

AMMI, Stability and GGE Biplot Analysis of Durum Wheat Grain Yield for Genotypes Tested under Some Optimum and High Moisture Areas of Ethiopia

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Abstract: The objective of this study was to examine the presence and type of genotype by environment interaction, evaluate the stability of the genotypes and to visualize the relation among test locations and genotypes using Additive Main effect and Multiplicative Interaction (AMMI) and genotype + genotype by environment (GGE) biplot analyses. The study includes twenty genotypes tested at seven locations using randomized complete block design with four replications during 2011/12 season. Genotype by environment interaction was examined using AMMI analysis and GGE biplot analysis. Stability of genotypes was also evaluated using cultivar superiority measure and Wricke's ecovalence. AMMI analysis showed significant ($P < 0.001$) effects of genotype, location and genotype by location interaction on grain yield. Location, genotype and genotype by location interaction, respectively accounted 73.5%, 1.8% and 6.8% of the variation in grain yield. 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. The mean squares of the first and the second interaction principal component axis was respectively highly significant ($P < 0.001$) and significant ($P = 0.01$). Hence, AMMI model with the first two IPCA was the best predictive model. The stability analysis using the parametric stability measures revealed that there were some stable genotypes with above average grain yield which could be promising candidate for release. The GGE biplot analyses revealed that the first and the second principal component explained 45.94% and 28.14% of the GGESS, respectively. On the 'which won where pattern' of the biplot, the test locations could be grouped in to two mega environments. Thus, mega environment-1 represented by the best performer genotype; Drought-tolerance (1/48)-off/14/2009, in terms of grain yield and which contributed significantly to the GEI included four of the seven locations whereas mega environment-2 by Drought-tolerance (1/48)-off/3/2009 represented two locations. Among the test locations Angacha and Arsi Robe were the most discriminating locations of the genotypes, while Hossana was the least and should not be included as a representative test location.

Key words: Genotype by environment interaction • Stability • AMMI • GGE biplot

INTRODUCTION

Durum wheat (*Triticum turgidum* var. *Durum*) is an endogenous tetraploid ($2n=4x=28$) wheat species which has been cultivated since ancient time in Ethiopia. The country is considered to be one of the centers of diversity for tetraploid wheat [1]. Durum wheat 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 [2]. 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 until the present time to develop varieties which are stable, high yielder, resistant to diseases and which can also meet the industrial quality standard. Therefore, multi environmental trials will be undertaken each year to evaluate 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 [3]. It occurs when two genotypes or cultivars respond differently to diverse environments. In such cases, the mean grain yield of genotypes across environments is not sufficient and meaningful indicator of the genotype performance [4]. A significant 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 [5]. The presence of GEI complicates breeding, testing and selection of superior genotypes [6]. Moreover, it 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 [7, 8]. Therefore, assessing any genotype or agronomic treatment without including its interaction with the environment is incomplete and limits the accuracy of yield estimates [9].

The knowledge of genotype by environment interaction can help breeders to minimize the cost of wider genotype evaluation by eliminating unwanted testing sites [7]. On the other hand, the presence of a large GEI could be an indication to include more testing sites for genotype evaluation. In countries like Ethiopia where the environmental variation is very high, a stable and adaptable variety is very much important. Therefore, wheat breeders should attempt to identify adaptive and stable genotypes to different environments to achieve faster genetic gain through evaluation of genotypes under multiple environments before release.

Multi-environment trials could be of a single or multiple year trial. Regardless of this, 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 [4]. 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 [4, 10].

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 and also has other important benefits in the analysis of multi-environment trial data. It can also be used to determine stability of genotypes across environments using principal component axis (PCA) scores and AMMI stability value (ASV) [6, 11]. Other parametric stability models are also available such as Wricke's ecovalence, superiority index, coefficient of variation, environmental variance and regression approach [12]. In Agriculture, stability refers to the desirable reaction of cultivated genotypes, forced and supported by humans, ensuring the similar yield level in different environmental conditions through small genotype-environmental interaction [13].

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 \times environment) by principal components analysis. The model is given by equation 1 [9].

$$Y_{ij} = \mu + G_i + E_j + (\sum_{k=1}^h \lambda_k \alpha_{ik} \beta_{jk}) + e_{ij} \quad (1)$$

The ANOVA result 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 (genotype + genotype by environment interaction) biplot analysis, which is another method of analysis, is a good method to fully explore multi-environment trials (METs) based on principal component analysis (PCA) [6]. Moreover, GGE biplot helps to effectively show the pattern of GEI of the data and it also shows which genotypes won in which environments and thus facilitates mega-environment identification [5].

The basic model for GGE biplot according to Yan [10] is:

$$y_{ij} - \bar{y} = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + e_{ij} \quad (2)$$

Durum wheat generally lacks stability in performance and shows inconsistent behavior when grown over a wide range of environments [11]. Because of this it would be important to evaluate the stability of genotypes in yield and other important traits before the variety release process.

The objective of the current study, therefore, was to examine the presence and type of GEI, evaluate the nature of stability of twenty durum wheat genotypes tested under optimum and high moisture areas of Ethiopia and to visualize the relation among test locations and genotypes using AMMI and GGE biplot analyses.

MATERIALS AND METHODS

The field experiment was carried out during the 2011/12 main season at seven major durum wheat growing locations of Ethiopia (Adet, Angacha, Arsi Robe, Chefe Donsa, Debre Zeit, Haramaya and Hossana) representing optimum and high moisture environments. Fifteen durum wheat genotypes including 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 150 kg ha⁻¹ and fertilizer rate was 100 kg ha⁻¹ Urea and diammonium phosphate (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 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 software, 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.

Then, the grain yield data was subjected to AMMI analysis using the GenStat 16th statistical software to assess both the additive and multiplicative variance. Stability analysis was done using the same statistical software and parametric stability measures; Wricke's ecovalence (Wi) and cultivars superiority measures (Pi) were used to evaluate the stability of genotypes. Genotypes with small values of Wi were contributed less to the GEI and considered stable; and those with low Pi values were in closer distance to the genotype with maximum mean yield and therefore were stable genotypes.

To graphically evaluate the relationship between environments (testers) and genotypes GGE biplot analysis was also executed using Gen stat 16th statistical software

to identify genotypes with wide and specific adaptability and to group environments to different mega-environments. Thus, from the GGE biplot genotypes located near the origin of the biplot are considered as widely adapted genotypes and those which are located far as specifically adapted. Moreover, locations which fell in 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 on 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 (73.50%) the largest parts of the variation in grain yield followed by genotype by location interaction (6.81%) and genotype (1.79%). Similar results were reported by Asrat *et al.* [3], Tesfaye *et al.* [5], Hints and Fetien [6], Tamene *et al.* [8] and Muez *et al.* [12] from GXE studies on soybean, bread wheat, barley, field peas and durum wheat. Likewise, Yan and Kang [4] 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 [3].

The multiplicative component of AMMI further revealed that the mean squares of the first interaction principal component axis (IPCA1) was highly significant ($P<0.001$) and significant ($P=0.01$) for the second interaction principal component axis (IPCA2),

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

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

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

Genotype	Mean Yield	R	Stability parameters			
			Pi	R	Wi	R
1. Drought-tolerance(1/48)-off/3/2009	3062	6	407439	5	1345665	14
2.DWSR-ETH/2009	2812	15	623820	14	307050	2
3.Drought-tolerance(1/24)-off/17/2009	2821	14	590369	13	398440	4
4.CD08-PANDZ/Off/106/2009	2923	12	502235	10	1077310	10
5. Drought-tolerance (1/24)-off/21/2009	3061	7	405117	4	1338684	13
6. Drought-tolerance (1/24)-off/19/2009	3068	5	328813	3	444609	5
7.DSP2009-OFF.F4/Off/1034/2009	3113	2	322230	2	251306	1
8.Drought-tolerance(1/48)-off/6/2009	2875	13	547767	12	389588	3
9.Drought-tolerance(1/24)-off/1/2009	2743	17	700682	17	933355	8
10.Drought-tolerance(1/48)-off/13/2009	3078	3	435217	8	518391	6
11.Drought-tolerance(1/48)-off/44/2009	2629	18	876776	18	592598	7
12.DSP2009-F4 /Off/1136/2009	2805	16	673353	16	1038151	9
13. Drought-tolerance (1/48)-off/14/2009	3257	1	313878	1	2702134	20
14.DSP2009-F6 /Off/1509/2009	2395	20	1330501	20	1612577	17
15. Drought-tolerance (1/48)-off/21/2009	3074	4	428380	7	1370150	15
16.Hitosa	2951	10	418059	6	1172302	12
17.Kilinto	2564	19	952580	19	1100290	11
18.Ude	2928	11	637732	15	1504819	16
19.Yerer	3041	8	493588	9	2400309	19
20.Local	3032	9	510407	11	2130825	18
Mean	2912					

R= Rank, Pi = Cultivar superiority measure, Wi = Wricke's ecovalence.

while the third interaction principal component axis (IPCA3) was not significant (Table 1). Hence, AMMI-II explained the observed GXE interaction. On the results of GXE study on bread wheat, only the first IPCA was found significant [6].

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 [6] and field pea [8]. The GXE in the current AMMI analysis contained 41908338 noise sum of square (3.84%) and 1049330021 pattern sum of square (96.16%) which was larger than the first two multiplicative terms (72.67%). 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. These results is in line with the previous findings reported by Asrat *et al.* [3], Hintsu and Fetien [6], Tamene *et al.* [8], Mulusew *et al.* [14].

Stability Analyses: The parametric stability measures of the 20 durum wheat genotypes tested at seven locations are presented on Table 3. Accordingly, cultivar superiority measures (P_i) and Wricke's ecovalence (W_i) values were used to evaluate the stability of genotypes in the this study.

Cultivar Superiority Measure (P_i): The smaller the value of the P_i , the less is the distance to the genotype with maximum mean yield and the better the genotype [15]. According to this method, genotype Drought-toler (1/48)-off/14/2009(G13) showed the least P_i value and was the most stable genotype followed by DSP2009-OFF.F4/Off/1034/2009 (G7), Drought-tolerance (1/24)-off/19/2009(G6) and Drought-tolerance (1/24)-off/21/2009 (G5). On the other hand, DSP2009-F6 /Off/1509/2009 (G14) was the genotype with the highest cultivar superiority measure and was the most unstable genotype with below average grain yield (Table 3).

Wricke's Ecovalence (W_i): 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 W_i values have smaller variations across environments and thus considered as stable [14]. Hence, DSP2009-OFF.F4/Off/1034/2009 (G7) was the most stable genotype according to this method; coupled with above average grain yield. Genotypes DWSR-ETH/2009 (G2), Drought-toler (1/48)-off/6/2009 (G8) and Drought-toler (1/24)-off/17/2009 (G3) were next to G7 in terms of stability because of lower W_i values, however these genotypes had below average grain yield. Genotype Drought-toler (1/48)-off/14/2009 (G13) showed the largest ecovalence indicating that this genotype was the least stable 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, GGE biplot analysis is the appropriate method to further exploit the current multi-environment trial data.

GGE biplot Analyses: The GGE biplot graphic analyses of the 20 durum wheat genotypes tested at seven locations are presented on Figures 1 and 2. The polygon in Fig.1 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) respectively explained 45.94% and 28.14% of the GGESS. The two principal component axis (PCA's) together explained 74.08% of the total variance (Fig.1 and 2). 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 [6], 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.1). On the other hand, G14 had a long vector from the origin, but performed poorly and contributed much to the GEI.

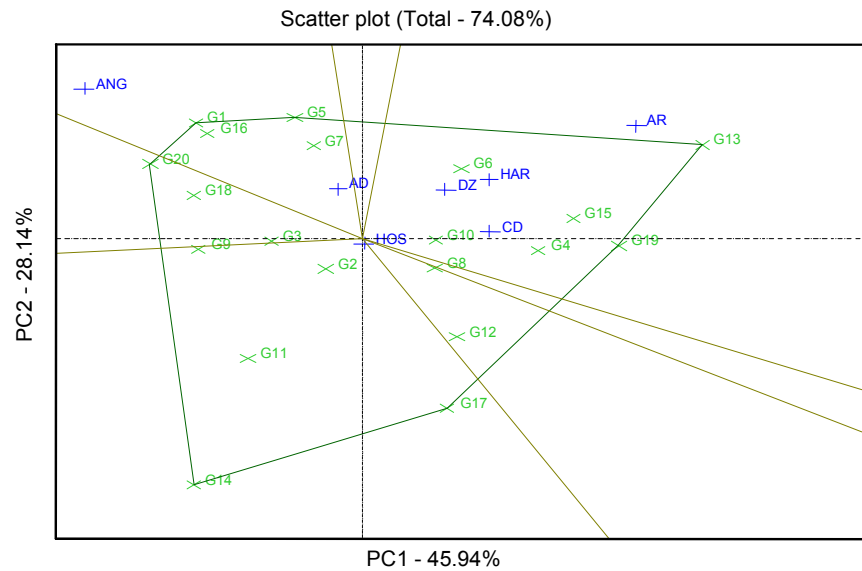


Fig. 1: 'Which won where' pattern of a biplot Where G= Genotypes (1-20 names on Table 2). While the name of locations: AD=Adet, ANG=Angacha, AR=Arsi Robe, CD=Chefe Donsa, DZ=Debre Zeit, HAR= Haramaya, HOS= Hosana.

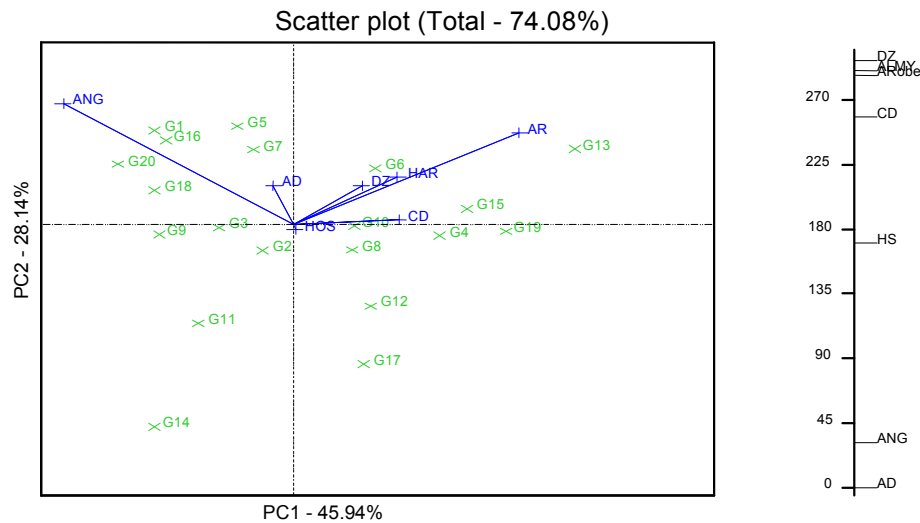


Fig. 2: Biplot indicating the relation among locations and genotypes. The abbreviation of locations and genotypes was similar to Figure 1.

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.1). 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 (Drought-toler (1/48)-off/14/2009), 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 (Drought-toler (1/48)-off/3/2009). Among the test locations, Hossana fell almost on the origin and this location was suggested as

the least representative test location. 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 [16], 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. 2). 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 [5]. 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. Therefore, these three locations could be grouped together as one mega environment (Fig.1 and 2). In addition, environments with long vectors are the most discriminating ones [16]. Therefore among the seven test locations, Angacha and Arsi Robe were the most discriminating environments as they had long vectors but, Hosana is the least discriminating environment. Chefe Donsa, Haramaya, Debre Zeit and Adet were moderate in their discriminating ability of the genotypes (Fig. 2).

CONCLUSIONS

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 (hence AMMI-II) was the best predictive model. The stability analysis using the parametric stability measures (P_i and W_i) 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). Regarding the test environments, the locations could be grouped in to 2 mega environments

(ME). Therefore, 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 location of the genotypes whereas Hossana was the least and should not be included as a test location representing optimum and high moisture areas of Ethiopia.

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