Singling Out Stable Wheat (*Triticum aestivum* L.) Genotypes through Genotype-Environment Interaction in Northern Ethiopia

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Authors' contributions

This work was carried out in collaboration between both authors. Authors BM and HH did data collection, data management, analysis and preparation of the manuscript. Both authors read and approved the final manuscript.

Original Research Article

ABSTRACT

A field trial was conducted using a triple lattice design with 25 bread wheat genotypes in order to identify high yielding stable wheat genotypes than the standard checks using stability analysis in six environments of Northern Ethiopia.In the current study, genotype, environment and genotype-environment interaction (G x E interaction) had significant effects on grain yield. The total sum of squares (TSS) split showed that the environmental effect was a predominant source of variation (76.13%), followed by genotype-environment interaction (G x E interaction) (16.17%) and genotypes (7.7%). AMMI analysis showed that the first two principal component axes (IPCA1 and IPCA2) of the interaction were highly

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significant (p<0.01) and explained 42.7 and 20.1% of the total variation, respectively. AMMI and GGE bi-plot method analyzes confirmed G 16 as an ideal genotype, whereas G 8 and G 22 are desirable genotypes; therefore, these three genotypes are recommended for verification experiments. The analysis of variance showed that genotype ETBW8480 yielded 10.2% more than the standard check Kingbird and 10.5% more than Kakaba. The GGE bi-plot analysis revealed that E-1 is the best environment (both discriminative and representative environments), which provides a useful test bed for selecting generally adapted genotypes.

1. INTRODUCTION

The self-polinating annual plant bread wheat (*Triticum aestivum* L.) belongs to the family of gramineous grasses (Poaceae family). It is widely grown as a stable food worldwide [1]. The most suitable altitude range for wheat production is between 1900 and 2700 meters above sea level [2]. It contains good nutrition profile with 12.1% protein, 1.8% lipids, 1.8% ash, 2.0% reducing sugars, 6.7% pentosans, 59.2% starch and 70% total carbohydrates and provides 314 Kcal/100 g of food [3]. Cereals are the most important food crops in Ethiopia, both in terms of production volume and area under cultivation. The proportion of Tef, corn, sorghum and wheat in the area under cereal cultivation was 23.85%; 3,023, 283.5 hectares;, 16.79%; 2,128,948.91 hectares; 14.96%; 1,896,389.29 or 13.38%; 1,696,907.05, respectively. In terms of production, the following crops accounted for the same percentage of grain production: corn (27.43%; 83,958,872.44 quintals), Tef (17.26%; 52,834,011.56 quintals), wheat (15, 17%; 46,429,657.12 quintals) and sorghum (16.89%; 51,692,525.40 quintals). The national average productivity of wheat in Ethiopia is 3046 kg/ha [4], but the experimental yield is over 5000 kg/ha. This yield gap may indicate that there is potential for productivity improvement by assessing the impact of GEI on wheat Genotype _ Environment Interaction (GEI) is a phenomenon related to the inconsistent performance under diverse environmental conditions, and it plays an important role in the performance of genotypes under different environments [5]. G-E interaction reduces the efficiency of selection and accuracy of varietal recommendation [6]. Due to this interaction of the genotype _ environment, it is necessary to study the genotype in the environment interaction before introducing new high-yielding genotypes with high stability in different environments.

In the Tigray region, there are a diverse agro ecologies process or systems that are suitable for wheat production, however, the average yield in the study area was 1983 kg/ha [4]. A shortage of improved varieties for different agro ecologies process or systems could be the major factor in the low yield. Mehari et al. [7] reported significant genotype-environment interaction (G x E interaction) in the Tigray region, and they suggested that to increase yield, genotypes should be tested in different agro ecological environments inside the region. Given the importance of GEI in its application for identifying reliable genotypes, this experiment was conducted with the objectives to estimate the effect of genotype, environment, and genotype-environment interaction (G x E interaction) on grain yield, and to assess the stability of bread wheat genotypes for yield in different environments

2. MATERIALS AND METHODS

2.1 Experimental Materials and Design

Twenty-five bread wheat genotypes (Table 1) obtained from the National Agricultural Institute of Ethiopia, along with two standard checks (Kakaba and Kingbird) were used. The experiment was conducted with each randomly assigned genotypes using a triple lattice design.

Seeds of the genotypes were planted with a plot size 2.5m*1.2m consisting of six rows, where spacing between rows was 20 cm. Planting was done by seed drill using a seed rate of 150 kg/ha for each genotype. Nitrogen (Urea) and blended fertilizers (NPKS) were applied at the rate of 100 kg/ha Urea in split, 1/3 at planting and the remaining 2/3 at the tillering stage of the crop, and 100 kg/ha blended (all at planting). All the experimental plots were agronomically treated alike.

Table 1. Names and parentage of plant materials

Entry	Name	Parentage
1	ETBW8484	MUTUS//WBLL1*2/BRAMBLING/3/WBLL1*2/BRAMBLING
2	ETBW8486	SNLG/3/EMB16/CBRD//CBRD/4/KA/NAC//TRCH
3	ETBW9026	AGUILAL/FLAG-3
4	ETBW9027	REYNA-29
5	ETBW9029	ND643/2*WBLL1/4/CHIBIA//PRLII/CM65531/3/SKAUZ/BAV92/5/BECARD
6	Kakaba	Kititati//Seri/Rayon
7	ETBW9034	MUTUS*2/HARIL #1
8	ETBW8492	KRICHAUFF/2*PASTOR//CHONTE
9	ETBW9015	SUP152//ND643/2*WBLL1/3/ND643/2*WBLL1
10	ETBW9016	SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
11	ETBW9051	CROC-1/AE.SQUARROSA (224) //OPATA/3/QAFZAH-21/4/SOMAMA-3
12	ETBW 8474	1447/PASTOR//KRICHAUFF/3/PAURAQ
13	ETBW 8475	WORRAKATTA/2*PASTOR//DANPHE #1
14	ETBW 8476	1447/PASTOR//KRICHAUFF/5/2*SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92
15	ETBW 8477	C80.1/3*BATAVIA//2*WBLL1/3/EMB16/CBRD//CBRD/4/CHEWINK #1
16	ETBW 8480	KA/NAC//TRCH/3/DANPHE #1
17	ETBW 8481	EMB16/CBRD//CBRD/4/BETTY/3/CHEN/AE.SQ//2*OPATA
18	ETBW 8506	AGUILAL/FLAG-3
19	ETBW 8507	DURRA-4
20	ETBW 7213	CHAM-4/SHUHA'S'/6/2*SAKER/5/RBS/ANZA/3/KVZ/HYS//YMH/TOB
21	ETBW 8511	BOW #1/FENGKANG 15/3/HYS//DRC*2/7C
22	ETBW 8512	BABAX/LR42//BABAX*2/3/KURUKU/4/KINGBIRD #1
23	ETBW 7871	PAURAQ/4/PFAU/SERI.1B//AMAD/3/WAXWING
24	ETBW 6940	UTIQUE 96/FLAG-1
25	King bird	THELIN # 2/TUKURU

Source; Ethiopian Institute of Agricultural Research

Table 2. Description of experimental sites

Location	Altitude (m.a.s.l)	Total annual rainfall (mm)	Temperature (^{0}C) min max		Latitude	longitude	Soil type
L/maichew	2118	782.8	10	29	14^0 06' 40.2''	038^0 45' 45.8''	Verti sol
Tahtay maichew	2090	656.6	12.6	25.51	$14^0$06'76.2''	$038^0$39'14.5''	Clay loam
Ahforom	2214	690.5	10.3	24.3	14^o06'40.2'' N	$039^0$04'15.6''E	Clay type

Source: National Meteorological Agency (Mekelle branch)

2.2 Description of the Experimental Sites

The experiment was conducted at three different environments, namely Laelay-maichew (Hatsebo), Tahtay-maichew (mai-siye), and Ahferom, under rain-fed conditions during the 2018 and 2019 main cropping seasons. These locations represent the varying agroecologies of the major wheat-growing areas of central Tigray. A description of the experimental areas is presented in Table 2.

2.3 Data Collection and Analysis

Five randomly selected plants from the four central rows of each plot were used for the data collection on a plant basis (plant height and spike length), and the averages of the five plants in each experimental plot were used for statistical analysis. The four central rows were used for data collection on a plot basis (days to 50%

heading, days to 90% maturity, grain yield, biomass yield, harvest index, thousand seed weight, and hectoliter weight).

2.4 Data Analysis

Before merging the data, the homogeneity of variances between environments was assessed using Bartlet's test, which established the validity of the combined ANOVA on the data [8]. To ascertain whether or not the data were regularly distributed, a normality test was also performed. Following the acquisition of homogenous and regularly distributed data, the grain yield data from the testing conditions was consolidated for additional combination analysis. [9] was used to do an analysis of variance (ANOVA) on the data, and Gene Stat 14th Edition was utilized to evaluate the GGE biplot pattern explorer. The AMMI analysis of variance condenses much of the magnitude of G x E interactions into one or a

few [10,11]. The [12] formula was utilized in the construction of the GGE biplot.

3. RESULTS AND DISCUSSION

3.1 ANOVA for Individual Environments

The analysis of variance conducted on individual environments revealed a statistically significant difference (p<0.01) among the bread wheat genotypes in terms of grain yield across all test locations (Table 3), indicating a strong possibility for selecting the most productive genotype/s. Notably, [13] observed substantial variability in grain yield among tested genotypes in diverse environments for bread wheat and [14] for cowpea. The highest grain yields were recorded at Tahtay-maichew 2018 (3613.9 kg/ha) and in 2019 (3587.6 kg/ha), and Ahforom 2019 (3242.3 kg/ha); attributed possibly to favorable rainfall distribution during the growing season (Table 3). Genotype ETBW8480 emerged as the highest performer at Tahtay-maichew 2018 (4330 kg/ha), followed by ETBW8475 (4196.3 kg/ha) and ETBW8477

(4182.8 kg/ha) with no significant differences. Similarly, at Tahtay-maichew 2019, genotypes ETBW8484, ETBW9015, and ETBW8480 exhibited high yields. Noteworthy top performers across different locations include ETBW8492 and ETBW8477 at Ahforom 2019, ETBW8480, ETBW8492, and ETBW8512 at Laelay-maichew 2018, ETBW8512, ETBW8484, and Kakaba at Ahforom 2018, as well as ETBW8492 and ETBW8512 at Laelay-maichew 2019 (Table 3).

In Laelay-maichew 2019, the genotypes displayed the lowest grain yield per hectare compared to the other environments, potentially due to excessive rainfall during the initial growth stage resulting in waterlogging. The findings suggest that different genotypes exhibit varying performance across distinct environments, indicating genotype-environment interactions (G x E interactions) influenced by variations among test locations. These results align with the observations of [13] regarding the diverse responses of bread wheat varieties in varying test environments

Table 3. Performance of genotypes for gain yield (kg/ha) at each location

Entry	Name	L/maichew (Hatsebo)		T/maichew		Ahforom	
		2018	2019	2018	2019	2018	2019
1	ETBW8484	2575.3c-g	1705.6b-i	3364.2f-i	4396.3a	2922.2ab	3347.3cd
2	ETBW8486	1882jkl	1616.1e-i	3084.5ij	3312.8e	2150.5de	3016.7cde
3	ETBW9026	2504.3d-h	1754.6b-h	3578d-i	3452.5e	2659.5a-e	2971.5cde
4	ETBW9027	1961.3i-l	1552.3ghi	3110.3ij	3373e	2291.3b-e	3533.5bc
5	ETBW9029	2010h-l	1643.8d-i	3294.3g-j	3582.5de	2210.8cde	3178.2cde
6	Kakaba	2763.7c-g	1778.8b-h	3486.3e-i	3402.3e	2917.5ab	3121cde
7	ETBW9034	2530.2d-g	1906.4bcd	4008.5a-e	4060.8a-d	2141.5e	3175.2cde
8	ETBW8492	3294.2ab	2326.9a	3374.2f-i	3645.5de	2082.2e	4497.3a
9	ETBW9015	2980.5a-d	1732.3b-h	3801.2a-g	4321.3ab	2174.7cde	3406.8cd
10	ETBW9016	2509.3d-h	1647.6c-i	3770.7a-g	3432.8e	2688.3a-e	3006cde
11	ETBW9051	2326.7f-j	1850.4b-e	3989.3a-e	3698.2cde	2098e	3318.3cd
12	ETBW8474	2282.3j-k	1834.6b-f	3268.7g-j	3668.3de	1357.7e	3376.7cd
13	ETBW8475	2432.3e-i	1858.3b-e	4196.3ab	3582.5de	2538.2a-e	2883.8de
14	ETBW8476	2574.2c-g	1631.6d-i	3244.8g-j	3371.2e	2326.2b-e	3300.3cd
15	ETBW8477	2821.3b-f	1503.4hi	4182.8abc	3348.5e	2392.8a-e	4047.5ab
16	ETBW8480	3356.5a	1645.1d-i	4330a	4221abc	2543.2a-e	3408.5cd
17	ETBW8481	3056.5abc	1727.1bh	3885a-f	3568.5de	2593a-e	3372cd
18	ETBW8506	2433e-i	1566.3f-i	3806a-g	3609.5de	2811.5abc	2569.5ef
19	ETBW8507	2490.5d-h	1935.9b	3610.3c-i	3456.8e	2384.2a-e	3480bcd
20	ETBW7213	1770.2kl	1929.2bc	3473.3e-i	3583.3de	2178.8cde	3243cd
21	ETBW8511	1736.3l	1697.6b-i	3139.3hij	3500e	2470.5a-e	2943.3cde
22	ETBW8512	2939.5a-e	2313.6a	4089.8a-d	3442.8e	2992a	3282.7cd
23	ETBW7871	2311.2f-j	1434.8i	2765.5j	3789b-e	2323.7b-e	2893.5de
24	ETBW6940	1917.5i-l	1830.9b-g	3775.3a-g	2048.3f	2791.5a-d	2232.3f
25	Kingbird	2296.5g-j	1846.9b-f	3716.5b-h	3790.8b-e	2506.8a-e	3400.2bcd
Mean		2470.2	1770.8	3613.9	3587.6	2421.9	3242.3
CV(%)		12.7	9.68	9.85	9.2	16.2	11.88
LSD (5%)		516.29**	282.08**	585.9**	545.1**	647.8**	634.2**
R² (%)		78	73	71	77	70	71

3.2 Combined Analysis of Variance

Combined analysis of variance unveiled highly significant differences (P ≤ 0.01) in grain yield among twenty-five bread wheat genotypes across six testing environments attributed to genotype, environment and (G x E interaction) (Table 4). The significance of G x E interaction could indicate that the performance of genotypes varied inconsistently across testing environments due to the distinct impact of the environment on the yield potential of genotypes. This outcome underscores the necessity for further study of G x E interaction to gain deeper insights into the nature of the interaction and to conduct stability analysis for discerning the consistency of genotypes across diverse environments. Yirga et al. [14] in cowpea and [13] in bread wheat similarly highlighted remarkably influence of environment, genotype and G x E interaction on the yield performance of bread wheat genotypes.

The combined analysis of variance also identified highly significant disparities (P < 0.01) among the evaluated bread wheat genotypes concerning traits such as grain yield, days to maturity, biomass yield, thousand seed weight, hectoliter weight, and grain protein content (Table 5). The findings demonstrated substantial distinctions in G x E interaction, emphasizing the considerable impact of the environment on the genotypes. Notably, genotype ETBW8480 exhibited the highest grain yield (3250.7 kg/ha) compared to the standard checks Kingbird (2920 kg/ha) and Kakaba (2910 kg/ha) based on the overall mean performance and has 10.2% yield advantage over the standard check kingbird and 10.5% over Kakaba (Table 5). Genotypes ETBW8492 (3203.4 kg/ha) and ETBW8512 (3176.7 kg/ha) also displayed superior grain yield compared to the standard checks. The observed significant G x E interaction necessitates further exploration of genotype by environment interaction, which is imperative for comprehending the underlying reasons for the interaction and conducting stability analysis to identify optimal and specifically adapted genotypes.

3.3 AMMI Model Analysis

High environmental variations and different genotype responses to variable environments are explained by the AMMI analysis of variance, which revealed significant effects of genotypes, environments, and G x E interaction (Table 6). The environmental effect explained the largest variation (76.13%), followed by interactions (16.17%) and genotype (7.7%) (Table 6). Large

percent of explained variation for environments showed that those were diverse, and that the majority of the variation in grain yield was caused by larg differences among the environmental means. This suggests that multi-location trials are crucial for identifying and choosing stable and high yielding varieties for both broad and narrow environments. This outcome supported the conclusions made by [15], where the variance caused by environment was greater that caused by genotype. [16] Found that the percentage of variation explained by environments, G x E interaction, and genotype was 51.97, 20.68, and 8.96 points, respectively. [7] Also discovered that the G x E interaction, genotypic variation, and large and significant environmental factors (78.29, 14.65, and 7.06%, respectively) all have an impact on the grain yield of bread wheat genotypes. Other similar results were also reported by [17].

The first two principal component axis (IPCA1 and IPCA2) of the interaction was highly significant different (p<0.01). IPCA1 and IPCA2 explain 42.7 and 20.1% of the interaction respectively, leading to a cumulative of 62.8% of the total variation and the rest 37.2% was contributed by the other principal components (Table 6). Many researchers also witnessed that the most accurate AMMI model prediction can be made using the first two IPCAs [12].

3.4 Which-Won-where View of the GGE bi-Plot Analysis

The GGE bi-plot analysis reveals the polygon view, which aids in identifying cross-over and non-crossover G x E interaction, as well as potential mega environments in multi-location yield trials [18]. When all environment markers fall within a single sector, it signifies that a single cultivar achieved high yield in all environments. Conversely, if the environment markers fall into different sectors, it indicates that different cultivars were successful in different environments [19] and [20]. Consequently, G22, G16, and G8 are considered vertex genotypes (Fig.1), as they perform the best in the environment lying within their respective sector in the polygon view of the GGE-bi plot. In the which-won-where view of the GGE biplot (Fig.1), the six environments are divided into three sectors with different winning cultivars. G22 emerges as the highest-yielding cultivar in E2 and E3 (although only slightly higher than several other cultivars with markers in proximity to G22), G16 excels as the highest-yielding cultivar in E1,

and G8 emerges as the highest-yielding cultivar in E5 and E6. This cross-over suggests that the target environments may be classified into different mega environments. However, it is important to note that repeatable environment grouping is necessary but not sufficient for asserting the presence of different mega-environments.

Table 4. Combined analysis of variance for grain yield

Source of variation	Degree of freedom	Mean square
Location (loc)	2	82268889.7**
Year (Yr)	1	46650.3ns
Treatment (Trt)	24	867579.5**
Loc*Trt	48	218859.9*
Yr*Trt	24	560705.5**
Yr*Loc*Trt	48	1227611.4**

Table 5. Combined means of grain yield and yield related traits of bread wheat genotypes tested at six environments

Entry	Name	GY (kg ha^{-1})	DM	BMY (kg ha^{-1})	TSW (gm)
16	ETBW8480	3250.7a	97.5fgh	9390a-d	31.7be
8	ETBW8492	3203.4ab	97.2fgh	9140a-h	32.3abc
22	ETBW8512	3176.7ab	99efg	9500abc	32bcd
9	ETBW9015	3069.5abc	99.3def	9250a-f	31.2b-f
1	ETBW8484	3068.5a-d	97.1fgh	9170a-g	31b-f
17	ETBW8481	3033.7a-d	99.2d-g	9080a-h	34.4a
15	ETBW8477	3049.4a-d	101.3b-e	9830a	31b-f
7	ETBW9034	2970b-e	96.5ghi	8920a-h	29.8efg
25	Kingbird	2920b-e	99.7c-f	8940a-h	30.5c-g
13	ETBW8475	2915c-f	102.2bc	8860b-i	31.5b-f
6	Kakaba	2910c-f	101.9bd	8580c-i	31.4b-f
19	ETBW8507	2892c-f	93.7i	8250ghi	32.4abc
11	ETBW9051	2880c-g	99.8c-f	9330a-d	31.8b-e
18	ETBW8506	2820d-h	101.2b-e	9140a-h	29.4fg
3	ETBW9026	2820d-h	98.7e-h	9190a-f	32.6ab
10	ETBW9016	2740e-l	101b-e	9560ab	30.3c-g
14	ETBW8476	2741e-l	102.6b	8640b-i	30.6b-g
20	ETBW7213	2696f-i	99.1eh	8470d-h	30.4c-i
5	ETBW9029	2653g-j	96.1hi	8220hi	30.1d-g
4	ETBW9027	2636hij	99.7c-f	8720b-i	29.7efg
12	ETBW8474	2631hij	98.8e-h	7940i	32bcd
23	ETBW7871	2586hij	106.5a	9080a-h	28.9g
21	ETBW8511	2581ij	105.5a	8360e-h	30.1e-i
2	ETBW8486	2510ji	106.6a	8400e-i	31.1b-f
24	ETBW6940	2432j	101.2b-e	8440e-i	30.7b-g
	Mean	2847.4	100	8899	31.1
	CV (%)	12.7	4.1	15	10.6

GY= gran yield, DM= days to maturity, BMY= biomass yield, TSW= 1000 seed weight, kg=kilogram, ha=hectare

Table 6. ANOVA for AMMI analysis

Source	f.d	M.S	% of explained Variation
Total	449	695944	
Genotypes	24	867579**	7.7
Environments	5	41224566**	76.13
Interactions	120	365036**	16.17
IPCA 1	28	667716**	42.7
IPCA 2	26	338275**	20.1
Residuals	66	247170**	2.13
Error	288	116051	

*fd = freedom degree; MS = mean squares; IPCA = interaction principal component analysis **,denotes highly significant difference*

3.5 Mean Vs. Stability Analysis

Evaluation of genotypes within a single mega-environment should encompass both mean performance and stability across environments. An ideal genotype would exhibit high mean performance and stability within a mega-environment [21]. In this study, the stability and yielding performance of 25 bread wheat genotypes were assessed using the average environment coordination (AEC) method, as depicted in Fig. 2. According to this method, the arrow on the AEC abscissa axis indicates the direction of higher mean performance of the genotypes, thereby ranking them based on mean performance. Consequently, the genotypes are ranked as follows: G16 > G8 > G22, with the highest average mean performance, followed by G9 > G1 > G17 > G15, and so on (Fig 2 and Table 5). In addition to mean performance, the stability of genotypes across testing environments is of great importance. A shorter genotype vector signifies greater stability of the genotype [21]. Consequently, genotype ETBW8480 exhibited the highest stability and yield, while G24 and G12 were identified as the least stable and low-yielding. Previous studies by [22,15] and [23] reported bread wheat genotypes with high mean yield performance and stability across environments. [24] also reported on genotypes with high mean yield and stability by testing 50 bread wheat genotypes across five environments

3.6 Evaluation of Genotypes Based on the Ideal Genotype

An ideal genotype should exhibit both high mean performance and stability across environments [22]. Fig. 3 illustrates the concept of an ideal genotype represented by the center of the concentric circles, which lies on the absolutely stable axis (AEA) in the positive direction and possesses a vector length equal to the longest vectors of the genotypes on the positive side of the AEA, indicating the highest mean performance. Therefore, genotypes that are located close to the ideal genotype are more desirable [20]. In this study genotypes 16, 15, and 21 were found to be stable. The ideal genotype can serve as a benchmark for selecting good genotypes comparatively. Genotypes that are far from the ideal genotype (first concentric circle) can be excluded in the early breeding cycle, while genotypes that are close to the first circle are significant for further activities [18].

Hence, G15, G17 and G9 are desirable and can be used for further breeding activities. Undesirable genotypes are those located far from the first concentric circle, namely G24, G2, G21, and G2. [25] assessed durum wheat genotypes and identified desirable genotypes that are important for breeding activities. Tekdal et al. [24] also reported desirable bread wheat genotypes that are located close to the ideal genotype.

3.7 Discriminating Capability and Representatives of Environments

Yan and Rajcan [26] stated that an ideal test environment would possess small PC2 scores, which would be more indicative of the overall environments, and large PC1 scores, which would have greater power in distinguishing genotypes in terms of genotypic main effects. An arrow pointing in this direction would symbolize such an optimal setting (Fig. 4). While it may be unlikely for such an ideal environment to exist in practice, it can still serve as a guide for selecting genotypes in trials with multiple environments. Hence, according to the graphical representation in Fig. 4, E1 represents the ideal environment (both discriminating and representative environment), making it suitable for testing and selecting widely adapted genotypes. On the other hand, E3 and E6 are the least representative environments (less suitable for selecting ideal genotypes) as they deviate significantly from the average environment coordinate. Although it may be challenging to find the ideal environment in the real world, these references can be used to select informative environments in multi-location trials [27,28].

3.8 Relationship among Test Environments

In addition, the cosine of the angle between the vectors of two environments can provide an approximation of the correlation between them. The presence of a wide obtuse angle (indicating strong negative correlations) among test environments suggests the presence of strong crossoverG x E interaction, while an acute angle indicates a positive correlation [20]. E3 and E6 displayed a strong negative correlation (Fig. 5), which could be attributed to the variability in rainfall distribution across different years. On the other hand, E6 showed a strong positive correlation (yielding identical information from both environments).
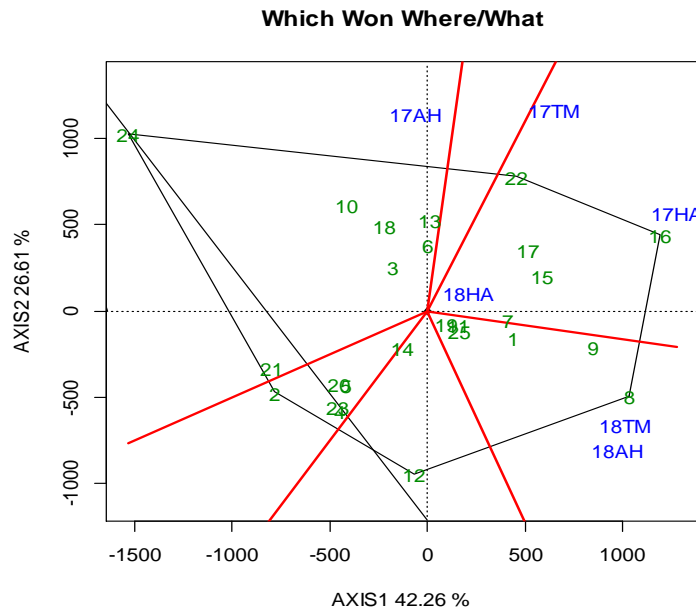
Which Won Where/What

Fig. 1. Which-won-where view of the Polygon view of the GGE by- plot analysis
E1 = 18HA, E2 = 18TM, E3 = 18AH
E4 =19HA, E5 = 19TM, E6 = 19AH
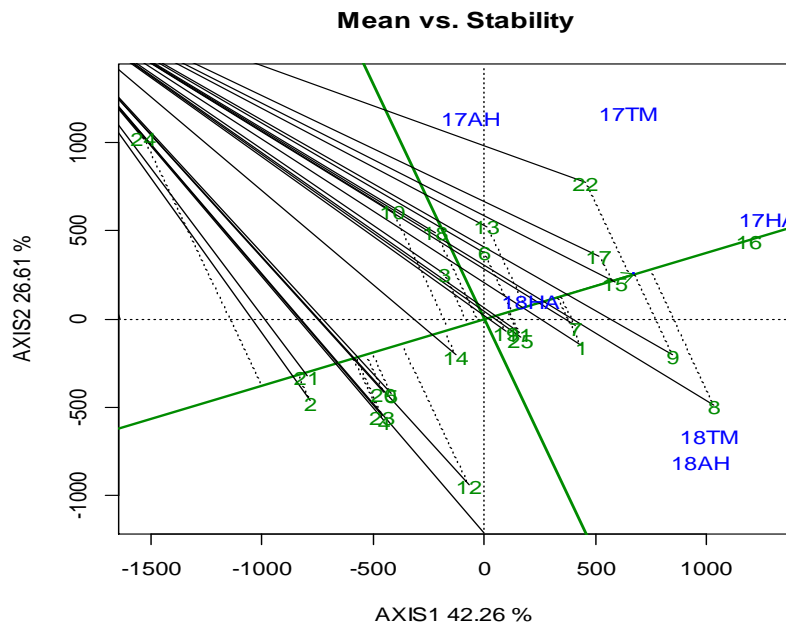
Mean vs. Stability

Fig. 2. "mean vs. stability" view of the GGE biplot based on data of 25 genotypes for the six environments
E1 = 18HA, E2 = 18TM, E3 = 18AH
E4 =19HA, E5 = 19TM, E6 = 19AH

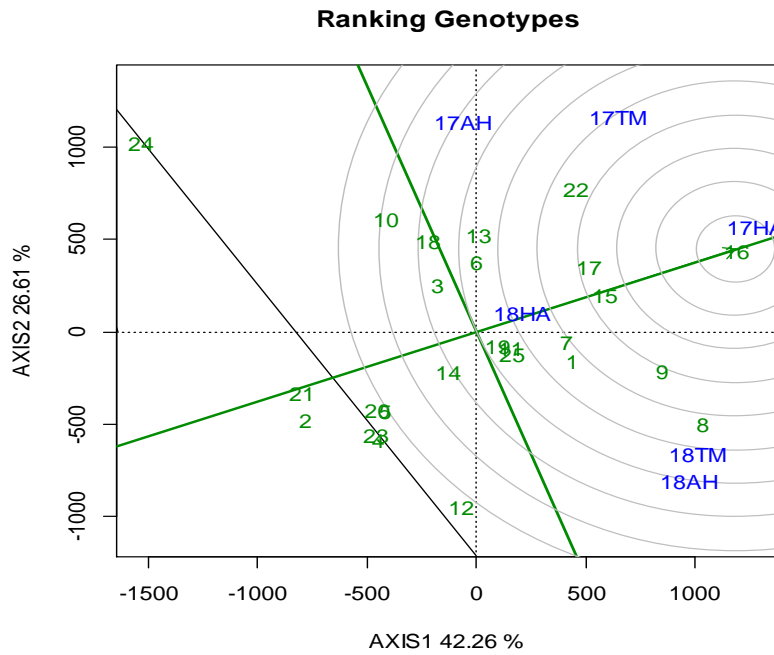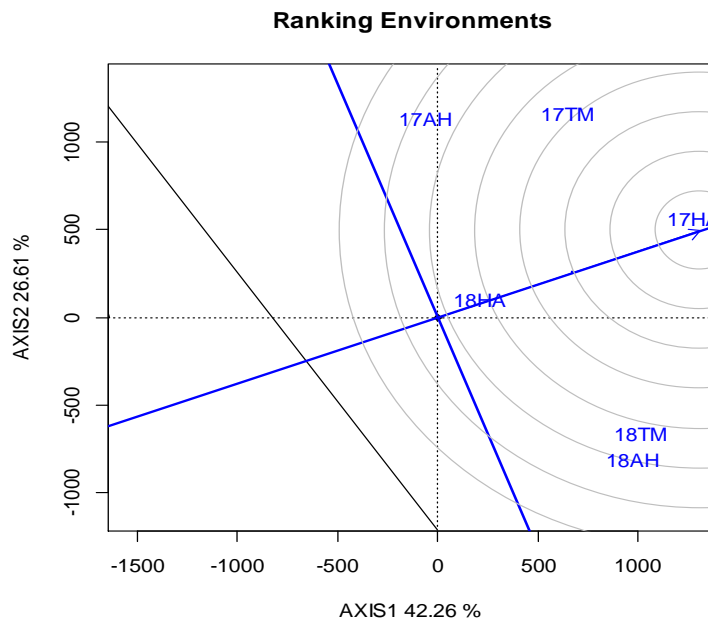Green colored numbers indicated genotype codes

Ranking Genotypes

Fig. 3. Evaluation based on the ideal genotype by GGE biplot with scaling focused on genotypes
E1 = 18HA, E2 = 18TM, E3 = 18AH
E4 =19HA, E5 = 19TM, E6 = 19AH

N.B Green colored numbers indicated genotype codes

Ranking Environments

Fig. 4. Evaluation of the ideal environment by GGE biplot with scaling focused on environment
E1 = 18HA, E2 = 18TM, E3 = 18AH
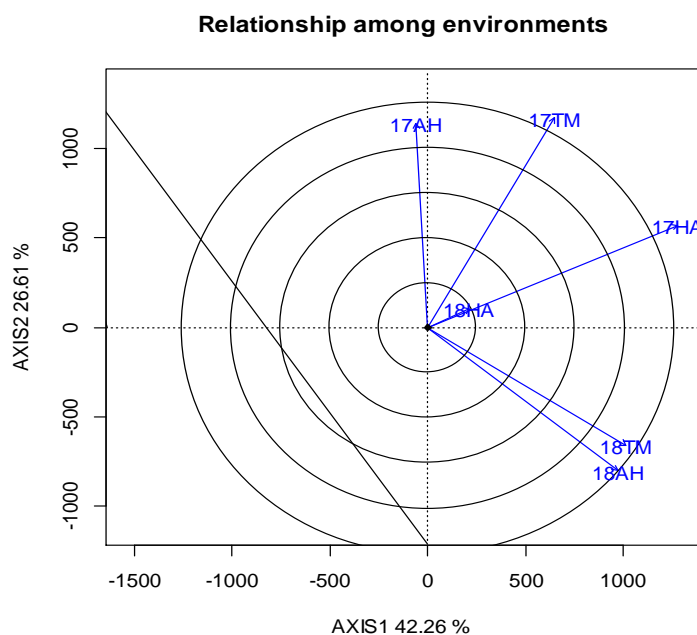*E4 =19HA, E5 = 19TM, E6 = 19AH*

Relationship among environments

Fig. 5. Discriminating vs representative environments
E1 = 18HA, E2 = 18TM, E3 = 18AH
E4 =19HA, E5 = 19TM, E6 = 19AH

4. CONCLUSION

An investigation was made to determine the effect of genotype-environment interaction (G x E interaction) on yield, and stability of bread wheat genotypes. Twenty-three bread wheat genotypes and two standard checks (Kakaba and Kingbird) were evaluated at six environments of the central zone of Tigray in the 2018 and 2019 main cropping season using triple lattice design with the objectives of assessing the effect of G x E interaction on yield and, identify desirable genotypes.

Combined analysis of variance showed significant differences for genotypes (7.7%), environments (76.13%), and G x E interaction (16.17%). The last one effect indicated the response of genotypes across the tested environments was different as well as the differential discriminating ability of the tested environments. From the tested environments, the highest mean grain yield (3613.9 kg/ha) was recorded at Tahtay-maichew 2018, followed by Tahtay-maichew 2019 (3587.6 kg/ha) and Ahferom 2018 (3242.3 kg/ha), however, the least mean grain yield was registered at Laelay-maichew 2019 (1770.8 kg/ha) because of the water logging problem during the growth stage. The significant G x E interaction could suggest further analysis of the sources of variation. Various statistical models were used to model the G x E interaction sources of variation. The AMMI analysis showed significant differences for genotype, environment, and G x E interaction. Therefore, both yield and yield stability performance of genotypes should be considered for selecting genotypes in a more precise and refined way. Accordingly, genotype, ETBW8480 is identified as the ideal genotype, while, ETBW8492, and ETBW8512 are desirable genotypes, therefore, both of them are promising genotypes, which are recommended for the variety verification trial to release the best variety/ties over the standard check variety.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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