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EFFECT OF GENOTYPE BY ENVIRONMENT INTERACTION ON BREAD WHEAT (*TRITICUM AESTIVUM L.*) GENOTYPES IN MIDLAND OF GUJI ZONE, SOUTHERN ETHIOPIA

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Abstract

Today, wheat is among the most important crops grown in Ethiopia, both as a source of food for consumers and as a source of income for farmers. Since Ethiopia is known for its diverse agro-ecology the performance of genotypes varies within and across environments and genotypes respond differently to different environments. Therefore, studies on Genotype by Environment (GxE) interaction help to determine whether or not a genotype is stable in performance over a range of environments. Therefore, this study was conducted to identify the best stable bread wheat genotype for midland areas of Guji Zone and analysis of the environment by GGE-biplot. In this experiment, 19 bread wheat genotypes were evaluated using RCBD with three replications at six different environments of midland Guji Zone of southern Ethiopia. The combined analysis of variance revealed that, there were highly significant differences among environments and among genotypes ($p<0.001$) for grain yield and yield components and for growth parameters except for days to emergence which was non-significant, indicating

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the presence of variability in genotypes as well as diversity of growing conditions at different locations. The GxE interaction was highly significant ($p<0.001$) for all traits except that of thousand seed weight (TSW) which is non-significant GxE interaction. Environments explained 89.89%, genotypes 8.29% and GxE 1.83% of the variability in grin yield. This shows that, the genotypes highly influenced by environment. Wadara2017 (E3) and Wadara2018 (E6) was the most biasing environment while Gobicha2018 (E5) followed by Dufa (2017) was the least discriminating environments. The environment grouped in to two mega environments. E1, E2 and E3 the same group and E4, E5 and E6 are the same group. ETBW8408 (G7) and ETBW8415 (G10) were high grain yield and found as stable, and therefore, recommended for wide adaptation. Again, the advanced ETBW8408 (G7) genotype was verified and released as new variety for wider production. Danda'a (G1) and ETBW8370 (G3) were low yielder and unstable genotypes. Those genotypes gave high grain yield, but unstable may be included in other breeding program, crossing.

INTRODUCTION

Today, wheat is among the most important crops grown in Ethiopia, both as a source of food for consumers and as a source of income for farmers. It is an important and most widely cultivated food crop in the world and quantity produced is more than that of any other crop, feeding about 40% of the world population.

Ethiopia is known for its diverse/heterogeneous agro-ecology. That is why genotypes performed differently within and across environments. When environmental differences are large, it may be expected that the interaction of genotypes with the environment will also be higher. This interaction may result in one cultivar having the highest yield in some environments while a second cultivar excels in others. Studies on Genotype x Environmental (GxE) interaction may help to determine whether or not a genotype is stable in performance over a range of environments. Genotype x Environmental Interaction (GEI) is useful to breeders as it can help determine if there is a

need to develop cultivars for all environments or specific cultivars for specific target environments [3]. GEI is said to occur when different cultivars or genotypes respond differently to diverse environments.

Significant G × E interaction component reduces correlations between genotypic and phenotypic values [9] and affects genetic improvement of quantitative traits. G x E interaction is one of the main complications in the selection of genotypes for broad adaptation. Numerous studies have shown that a proper understanding of the environmental and genetic factors causing the interaction as well as an assessment of their importance in the relevant G x E system could have a large impact on plant breeding [11]. G x E interaction occurs universally when genotypes are evaluated in several different environments [1, 2, and 12].

Different statistical model were used to describe the effect of GEI and facilitate genotype recommendations in MET such as stability variance [15], coefficient of variability and AMMI have been commonly used to analyze MET data to reveal patterns of GEI. Yan *et al*. [17] proposed another methodology known as GGE biplot for graphical display of GEI pattern of MET data with many advantages. GGE biplot analysis considers both genotype and GEI effects and graphically displays GEI in a two way table. GGE biplot is an effective method based on principal component analysis to fully explore MET data. It allows visual examination of the relationships among the test environments, genotypes and the GEI [2]. The main objective of this study is to identify the best performing high yielding stable bread wheat genotype for selected environments.

MATERIALS AND METHODS

Nineteen (13 advanced lines and 6 released varieties) of bread wheat genotype were evaluated across six environments in 2017 /2018 main cropping seasons.

The field experiment was laid out in RCBD with three replications. The experimental field plot was 6 rows of 2.5 m long with a 0.2 m inter-row spacing. 45g $plot^{-1}$of seed was used. The fertilizer application and other crop management practices were done as per recommendations of each test

locations. Weeding was conducted based on its appearance, twice for some locations and more for others.

Table 1: Lists of bread wheat genotypes and environments included in the study and their codes

S.N	Genotype	Gen.Code	Category	S.N	Environments	Env. code
1	Danda'a	G1	Standard check	1	Dufa2017	E1
2	ETBW8369	G2	Advanced breeding line	2	Gobicha2017	E2
3	ETBW8370	G3	Advanced breeding line	3	Wadara2017	E3
4	ETBW8373	G4	Advanced breeding line	4	Dufa2018	E4
5	ETBW8383	G5	Advanced breeding line	5	Gobicha2018	E5
6	ETBW8407	G6	Advanced breeding line	6	Wadara2018	E6
7	ETBW8408	G7	Advanced breeding line			
8	ETBW8412	G8	Advanced breeding line			
9	ETBW8413	G9	Advanced breeding line			
10	ETBW8415	G10	Advanced breeding line			
11	ETBW8420	G11	Advanced breeding line			
12	ETBW8427	G12	Advanced breeding line			
13	ETBW8428	G13	Advanced breeding line			

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14	ETBW8444	G14	Advanced breeding line			
15	Hidase	G15	Standard check			
16	Kakaba	G16	Standard check			
17	Kubsa	G17	Standard check			
18	Ogolcho	G18	Standard check			
19	PBW-343	G19	Standard check			

Collected data

Days to heading: The number of days from date of emergence to the stage where 50% of the spikes have fully emerged from the flag leaf.

Days to maturity: The number of days from emergence to the stage when 90% of the plants in a plot have reached physiological maturity (is stages at which the crop stops physiological activities, green parts of the plant turned to yellow and grain becomes hard/ dough stage of grain development).

Grain yield (kg): Grain yield obtained from the central four rows of each plot and converted to tons per hectare at 12.5% moisture content.

1000-kernel weight: Weight of 1000 seeds in gram at moisture content of 12.5% (standard moisture level for bread wheat).

Plant height: The average height in cm from ground level to the base of the head/spike.

Spike length: The average spike length in cm from its base to the tip excluding awns.

Statistical Analysis

The collected raw data were used to combine analysis of variance (ANOVA) to determine the effects of environment, genotype and GEI. Before

combine the data Bartlett's test was used to determine the homogeneity of variances between environments to determine the validity of the combined ANOVA on the data and the data collected was homogenous.

Collected raw data is subjected to GenStat software version 18 and R-Software for analysis.

ANOVA model for data combined over environments will be as follows

$Yijk = \mu + G_i + E_j + GE_{ij} + Bk(j) + e_{ijk}$.

Where, Yijk = observed value of genotype i in block k of environment j, μ = grand mean of the experiment, Gi = the effect of genotype i, Ej = environment effect, GEij = the interaction effect of genotype i with environment j, Bk(j) = the effect of block k in location j, eijk = error (residual) effect of genotype i in block k of environment j.

RESULT AND DISCUSSION

Combined analysis of variance (ANOVA) showed very highly significant differences among environments, genotypes and highly significance differences for GE interactions for grain yield and other traits (Table 3). This result is supported with the finding of Aliyi *et al.* [1] and Gadisa *et al.* [7] who reported that the combined analysis of variance over five and six locations (respectively), showed highly significant variations among the genotypes in all studied traits.

This tells us grain yield of bread wheat was highly influenced by environmental factors. These results were in agreement with the works of Aliyi [1], Mohamed [14] and Melkamu *et al.* [13] who reported that bread wheat grain yield was significantly affected by environment. This result also showed the presence of high genetic variability among the tested genotypes and the inconsistency of their performance over years across locations. Similarly Aliyi *et al* [1] and Melkamu *et al.* [13] reported that the bread wheat genotypes they studied had wider genetic variability for all traits investigated.

Table 2: ANOVA table

Traits	Source of variation						
	Env't(5)	Rep(evn't)(12)	Genotype(18)	GEI(90)	Error(226)	Means	CV%
DH	15511.757***	3.415	221.474***	161.062***	9.285	68.21	4.47
DM	22548.01***	2.69	2111.26***	1893.47***	13.11	120.65	3.00
PH	504.64***	54.85	142.79***	65.04***	39.22	74.04	8.46
SL	19.7631***	0.0828	3.4664***	0.5572	0.4417	7.39	8.99
GYLD	1963.05***	228.99	181.03***	39.59**	25.53	2.26	22.40
TSW	2377.02***	3.50	75.21	63.48	52.14	37.99	19.10

***very highly significant p<0.001, ** highly significant (p<0.01), * significant p<0.05 and ns non-significant:

HD = days to heading, MD = days to maturity, PH = plant height, SL= spike length, TKW= thousand kernel weight, GY = grain yield and CV = coefficient of variation.

Mean Comparison of the Genotypes over Locations

Mean performance of the genotypes for agronomic (phenology, growth, yield and yield components) traits across locations are discussed as below.

Mean comparison of genotypes in Phenology

Genotypes showed variation for days to heading that ranged from 60.17 to 76.89 while days to maturity ranged from 111.6 to 163.9 (table 3). The

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genotypes those early in maturity are preferred for those locations where this study was conducted. This is due to the shortage of rain fall at these locations.

Mean comparison of genotypes in growth characters

Tested genotype showed variation for growth character (plant height and spike length**).** Plant height ranged from 65.99 to 77.17 cm, and spike length ranged from 6.713 to 8.310 cm across environments (Table 3).

Mean comparison in grain yield and yield components

High grain yield from combined data across environments was obtained from genotype ETBW8408 (2.7ton/ha) followed by the genotype ETBW8415 (2.6ton/ha) and PBW-343 (2.56ton/ha). The lowest grain yield was harvested from the genotype Danda'a (1.9ton/ha) (Table 4).

The advanced genotype ETBW8408 was evaluated by variety releasing committee of Ethiopian agricultural ministry. This genotype was released and registered as new variety. The new name is given as 'Adola-1' variety. The studied genotypes showed high variability in grain yield. This result was in agreement with those obtained by Aliyi *et al*., [1] and Zecevic*et al*., [19] who reported that genotypes showed high variability in grain yield across environments.

Table1: Combined means of grain yield and some agronomic traits of bread wheat across environments.

No	GENO	GYLD(ton/ha)	DH	DM	PH(cm)	SL(cm)	TKW
1	Danda'a	1.59	69.67	119.4	76.71	7.509	39.24
2	ETBW8369	2.58	67.78	120.9	74.59	7.814	38.40
3	ETBW8370	1.95	74.50	116.2	74.60	7.204	40.18
4	ETBW8373	1.67	67.33	117.0	75.44	8.012	36.41
5	ETBW8383	2.29	69.06	111.6	75.54	7.182	39.74
6	ETBW8407	2.47	66.50	121.7	76.66	8.310	37.20
7	**ETBW8408**	2.73	60.17	122.9	75.18	7.496	39.31
8	ETBW8412	2.38	67.67	116.2	77.17	8.033	39.09

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9	ETBW8413	2.42	66.83	163.9	76.74	7.084	37.38
10	ETBW8415	2.60	76.89	117.7	75.59	6.854	36.42
11	ETBW8420	2.48	67.83	122.1	71.77	7.213	34.98
12	ETBW8427	2.08	67.67	119.4	70.71	7.801	39.16
13	ETBW8428	2.03	68.78	115.2	70.62	7.296	34.96
14	ETBW8444	2.44	63.50	117.8	73.52	7.611	37.82
15	Hidase	2.48	67.17	116.5	75.62	7.288	38.18
16	Kakaba	2.50	66.83	119.3	74.49	6.944	39.82
17	Kubsa	2.13	70.83	116.3	71.33	7.163	35.01
18	Ogolcho	2.01	68.33	118.6	65.99	6.713	36.02
19	PBW-343	2.56	68.61	119.7	74.42	6.968	42.56
Means		2.26	68.21	120.65	74.04	7.39	37.99
CV%		22.40	4.47	3.00	8.46	8.99	19.10
LSD (5%)		8.13	2.00	2.38	4.11	0.44	4.74

Grain Yield Stability analysis

GGE Bi-plot for Evaluation of Environments and Genotypes

Evaluation of genotypes relative to ideal genotypes

From the concept of stability parameters, genotypes nearest to concentric of the circle is supposed to be stable and as the same time high grain yielder. Based on this concept, from this study, ETBW8415 genotype is the nearest to the arrow and is considered to be the "ideal" genotype and the highest yielding genotype followed by ETBW8408. A genotype is more desirable (high yielding) if it is located closer to the ideal genotype along PCA1 and undesirable (low yielding) if it is located far from the ideal genotype. Genotypes above PCA1=0 give above-average yield while those below PCA1=0 give below-average yield. The result f this research showed that 42.1 % of genotypes included here were gave below average yield, while 52.63 % them were yielded above average yield. From example, Danda'a and ETBW8373 were among low yielding genotype, while and ETBW8415 and ETBW8408 were from high yielding. The genotypes those mostly far away

from ideal genotype was most unstable genotypes (figure 1). Similar result was reported by Aliyi *et al*., [1], Kaya *et al*., [10] and Farshadfar *et al*., [4].

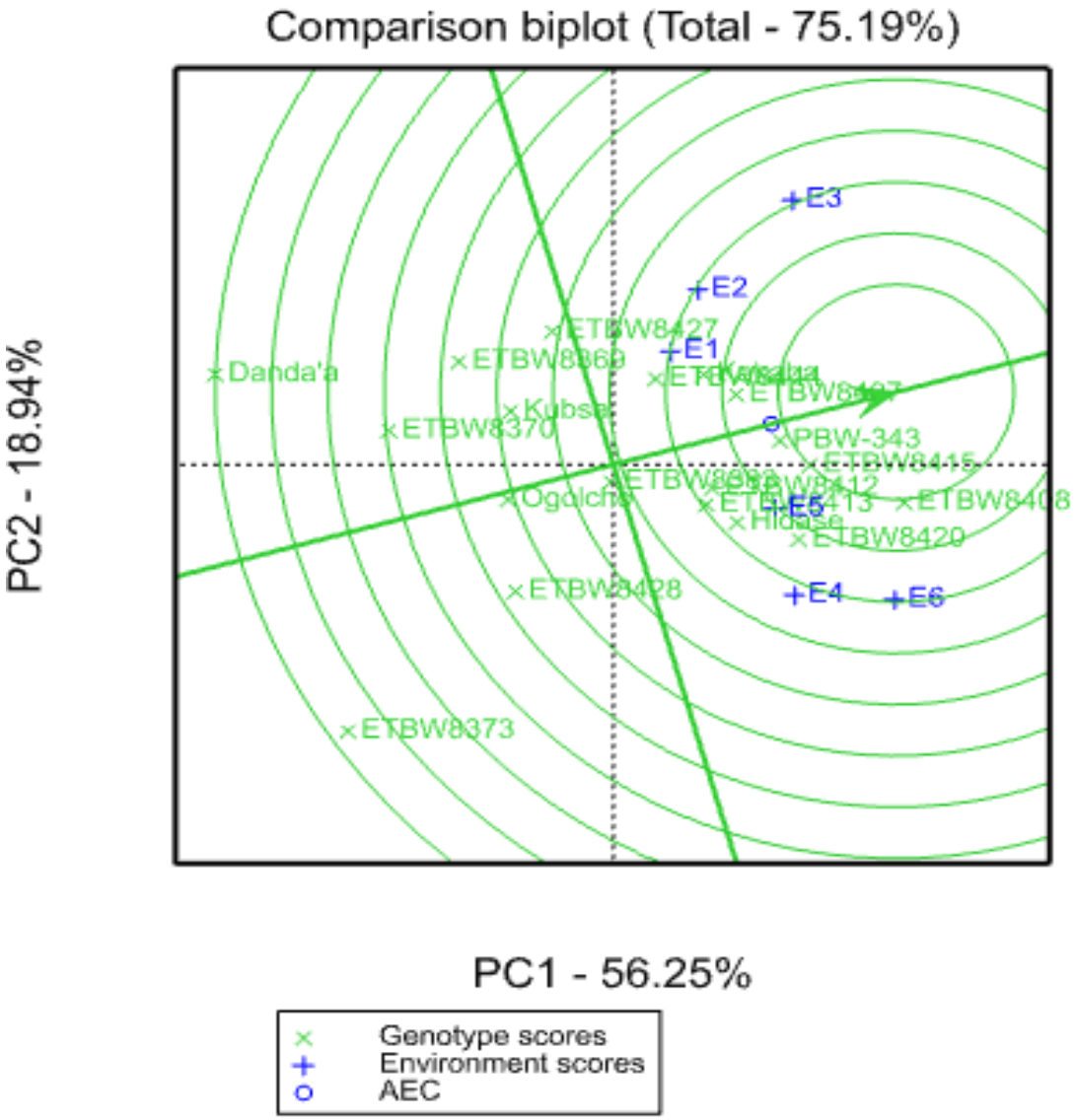


Figure1. GGE-bi-plot showing the "ideal" genotype.

Evaluation of environments relative to the ideal environments

From GGE-biplot comparison for environments under this study, E5 (Gobicha2018) had the longest vector with small PCA2, and fell into the center of the concentric circles and is considered as an ideal environment in terms of being the most representative of the overall environments and the

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most powerful to discriminate genotypes (Figure 2). From figure 2, it shows that, E6 (Wadara2018) was closer to the ideal environments (E5) and is considered as suitable to select widely adapted genotypes. E1 (Dufa17) and E2 (Gobicha17) were far from the ideal environment and are considered to be unsuitable environments to select desirable genotypes (Figure 2). This result is in line with the findings of Aliyi *et al* [1], [17] Yan and Rajcan [16], Yan *et al*. [18] and Fiseha *et al*. [5]

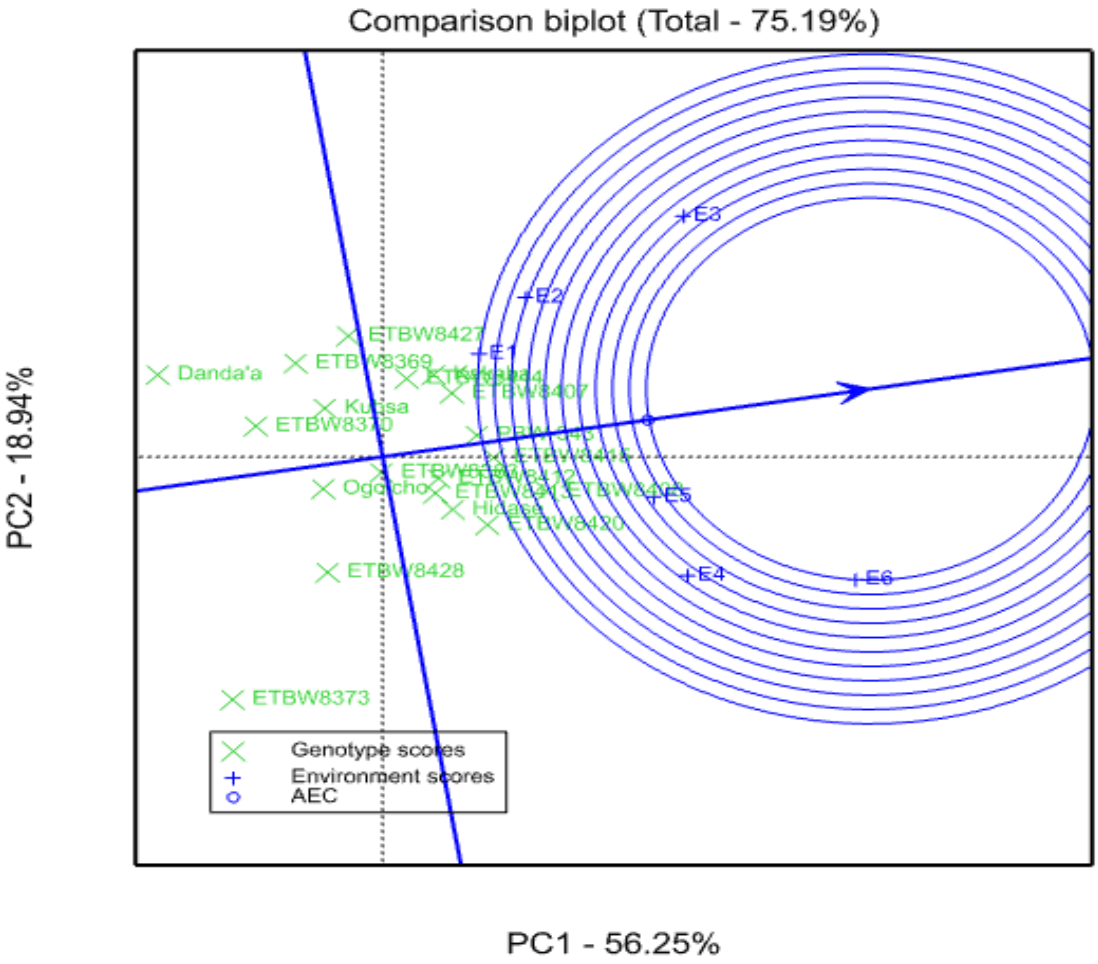


Figure2. GGE-biplot based on the ranking of environments relative to an ideal environment

'Which-Won-Where' Pattern and Mega-environment Identification

The polygon view of the GGE biplot was constructed to show which genotypes performed best in which environment (Figure3). PC1 (52.51%) and

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PC2 (24.67%) accounted for 75.19% of the G + GE variation for grain yield of the genotypes evaluated at six environments (three locations for two years). The vertices of the polygon were the genotype markers located farthest away from the biplot origin in various directions, such that all genotype markers were contained within the resulting polygon. Based on this truth, five genotypes were identified as the markers which are farthest away from the biplot origin and the remaining fourteen genotypes lied within this polygon. The vertex genotypes were the best or the poorest genotypes in the test environments since they had the shortest or longest distance from the origin of the biplot on the opposite side of the environments. For example, from marker genotypes ETBW8408 is the best genotype as it has the shortest distance to the origin of biplot on the same side of all environments and genotypes like ETBW8373 and Danda'a were the poorest genotypes as they have the longest distance from the origin of biplot on the opposite side of all environments (figure 3).

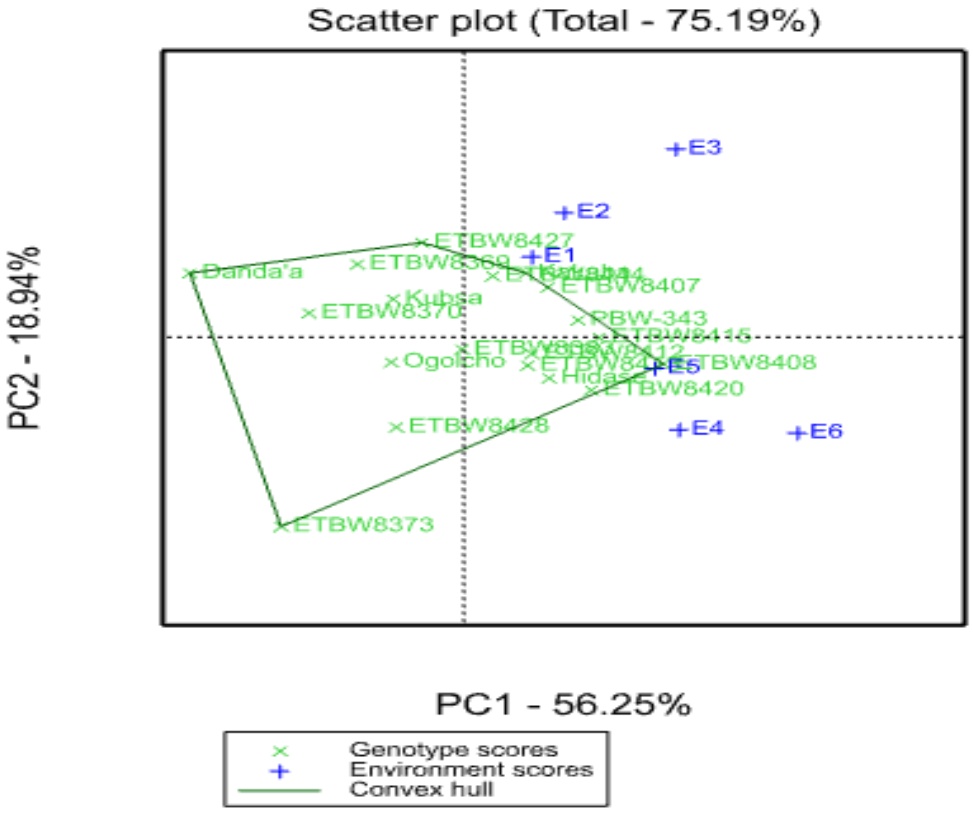


Figure3. 'Which-Won-Where' Pattern and Mega-environment Identification.

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CONCLUSIONS AND RECOMENDATIONS

In the study, 19 bread wheat genotypes were tested at three locations for two years in mid land Guji Zone of Southern Ethiopia.

From the combined analysis of variance, the effects of environments, genotypes and G x E were highly significant for grain yield. This implies that, environment influence yield performance of bread wheat in Ethiopia and the genotypes respond differently to these environments. From those genotypes included in this study, genotypes like ETBW8408 and ETBW8415 were the most desirable genotypes across tested environments.

ETBW8408 was advanced both by yield performance and stability and therefore released and registered as new variety after it was evaluated by evaluation committees of Ethiopian ministry of agriculture for commercial production. Then, the new name 'Adola-01' is given for this genotype and currently it is widely under production. While, the other advanced stable and high yielding genotypes were not selected due to high disease reaction and together, with those genotypes specifically adapted to specific environments were recommended to include in breeding programs.

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