sensitive to environmental changes and this necessitates screening of cultivars for wide and specific adaptation. Based the one year data the genotype Digelu were stable accompanied with higher yield but in order to recommended appropriate genotypes to the south Eastern Ethiopia, repeating the trial is vital.

Key words: AMMI · Bread wheat · Genotype-by- environment interaction · Stability

INTRODUCTION

Bread wheat *(Triticum aestivum* L.), together with durum *(Triticum turgidum* L.) are the most widely distributed crops worldwide and of primary importance for human nutrition [1]. Its high productivity contributed to the prevention of widespread food shortage and stabilized the food security of countries like Asia, Latin America and to some extent in Africa [2].

Ethiopia is the second largest wheat producer, after South Africa, in Sub- Saharan Africa. Wheat covers an area of 1453817 ha with production of 2537639.8 t [3].Wheat has been one of the major cereals of choice, dominating the food habit and dietary practices and known to be a major source of energy and protein for the highland population [4].

The regions identified as highly suitable for wheat production include Arsi, South - Shewa, West- Shewa, North - Shewa, Ilubabor and Western - Harerge, Sidamo, Tigray, North - Gonder, Bale and Gojam. In some regions wheat covers an area of 101092.5 ha with production of 138719.28 t and ranks fourth next to maize, sorghum and barely in terms of productivity; fourth in terms of production next to sorghum, teff, barley and third in area production next to teff, sorghum [5].

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Average national grain yield of wheat in Ethiopia is estimated to be around 2.2 t/ha, National average yield is1.8 t/ha in the Arsi Zone region [3]. which is lower as compared to the world average productivity, which is 2.7 t/ha [6]. which is far below from experimental yields of over 5 t ha^{-1} [7]. This is because of the many production constraints of which the major ones include: poor soil fertility, high incidence of weeds, pests and diseases, drought and shortage of well-adapted improved varieties. All these constraints result in yield fluctuation from season to season and from location to location [8]. Thus the huge gap between the research centers by which the genotype being released and the target environment farmers' field could be due to the less representation production environment that leads to the significant genotype by environment interaction.

The National wheat breeding program in Ethiopia had started about half a century ago [8]. Nationally, still 41 improved bread wheat varieties had been released. Testing of nationally released and exotic introduced wheat genotypes have been continously under going by the Kulumsa Agricultural Research Institute (KARI) for their high yielding performance and adaptation.

The GxE interaction reduces association between phenotypic and genotypic values and thus, a genotype that performs well in a given environment may not necessarily respond well in other environment. So if environments are sufficiently different, GxE interaction can result in different yield ranking of evaluating genotypes. In addition, the relationship between selection environments and target production environment had been a fundamental problem because many of the selected activities performed by the conventional approach are in on-stations which are good production environments [9]. Multi-environment yield trails are essential in estimation of genotype by environment interaction (GEI) and identification of superior genotypes in the final selection cycles [10,11].

Different methods are commonly used to analyze multi location yield trial data to reveal patterns of genotype by environment interaction. The additive main effects and multiplicative interaction (AMMI) model gives good insight in separating complicated patterns of genotypic by environment interaction by using combining the classical analysis of variance and the principal component analysis [12].This study is initiated with the objective of to evaluate the yield performance and stability of bread wheat genotypes.

MATERIALS AND METHODS

Experimental Design: The trial was conducted in six locations during 2013 crop season and the detailed descriptions of the locations (Table 1). 22 bread wheat genotypes (Table 2) were laid out in randomized complete block design (RCBD) with four replications. A total of 6 rows with row spacing of 0.2m and with a total plot size of 1.2 meter by 2.5 meter and spacing between plots was 0.5 meter while spacing between block was maintained at 1 meter. Seed rate of 150 kg ha^{-1} and planting was made by drilling to the six rows. A fertilizer rate of 41 kg N ha^{-1} and 46 kg P_2O_5 ha^{-1} of split application were used during sowing and tillering period and data for yield were collected from the four middle rows.

Statistical Analysis: The additive main effect and multiplicative interaction effect (AMMI) were done based on the model suggested by [13].Using the crop stat 7.2 software released by the international rice research institute

$$y_{ij} = \mu + G_i + E_j + (\sum_{1}^{n} K_n U_{ni} S_{nj}) + Q_{ij} + e_{ij}$$

where: (i = 1, 2……….22: j = 1…….6); Y_{ij} = The performance of the i^{th} genotype in the j^{th} environment; μ= The grand mean; G_i = Additive effect of the i^{th} genotype (genotype mean minus the grand mean); K_n = Eigen value of the PCA axis n,; E_j = Additive effect of the j^{th} environment (environment mean deviation); U_{ni} and S_{nj} = Scorer of genotype i and environment j for the PCA axis n; Q_{ij} = Residual for the first n multiplicative components and ; e_{ij} = error.

To see the yield stability analysis, the formula suggested by [14] was used and the output of the crop stat software was calculated using the Microsoft excels 2010.

$$ASV = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}}(IPCA1score)^2 + \left[IPCA2sccore\right]^2}$$

where

ASV= AMMI stability value

IPCA1 = interaction principal component analysis 1.

IPCA2 = interaction principal component analysis 2.

SSIPCA1 = sum of square of the interaction principal component one.

SSIPCA2 = sum of square of the interaction principal component two.

Table 1: Description of the study site

Locations	Annual Rainfall (mm)	Altitude (m.a.s.l.)	Latitude	Longitude	Temperature(°C)	Soil type
Kulumsa	832	2200	08^0 01' 10"N	39^0 09' 11"E	10.5-22.8	Luvisol
Bokoji	1020	2809	08^0 31' 60"N	39^0 15' 0"E	7.9-18.6	Nithosols
Asassa	620	2340	07 07 N'	39 11 56 E'	5.8-23.6	Clay loam
Holeta	872	2400	09 04 N'	38 29 E'	10.1-36.4	Red
Sinana	834	2600	$07^0$4' 60"N	$40^0$12'0"E	10-22	clay
Areka	633	1751	07^0 4'0.0"N	37^0 $42^0$0.0"E	15-30	Sandy loam

Source: BoARD (2013)

Table 2: Pedigree and Selection history of materials used in this study

Entry	Genotype	Pedigree
1	Danda'a	Breeder Seed (Check)
2	ETBW 6728	ROELFS F2007
3	ETBW 6729	TRCH/SRTU/5/KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES
4	ETBW 6730	WAXWING*2/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1
5	ETBW 6731	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/PARUS/6/FRET2*2/KUKUNA
6	ETBW 6732	PBW343*2/KUKUNA*2//YANAC
7	ETBW 6733	FRET2/KUKUNA//FRET2/3/PARUS/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
8	ETBW 6734	ROLF07*2/KIRITATI
9	ETBW 6735	ROLF07/YANAC//TACUPETO F2001/BRAMBLING
10	ETBW 6736	WBLL1/KUKUNA//TACUPETO F2001/5/WAXWING/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
11	ETBW 6737	WAXWING/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1
12	ETBW 6738	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1
13	ETBW 6739	SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI
14	ETBW 6740	PBW343*2/KHVAKI//PARUS/3/PBW343/PASTOR
15	ETBW 6741	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/PFAU/WEAVER//BRAMBLING
16	ETBW 6742	WBLL1//UP2338*2/VIVITSI
17	ETBW 6743	WAXWING/WHEAR//WAXWING/KIRITATI
18	ETBW 6744	FRET2/KUKUNA//FRET2/3/YANAC/4/FRET2/KIRITATI
19	ETBW 6745	TRCH//PRINIA/PASTOR
20	ETBW 6746	BAV92//IRENA/KAUZ/3/HUITES/4/DOLL
21	ETBW 6747	PBW343*2/KUKUNA//PARUS/3/PBW343*2/KUKUNA
22	Digelu	Breeder Seed (Check)

RESULTS AND DISCUSSION

Additive Main Effect and Multiplicative Interaction Analysis: The AMMI for the additive main effect showed a significant variance (P<0.01) for the locations, genotypes and genotype by location interaction (Table 3). The environment captured the maximum sum of squares 51.97 % followed by the genotype by location interaction sum of squares which (20.68 %) and the genotype sum of square were the least (8.97%).The large sum of squares for environment showed that the environment was diverse with large differences among environmental means and caused variation in performance of the genotypes and this could be attributed due to the unequal distribution of rain fall in the growing season and heterogeneity of location in soil type and altitude range in discriminating the performance of genotypes. Large environmental sum of squares was reported by [15, 10] that who found very large and significant environmental sum of squares.

The AMMI analysis (Multiplicative effect) was further demonstrated three significant interaction principal components and according to the significant F-test provided by [16] the three multiplicative interaction principal components was significant (P<0.01) where the remaining interaction principal component was not significant the result was not in agreement with [17] recommended an AMMI model with the first three IPCAs predicates the genotype by enviroment interaction. adequately predict model fitness of the additive main effect and multiplicative interaction (AMMI). The adequate number of interaction principal component in the AMMI model affected by type of traits measured, crop type but according to [18, 19] in multi location yield trial the pattern of interaction is mainly explained by the two interaction principal component analysis and using the two interaction principal component the genotypes can be recommend.

Table 3: AMMI analysis of variance for grain yield of 22 bread wheat genotypes in six locations, in the production year 2013/2014 in South Eastern Ethiopia

Source	df	SS	MS	%SS
Total	527	36017	68.3	
Treatments	131	27064	206.6**	75.14
Genotypes	21	897	42.7**	8.97
Environments	5	18718	3743.7**	51.97
Block	18	419	23.3**	
Interactions	105	7448	70.9**	20.68
IPCA1	25	4526	181**	60.77
IPCA2	23	1169	50.8**	15.70
IPCA3	21	985	46.9**	13.23
IPCA4	19	534	28.1^{ns}	7.17
IPCA5	17	234	13.7^{ns}	5.17
IPCA6	15	0	0^{ns}	0
Error	378	8535	22.6	

** significant at $p \leq 0.01$, ns = not significant

The AMMI analysis of variance (Multiplicative effect) was further broken by decomposing it into principal components (Table3). The first principal component (IPCA1 explained 60.77% of the genotype by environment interaction and the AMMI 1 had a model fitness of 89.2 % of the treatment sum of square in the genotype by environment interaction of the bread wheat genotypes and 8.97% was explained due to noise. Hence the genotype by environment data of the 22 bread wheat genotype were best explained by AMMI 1 The result of the study was in agreement with [20] that the AMM2 had better fitness in food barley.

AMMI 1 Biplot Analysis: The AMMI analysis provides a graphical representation (biplot) to summarize information on main effects and interactions effect of both genotypes and environments simultaneously. The intimacy between pairs of locations or pairs of genotypes in the biplot is proportional to their similarity for genotype by location interaction effects [21]. The interaction principal component 1 (IPCA1) represented in the y- axis where as the genotype and environment mean represented on the x-axis (Figure 1). Genotypes or Location located in the right side of the midpoint of the perpendicular line have higher yields than genotypes or location placed to the left side of the perpendicular line (grand mean).

Genotypes or Environments located in the right side of the midpoint of the perpendicular line have higher yields than those on the left side hence genotypes G22 (Digelu), G12 (ETBW6738),G4(ETBW6730), G19 (ETBW6745),G20 (ETBW6746) and G13 (ETBW6739) were higher yielder genotypes with mean grain yield of (44.66,44,44.15,43.62,45.91 Qt/ha) respectively. The genotypes G1 (Danda'a), G6 (ETBW 6732) and G21(ETBW6747) were genotypes with lower mean grain yield.

The genotype G22 (Digelu), G12 (ETBW6738), G4 (ETBW6730), G17 (ETBW6743) and G21 (ETBW6747) was located near to the origin with lower contribution to the magnitude genotype by environment interaction implying that the genotypes were stable. The genotypes G1 (Danda'a), G10 (ETBW 6736) G6 (ETBW6732) and G21 (ETBW6746) they were the most unstable genotypes (Fig 1).

The testing locations E5 (Asassa), E4 (Kulumsa), E6 (Bokoji) and E1(Holeta) were favorable testing location located to the right side of the grand mean where as the only testing location E3(Areka) was un favorable testing location placed to the left Side of the perpendicular line (grand mean). The testing location E3 (Areka) was located distant from the origin implying the testing locations had higher contribution to the magnitude of genotype by environment interaction and caused unstable genotype performance. The testing locations E5 (Asassa) and E4 (Kulumsa) were nearly placed to the origin with lower contribution to genotype by environment interaction and implying the testing locations had less contribution to the genotype by location interaction and contributes to the stable performance of the genotypes. The AMMI biplot analysis the first interaction principal component(IPCA1) had explained 60.77% of the genotype by enviroment interaction and AMMI1 had a model fitness of 89.2% of the treatment sum square in the genotype by enviroment interaction of bread wheat genotypes and 8.97% was explained the noise. The genotype by enviroment interaction of the bread wheat genotypes the AMMI 1 model gives the best model fit. The result of the study

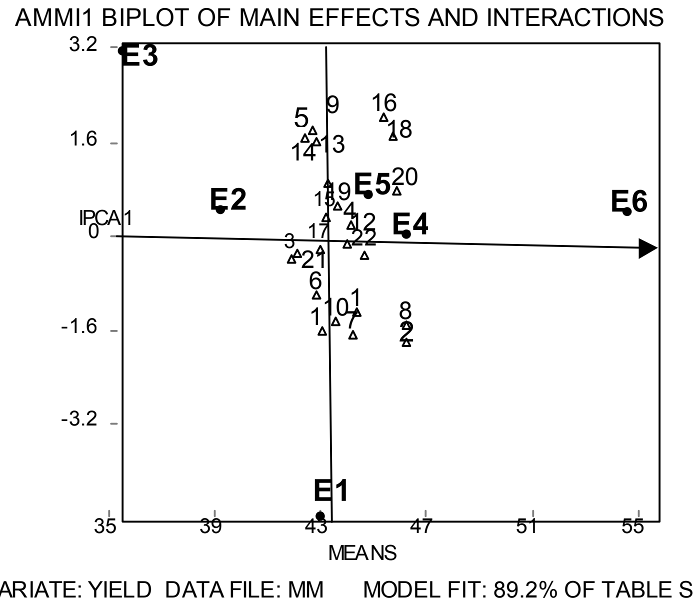

Fig. 1: AMMI biplot for grain yield of 22 bread wheat genotypes tested in six locations of South East Ethiopia
Genotypes plotted as G1, G2 and G3 …and Enviroment plotted as Hol, Si, Are, Kul, Asas and Bok N.B. abbreviations in the Biplot are mentioned as follows:
Genotypes: G1 = Danda'a, G2 =ETBW6728, G3 = ETBW6729, G4 = ETBW6730, G5= ETBW6731,G6= ETBW6732, G7 = ETBW6733, G8 = ETBW6734, G9= ETBW6735,G10= ETBW6736,G11= ETBW6737, G12= ETBW6738, G13= ETBW6739, G14= ETBW6740,G15= ETBW6741, G16= ETBW6742,G17= ETBW6743, G18= ETBW6744,G19= ETBW6745,G20= ETBW6746, G21= ETBW6747 and G22= Digelu
Environments: E1 = Holeta, E2 = Sinana, E3 = Areka, E4 = Kulumsa, E5= Asassa, E6= Bokoji

Table 4: AMMI stability value for yield of 22 bread wheat genotypes in six testing locations, in the production year 2013/14 during main cropping season

Genotype	Gm	IPCA1	IPCA2	ASV	Rank
Danda'a	44.38	-1.27786	1.33862	-1.81	1
ETBW 6728	46.28	-1.79806	-0.26947	4.70	21
ETBW 6729	41.92	-0.36901	0.21094	-0.56	8
ETBW 6730	44.15	0.18712	0.94152	0.43	12
ETBW 6731	42.74	1.82082	-0.38154	-4.06	3
ETBW 6732	42.84	-0.98481	-0.39517	1.68	16
ETBW 6733	44.26	-1.66424	-0.9284	2.55	19
ETBW 6734	46.26	-1.50209	-0.98992	2.22	17
ETBW 6735	42.88	1.62932	0.01803	15.49	22
ETBW 6736	43.61	-1.44632	0.75188	-2.26	5
ETBW 6737	43.09	-1.6206	-1.14472	2.36	18
ETBW 6738	44	-0.12151	0.90872	-0.34	11
ETBW 6739	42.39	1.68251	0.63706	2.92	20
ETBW 6740	43.31	0.91047	1.00576	1.29	15
ETBW 6741	43.18	0.31643	-0.40548	-0.45	10
ETBW 6742	45.39	2.02295	-1.08007	-3.14	4
ETBW 6743	43	-0.21457	1.53483	-0.58	7
ETBW 6744	45.78	1.72196	-0.20315	-5.05	2
ETBW 6745	43.62	0.50953	0.11778	1.09	14
ETBW 6746	45.91	0.77984	-1.67056	-1.26	6
ETBW 6747	42.14	-0.26972	-0.86663	0.51	13
Digelu	44.66	-0.31217	0.86997	-0.55	9

was in agreement with [22] in food barley and similar reports was been made by [23] in Evaluation of yield and seed requirements stability of bread wheat that the AMMI2 had better fitness in bread wheat genotypes and deviation of current study with the previous authors could explained the genotype by enviroment interaction.

AMMI Stability Value (ASV): The Bread wheat genotypes showed significant genotype by testing location interaction effect and the additive and multiplicative interaction effect stability analysis (ASV) implied to decompose the interaction effect. Considering mean grain yield as a first criteria for evaluating the bread wheat genotypes ETBW6728 was with a higher mean grain yield (46.28Qt/ha) followed by the genotypes ETBW6734 and ETBW6746 with the mean grain yield of (46.26 and 45.91 Qt/ha) while the genotypes ETBW6729, ETBW6747 and ETBW6742 was with low mean yields across the testing locations (Table 2). The interaction principal component one (IPCA1) scores and the interaction principal component two in the AMMI model are indicators of stability [14].

Considering the first interaction principal component (IPCA1) the genotypes ETBW6728, were the most stable genotype with IPCA1 value (-1.79) followed by ETBW6733, ETBW6737 and ETBW6734 with IPCA1 value of (-1.66,-1.62and -1.50). When the second interaction principal component (IPCA2) was considered ETBW6746 was the most stable genotype with interaction principal component value (-1.67) followed by the genotype ETBW6737 with the IPCA2 value (-1.14).

The two principal components have their own extremes, but calculating the AMMI stability value (ASV) is a balanced measure of stability [14]. The Genotypes with lower ASV values is considered more stable and genotypes with higher ASV are unstable. According to the ASV ranking in the (Table 2) the genotype Danda'a was the most stable with an ASV value of (-1.81) followed by the genotype ETBW6744 with ASV value (-5.05).The genotypes ETBW6735 was the most unstable with ASV value (15.49). The Stable genotypes was followed with mean grain yield above the grand mean and this result was in agreement with [17] who has used ASV as one method of evaluating grain yield stability of bread wheat varieties in Tigray and similar reports been made by [22, 24] in barley in Tigray and bread wheat Using AMMI stability value.

CONCLUSION

The AMMI analysis for the additive main effect and multiplicative interaction effect revealed significant variance for Genotype, location and genotype by location interaction. For the study of genotype by environment interaction of the 22 bread wheat genotypes across six locations the AMMI1 gives the best model fitness.

In multi-location, adaption trial considering both the stability and mean grain yield is vital. According to the ASV and AMM1 biplot the bread wheat genotypes ETBW6742, ETBW6730 and ETBW6732 were stable genotypes coupled with higher mean grain yield greater than the grand mean.

The genotypes Danda'a, ETBW6732 and ETBW6747 were unstable with lower mean grain yield less than the grand mean. Using the AMMI 1 biplot analysis E2 (Sinana), E5 (Asassa), E6 (Bokoji), E4 (Kulumsa) and E1 (Holeta) were favorable testing locations while the testing location Areka was unfavorable on some response variables.

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