Genotype by Environment Interaction and Stability Analysis for Grain Yield of Durum Wheat Genotypes Evaluated in Ethiopia

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Abstract

The objective of this study was to examine the genotype by environment interaction and evaluate the stability of genotypes using Additive Main effect and Multiplicative Interaction (AMMI) and genotype and genotype by environment (GGE) biplot analyses. Accordingly, twenty genotypes were evaluated across seven locations using RCBD with four replications during 2011/12 main cropping season. Stability of genotypes was calculated using cultivar superiority measure, Wricke's ecovalence and AMMI stability values. AMMI analysis showed significant ($P<0.001$) effects of genotype, location and genotype by location interaction for grain yield. Location, genotype and genotype by location interaction accounted 74%, 2% and 7% of the variation in grain yield, respectively. The mean squares of the first and second interaction principal component axis were highly significant at $P\leq0.001$ & $P\leq0.01$, respectively. Hence, AMMI model with the first two IPCA was the best predictive model. The stability analysis revealed that genotype 7 (G7) was highly stable with above average grain yield and can be a promising candidate for release. The GGE biplot analyses revealed that the first and second principal component explained 46% and 28% of the GGE sum square, respectively. On the 'which won where pattern' of the biplot, the test locations were grouped in to two mega environments. Mega environment-1 included four of the seven locations and represented by the best performer genotype G13. Whereas, mega environment-2 included two locations and represented genotype G1. Among the test locations, Angacha and Arsi Robe were the most discriminating locations while Hossana was the least and should not be included as a test location.

Key words: Genotype by environment interaction. Stability. AMMI. GGE biplot.IPCA.

Introduction

Durum wheat (*Triticum turgidum var. Durum*) is an indigenous tetraploid (2n=4x=28) wheat species which has been cultivated since ancient time in Ethiopia (Tesfaye and Getachew, 1991). The country is considered to be one of the centers of diversity for tetraploid wheat (Vavilov, 1951). This crop is traditionally produced in the heavy black clay soils (vertisols) under rain fed conditions between an altitude range of 1800 and 2800 meters above sea level (Tesfaye and Getachew, 1991). As this crop is an industrial crop meant for the production of pasta and related products, yield and quality are equally important. However, these important traits are affected by genetic and environmental factors. For this reason, efforts have been made to develop varieties which are stable, high yielder, resistant to diseases and meet quality standard for agro-industries. Therefore, conducting multi environmental trials are crucial to evaluate and identify stable high yielding genotypes for the aforementioned and other important traits.

Plant breeding programs undertake multi-environment trials to evaluate the performance of genotypes at various environmental conditions and select the best performing ones for release as a variety. Moreover, multi-environment trials were carried out to determine if the test environments could be subdivided in to different mega-environments for meaningful cultivar evaluation and recommendation. However, the selection of many crop varieties including durum wheat suitable for the production environment is often challenged by the presence of genotype by environment interaction in the variety development process. Genotype by environment interaction (GEI) is the differential or inconsistent phenotypic performance of genotypes across environments (Asrat *et al.*, 2009). In such cases, the mean grain yield of genotypes across environments is not sufficient and meaningful indicator of the genotype performance (Yan and Kang, 2003). Genotype by Environment Interaction (GEI) could be a non-crossover type where the ranking of genotypes remains constant across the test environments and the interaction is significant because of the change in the magnitude of the response or a crossover type where a significant change in rank occurs from one environment to another (Tesfaye *et al.*, 2008). The presence of GEI reduces the association between genotype and phenotype which leads to change in relative ranking and stability differences of genotypes across environments, and also diminishes the genetic progress expected from plant breeding (Ayalneh *et al.*, 2013; Tamene *et al.*, 2013). Therefore, assessing any genotype or agronomic practices without including its interaction with the environment is incomplete and limits the accuracy of yield estimates (Crossa, 1990). The universal phenomenon in all regional yield trial is that E (Environment) is the predominant source of yield variation, and G (Genotype) and GEI (Genotype by Environment interaction) are relatively small (Yan and Kang, 2003). According to these authors, E is irrelevant for cultivar evaluation although its effect is large. However, G and GE are relevant to meaningful cultivar evaluation and they should be considered simultaneously in making selection decision (Yan and Kang, 2003; Yan, 2001).

A number of statistical procedures are available to analyze data from multi-environment trials. Among others, Additive Main effect and Multiplicative Interaction (AMMI) analysis is a useful method to clarify genotype by environment interaction. It can also be used to determine stability of genotypes across environments using principal component axis (PCA) scores and AMMI stability value (ASV) (Hintsa and Fetien, 2013; Jemanesh *et al.*, 2007). However, the additive component of AMMI can give an indication whether the GEI is significant or not, but not on the insight as to which genotypes and environments contributed to the GEI. Therefore, the GGE biplot analysis is a good method to fully explore multi-environment trials (METs) based on principal component analysis (PCA) (Hintsa and Fetien, 2013).

Durum wheat lacks stability in its performance when grown over a wide range of environments (Jemanesh *et al.*, 2007) and thus GEI is a challenge in the improvement of many crops including durum wheat. Therefore, the objective of the current study was to examine the presence and type of GEI; and evaluate the stability of twenty durum wheat genotypes tested under different environments of Ethiopia, using AMMI and GGE biplot analyses.

Materials and methods

Experimental set up

The field experiment was carried out during the 2011/12 main season at seven major durum wheat growing locations in Ethiopia (Adet, Angacha, Arsi Robe, Chefe Donsa, Debre Zeit, Haramaya and Hossana) representing optimum and high rainfall environments. Fifteen durum wheat genotypes along with four standard checks (Ude, Kilinto, Yerer and Hitosa) and a local check were evaluated using randomized complete block design (RCBD) with four replications. The plot area was six rows of 2.5 m long with inter-row spacing of 20 cm. The seed rate was 150kgha^{-1} and fertilizer rate was 100/100 kgha^{-1} Urea/DAP with split application of urea (half at planting and half at the end of tillering). Other agronomic practices were applied as per the recommendations for each location. The central four rows were harvested to measure grain yield and other agronomic traits and grain yield was considered for the current analysis.

Statistical analysis

Statistical analyses were done using GenStat 16th edition statistical software. Before undertaking the combined analysis of variance over environments (locations), the homogeneity of residual variance test was carried out by using Leven's test of the SAS statistical procedure, SAS version 9.1.3.; and normality test was undertaken using the GenStat 16th edition statistical software residual plot procedure. Accordingly, the data were found homogenous and normally distributed.

AMMI analysis: The grain yield data was subjected to AMMI analysis using the GenStat 16th statistical software. AMMI analysis first fits the additive main effects of genotype and environment using the traditional analysis of variance and then describes the non-additive part (genotype × environment) by principal components analysis. The model is given by equation 1 (Crossa, 1990).

$$Yij = \mu + Gi + Ei + (\sum_{n-1}^{h} knvnisnj) + eij$$

Where Yij = the mean yield of the i^{th} genotype at the j^{th} environment, μ= the grand mean yield, Gi= the genotype effect, Ei= the environment effect, $\sum_{n-1}^{h} knvnisnj) = GEij$ the interaction effect of the genotype and environment, kn= the singular value of the n^{th} axis, vni=the eigenvector of the i^{th} genotype for the n^{th} axis, snj=the eigenvector of the j^{th} environment at for the n^{th} axis and eij = the average of the random errors associated with the n^{th} plot that receive the i^{th} genotype at the j^{th} environment.

Stability analysis: to evaluate the stability of genotypes, Wricke's ecovalence (Wi) and cultivars superiority measures (Pi) were analyzed using GenStat 16th statistical software whereas AMMI Stability Value (ASV) was calculated by the formula suggested by Purchase (1997) using Microsoft Excel.

$$\mathrm{ASV} = \sqrt{\frac{\mathrm{SSIPCA1}}{\mathrm{SSIPCA\,2}}(\mathrm{IPCA1}_{\mathrm{score}})^2 + [\mathrm{IPCA2}_{\mathrm{score}}]^2}$$

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 1, SSIPCA2 = Sum of square of the interaction principal component 2

GGE biplot analysis: to graphically evaluate the relationship between environments (testers) and genotypes, GGE biplot analysis was also executed using GenStat 16th statistical software. The basic model for GGE biplot according to Yan (2001) is:

$$Yij - \overline{YJ} = \lambda_1 \xi_{i1} \eta_{j_1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where Yij= the average yield of the genotype i in the environment j, $\overline{YJ}$ = the average yield over all genotypes in environment j, λ_1 and λ_2 = the singular values of PC1 and PC2 respectively, ξ_{i1} and ξ_{i2} = the PC1 and PC2 scores, respectively for genotype i, η_{j_1} and η_{j2} = the PC1 and PC2 scores, respectively for environment j, ε_{ij} = the residual of the model associated with the genotype i in environment j.

From the result of this analysis genotypes with wide & specific adaptability were identified and environments were grouped to different mega-environments. Thus, genotypes located near the origin of the biplot are considered as widely adapted and those which are located far from the origin of the biplot are specifically adapted. Moreover, locations which fell in the same sectors of the polygon version of the biplot were grouped as same mega-environment.

Results and discussion

Additive main effect and multiplicative interaction (AMMI) analysis:

The AMMI analysis of variance for grain yield (kg ha^{-1}) of 20 durum wheat genotypes tested at seven locations is presented in Table 1. Considering the additive component of the analysis, the result showed significant (P<0.001) effects of genotype, location and genotype by location interaction on grain yield. Location accounted the largest parts of the variation in grain yield (73.50%) followed by genotype by location interaction (6.81%) and genotype (1.79%). Similar results were reported by Asrat *et al*. (2009) on soybean, Tesfaye *et al*. (2008) on bread wheat, Hintsa and Fetien (2013) on barley, Tamene *et al.* (2013) on field peas and Muez *et al.* (2014*)* on durum wheat. Likewise, Yan and Kang (2003) also reported environment as the predominant source of variation. In the current study, the largest variation in yield explained by environments indicated the presence of different environments that can be sub-grouped into mega-environments.

The average environmental grain yield across genotypes ranged from 1123 kg ha^{-1} at Adet to 4577 kg ha^{-1} at Angacha, while the average genotype grain yield across environments ranged from 2805 kg ha^{-1} for genotype G12 to 3257 kg ha^{-1} for genotype G13 (Table 2). Moreover, this study revealed that the magnitude of the GEI sum of squares was about four times larger than that for genotypes indicating the differential responses of genotypes across environments. The GEI in the current analysis was a cross-over type whereby a change in the ranking of genotypes was observed across the test environments (Table 2). This condition limits the selection and recommendation of genotypes for a target environment because of the difficulty to interpret yield based on genotype and environment means alone (Asrat *et al.,* 2009).

The multiplicative component of AMMI further revealed that the mean squares was highly significant ($P \leq 0.001$) for the first interaction principal component axis (IPCA1) and significant ($P \leq 0.01$) for the second interaction principal component axis (IPCA2), while the third interaction principal component axis (IPCA3) was not significant (Table 1). Hence, the first two PCA explained 72.67% of the total G x E interaction.

The first and the second principal component axis explained 56.04% and 16.63% of the GEI sum of squares, respectively. Furthermore, the first interaction principal component axis sum of squares was greater than the second indicating the presence of differences in grain yield performance of the genotypes as a result of GEI. This finding is in agreement with that reported for bread wheat (Hintsa and Fetien, 2013) and field pea (Tamene *et al.,* 2013).

Table 1: AMMI analysis of variance for grain yield of durum wheat genotypes tested at seven locations.

Source of variation	Degrees of freedom	Sum of squares (SS)	Mean squares (MS)	Proportion of explained variance (%)
Total	559	1329089819	2377620	
Genotypes	19	23789314	1252069***	1.79
Location	6	976934823	162822470***	73.50
Block	21	91172230	4341535***	-
Interactions	114	90514222	793984***	6.81
IPCA1	24	50728086	2113670***	56.04
IPCA2	22	15053919	684269*	16.63
IPCA3	20	10295911	514796NS	11.37
Residuals	48	14436305	300756	-
Error	399	146679231	367617	-

*. **, ***Significant at P<0.05, P<0.01 and P<0.001, respectively; NS=non-significant

The first and the second IPCA together explained 72.67% of the variability in grain yield of durum wheat due to GEI and were significant, but the third IPCA accounted for 11.37% of the GEI sum of square and was non-significant. Therefore, AMMI with the first and the second IPCA was the best predictive model for cross validation of the yield variation explained by the GEI whereas the third IPCA and residuals were considered as a noise. Several authors took the first two IPCAs for GGE biplot analysis for different crops (Asrat *et al.,* 2009; Hintsa and Fetien ,2013; Tamene *et al.,*2013;and Mulusew *et al.,*2014).

Stability analyses:

The stability result of the 20 durum wheat genotypes measured using cultivar superiority (Pi), AMMI stability values and Wricke's ecovalence (Wi) methods are presented on Table 3.

Cultivar superiority measure (Pi)

The smaller the value of the Pi, the less is the distance to the genotype with maximum mean yield and the better the genotype (Martin, 2004). Accordingly, genotype G13 showed the least Pi value and was the most stable genotype followed by G7, G6 and G5. On the other hand, G14 was the genotype with the highest cultivar superiority measure and thus the most unstable genotype with below average grain yield (Table 3).

Wricke's ecovalence (Wi)

This method defined the concept of ecovalence, to describe the stability of a genotype as the contribution of each genotype to the GEI sum of squares. Genotypes with low Wi values have smaller variations across environments and thus considered as stable (Mulusew *et al.*, 2014). Hence, G7 was the most stable genotype according to this method; coupled with above average grain yield. Similarly, genotypes G2, G8 and G3 showed relatively stable performance across locations but their yield potential is below average (Tables 2 and 3). Genotype G13 showed the largest ecovalence indicating that this genotype was the least stable according to this method (Table 3).

AMMI stability value (ASV)

The ASV of 20 durum wheat genotypes tested at seven locations is presented on table 3. The interaction principal component analysis one (IPCA1) and two (IPCA2) scores are indicators of stability, but these two scores have their own extremes. Therefore, calculating ASV is a balanced measure of stability (Muez *et al.*, 2014). Accordingly, genotypes with lower ASV values are stable and those with higher values are unstable. Genotype G2 with the lowest ASV value was the most stable genotype followed by G8, G3 and G7. Genotype G13 was the most unstable genotype according to this method (Table 3).

Since the variation in yield explained by location was large in this study, and this is not useful in cultivar evaluation and mega-environment analysis, AMMI and GGE biplot analysis are appropriate methods to further exploit the current multi-environment trial data.

AMMI biplot analyses

The AMMI biplot of 20 durum wheat genotypes evaluated at seven environments is presented in Figure 1. According to Zobel *et al.,* (1988), when a genotype and an environment have the same sign on the PCA axis, their interaction is positive; but if different, their interaction is negative. If a genotype or environment has an IPCA score of nearly zero it has small interaction effects. Accordingly, Haramaya and Chefe Donsa differ in main effects but not in interaction, since the mean yield differs but the IPCA score do not (Fig.1). Angacha and Haramaya differ in interaction but not in main effects. Adet and Chefe Donsa differ both in the interaction and main effects (Fig 1). On the other hand, G10, G6, G8, G12 and G17 had the same sign on the IPCA score with the locations Debere Zeit, Chefe Donsa and Haramaya. The genotypes G4, G15, G19 and G13 had same sign of IPCA score with the locations Chefe Donsa , Arsi Robe and Haramaya. This indicates that these locations had positive interactions with the corresponding genotypes. The location Hossana and the genotype G2 had an IPCA score of nearly zero which indicates that this location and genotype has small interaction with the test genotypes and locations, respectively (Fig.1).

Table 2. Mean grain yield (kg/ha) and rankings of durum wheat genotypes across seven locations

Genotypes	Code	Adet	Haramaya	Angacha	Arsi Robe	Chefe Donsa	Debre Zeit	Hossana	Mean
1. Drought-tolerance (1/48)-off/3/2009	G1	1013	4694	5761	3508	2933	1778	1746	3062
2. DWSR-ETH/2009	G2	1156	4658	4445	3416	2544	1848	1621	2812
3. Drought-tolerance (1/24)-off/17/2009	G3	1041	4574	4889	3285	3013	1684	1260	2821
4. CD08-PANDZ/Off/106/2009	G4	698	4648	3973	4306	3071	2141	1623	2923
5. Drought-tolerance (1/24)-off/21/2009	G5	1381	4481	5317	3800	2919	2446	1081	3061
6. Drought-tolerance (1/24)-off/19/2009	G6	1391	4909	4553	4275	3210	1708	1431	3068
7. DSP2009-OFF.F4/Off/1034/2009	G7	1508	4647	5145	3778	3118	1929	1666	3113
8. Drought-tolerance (1/48)-off/6/2009	G8	1122	4882	4125	3814	2794	1663	1728	2875
9. Drought-tolerance (1/24)-off/1/2009	G9	1080	3983	2108	3193	3036	1646	1155	2743
10. Drought-tolerance (1/48)-off/13/2009	G10	1454	4897	4241	3768	3047	1899	2243	3078
11. Drought-tolerance (1/48)-off/44/2009	G11	1105	3802	4353	3075	2783	1471	1816	2629
12. DSP2009-F4 /Off/1136/2009	G12	758	4650	3882	3751	3215	1244	2135	2805
13. Drought-tolerance (1/48)-off/14/2009	G13	1096	4996	3963	5288	3646	2007	1801	3257
14. DSP2009-F6 /Off/1509/2009	G14	626	3843	4015	2209	2869	1372	1828	2395
15. Drought-tolerance (1/48)-off/21/2009	G15	1234	5410	3926	4278	3219	1796	1654	3074
16. Hitosa	G16	1680	4285	5519	3691	2612	1535	1771	2951
17. Kilinto	G17	1150	4310	3447	3295	3259	1450	1221	2564
18. Ude	G18	1420	4347	5207	3650	2351	1194	1750	2928
19. Yerer	G19	704	4343	3853	4543	3870	2360	1617	3041
20. Local	G20	848	4438	5819	3293	3166	1430	2231	3032
Mean		1123	4540	4577	3716	3037	1734	1669	2912

Bold and underlined means indicate genotypes which ranked first in the respective locations

Table 3: Mean grain yield (kg/ha), stability parameters and their rank orders for twenty durum wheat genotypes tested at seven location in 2011/12.

				Stability parameters					
Genotype	Code	Mean Yield	R	Pi	R	Wi	R	ASV	R
1. Drought-tolerance(1/48)-off/3/2009	G1	3062	6	407439	5	1345665	14	32.2	17
2.DWSR-ETH/2009	G2	2812	15	623820	14	307050	2	3.7	1
3.Drought-tolerance(1/24)-off/17/2009	G3	2821	14	590369	13	398440	4	13.7	3
4.CD08-PANDZ/Off/106/2009	G4	2923	12	502235	10	1077310	10	28.3	14
5. Drought-tolerance (1/24)-off/21/2009	G5	3061	7	405117	4	1338684	13	24.8	11
6. Drought-tolerance (1/24)-off/19/2009	G6	3068	5	328813	3	444609	5	14.7	6
7.DSP2009-OFF.F4/Off/1034/2009	G7	3113	2	322230	2	251306	1	13.8	4
8.Drought-tolerance(1/48)-off/6/2009	G8	2875	13	547767	12	389588	3	12.7	2
9.Drought-tolerance(1/24)-off/1/2009	G9	2743	17	700682	17	933355	8	24.0	10
10.Drought-tolerance(1/48)-off/13/2009	G10	3078	3	435217	8	518391	6	14.4	5
11.Drought-tolerance(1/48)-off/44/2009	G11	2629	18	876776	18	592598	7	15.6	7
12.DSP2009-F4 /Off/1136/2009	G12	2805	16	673353	16	1038151	9	23.9	9
13. Drought-tolerance (1/48)-off/14/2009	G13	3257	1	313878	1	2702134	20	47.3	20
14.DSP2009-F6 /Off/1509/2009	G14	2395	20	1330501	20	1612577	17	28.1	13
15. Drought-tolerance (1/48)-off/21/2009	G15	3074	4	428380	7	1370150	15	30.5	16
16.Hitosa	G16	2951	10	418059	6	1172302	12	29.8	15
17.Kilinto	G17	2564	19	952580	19	1100290	11	23.6	8
18.Ude	G18	2928	11	637732	15	1504819	16	27.4	12
19.Yerer	G19	3041	8	493588	9	2400309	19	38.9	19
20.Local	G20	3032	9	510407	11	2130825	18	37.8	18

R= Rank, Pi = Cultivar superiority measure, Wi = Wricke's ecovalence, ASV = AMMI stability value

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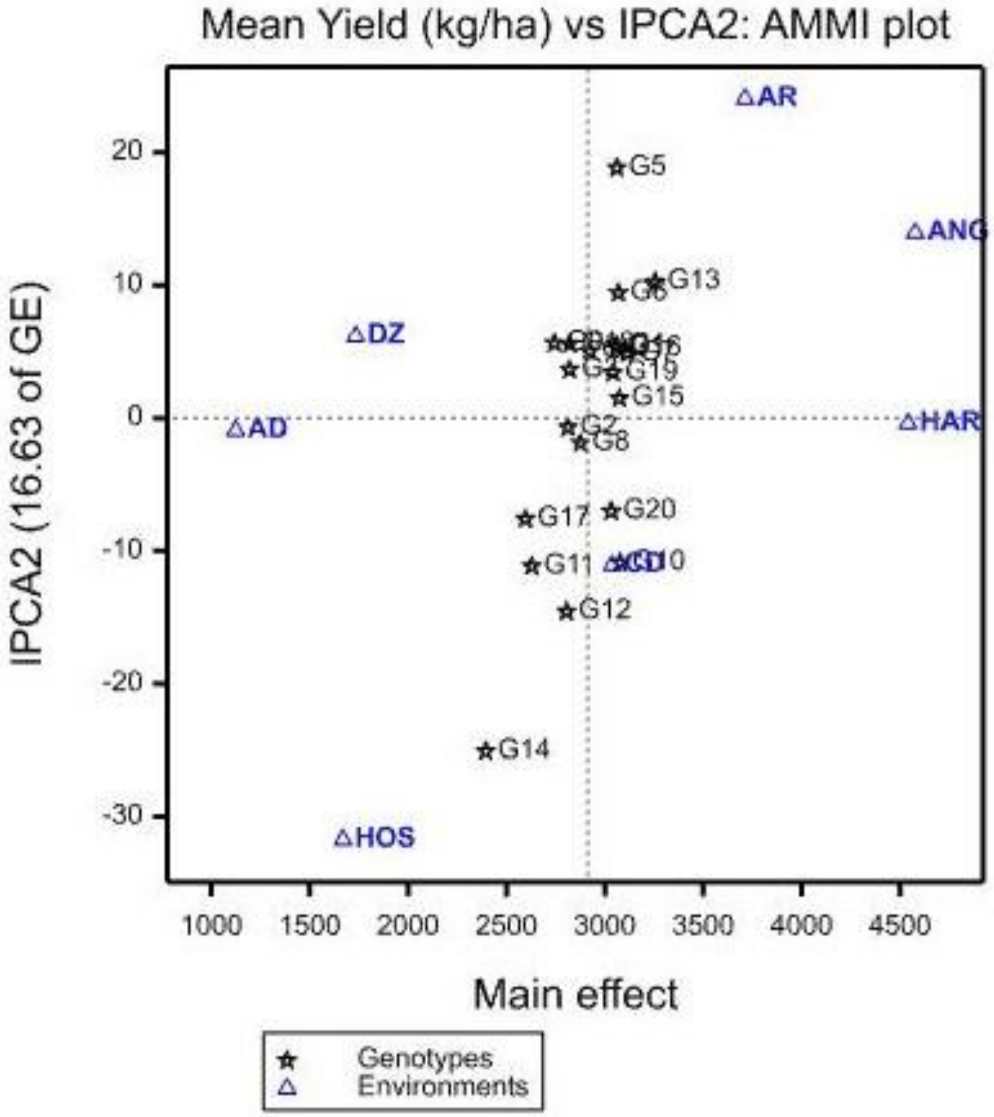

Key: G= Genotypes (1-20 names on Table 2).While the name of locations: AD=Adet, ANG=Angacha, AR=Arsi Robe, CD=Chefe Donsa, DZ=Debre Zeit, HAR= Haramaya, HOS= Hosana

.**Fig. 1.** AMMI biplot of durum wheat genotypes indicating main and interaction effects of genotype and environment.

Genotype and genotype by environment interaction (GGE) biplot analyses

The GGE biplot graphic analyses of the 20 durum wheat genotypes tested at seven locations are presented on Figures 2 and 3. The polygon in Fig. 2 was formed by connecting a straight line to the vertex genotypes while the rest of the genotypes fall inside the polygon. The vertex genotypes were G1, G13, G14, G17 and G20. Accordingly, the results of the present study revealed that the first principal component (PC1) and the second (PC2) explained 45.94% and 28.14% of the genotype and genotype by environment sum of squares (GGESS), respectively. The two principal component axis (PCA's) together explained 74.08% of the total variance (Fig.2 and 3). Statistically, stable genotypes and locations were located near the origin of the biplot with the two IPCA scores of almost zero. The genotype, G10 was slightly closer to the origin and showed medium stability with above average grain yield. Seven genotypes (G1, G5, G13, G19, G17, G14 and G20) were located far from the origin indicating that they are more responsive to the environmental change and are adapted to specific environments. According to Yan and Tinker (2006), the line from the origin of the biplot to the genotype indicates the difference in yield of genotypes from the grand mean, and genotypes with long vectors could be of good or poor performance. Accordingly, G13 was the best performer in terms of grain yield and contributed a lot to the GEI. However, this genotype was specifically adapted because of its farness from the origin of the biplot (Fig.2). On the other hand, G14 had a long vector from the origin, but performed poorly and contributed much to the GEI.

On the 'which won where pattern' of the biplot, the lines from the origin of the biplot perpendicular to the sides of the polygon divided the polygon it to 4 sectors (Fig.2). The test locations fell in to 2 of the 4 sectors. Therefore, Arsi Robe, Haramaya, Debre Zeit and Chefe Donsa fell in one sector and the vertex genotype for this sector was G13, indicating this genotype to be higher yielding at these four locations. Likewise, Angacha and Adet fell in another sector and the vertex genotype was G1. Therefore, the current test locations could be grouped in to two mega environments; ME1 represented by G13 included four locations (Arsi Robe, Debre Zeit, Chefe Donsa and Haramaya); whereas ME2 by G1 corresponded to Angacha and Adet.

According to Yan and Tinker (2006), the lines that connect the environment to the biplot origin are called environment vectors and the cosine between the vectors of two environments indicates the correlation between them. In view of that, the current study revealed that Adet was positively correlated with Debre Zeit, Haramaya and Arsi Robe because of the presence of an acute angle between Adet and the indicated locations. Moreover, Debre Zeit and Haramaya, Debre Zeit and Arsi Robe, Debre Zeit and Chefe Donsa, Haramaya and Arsi Robe, Haramaya and Chefe Donsa were positively correlated (Fig. 3). This indicates that the same information about the genotypes could be obtained from these environments. Under such cases indirect selection for grain yield can be practical across the test environments (Tesfaye et al., 2008). However, the consistency of the close association between the locations should be proven by analyzing the data across years.

Angacha and Chefe Donsa were strongly negatively correlated because of a large obtuse angle between them. This indicates the presence of a strong crossover GEI. Angacha and Debre Zeit were not correlated, because of the right angle between their vectors (Fig.2). On the other hand, the similarity between two environments is determined by the length of the vectors and the cosine of the angles between them. Accordingly, Haramaya and Chefe Donsa were similar environments. Debre Zeit had some level of similarity with Haramaya and Chefe Donsa.

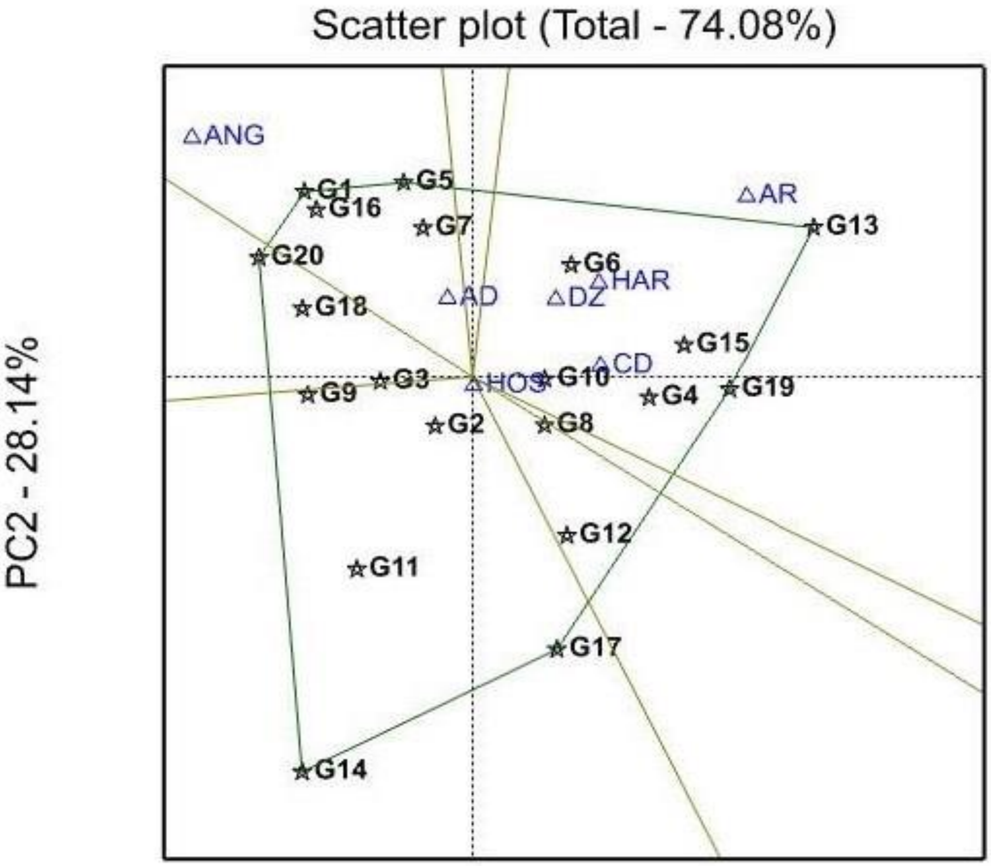

Fig. 2. 'Which won where' pattern of a biplot. The abbreviation of locations and genotypes was similar to Figure 1.

Therefore, these three locations could be grouped together as one mega environment (Fig.2 &3). In addition, environments with long vectors are the most discriminating ones (Yan and Tinker, 2006). Therefore among the seven test locations, Angacha and Arsi Robe were the most discriminating environments as they had long vectors but, Hosana was the least discriminating environment. Chefe Donsa, Haramaya, Debre Zeit and Adet were moderate in their discriminating ability of the genotypes (Fig. 3).

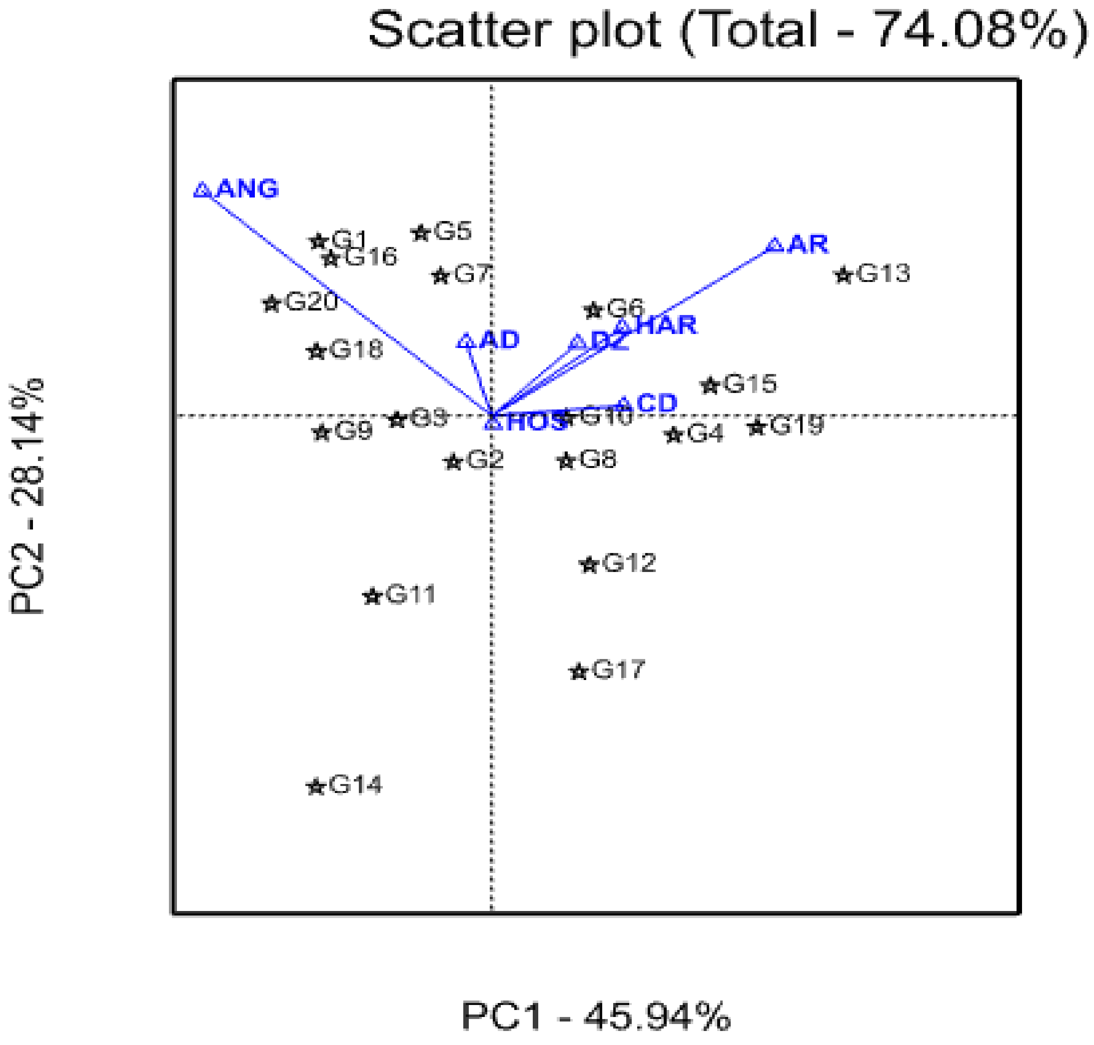

Fig. 3. Biplot indicating the relation among locations and genotypes. The abbreviation of locations and genotypes was similar to Figure 1.

Conclusion

The current analysis of multi-environment field experiment data on durum wheat grain yield revealed the presence of GEI with the largest variation accounted by location followed by GEI. The GEI was a cross-over type whereby the rankings of the genotypes changed across the test locations. The AMMI analysis of the current data showed AMMI model with the first two IPCA (AMMI-II) was the best predictive model. The stability analysis using the parametric stability measures revealed that genotype G7 was a stable genotype with above average grain yield and could be a candidate for release. The genotype G10 showed medium stability and above average grain yield. G13 was the highest yielder genotype with specific adaptation to some of the test locations (Arsi Robe, Debre Zeit, Haramaya and Chefe Donsa). The test locations could be grouped in to 2 mega environments (ME) such that Arsi Robe, Debre Zeit, Chefe Donsa and Haramaya were grouped as ME1 and Angacha and Adet as ME2. Among the test locations Angacha and Arsi Robe were the most discriminating locations of the genotypes whereas Hossana was the least and should not be included as a test location for optimum and high moisture trials.

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