

Genotype by environment interaction and stability analyses of durum wheat elite lines evaluated in Ethiopia

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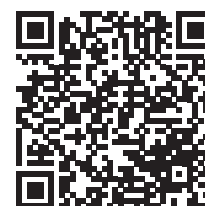
Abstract: Identifying a stable high-yielding variety is challenging. This paper reports high-yielding and stable durum wheat candidates identified using AMMI, GGE biplot models, and stability parameters. Twenty-five lines were evaluated in 13 environments in 2018 and 2019 using a triplicate row-column design. AMMI, stability, and GGE biplot analyses were conducted using packages in the R statistical software. AMMI indicated highly significant effects of environments, genotypes, and their interactions on grain yield. The highest proportion of the total sum of squares accounted for by the environment (42.3%), followed by the genotype by environment interaction (26.7%), may suggest the presence of diverse environments grouped into mega-environments. The environments fell into three sectors on the which-won-where view of the biplot and they were grouped into two mega-environments. Genotypes 5 and 15 were the highest yielding and most stable among all and are recommended as candidate varieties for the midlands to highlands of Ethiopia.

Keywords: Durum wheat, stability, AMMI, GGE biplot

INTRODUCTION


Durum wheat (*Triticum durum* Desf.) is an important tetraploid wheat species produced for industrial purposes and for preparation of traditional foods consumed in different countries. Durum has been produced in Ethiopia since ancient times (Tesemma and Belaye 1991). The country is endowed with diverse landraces adapted mainly to the highland Vertisol areas (Tefaye 1988). Ethiopia is known as the center of diversity for tetraploid wheat, and it is the secondary center of origin of durum wheat (Kabbaj et al. 2017, Hodson et al. 2020). Tefaye (1988) reported that durum wheat occupied 60% to 70% of the total wheat area around the mid-1980s, and landraces have been dominant over improved varieties, estimated to account for under 10% of the durum wheat area. The proportion of durum wheat in the total wheat-growing area has decreased dramatically due to the introduction of semi-dwarf fertilizer-responsive bread wheat varieties, and the largest share between the two species shifted to bread wheat (Hodson et al. 2020). However, the durum wheat area is expected to increase due to urban-related demand for pasta products and expansion of irrigated wheat in Ethiopia (Letta et al. 2013).

Durum wheat breeding activity mostly deploys elite lines from different sources, which vary in performance across environments. This difference in



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performance may be due to the effect of the genotype by environment interaction (GEI) (Lule et al. 2014). Hence, varieties should be tested under multiple environments to evaluate their performance regarding important traits and their stability across these environments (Yan and Tinker 2006). A stable genotype is a genotype which is high yielding with minimum fluctuation in performance when grown in diverse environments (Zerihun et al. 2016). In identifying a stable and high yielding variety, breeders face difficulties in selection decisions because of the GEI. Therefore, proper analysis of multi-environment trial data and exploitation of genotypes that performed differently in diverse environments is crucial for progress in breeding (Gauch 2006).

Traditional ANOVA is not sufficient for modeling GEI and detecting genotypes with stable performance. However, multivariate statistical analysis models are suitable for identifying stable genotypes, grouping mega-environments, and ranking genotypes based on their performance (Dehghani et al. 2006). Among those models, the additive main effects and multiplicative interaction (AMMI) model and the genotype main effect and genotype by environment interaction (GGE) biplot are the statistical methods most extensively used for modeling GEI and increasing the efficiency of selection in yield trials and group environments in multi-environment trials of cereal crops, including wheat (Zerihun et al. 2016), barley (Pour-Aboughadareh et al. 2022), sorghum (Enyew et al. 2021), and maize (Katsenios et al. 2021). The AMMI model includes both the main (additive) effect and interaction (multiplicative) effect in the results of analysis, and the GGE biplot visualizes multi-environment trial data for better identification of winning genotypes in test environments (Yan and Tinker 2006). Therefore, the objective of this study was to conduct genotype by environment interaction analyses on multi-environment trials of elite durum wheat lines using the AMMI and GGE biplot and identify candidates with high and stable yield across environments.

MATERIAL AND METHODS

Test environments, planting materials, and experimental design

Twenty-five durum wheat genotypes, including three standard checks (Boohai, Utuba, and Tesfaye), were evaluated in 13 environments (location by year) in the 2018 and 2019 crop seasons (Supplemental Table 1). The test environments were AD-18 and AD-19 (Adet 2018 and 2019), CD-18 and CD-19 (Chefe Donsa 2018 and 2019), DZ-18 and DZ-19 (Debre Zeit 2018 and 2019), GN-18 and GN-19 (Gondar 2018 and 2019), HL-18 and HL-19 (Holeta 2018 and 2019), MJ-18 and MJ-19 (Minjar 2018 and 2019), and KU-19 (Kulumsa 2019).

The genotypes were arranged using a row-column design in three replications. Plot size was 6 rows of 2.5 m length, with a 0.2-m between-row spacing. A seeding rate of 125 kg ha⁻¹ was used and urea was applied at a rate of 200 kg ha⁻¹ in two split applications, half at planting and the remaining half at the tillering stage. Diammonium phosphate (DAP) was applied at a rate of 100 kg ha⁻¹ in one application at sowing. Hand weeding was performed three times in each environment. Data on different agronomic and phenological traits were recorded. Grain yield was measured in grams per plot using a digital scale and then converted to kilograms per hectare for purposes of analysis.

Statistical analysis

Data was analyzed using the R version 4.1.2 statistical software (R Core Team 2021). Analysis of variance (ANOVA) was carried out on the multi-environment data using the *aov* function of the R package *car* (Fox and Weisberg 2019) to observe the significance of the genotype by environment interaction. The *GGEModel* function of the R statistical package *GGEBiplots* was applied to the genotype by environment data matrix (Dumble 2022). Then the *WhichWon* function was fit to the output to plot the “which-won-where” view of the GGE biplot. The *EnvRelationship* function of the *GGEBiplots* package was used to plot the environment relationship; the *DiscRep* function to plot discrimination ability and representativeness, and the *MeanStability* function to create the discrimination ability and representativeness view and stability plots, respectively. AMMI analysis was performed using the *AMMI* function of the *agricolae* package (Mendiburu 2017). Genotype stability was further evaluated using other stability parameters; the coefficient of variation (CV) (Francis and Kannenberg 1978), Shukla stability variance (Shukla 1972), AMMI Stability Value (ASV) (Purchase et al. 2000), ecovalence (Ecoval) (Wricke 1962), and deviation from joint regression analysis (Sij) (Eberhart and Russell 1966) were estimated using the *metan* R statistical software package (Olivoto and Lúcio 2020).

RESULTS AND DISCUSSION

Yield performance

The distribution of grain yield of the twenty-five genotypes varied across the thirteen environments (Figure 1). Among the test environments, the mean grain yield of genotypes was the highest (4716.6 kg ha⁻¹) at Chefe Donsa in 2019, whereas it was the lowest at Kulumsa in 2019 (2297.5 kg ha⁻¹) (Table 1). The higher grain yield at Chefe Donsa may be due to a longer growth period, providing an extended time for assimilate production during the grain-filling period. This is in agreement with Richards (2000), who indicated that an extended photosynthesis period increases both biomass and grain yield. The highest performing genotypes differed across environments. The yield ranged from 1345.8 kg ha⁻¹ for genotype-24 at AD-19 to 6335 kg ha⁻¹ for genotype-10 at CD-19 (Table 1). The difference in the performance of genotypes across the different test environments is a consequence of the genotype by environment interaction, leading to large variations in grain yield.

The distribution of grain yield across all environments was close to normal, which corroborates the quantitative nature of grain yield (Supplementary Figure 1). Correlation among the environments shows that the mean grain yield of genotypes in each location was correlated with the same location in a different year (Figure 2). Holeta (HL-18, HL-19) and Gonder (GN-18 and GN-19) were correlated with each other; and AD-18, AD-19, and GN-18 were correlated with each other, suggesting that genotypes selected in one environment perform well in another environment. That indicates the possibility of selecting genotypes based on the mean across these environments.

Additive Main Effects and Multiplicative Interaction (AMMI) model

AMMI analysis revealed highly significant effects of environments, genotypes, and their interactions on grain yield ($P < 0.001$). Considering the multiplicative component of AMMI, the sum of squares due to the GEI is further divided into five significant Interaction Principal Components (PC-1 to PC-5) of the (Table 2). The highest proportion of the total sum of squares was accounted for by the environment (42.3%), followed by the genotype by environment interaction (26.7%) (Table 2). This agrees with the result expected in GEI analysis as described by Gauch (2006). The highest magnitude of the sum of squares from the environment suggests that the test environments are diverse and affect expression of the grain yield trait. The highest proportion of variation from environment, followed by the GEI, is in agreement with results from barley (Pour-Aboughadareh et al. 2022) and durum wheat grain yield (Mohammadi et al. 2015). Higher sum of squares due to the genotype by environment interaction compared to the genotype effect indicates the presence of mega-environments (Figure 2).

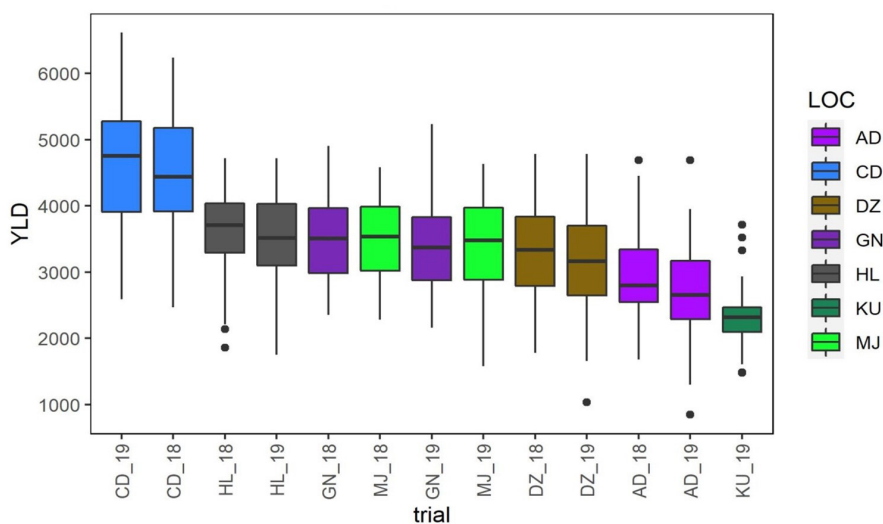


Figure 1. Box plot of durum wheat grain yield in kg ha⁻¹ across thirteen environments (year by location).

Table 1. Mean grain yield performance (kg h⁻¹) of durum wheat genotypes evaluated across thirteen environments in Ethiopia

Gen. No.	Environment													Mean
	AD_18	AD_19	CD_18	CD_19	DZ_18	DZ_19	GN_18	GN_19	HL_18	HL_19	KU_19	MJ_18	MJ_19	
1	1812.7	1537.2	4938.0	4863.3	3400.7	3298.3	3035.3	3043.7	3293.0	3383.8	2111.0	2345.0	2170.0	3017.8
2	3049.7	3049.7	4075.0	4075.0	2721.7	2721.7	3632.7	3632.7	3995.0	3995.0	2395.3	3723.3	3723.3	3445.4
3	2348.0	1561.2	4437.3	4648.3	2414.3	2271.7	2485.7	2322.8	2181.0	2101.7	1620.7	3218.3	3286.7	2684.4
4	2341.0	2139.2	4261.7	4226.7	3150.0	3168.3	2854.7	2720.2	2436.7	2475.8	1869.0	3380.7	3448.3	2959.4
5	4035.0	3657.0	5723.7	5523.3	4500.0	3493.3	4354.2	3456.0	4215.8	3875.3	1986.0	3880.0	3680.0	4029.2
6	3231.5	2781.8	4843.3	5610.0	4348.3	4181.7	2784.3	2587.3	3757.7	3402.2	2036.7	4040.0	3890.0	3653.4
7	2827.3	2024.8	4956.7	4923.3	3141.3	2673.3	3028.0	2662.7	3890.0	3758.8	2245.0	3045.0	2645.0	3217.0
8	2856.3	2854.2	5091.7	5091.7	4270.0	4270.0	3235.0	3235.2	3617.7	3617.7	2387.7	3151.7	3151.7	3602.4
9	3179.7	2846.5	4001.7	4168.3	3776.0	3696.7	3735.0	3268.7	3763.7	3497.0	2473.7	3478.3	3111.7	3461.3
10	2761.7	2920.2	6071.5	6335.0	3927.3	3871.7	3794.0	3665.7	3077.0	2879.7	2404.0	3412.0	3243.3	3720.2
11	2894.7	2577.5	3994.3	4301.7	4165.7	3945.0	2893.3	2521.7	3106.0	2932.3	2328.7	3273.3	2831.7	3212.8
12	2869.0	2868.0	5347.3	5531.7	3578.0	3498.3	3326.0	3307.8	3903.3	3866.0	2427.3	3489.7	3360.0	3644.0
13	3106.3	2434.5	4214.3	4385.0	3245.3	3113.3	3683.3	3687.0	4050.3	4073.3	2704.0	4051.0	3868.3	3585.8
14	3499.7	3319.0	4322.3	4490.0	3957.0	3820.0	3591.3	3470.7	3486.7	3387.3	2272.3	3995.0	3895.0	3654.3
15	4044.3	3901.7	5597.0	5627.5	3874.7	3208.3	4413.3	3938.7	3743.0	3044.7	3522.7	3873.3	3204.5	3999.5
16	3854.3	3855.8	4350.3	4516.3	2865.3	2866.7	4169.7	4173.2	4002.3	4004.1	1598.0	3429.0	3429.0	3624.2
17	3155.7	3099.7	2790.7	3060.0	2533.0	2148.3	4467.3	4592.0	3807.7	3765.8	2313.7	3940.0	4030.0	3361.8
18	2588.7	2398.3	3956.0	4500.0	3088.3	2880.0	3678.0	3729.0	3399.3	3350.0	2486.7	4032.3	3976.7	3389.5
19	2603.7	2008.3	4649.7	4616.7	2504.0	2841.7	3131.0	3105.8	3446.0	3468.8	2370.7	3627.0	3588.3	3227.8
20	3177.7	3203.7	4882.7	5262.5	3363.0	3353.3	3368.3	3376.0	4338.7	4402.5	2302.0	3365.3	3465.0	3681.6
21	2393.0	2333.8	4377.3	4885.0	2069.3	2236.7	4199.0	4499.3	4508.7	4490.3	2234.7	2876.3	2641.7	3365.0
22	2765.0	2630.0	4620.0	4848.3	3001.0	2898.3	3854.5	3856.5	3503.3	3480.5	2277.0	3361.7	3156.7	3404.1
23	3060.0	2893.8	4931.7	5395.0	3583.3	3626.7	2969.0	2800.7	3389.0	3422.5	2211.7	3573.3	3303.3	3473.8
24	2123.3	1345.8	3438.3	3438.3	2779.0	2246.7	3248.7	3720.8	3838.7	3865.7	2584.3	3609.0	3350.0	3045.3
25	3501.2	3501.2	3498.0	3591.7	3426.3	3746.7	3760.7	3760.7	3747.3	3747.3	2275.3	3430.0	3430.0	3493.6
Mean	2963.2	2709.7	4534.8	4716.6	3347.3	3203.1	3507.7	3405.4	3619.9	3531.5	2297.5	3504.0	3355.2	3438.2
Min	1812.7	1345.8	2790.7	3060.0	2069.3	2148.3	2485.7	2322.8	2181.0	2101.7	1598.0	2345.0	2170.0	2684.4
Max	4044.3	3901.7	6071.5	6335.0	4500.0	4270.0	4467.3	4592.0	4508.7	4490.3	3522.7	4051.0	4030.0	4029.2
LSD	671.8	565.9	1006.7	1199.6	762.5	889.5	713.7	630.5	590.3	646.5	217.6	523.2	662.1	208.9

Which-won-where, GGE biplot and environment relationship

The “which-won-where” view of the GGE biplot explained 65.5% of the total variation, 35.5% of which was explained by PC1 and 29.9% by PC2 (Figure 2). The genotypes in the vertex (five genotypes) formed a five-sided polygon. The lines drawn from the center perpendicular to the sides of the polygon divided the biplot into five sectors, and the thirteen environments fell into three of the five sectors (Figure 3). For environments within a sector, the winning genotype was located at the vertex of the sector. The winning genotype in Sector 1 was genotype 10, and this sector included environments CD-18, CD-19, DZ-18, and DZ-19 (Figure 2). The second sector was represented by AD-18, AD-19, KU-19, MJ-18, MJ-19, and the winners were genotypes 5 and 15. The third sector included HL-18, HL-19, GN-18, and GN-19; and genotype 17 was the winner (Figure 2). This suggests that the four winning genotypes in the respective sectors are adapted to the environments located in that sector. Genotypes 24 and 3 were in the fourth and fifth sectors, respectively, where no environment was shown (Figure 2). These two genotypes (24 and 3) with the other five genotypes (1, 4, 7, 11, 19), that fell in Sector 5, might adapt to a different environment than the test environments considered in this study.

The plot of environment relationship clearly indicated the presence of two mega-environments (Figure 2). Nine of the thirteen environments (MJ-18, MJ-19, GN-18, GN-19, AD-18, AD-19, HL-18, HL-19, and KU-19) were in one group, while the remaining four environments (DZ-18, DZ-19, CD-18, and CD-19) fell in another group (Figure 2). A similar grouping of CD and DZ was reported by Shitaye (2015). The grouping of environments may suggest the need for planning different

Table 2. Analysis of variance of grain yield of durum wheat genotypes using the Additive Main Effects and Multiplicative Interaction Model

Sources of variation	df	SS	MSS	F-value	Pr > F	Sum of squares explained (%)		
						Total variation	G×E explained	G×E cumulative
Env	12	3.76E+08	31354741	27.92	8.48E-12	43.4		
Rep(env)	26	29195324	1122897	4.98	5.08E-14	3.4		
Gen	24	90246396	3760267	16.68	1.93E-52	10.4		
Env: Gen	288	2.31E+08	801147	3.55	4.12E-40	26.6		
Residuals	624	1.41E+08	225354.1			16.2		
PC1	35	1.06E+08	3018951	13.4	0		45.8	45.8
PC2	33	44947522	1362046	6.04	0		19.5	65.3
PC3	31	27284980	880160.6	3.91	0		11.8	77.1
PC4	29	23701341	817287.6	3.63	0		10.3	87.4
PC5	27	14237308	527307.7	2.34	2.00E-04		6.2	93.5

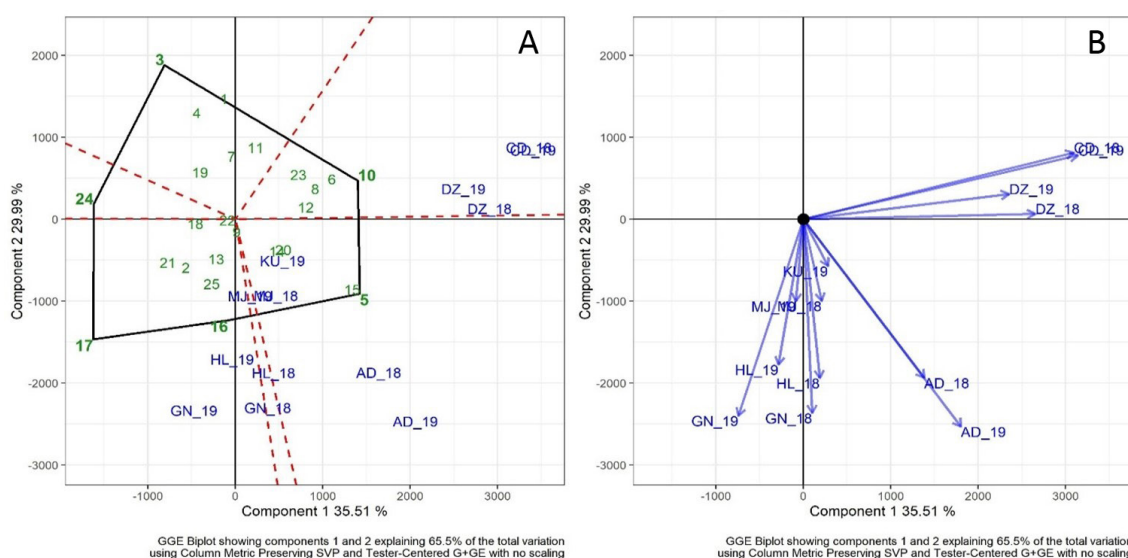


Figure 2. “Which -Won -Where” (A) and environment relationship (B) view of GGE plot of durum wheat genotypes evaluated across thirteen environments.

sets of trials based on the agroecology of the environments in the future. However, this result should be confirmed with trials of an additional year. A large obtuse angle was observed between CI-18, CD-19, and GN-19, indicating a negative correlation between test environments and a strong cross-over GEI, as described in Yan and Tinker (2006).

Discriminating ability and representativeness of test environments for durum wheat grain yield

The environment vectors for CD-18, CD-19, DZ-18, DZ-19, AD-19, AD-18, GN-19, and GN-18 were long for discriminating ability and representative view of the GGE biplot, indicating that these eight environments are the most discriminating (informative) environments (Figure 3). The positive relationship between the length of the environment vector and discriminating ability was previously reported by Yan and Tinker (2006). The smallest circle in the biplot was for KU-19, suggesting that this environment is the average environment (Figure 3). The arrow on the straight line passing through the origin of the GGE biplot aligned with this environment. Moreover, KU-19 had the smallest angle with the average environment axis (AEA), the line that passes through the origin of the biplot (Figure 3). Hence, KU-19 was the most representative, and genotypes selected in this environment will likely perform well in the other environments of the

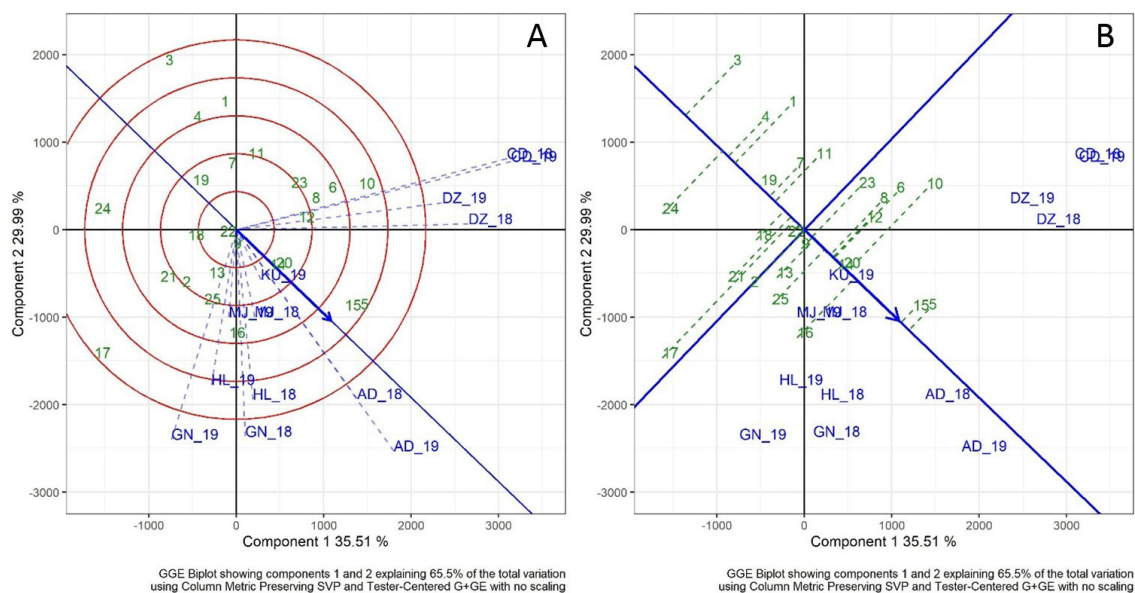


Figure 3. Discriminating ability versus representativeness of environments (A) and mean performance stability of durum wheat genotypes across thirteen environments (B).

same group (Yan and Tinker 2006, Nai-yin et al. 2014). CD-18, CD-19, and GN-19 were the least representative (larger angle with the AEA), but discriminating environments which indicate that these environments are suitable for selecting specifically adapted genotypes. AD-18, AD-19, and DZ-18 were among those with long vectors and small angles with the AEA, suggesting that these environments are both discriminating (informative) and representative, which means they are useful for selecting widely adapted genotypes (Figure 3) (Yan and Tinker 2006).

Stability of durum wheat genotypes

Figure 3 shows an arrow in the mean performance and stability parameter in the plot of durum wheat genotypes across the 13 environments, pointed to a genotype with higher mean yield across environments. Genotype 5 was close to this arrow, indicating that this genotype had the highest mean yield ($4020.2 \text{ kg ha}^{-1}$), followed by genotype 15 ($3999.5 \text{ kg ha}^{-1}$). Genotype 2 had mean grain yield similar to the overall mean and was highly stable; while genotype 17 was highly unstable. Genotype 19 and 20 were the most stable genotypes, but both had yield below the overall mean. Genotype 15 and 5 combine higher stability with higher mean yield (Figure 3, Table 3). Hence, genotype 5 and 15 are suggested candidates for cultivar release, and they can also be used as parents in a crossing program.

Genotype stability was further evaluated using different stability parameters. Genotypes with minimum values of CV, Shukla, ASV, Ecovalence, and Sij were considered stable. The most stable genotype based on the CV (genotype 25) ranked 18th for Shukla and Ecovalence, 8th for Sij, and 4th for ASV; but this genotype is a check variety, which was outyielded by 10 genotypes. This may indicate that identifying a genotype that combines high yield and stability is challenging. The highest yielding genotype (genotype 5) ranked 12th based on CV and ASV, and 14th for Shukla, Ecovalence, and Sij, suggesting that this genotype had moderate stability (Table 3). The second highest yielding genotype (genotype 15) showed inconsistency in the ranking of stability parameters, yet this genotype looks stable if CV and ASV are considered (Table 3).

This paper was a general analysis of the genotype by environment interaction on grain yield of durum wheat elite lines using AMMI and GGE biplot analyses and yield stability parameters of elite durum wheat genotypes. AMMI and GGE biplot analyses revealed significant GEI, and the interaction was a crossover type. The environments are grouped into two mega-environments, nine of the environments in one group and four in another. Genotypes with the highest stability did not have the highest yield in this study. The highest yielding genotypes, 5 and 15, are genotypes with

Table 3. Mean grain yield, stability parameters, and rankings of durum wheat genotypes across thirteen environments

Gen	Yield (kg ha ⁻¹)	Rank	CV	Rank	Shukla	Rank	Ecoval	Rank	Sij	Rank	ASV	Rank
1	3017.8	23	34.7	24	338344.2	19	11590510	19	192842.4	18	38.7	18
2	3445.4	14	16.9	4	168152.5	11	5953760	11	66767.97	11	61.1	24
3	2684.4	25	35.8	25	254737.7	15	8821462	15	147725	16	34.5	14
4	2959.4	24	25.1	18	142898.9	10	5117363	10	79903.87	13	27.3	13
5	4029.2	1	23.3	12	216480.9	14	7554398	14	112275.3	14	27.3	12
6	3653.4	6	27.1	20	368567.1	21	12591492	21	277785	21	19.2	6
7	3217.0	20	28.7	21	171343.4	12	6059446	12	63065.96	10	15.7	5
8	3602.3	9	23.5	13	206393.9	13	7220317	13	137453	15	36.8	16
9	3461.3	13	13.7	2	101983.3	4	3762236	4	-18672.3	2	96.8	25
10	3720.2	3	32.2	22	506169.1	23	17148872	23	256610.2	19	23.0	10
11	3212.8	21	20.8	8	274259.2	16	9468014	16	175584.8	17	7.3	1
12	3644.0	7	24.6	16	97047.74	2	3598772	2	-18190.5	1	39.4	19
13	3585.9	10	17.0	5	111612.9	6	4081168	6	32168.28	7	8.6	2
14	3654.3	5	15.0	3	122735.4	7	4449546	7	22168.11	4	57.8	23
15	3999.5	2	20.3	7	327696.9	17	11237872	17	261919.7	20	12.3	3
16	3624.2	8	22.0	10	348465.8	20	11925738	20	278077.5	22	35.0	15
17	3361.8	18	23.8	14	961227.6	25	32220408	25	604615.5	25	50.5	22
18	3389.5	16	19.6	6	140222.9	9	5028734	9	68495.02	12	40.6	20
19	3227.8	19	24.7	17	101764.8	3	3755000	3	29969.3	5	27.1	11
20	3681.6	4	21.9	9	105076.6	5	3864688	5	31504.24	6	22.7	9
21	3365.0	17	33.1	23	650359.1	24	21924444	24	559413	24	22.1	7
22	3404.1	15	22.0	11	48895.32	1	2003964	1	-19501.4	3	49.3	21
23	3473.8	12	24.5	15	134723.5	8	4846594	8	52209.84	9	22.7	8
24	3045.3	22	25.4	19	446040.6	22	15157416	22	346364.7	23	37.9	17
25	3493.6	11	11.2	1	331026	18	11348132	18	49470.29	8	13.4	4

moderate stability, and we recommend both of them as candidates for variety verification for the midland to highland areas of Ethiopia and as parents in crossing of in the wheat breeding program.

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