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Genotype X Environment Interaction and Stability Analysis for Grain Yield of Bread Wheat (*Triticum aestivum*) Genotypes Under Low Moisture Stress Areas of Ethiopia

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Abstract: A multi-locations' experiments were carried out from 2018 to 2019 main cropping seasons in moisture stress areas of Ethiopia to estimate the genotype x environment interaction and to select stable and adaptable variety/ies for grain yield of bread wheat. The genotypes consisted of 23 genotypes and two standard checks arranged in alpha lattice design replicated three times. Data were taken for agronomic traits and diseases. Analysis of variances and stability analysis were carried out for grain yield using R software. Combined analysis of variance showed a highly significant ($p \leq 0.01$) difference among the genotypes, locations, and GEI for grain yield suggesting a differential response of genotypes across testing environments. The grand mean yield over nine environments was 5251.90 kg ha^{-1} and the mean yield of genotypes across nine environments ranged from 1539.29 kg ha^{-1} in 2018 at Dhera to 7621.87 kg ha^{-1} in 2018 at Kulumsa, respectively. The recorded mean yield of the standard check Deka (5066.543 kg ha^{-1}) and Ogolcho (4018.39 kg ha^{-1}) was below the grand mean yield of genotypes across environments. The Genotypes ETBW 9136 (5731.79 kg ha^{-1}), ETBW 9139 (5844.87 kg ha^{-1}), ETBW 9646 (5754.01 kg ha^{-1}), ETBW9172 (5634.01 kg ha^{-1}), ETBW9641 (5545.03 kg ha^{-1}), ETBW 9080 (5545.31 kg ha^{-1}) and ETBW9396 (5467.04 kg ha^{-1}) gave the highest mean grain yield across environments, whereas the standard check Ogolcho recorded lowest mean grain yield across environments. The first four principal components of the GEI explained 85.6% of the variation. Additive main effects and multiplicative interaction (AMMI) stability parameters revealed that the genotypes ETBW 9080 (G11), ETBW 9172 (G12), ETBW 9646 (G19), ETBW 9396 (G13), ETBW 9452 (G14), ETBW 9136 (G5) and ETBW 9139 (G6) were high yielder and more stable inferring little interaction of genotypes with the environment whereas Ogolcho (G25), ETBW 9119 (G3), ETBW 9647 (G20) and ETBW 9065 (G8) was low yielder and unstable suggesting high interaction with the environments. Based on stability parameters and other agronomic traits, the genotypes viz. ETBW 9396 (G13) and ETBW 9080 (G11), were proposed for variety verification and possible release in 2021.

Keywords: Ethiopia, Genotype by Environment Interaction, Grain Yield, Moisture Stress Areas, Stability Analysis, Triticum Aestivum

1. Introduction

Wheat (*Triticum spp.*) is one of the most important cereal crops cultivated in Ethiopia. The production and productivity of wheat have increased by 14% due to the use of full packages for the last decade in Ethiopia [9]. The current wheat productivity is 2.7 tons per hectare but the potential yield could be more than 5.0 tons per hectare [3, 13]. However, due to a higher increment in demands, about 37% (1.7 million tons) wheat grain deficit was observed during the 2018 budget year in Ethiopia (https://www.world-grain.com/articles/11880-ethiopias-wheat-production-to-increase/accessed in Nov. 2019). The yield gap observed could be attributed to different factors of which is lack of high yielder varieties sustainably tolerant to diseases and pests, tolerant to low pH and waterlogged areas and lack of use of full packages and knowledge of production in the farming communities. The Varietal differences in relation to Al tolerance exist in wheat; and the integrated use of all the available resources including acid tolerant and crop species, which improve and sustain soil and agricultural productivity, is of great practical significance [12]. Biotic factors viz. fungal diseases, rusts (*Puccinia. spp.*) are the devastating rust diseases which highly affecting wheat production of wheat in Ethiopia [18].

Multi-environment trials are important in plant breeding for evaluating genotypes for their overall stability and adaptability in the presence of genotype by environment (GE) interaction. An understanding of GE interaction is important at all stages of plant breeding, including ideotype design, parent selection, selection based on traits, including grain yield [19]. The G × E study is important in presence various agro-ecologies. Significant G × E interaction is a consequence of variations in the extent of differences among genotypes in diverse environments (called as a qualitative or rank changes) or variations in the comparative ranking of the genotypes (called as a quantitative or absolute differences between genotypes) [5, 6, 8].

Low moisture stress is becoming important in bread wheat producing areas of Ethiopia. In view of the problems, two product concepts (low moisture areas and high moisture areas) were designed in wheat breeding program at Kulumsa Agricultural Research Center and genotypes were selected based on the different agronomic traits viz. low sensitivity to low moisture stresses, early maturity and other agronomic traits. Therefore, a multi-locations trials were designed with the objectives to estimate the magnitude of genotype by environment interactions; and to select best genotypes with stable and adaptable to the tested environments.

2. Materials and Methods

2.1. Experimental Sites' Descriptions

The experiments were conducted at nine environments viz. Dhera, Melkasa, Asasa, Kulumsa and Atsela during 2018 and at Dhera, Melkasa, Kulumsa and Asasa during 2019 cropping season. The descriptions of the locations are listed in Table 1.

Table 1. *List of test locations and their descriptions.*

Experimental site	Geographic position		Altitude	2018			2019		
	Latitude	Longitude		Temperature (°C)		Rain fall (mm)	Temperature (°C)		Rainfall (mm)
				Min	Max		Min	Max	
Kulumsa	08°01′10″N	39°09′11″E	2200	11.85	23.48	850	11.0	24.0	939.0
Asasa	07°07′09″N	39°11′50″E	2340	6.92	18.11	640	7.0	21.0	640.0
Dhera	08°19′10″N	39°19′13″E	1650	14.00	27.80	680	-	-	-
Melkasa	08°24′N	39°12′E	1550	13.60	28.60	763	-	-	-

Note: Sources (KARC; 2019; MARC, 2019)

2.2. Experimental Design and Data Management

Twenty-five genotypes including two standard checks were grown in Alpha-Lattice Design with three replications (Table 2). Each experimental unit consisted of six rows of 2.5 m length with 20 cm spacing between rows; 1 m and 1.5 m spaces were left between adjacent plots and replications, respectively. Data were collected from the entire plot for the parameters days to heading, days to maturity, grain yield, 1000 kernel weight, hectoliter weight, and from randomly sampled plants for the character; plant height. A seed rate of 125 kgha^{-1} was used at all locations. Fertilizers were applied based on the specific site recommendations and weeding were done uniformly to all plots in each location as necessary. Yellow rust (*Puccinia striformis*f. sp. *tritici*.) and stem rust (*P. graminis*) data, were recorded using the modified Cobb scale [15]. Disease severity was estimated which was used to determine the percentage of possible tissue infected and the maximum disease severity and reaction record were taken at each testing location for each genotype.

2.3. Statistical Analyses

Additive main effects and multiplicative interaction (AMMI) method integrates analysis of variance and principal components into a unified approach [2; 11]. AMMI method first fits the additive main effects of genotypes and environments by the usual analysis of variance and then describes the non-additive part, genotype by environment interaction, by principal component analysis. Data were subjected to analysis after checking for required assumptions of normality, homogeneity of variance using respective tests. The AMMI analysis was performed using the model suggested by Gauch and Zobel [11] for genotypes and environments is:

$$Yij = \mu + gi + ej + \sum_{k=1}^{n} \Lambda_k \, a_{ik} y_{jk} + e_{ij}$$

Table 2. *List of studied bread wheat genotypes.*

Entry No.	Genotype	Pedigree
G1	DAKA	Check
G2	ETBW 9116	PFAU/MILAN/5/CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/ VEE#7/BOW/4/PASTOR/6/KINGBIRD #1
G3	ETBW 9119	ELVIRA/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI/6/VEE/PJN//KAUZ/3/PASTOR/7/TILHI/4/CR OC_1/AE.SQUARROSA (213)//PGO/ 3/CMH81.38/2*KAUZ/8/PICAFLOR #2
G4	ETBW 9128	FRNCLN*2/BECARD
G5	ETBW 9136	92.001E7.32.5/SLVS/5/NS-732/HER/3/PRL/SARA//TSI/VEE#5/4/ FRET2/6/SOKOLL/3/PASTOR//HXL7573/2*BAU
G6	ETBW 9139	KA/NAC//TRCH/5/W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1
G7	ETBW 9149	PRL/2*PASTOR/6/TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU #1
G8	ETBW 9065	FALCIN/AE.SQUARROSA (312)/3/THB/CEP7780//SHA4/ LIRA/4/ FRET2/5/DANPHE #1/11/CROC_1/AE.SQUARROSA (213)//PGO/10/ ATTILA*2/9/KT/BAGE//FN/U/3/BZA/4/TRM/5/ALDAN/6/SERI/7/VEE#10/8/OPATA
G9	ETBW 9077	SHORTENED SR26 TRANSLOCATION//2*WBLL1*2/ KKTS/3/BECARD
G10	ETBW 9078	SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
G11	ETBW 9080	KACHU//WHEAR/SOKOLL
G12	ETBW 9172	ND643/2*WBLL1//KACHU
G13	ETBW 9396	BOUSHODA-1/4/CROC-1/AE.SQUARROSA (205)//KAUZ/3/SASIA
G14	ETBW 9452	REBWAH-19/HAAMA-14
G15	ETBW 9543	KFA//PBW343/PASTOR/3/PBW343*2/KUKUNA/4/PBW343*2/KUKUNA*2//FRTL/PIFED/5/PBW343*2/ KUKUNA*2//FRTL/PIFED
G16	ETBW 9545	ATTILA*2/PBW65*2//MURGA/4/MUU #1//PBW343*2/KUKUNA/3/MUU/5/ATTILA*2/PBW65//MURGA
G17	ETBW 9641	MELON//FILIN/MILAN/3/FILIN/4/PRINIA/PASTOR//HUITES/3/MILAN/OTUS//ATTILA/3*BCN/5/MEL ON//FILIN/MILAN/3/FILIN
G18	ETBW 9642	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/WHEAR/SOKOLL
G19	ETBW 9646	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/PARUS/PASTOR
G20	ETBW 9647	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/MEX94.2.19//SOKOLL/WBLL1
G21	ETBW 9648	PUB94.15.1.12/FRTL//92.001E7.32.5/SLVS
G22	ETBW 9650	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/GLADIUS
G23	ETBW 9651	KACHU*2/3/ND643//2*PRL/2*PASTOR
G24	ETBW 9652	PFUNYE #1/KINGBIRD #1
G25	OGOLCHO	Check

Where, Yij is the mean yield of the i^{th} genotype in the j^{th} environment; μ is the general mean; gi is the i^{th} genotypic effect; ej is the j^{th} location effect; λn is the eigenvalue of the PCA axis n; a_{ik} and y_{jk} are the i^{th} genotype j^{th} environment PCA scores for the PCA axis n; e_{ij} is the residual; n' is the number of PCA axis retained in the model. Therefore, the interaction effect can be calculated as;

$$(GXE)ij = yij - yi - yj - y..$$

AMMI Stability Value (ASV): ASV indicates the distance from zero in the two-dimensional plot of IPCA1 score against IPCA2 score in the AMMI model [16].

The ASV was calculated using the formula suggested by purchase [16]

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}}(IPCA1)^2\right]^2 + (IPCA)^2}$$

The larger the ASV value, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller ASV values indicate more stable genotypes across environments [16].

Where; SS_{IPCA1} is sum of square of interaction principal component 1 and SS_{IPCA2} IS sum of square of interaction principal component 2.

Yield Selection Index (YSI): Stability is not the only parameter for selection as most stable genotypes and would not necessarily give the best yield performance. Therefore, based on the rank of mean grain yield of genotypes (rYi) across environments and rank of AMMI stability value (rASVi). A genotype with the least YSI is considered as the most stable [7]. Yield selection index (YSI) was calculated for each genotype as:

$$YSI = rASVi + \text{rYi}$$

Eberhart and Russell regression model: The regression coefficient (bi) and deviation from regression (S^2d) of genotype mean across environments index were computed as suggested by [4]. The analysis was performed using R statistical software.

3. Results and Discussion

3.1. Additive Main Effects and Multiple Interaction (AMMI) Model for Grain Yield

Combined analysis of variance showed that highly significant (p≤0.01) differences among the genotypes, environments, GEI and the first four Principal Components (PCs) for grain yield suggesting differences among environments and differential response of genotypes across testing environments (Table 3). The first four interaction principal components (IPCA) of the GEI explained 82.1% of the total variation and 40.5% is explained by IPCA1 followed by 16.7%, 15.2%, and 9.7% for IPCA2, IPCA3, and IPCA4, respectively. The most accurate model for AMMI can be predicted by using the first two PCAs [10]. In this, the first two IPCAs were used to show genotype by environment interaction and placement on the biplots (Figure 1). The greater the IPCA scores (positive or negative) as it is a relative value, the more specifically adapted a genotype is to certain environments. The more IPCA scores approximate to zero, the more stable the genotype is across environments sampled [16; 1]. Accordingly, the genotypes ETBW 9080 (G11), ETBW 9172 (G12), ETBW 9646 (G19), ETBW 9396 (G13), ETBW 9452 (G14), ETBW 9136 (G5) and ETBW 9139 (G6) were relatively located near to the origin of the biplot and hence better stable (little interaction of genotypes with the environment) and widely adaptable genotypes across environments. Whereas the genotypes Ogolcho (G25), ETBW 9119 (G3), ETBW 9647 (G20) and ETBW 9065 (G8) far from the origin of biplot suggesting less stability (high interaction of genotypes with the environments) and have specific adaptability to certain environments.

Table 3. *AMMI analysis of variance for grain yield (kg ha^{-1}) of 25 bread wheat genotypes.*

Source of variation	Df	Sum Squares	Mean Squares	% Explained
ENV	8	2924185793	365523224***	
REP (ENV)	18	29803986	1655777***	
GEN	24	102570244	4273760***	
ENV x GEN	192	274195518	1428102***	
PC1	31	110968396	3579625.7***	40.5
PC2	29	45899417	1582738.5***	16.7
PC3	27	41715720	1545026.7***	15.2
PC4	25	26482907	1059316.3**	9.7
Residuals	432	266347198	616544	

Note: Df- degrees of freedom.

3.2. Mean Grain Yield Performances of the Genotypes Across the Tested Environments

The mean grain yield of the 25 genotypes showed a wide range of variation in the different environments. The grand mean yield over nine environments was 5252 kg ha^{-1} and the mean yield of genotypes across nine environments ranged from 1539 kg ha^{-1} at Dhera in 2018 to 7622 kg ha^{-1} at Kulumsa in 2018, respectively. The recorded mean yield of the standard checks; Daka (5067 kg ha^{-1}) and Ogolcho (4018 kg ha^{-1}) were below the grand mean yield of genotypes across environments implying the possibility to select superior candidate genotypes better than the st. check varieties. The Genotypes ETBW 9136 (5732 kgha^{-1}), ETBW 9139 (5845 kg ha^{-1}), ETBW 9646 (5754 kg ha^{-1}), ETBW9172 (5634 kgha^{-1}), ETBW9641 (5545 kgha^{-1}), ETBW 9080 (5545 kgha^{-1}) and ETBW9396 (5467 kgha^{-1}) gave the highest mean grain yield across environments, whereas the standard check Ogolcho recorded lowest mean grain yield across environments (Table 4).

3.3. AMMI Stability Value (ASV) and Yield Selection Index (YSI)

The genotype with lower ASV values is considered more stable and genotypes with higher ASV are unstable. The analysis using AMMI stability value revealed that ETBW 9172 (7.30), ETBW 9396 (6.18), ETBW 9452 (4.77), ETBW 9646 (4.93), ETBW 9651 (9.89), ETBW 9652 (2.99), ETBW 9139 (4.21) and ETBW 9077 (8.47) were among genotypes with lower ASV values, indicating those genotypes were more stable than the others. However, the genotype OGOLCHO (102.08), ETBW 9119 (38.89), ETBW 9065 (31.31), ETBW 9545 (28.28) had the highest AMMI stability values inferring those genotypes were classified under the least stable genotypes. Stability is not the only parameter for selection, because the most stable genotypes would not necessarily give the best yield performance [14] hence there is the need to use the Yield Selection Index (YSI) which incorporate both mean yield and stability of genotypes. It was applied to identify high yielding and stable genotypes in cereal crops like maize [4] and durum wheat [14]. Accordingly, the Yield selection index revealed that the genotype ETBW 9139, ETBW 9646, ETBW 9396, and ETBW 9172 are the best and top-ranking genotypes integrating both stability and grain yield performance parameters. This result is also confirmed by conducting further analysis using the Eberhart and Russell regression model for the proper recommendation of the genotypes. The genotypes ETBW 9172, ETBW 9396, ETBW 9641, and ETBW 9646 had regression coefficients approaching one and deviation from regression approaching zero implying that they are stable and widely adaptable than the other genotypes which highly agreed with AMMI model. The genotypes ETBW 9396 and ETBW 9646 selected as high yielding and stable by AMMI model are also selected by Eberhart and Russell regression model (Table 5).

Table 4. *Mean grain yield (kg ha^{-1}) performance of the 25 genotypes of bread wheat tested in nine environments.*

Genotype	KU18	AA18	DH18	MK18	AT18	KU19	AA19	DH19	MK19	MEAN
DAKA	8040	5864	1818	1300	6317	6282	7759	4144	4074	5067
ETBW 9116	6991	5484	2746	1649	7012	6842	6446	4006	3874	5006
ETBW 9119	7012	6470	1923	1711	7205	5473	5536	4090	4090	4835
ETBW 9128	7417	4917	841	929	5708	7342	6808	4756	4419	4793
ETBW 9136	7708	6894	2377	2201	5995	7671	8123	5452	5164	5732
ETBW 9139	8100	6791	1114	2868	7375	7179	7932	4916	6329	5845
ETBW 9149	7412	5812	1343	1242	5838	7919	6188	4574	5113	5049
ETBW 9065	6731	7038	1086	1620	6998	5976	8386	5687	4879	5378
ETBW 9077	7232	4702	1921	2212	7555	6047	7273	4458	4817	5135
ETBW 9078	7703	4674	1271	2721	6127	6609	7040	4936	3721	4978
ETBW 9080	7706	6868	1713	2507	5100	7519	8186	4996	5314	5545
ETBW 9172	8301	6464	1913	2139	6775	6510	7360	5828	5416	5634
ETBW 9396	7827	6327	1167	2418	6360	7429	7210	5256	5211	5467
ETBW 9452	7903	5689	1031	2521	7045	6607	6982	5618	4986	5376
ETBW 9543	7714	6280	1449	1629	7732	6290	7044	4110	4542	5199
ETBW 9545	8314	5428	1089	1158	6408	7382	8202	4591	3914	5165
ETBW 9641	7788	5943	1852	2547	6942	6308	8393	5063	5114	5550
ETBW 9642	8157	5210	1240	1993	6778	7319	7747	4788	5240	5386
ETBW 9646	8397	5972	1706	2697	6825	6909	7653	5979	5649	5754
ETBW 9647	7731	4280	1564	2727	6708	7512	7688	4357	5916	5387
ETBW 9648	8394	6279	2484	2380	6637	6093	7974	5567	5598	5712
ETBW 9650	7992	4559	1188	1512	7685	6874	7409	5249	5320	5310
ETBW 9651	6919	6306	1021	1369	5845	6549	7004	3709	4977	4855
ETBW 9652	7467	5510	1424	1594	6743	7053	7174	4502	4638	5123
OGOLCHO	5590	4072	1200	792	7027	6484	1558	4279	5163	4018
Mean	7622	5753	1539	1937	6670	6807	7163	4836	4939	5252
CV (%)	5.92	13.42	31.06	47.13	13.70	13.18	8.21	8.33	19.41	14.95
LSD (5%)	801	1391	1090	ns	ns	ns	966	677	ns	

Note: KU18- Kulumsa 2018; AA18_ Asasa 2018; DH18_ Dhera 2018; MK18_ Melkasa 2018; AT18_ Atsela 2018; KU19_ Kulumsa 2019; AA19_ Asasa 2019; DH19_ Dhera 2019; MK19_ Melkasa 2019.

Table 5. *Stability parameters and the rank of genotypes tested for grain yield.*

S/No.	Genotype	bij	S^2dij	ASV	YSI	Mean grain yield (kg ha^{-1})	Y rank
1	DAKA	1.06	106253.30	21.50	37	5067	8
2	ETBW 9116	0.86	251329.72	18.29	37	5006	6
3	ETBW 9119	0.86	466019.18	38.90	47	4835	3
4	ETBW 9128	1.10	16019.92	17.82	39	4793	2
5	ETBW 9136	0.97	154110.38	16.49	16	5732	23
6	ETBW 9139	1.07	103245.50	4.21	3	5845	25
7	ETBW 9149	1.03	241996.10	18.18	35	5049	7
8	ETBW 9065	1.06	576631.12	31.32	34	5378	15
9	ETBW 9077	0.92	167188.90	8.47	23	5135	10
10	ETBW 9078	0.93	195231.34	11.05	30	4978	5
11	ETBW 9080	0.97	505655.56	27.75	28	5545	19
12	ETBW 9172	0.98	-37970.73	7.30	11	5634	21
13	ETBW 9396	1.02	-57483.87	6.18	13	5467	18
14	ETBW 9452	1.00	-9718.48	4.77	15	5376	14
15	ETBW 9543	1.07	118148.19	17.46	28	5199	12
16	ETBW 9545	1.22	78965.93	28.28	37	5165	11
17	ETBW 9641	0.98	27637.70	18.81	24	5550	20
18	ETBW 9642	1.10	-87313.60	15.84	22	5386	16
19	ETBW 9646	0.99	-54204.30	4.94	6	5754	24
20	ETBW 9647	0.97	446791.96	25.59	29	5387	17
21	ETBW 9648	0.92	75084.50	14.38	15	5712	22
22	ETBW 9650	1.12	177172.22	13.58	23	5310	13
23	ETBW 9651	1.03	79368.60	9.89	30	4855	4
24	ETBW 9652	1.05	-170007.71	2.99	18	5123	9
25	OGOLCHO	0.71	3153092.50	102.09	50	4018	1

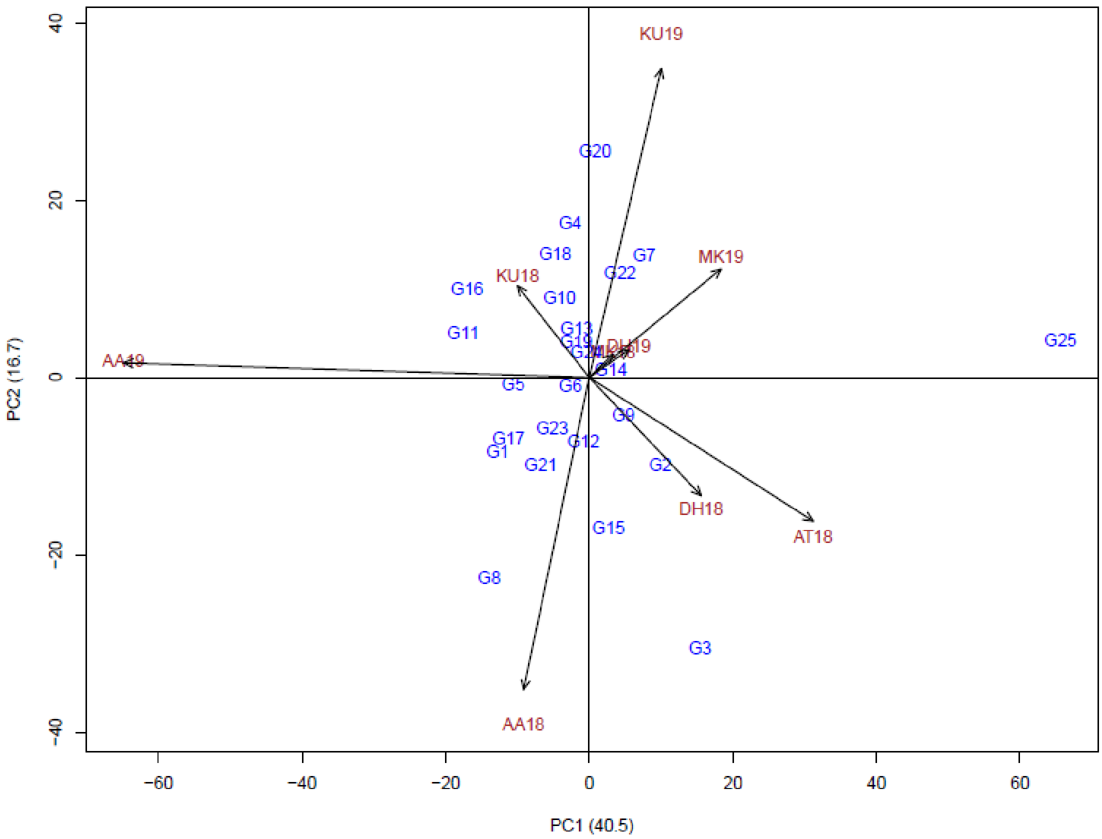

Figure 1. *GGE biplot analysis for the first two IPCA scores of the genotype x environment interaction for mean grain yield.*

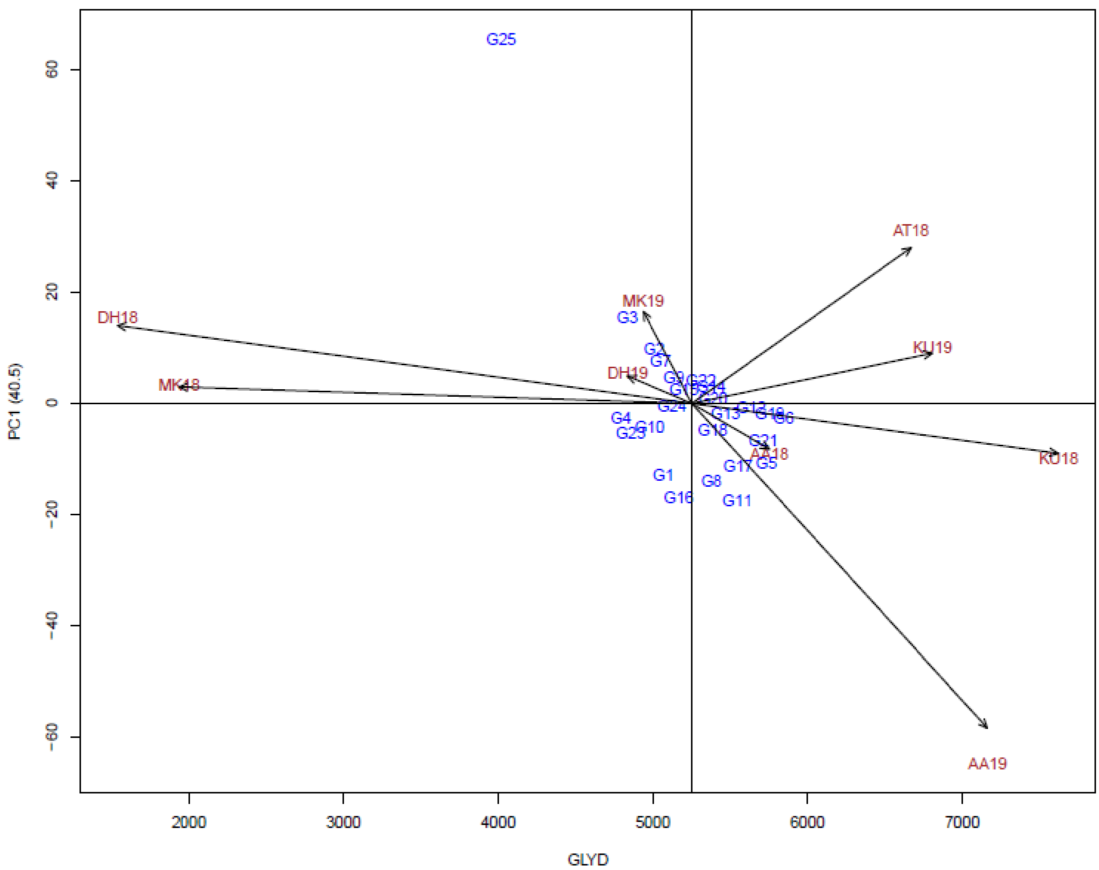

Figure 2. *GGE biplot analysis for the mean yield (kg ha^{-1}) with first IPCA score of the genotype x environment interaction.*

3.4. Mean Performance of the Genotypes for Other Important Agronomic Traits

A mean for days to heading of genotypes was ranged from 57 to 65 days with an average value of 60.11 days which indicates almost all genotype had the narrow range of heading dates. Similarly, there was little difference between genotypes for days to maturity confirming that the tested genotypes can be categorized under similar maturity groups. Plant height varied from 82 to 93 cm with minimum values in genotypes ETBW 9651 and the maximum was for ETBW 9646. The mean 1000 kernel weight ranged from 28 g (ETBW 9396 and OGOLCHO) to 38 g (ETBW 9545) with an average value of 32.75 g. The genotype ETBW 9545 (22.5 % and 35%), ETBW 9647 (19% and 32%) ETBW 9080 (19% and 32%) had TKW advantage than the st. checks DEKA and OGOLCHO, respectively. Hectoliter weight provides a rough estimate of flour yield potential in wheat and is important to millers just as grain yield is important to wheat producers. The value the trait ranged from 64 kg/hl (OGOLCHO) to 69 hg/hl (ETBW 9136, ETBW 9080, ETBW 9646 and ETBW 9651) (Table 6).

Table 6. *Combined mean performance of bread wheat for some important agronomic traits tested across 9 environments from 2018 to 2019 cropping seasons.*

S/No	Genotype	DTH	DTM	PHT (cm)	TKW (g)	HLW (kg/hl)
1	DEKA	62	110	89	31	66
2	ETBW 9116	65	110	86	31	67
3	ETBW 9119	63	110	86	29	67
4	ETBW 9128	61	110	85	30	66
5	ETBW 9136	60	107	91	35	69
6	ETBW 9139	58	107	85	34	68
7	ETBW 9149	60	108	85	35	67
8	ETBW 9065	58	108	90	32	68
9	ETBW 9077	60	109	83	31	68
10	ETBW 9078	60	108	84	30	68
11	ETBW 9080	59	108	87	37	69
12	ETBW 9172	61	108	86	32	68
13	ETBW 9396	59	107	83	28	68
14	ETBW 9452	59	108	84	36	68
15	ETBW 9543	59	110	83	32	67
16	ETBW 9545	57	107	83	38	68
17	ETBW 9641	60	108	91	36	67
18	ETBW 9642	60	108	89	35	68
19	ETBW 9646	60	109	93	36	69
20	ETBW 9647	60	109	89	37	68
21	ETBW 9648	59	109	90	32	68
22	ETBW 9650	60	108	89	34	68
23	ETBW 9651	58	107	82	31	69
24	ETBW 9652	61	110	86	29	67
25	OGOLCHO	62	109	92	28	64
Mean		60.11	108.43	86.89	32.75	67.63
LSD (5 %)		1.81	1.98	3.50	2.81	2.00
CV (%)		4.10	2.07	6.78	9.69	2.57

Note: DH=Days to 75% heading; DM=Days to 95 % maturity; PHT=Plant height (cm); TKW=Thousand kernel weight (g); HLW=Hectoliter weight; YLD=Grain Yield (t/h

3.5. Severity and Response of Genotypes to Yellow and Stem Rust

The level of severity values and response were slightly different at each location and years indicating that the level of the rust's disease severity is dependent on the suitability of the environments. As was indicated by the Yield selection index the genotype, ETBW 9646, ETBW 9396, and ETBW 9172 were stable and top-yielding genotypes. But except ETBW 9396 the top-ranking and stable genotype have weak resistance to yellow and stem rust when the environment is appropriate for the occurrence of the disease. The degree of wheat susceptibility to yellow rust varied across locations due to variation in virulence spectra of the pathogen and climatic conditions for the pressure [17]. The highest yellow and stem rust disease score observed in the 2019 cropping season at kulumsa indicating this environment was highly suitable for buildup of both yellow and stem rust disease (Table 7). Among the studied genotypes relatively showed the best stability and score high mean grain yield; the genotype ETBW 9080 and ETBW 9396 were relatively recorded low yellow rust and stem rust score over location and years. These two genotypes were selected and proposed for variety verification and possible release in 2020.

Table 7. *Mean severity percentage of yellow rust and stem rust on 25 bread wheat genotypes.*

S/No.	Genotype	KU18YR	KU18Sr	AA18Yr	AA18Sr	MK18Sr	KU19Yr	KU19Sr	AA19Yr
1	DEKA	1MRMS	5MSMR	5MSMR	15MSMR	15SMS	30MSS	50S	15MSMR
2	ETBW 9116	0	1MS	5MSMR	5MSMR	10SMS	5MSMR	40S	1MR
3	ETBW 9119	5MS	10MSS	10MSS	10MR	15S	60S	50S	10MRMS
4	ETBW 9128	5MSMR	5S	5MSMR	60S	20S	50S	50S	5MS
5	ETBW 9136	1MR	5S	5MSMR	40MSS	15SMS	5MSMR	50S	5MRMS
6	ETBW 9139	5MR	10MSS	10MSMR	20MSS	154SMS	60S	50S	15S
7	ETBW 9149	5MR	1MS	1MSMR	5MR	5MSMR	5MSMR	40S	5MS
8	ETBW 9065	1MR	1MS	5MR	30MS	15SMS	60S	30S	1MR
9	ETBW 9077	30MSS	1MS	10MSS	20MSMR	10MRMS	40S	40S	10MS
10	ETBW 9078	5MSMR	0	10MSMR	10MSMR	5MSMR	15MSS	50S	15MS
11	ETBW 9080	1MR	5MS	1MSMR	10MSMR	15SMS	10MSMR	15MSS	5MR
12	ETBW 9172	5MRMS	5MSS	5MSMR	10MSMR	10MSMR	15MSMR	50S	1MR
13	ETBW 9396	5MRMS	0	1MSMR	1RMR	1MRMS	1MR	15S	5MSMR
14	ETBW 9452	1MR	0	15MSMR	0	1MRMS	60S	40S	1MR
15	ETBW 9543	15MRMS	0	20MSS	10MRMS	5MSMR	50S	30S	10MSS
16	ETBW 9545	15MRMS	1MR	15MSMR	10MS	1MRMS	5MSMR	50S	10MS
17	ETBW 9641	0	20S	5MSMR	60S	20SMS	40S	80S	1MR
18	ETBW 9642	1MR	10MSS	5MSMR	60S	15SMS	5MSMR	70S	1MR
19	ETBW 9646	1MR	20S	5MSMR	40MSS	30S	10MSMR	70S	1MRMS
20	ETBW 9647	1MR	10S	5MSMR	70S	30S	15MSS	50S	1MSMR
21	ETBW 9648	5MRMS	15S	10MSMR	10RMR	1MRMS	60S	30MSS	15MS
22	ETBW 9650	1MSMR	15S	5MSMR	60S	20S	60S	30S	1MR
23	ETBW 9651	5MR	1MSMR	5MSMR	20MS	1MRMS	60S	30S	5MSMR
24	ETBW 9652	5MRMS	1MSMR	5MSMR	10MRMS	5SMS	60S	60S	10MSMR
25	OGOLCHO	10MSMR	40s	20MSMR	50S	30S	40S	70S	90S

Note: Yr= Yellow rust, Sr= Stem rust, KU= kulumsa, AA=Asasa, MK=Melkasa, R –Resistant, MR- Moderately resistant, MS- Moderately susceptible, S- Susceptible

4. Conclusion

Due to changes in climatic factors and/or weather variabilities, most of the wheat producing regions in Ethiopia became low moisture stress areas. Hence, there is a need to develop varieties which could adapt to this short growing cycles. In view of this 25 bread wheat genotypes including two st. checks were evaluated in 9 environments from 2018 to 2019 cropping seasons with the objectives to estimate the magnitude of genotype by environment interaction and to select stable and adaptable varieties across the tested environments. The combined analysis of variance showed a highly significant ($p \leq 0.01$) differences among the genotypes, environments, and GEI for grain yield suggesting a differential response of genotypes across testing environments. The grand mean yield over nine environments was 5252 kg ha^{-1} and the mean yield of genotypes across nine environments ranged from 1539 kg ha^{-1} in 2018 at Dhera to 7622 kg ha^{-1} in 2018 at Kulumsa. The genotypes ETBW 9136 (5732 kg ha^{-1}), ETBW 9139 (5845 kg ha^{-1}), ETBW 9646 (5754 kg ha^{-1}), ETBW9172 (5634 kg ha^{-1}), ETBW9641 (5545 kg ha^{-1}), ETBW 9080 (5545 kg ha^{-1}) and ETBW9396 (5467 kg ha^{-1}) gave the highest mean grain yield across environments, whereas the standard check Ogolcho recorded lowest mean grain yield across environments. The first four principal components of the GEI explained 85.6% of the total variations. Additive main effects and multiplicative interaction (AMMI) stability parameters revealed that the genotypes ETBW 9080 (G11), ETBW 9172 (G12), ETBW 9646 (G19), ETBW 9396 (G13), ETBW 9452 (G14), ETBW 9136 (G5) and ETBW 9139 (G6) were high yielders and more stable inferring little interaction of genotypes with the environment whereas Ogolcho (G25), ETBW 9119 (G3), ETBW 9647 (G20) and ETBW 9065 (G8) was low yielder and unstable suggesting high interaction with the environments. Based on the results of grain yield stability parameters and other agronomic traits including diseases resistances, the genotypes viz. ETBW 9396 (G13) and ETBW 9080 (G11), were selected for candidate varieties for variety verification and possible release in 2021 for low moisture stress areas of Ethiopia.

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