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Stability and Performance Evaluation of Advanced Bread Wheat (*Triticum aestivum* L.) Genotypes in Low to Mid Altitude Areas of Ethiopia

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ABSTRACT

Twenty three advanced bread wheat genotypes have been evaluated against two released bread wheat varieties in 2018–19 and 2019–20 in nine diverse environments of Ethiopia. The experiment was laid out using alpha lattice design with three replications. Ten stability models were employed in order to assess stability and performance of 23 advanced bread wheat genotypes. Combined analysis of variance for grain yield has revealed that the environments, the genotypes and GEI effects were significantly different (p<0.001). In the present study, Environments, GEI and Genotypic effects accounted for 88.6%, 8.3% and 3.1% of the total grain yield variation, respectively. Twelve bread wheat genotypes, ETBW 9136, ETBW 9139, ETBW 9065, ETBW 9080, ETBW 9172, ETBW 9396, ETBW 9452, ETBW 9641, ETBW 9642, ETBW 9646, ETBW 9647 and ETBW 9648 produced grain yield that raged from 5.4 to 5.8 t ha^{-1}, indicating their superior yielding potential. ETBW 9136, ETBW 9139, ETBW 9172, ETBW 9396, ETBW 9452, ETBW 9641, ETBW 9642 and ETBW 9646 were the most stable bread wheat genotypes as confirmed by five to ten stability models. However, ETBW 9452, ETBW 9641, ETBW 9642, ETBW 9646, ETBW 9647 and ETBW 9648 were susceptible to either stem rust or yellow rust or both. Providentially, ETBW 9136, ETBW 9139, ETBW 9172 and ETBW 9396 were superior yielding, stable, resistant and moderately resistant to wheat rusts. Thus, these four genotypes were the most promising advanced bread wheat genotypes to be verified and released in low to mid altitude areas of Ethiopia.

KEYWORDS: Bread wheat, Ethiopia, gei, yield stability

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1. INTRODUCTION

Wheat is strategic, economic, industrial, commercial, political and food security commodity in Ethiopia. Thus, the demand for wheat has been increasing in the country (Cockx et al., 2019, Tadesse et al., 2018, Abebe et al., 2022). Wheat is a major source of energy, starch, protein, vitamins, minerals, dietary fiber and phytochemicals (Kumar et al., 2011, Shewry and Hey, 2015).

In Ethiopia, wheat is produced on a total area of 2.1 mha of land with a total production of 6.7 mt with average productivity of 3 t ha^{-1} and 4 t ha^{-1} under rain fed and irrigation conditions, respectively (Hodson et al., 2020, CSA, 2022, Tadesse et al., 2022). However, Ethiopia is not self sufficient in wheat production for she is filling the demand gap of 15% through wheat import (Shiferaw et al., 2011, Brasesco et al., 2019, Hodson et al., 2020, Tadesse et al., 2022). On the other hand, Ethiopian government is determined to fill the demand gap through production of wheat during off-season in existing environments by using irrigation and expansion of wheat production in non-traditional wheat growing areas specially in lowlands. Lack of high yielding and stable varieties adapted to wide range of environments (Gadisa et al., 2020, Abebe et al., 2022), drought and heat stresses, resistant to diseases specially rusts, and factors such as poor soil fertility, sum-optimal use of agronomic practices, erratic rainfall and increased costs of inputs are the most limiting factors for wheat production in the low to mid altitude areas of Ethiopia (Habte et al., 2014, Shiferaw et al., 2014, Brasesco et al., 2019, Hodson et al., 2020, Adugnaw and Dagninet, 2020). Aforementioned factors complicated selection of crop varieties for production environment and contributed to the complexity of genotype×environment interaction (GEI) in the variety development process (Asfaw, 2009). Hence, multi-environment trials (METs) are essential to evaluate genotypes and select superior ones for high yield, relatively stable and other important traits (Ebdon and Gauch, 2002, Kaya et al., 2006, Ahmadi et al., 2012, Mitrovic et al., 2012, Sajid & Mohammd, 2018).

Both yield and stability of performance should be considered simultaneously in order to reduce the effects of GEI and to make selection of genotypes more precise (Ashrei and Ghareeb, 2015). A genotype is stable if it possesses a constant performance across diverse environments and its contribution to G×E interaction is small (Becker and Leon, 1988, Fasahat et al., 2015, Assefa et al., 2020).

The Ethiopian wheat research program is striving to develop high yielding, stable, diseases resistant with acceptable end use quality wheat varieties for different agro-ecologies. Of course, the program is able to release more than 100 wheat varieties for different agro-ecologies of Ethiopia in five decades of concerted research efforts & endeavors (MoANR, 2021, Tadesse et al., 2022). However, majority of these varieties are becoming susceptible to rust diseases and put out of production in a few years of their release. Because, yellow and stem rusts epidemics have frequently occurred in Ethiopia (Solh et al., 2012, Singh et al., 2015, Hei et al., 2018, Tolemariam et al., 2018, Meyer et al., 2021). Currently, Ethiopia is becoming factories for production of new and virulent rust pathogens inoculums and wheat farmers are reaching on a situation where they cannot produce wheat without application of fungicides. Thus, wheat research program is persistently introducing thousands of germplasms and advanced lines annually from International Research Institutes and evaluate these materials in series of nurseries and yield trials. The objective of the present study is therefore to identify high yielding, stable and rusts resistant advanced bread wheat genotypes for use in low to mid altitude areas of Ethiopia.

2. MATERIALS AND METHODS

2.1. Planting materials and test locations

Twenty three advanced bread wheat genotypes were evaluated against two checks ('*Deka*' and '*Ogolcho*') at five locations and/or nine environments in moisture stress areas of Ethiopian in 2018–19 and 2019–20 cropping seasons. Sowing and harvesting of tested materials were carried out from first week of June to mid July and from last week of October to last week of November, respectively. Description of five test locations and advanced bread wheat genotypes were presented in Tables 1 and 2, respectively.

2.2. Experimental design and layout

The treatments were evaluated using alpha lattice design with three replications. Each entry was planted at a seed rate of 125 kg ha^{-1} in six rows of 20 cm spacing and 2.5 m long. Fertilizer application and other crop management practices were applied as per the local recommendations for each testing locations. Data on diseases and grain yield were recorded.

2.3. Statistical methods

There are various methods for describing and dynamically interpreting the effects of GEI along with identifying and recommending stable genotypes (Changizi et al., 2014). A combined analysis of variance was first undertaken across the test environments. Then, parametric stability parameters such as coefficient of variability (Francis and Kannenberg, 1987), linear regression coefficient (Finlay and Wilkinson, 1962), deviation from regression coefficient mean square (Eberhart and Russell, 1966), stability variance (Shukla, 1972), the genotypic eccovalence (Wricke, 1962), coefficient of determination (Pinthus, 1973), adjusted linear regression coefficient and deviation (Perkins and

Table 1: List of test locations and their description

Location	Geographic position			Temperature (oC)		Rainfall (mm)
	Latitude	Longitude	Altitude	Min.	Max.	
Kulumsa	08°01'10''N	39°09'11''E	2200	10.5	22.8	820
Asasa	07°07'228''N	39°11'932''E	2360	5.8	23.6	620
Atsela	-	-	-	-	-	
Dhera	08°19'10''N	39°19'13''E	1650	14	27.8	680
Melkasa	8°33’ N	39°17’ E		15.2	27.5	763

-: Data not available

Table 2: List of advanced bread wheat genotypes evaluated in nine environments in Ethiopia and their pedigrees

Genotype id	Genotype	Pedigree
1	DEKA	Check
2	ETBW 9116	PFAU/MILAN/5/CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/VEE#7/BOW/4/PASTOR/6/KINGBIRD #1
3	ETBW 9119	ELVIRA/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI/6/VEE/PJN//KAUZ/3/PASTOR/7/TILHI/4/CROC_1/AE.SQUARROSA (213)//PGO/3/CMH81.38/2*KAUZ/8/PICAFLOR #2
4	ETBW 9128	FRNCLN*2/BECARD
5	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
6	ETBW 9139	KA/NAC//TRCH/5/W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1
7	ETBW 9149	PRL/2*PASTOR/6/TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU #1
8	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
9	ETBW 9077	SHORTENED SR26 TRANSLOCATION//2*WBLL1*2/KKTS/3/BECARD
10	ETBW 9078	SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
11	ETBW 9080	KACHU//WHEAR/SOKOLL
12	ETBW 9172	ND643/2*WBLL1//KACHU
13	ETBW 9396	BOUSHODA-1/4/CROC-1/AE.SQUARROSA (205)//KAUZ/3/SASIA
14	ETBW 9452	REBWAH-19/HAAMA-14
15	ETBW 9543	KFA//PBW343/PASTOR/3/PBW343*2/KUKUNA/4/PBW343*2/KUKUNA*2//FRTL/PIFED/5/PBW343*2/KUKUNA*2//FRTL/PIFED
16	ETBW 9545	ATTILA*2/PBW65*2//MURGA/4/MUU #1//PBW343*2/KUKUNA/3/MUU/5/ATTILA*2/PBW65//MURGA
17	ETBW 9641	MELON//FILIN/MILAN/3/FILIN/4/PRINIA/PASTOR//HUITES/3/MILAN/OTUS//ATTILA/3*BCN/5/MELON//FILIN/MILAN/3/FILIN
18	ETBW 9642	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/WHEAR/SOKOLL
19	ETBW 9646	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/PARUS/PASTOR
20	ETBW 9647	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/MEX94.2.19//SOKOLL/WBLL1
21	ETBW 9648	PUB94.15.1.12/FRTL//92.001E7.32.5/SLVS
22	ETBW 9650	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/GLADIUS

Table 2: Continue...

Genotype id	Genotype	Pedigree
23	ETBW 9651	KACHU*2/3/ND643//2*PRL/2*PASTOR
24	ETBW 9652	PFUNYE #1/KINGBIRD #1
25	OGOLCHO	Check

Jinks, 1968), cultivar superiority measure (Lin and Binns, 1988), nonparametric stability statistics (Nassar and Huehn, 1987) and the Additive Main effect and the Multiplicative Interaction effect (AMMI) (Yan, 2011) were analyzed by using a comprehensive free software (Pacheco et al., 2016), which calculates the most parametric and non-parametric stability statistics.

3. RESULTS AND DISCUSSION

AMMI analysis of variance for grain yield for 25 advanced bread wheat genotypes evaluated across nine environments revealed that the environments, the genotypes and GEI effects were significantly different ($p<0.01$). Several authors reported similar findings in bread wheat (Kaya et al., 2002, Ahmadi et al., 2012, Farshadfar and Sadeghi, 2014, Hassan, et al., 2017, Singh et al., 2019, Gadisa et al., 2020), durum wheat (Mohammadi et al., 2007), barley (Zerihun, 2012), maize (Haruna et al., 2017), sorghum (Rakshit et al., 2012), soybean (Asrat, 2009), mungbean (Thangavel et al., 2011), field pea (Tamene et al., 2013), chickpea (Assefa et al., 2017), cowpea (Tariku, 2018), linseed (Adane and Abebe, 2018), lentil (Mohebodini et al., 2006) and cassava (Aina et al., 2009, Boakye et al., 2013) suggesting the existence of wide variability among environments, among genotypes and the possibility of selection for high yielding, best performing and stable genotypes. The present results showed that 88.6% of the total sum of squares (SS) was attributed to environmental effects, only 3.1 and 8.3% to genotypes and GEI effects, respectively. A large SS for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield (Table 3). Significant GEI indicated that each genotype interacted differently at each location. The presence of GEI mainly attributed to different factors such as soil type, pests, altitude, rainfall, temperature and humidity. The GEI effect was 2.7 times greater than the genotypic effects indicating the existence of differential response of genotypes to changes in the growing environments and the discriminating ability of environments. The significant GEI effects also demonstrated the necessity of evaluating bread wheat genotypes at multi locations in order to explore the response of genotypes for wide or specific adaptability. Similar results have been reported by several authors for several crops (Kaya et al., 2002, Aina et al., 2009, Zerihun, 2012, Tamene et al., 2013, Farshadfar and Sadeghi, 2014, Hassan, et al., 2017, Assefa et al., 2017, Gadisa et al., 2020).

3.1. AMMI 1 analysis

Highly significant differences among environments, genotypes and GxE interaction explained 88.6%, 3.1% and 8.3% total sum of squares, respectively (Table 3). The significant GE interaction sum of squares further partitioned into four significant Interaction Principal Component Axes (IPCAs) and a residual term. The first four interaction principal component analysis explained 41.3%, 16.5%, 15.5% and 9.9% of the GE interaction variation, respectively. Similar results were reported by Ahmadi et al. (2012), Golkari et al. (2016) and Jeberson et al. (2017) in wheat, by Mortazavian et al. (2014) in barley and by Yayis et al. (2014) in field pea.

These four IPCAs revealed 83.1% of variation of the total sum of squares due to the interaction. The remaining 16.9% of the interaction effect being the residual, therefore, not interpreted and hence removed (Purchase et al., 2000). The variation contributed by these four IPCAs showed differential performance of genotypes for grain yield across locations. However, for the confirmation of the variation revealed by GE, the first two multiplicative component axes were sufficient (Gauch, 2006), which explained 57.8% of the total GE variation among the wheat genotypes in the present study. This

Table 3: AMMI analysis of variance for grain yield of 25 bread wheat genotypes evaluated across nine environments in Ethiopia in 2018–19 and 2019–20

	DF	SS	MS	PROBF	percentage Explained
ENV	8	2894.949	361.8686	0	88.55526
GEN	24	102.3034	4.26264	0	3.12942
ENV× GEN	192	271.8351	1.41581	0	8.31532
PC1	31	111.9703	3.61195	0	41.29991
PC2	29	44.68134	1.54074	0	16.48058
PC3	27	41.8912	1.55153	0	15.45144
PC4	25	26.84646	1.07386	0.00264	9.90224
Residuals	446	293.4483	0.65796	NA	0

is due to the prominent reduction of dimensionality and graphical visualization for the adaptation of the genotypes (Annicchiarico, 2002). The IPCA scores of a genotype in AMMI analysis are an indication of the stability of a genotype across environments. The greater the IPCA scores, either positive or negative, the more specifically adapted a genotype to certain environments. The more IPCA scores approximate to zero, the more stable a genotype is across environments. Hence, genotypes ETBW 9172 (G12), ETBW 9652 (G24), ETBW 9077 (G9), ETBW 9543 (G15), ETBW 9396 (G13), ETBW 9452 (G14), ETBW 9646 (G19), ETBW 9647 (G20), ETBW 9650 (G22), ETBW 9651 (G23), ETBW 9642 (G18), ETBW 9139 (G6) and ETBW 9128 (G4) were stable genotypes as their IPCA scores were closer to zero (Figure 1). Genotypes ETBW 9139 (G6), 9172 (G12), 9396 (G13), 9452 (G14), 9642 (G18), 9646 (G19) and 9647 (G20) were stable and promising bread wheat genotypes as they produced a grain yield that ranged from 5.4 to 5.8 t ha^{-1}. On the other hand, genotypes ETBW 9080 (G11), ETBW 9545 (G16), ETBW 9065 (G8), Deka (G1), ETBW 9641 (G17), ETBW 9136 (G5) and ETBW 9119 (G3) were unstable. Genotypes ETBW 9080 (G11), ETBW 9545 (G16), ETBW 9136 (G5), ETBW 9065 (G8) and ETBW 9641 (G17) were specifically adapted to Kulumsa-2018 (E1), Asasa-2018 (E2) and Asasa-2019 (E7). Genotype Ogolcho (G25) was exceptionally highly unstable and lowest yielder.

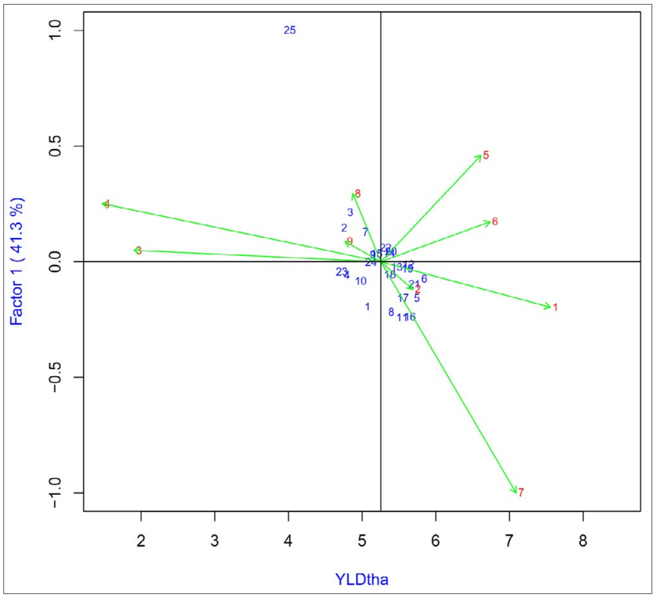

Figure 1: AMMI 1 bi plot showing the main (main effect) versus stability (IPC1) view of both genotypes and environments on grain yield. Where, E1=Kulumsa-2018, E2=Asasa-2018, E3=Melkasa-2018, E4=Dhera-2018, E5=Atsela-2018, E6=Kulumsa-2019, E7=Asasa-2019, E8=Melkasa-2019, E9=Dhera-2019. Genotypes designation was as indicated in Table 2

3.2. *AMMI 2 analysis*

AMMI 2 bi plot was generated using genotypic and environmental scores of the first two AMMI multiplicative components to cross validate the interaction pattern of 25 bread wheat genotypes within nine environments. Connecting vertex cultivars markers in all direction form a polygon, so that all genotypes are contained within the polygon and a set of straight lines that radiate from the pi plot origin to intersect each of the polygon sides at right angles form sectors of genotypes and environments (Yan, 2011). Figure 2 cross validated the interaction patterns of the 25 bread wheat genotypes evaluated in nine diverse environments. The distance from the origin (0, 0) are indicative of the amount of interaction that was exhibited by genotypes either over environments or environments over genotypes (Yan and Tinker, 2006). With the current data set, genotypes ETBW 9647 (20), Ogolcho (25), ETBW 9119 (3), ETBW 9065 (8), ETBW 9080 (11) and ETBW 9545 (16) exhibited a highly interactive behavior whereas Melkasa-2018 (E3) and Dhera-2019 (E9) were the least interactive of all environments against Asasa-2019 (E7) which was the most interactive of all environments.

The orthogonal projections of the genotypes over the environmental vector showed clear genotypes-environment affinity. Environments with in the same sector are assumed to share the same winner genotypes. The best genotypes with respect to Kulumsa-2019 (E6)

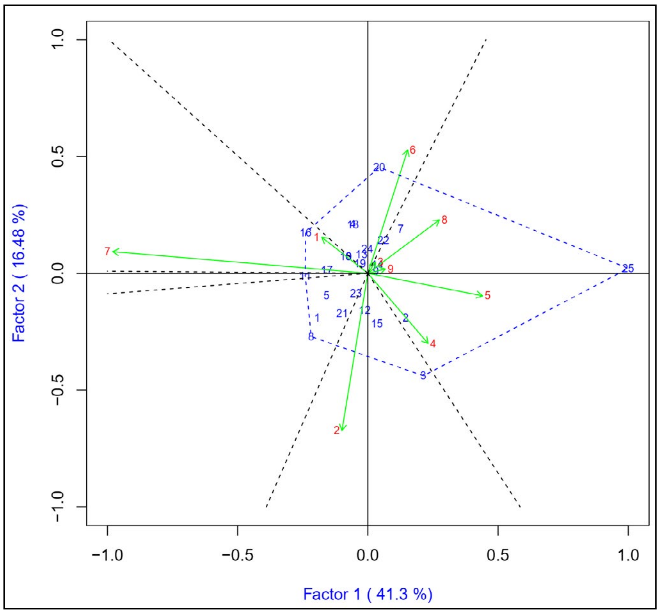

Figure 2: AMMI bi plot analysis showing the mega environments and their respective high yielding genotypes. Where, E1=Kulumsa-2018, E2=Asasa-2018, E3=Melkasa-2018, E4=Dhera-2018, E5=Atsela-2018, E6=Kulumsa-2019, E7=Asasa-2019, E8=Melkasa-2019, E9=Dhera-2019. Genotypes designation was as indicated in Table 2

was ETBW 9647 (G20). Ogolcho (G25) best performed at Dhera-2018 (E4), Atsela-2018 (E5) and Melkasa-2019 (E8). Similarly, ETBW 9119 (G3) best performed at Asasa-2018 (E2), while ETBW 9545 (G16) was the best for Asasa-2019 (E7) (Figure 2). On the other hand, genotypes like ETBW 9065 (G8), ETBW 9080 (G11) and Deka (G1) fall in sectors where there was no environment at all, indicating their poor adaptation to any of the testing environments. Genotypes, ETBW 9077 (G9), ETBW 9078 (G10), ETBW 9172 (G12), ETBW 9396 (G13), ETBW 9452 (G14), ETBW 9646 (G19), ETBW 9650 (G22), ETBW 9651 (G23) and ETBW 9652 (G24) showed lower fluctuations to both spatial and temporal changes in the growing environments. ETBW 9172 (G12), ETBW 9396 (G13), ETBW 9452 (G14) and ETBW 9646 (G19) were promising genotypes as they produced a grain yield that ranged from 5.4 t ha^{-1} to 5.8 t ha^{-1}. Similar findings have been reported by (Asrat et al., 2009, Tamene et al., 2013, Assefa et al., 2017, Adane and Abebe, 2018).

Environments viz. Dhera-2018 (E4), Atsela-2018 (E5), Kulumsa-2019 (E6) and Melkasa-2019 (E8) were associated with their higher positive IPC1 values, indicating their higher discriminative ability. Environment Asasa-2019 (E7) characterized by largest IPC1 value, was completely the opposite in its ability to discriminate the genotypes. Based on their proximity to the origin Melkasa-2018 (E3) and Dhera-2019 (E9) showed lowest genotypic discriminative ability and proved to be more representative of the average environment. On the other hand, environments Asasa-2018 (E2), Dhera-2018 (E4), Atsela-2018 (E5), Kulumsa-2019 (E6), Asasa-2019 (E7) and Melkasa-2019 (E8) demonstrated higher genotypic discriminating ability and found to be less representative of the average environment (Figure 2). And environments including Melkasa, Atsela and Dhera were clustered into a single sector, indicating the consistency in performance of genotypes in these locations. These locations could be considered as a separate mega environments for bread wheat variety evaluation. Similar results were reported by Tamene et al. (2013).

3.3. Francis and kannenberg stability model (CV)

Genotypes with low CV and high mean grain yield were considered as most stable and desirable. Accordingly, bread wheat genotypes such as ETBW9116, ETBW9136, ETBW9139, ETBW9077, ETBW9080, ETBW9172, ETBW9641, ETBW9646 and ETBW9648 were the most stable genotypes. Except genotypes ETBW9116 and ETBW9077 all listed genotypes were the most stable and desirable genotypes as they had the lowest CV and produced highest grain yield that ranged from 5.5 to 5.8 t ha^{-1} (Table 4). Similar to the present findings Abebe et al. (2022) identified six stable and desirable advanced bread wheat genotypes by evaluating 30 advanced bread wheat genotypes across 18 environments in optimum areas of Ethiopia. Likewise, Gadisa et al. (2021) identified seven best performing and stable varieties of bread wheat by evaluating 15 commercial varieties across 21 environments. Besides, Ahmed et al. (2016) identified four stable and two unstable bread wheat genotypes by evaluating 14 bread wheat genotypes across 12 environments. Moreover, Mohammadi and Mohmoodi (2008) identified five stable and high yielding barley genotypes by evaluating 13 barley genotypes across 18 environments. In the present study, genotypes such as Deka, ETBW9128, ETBW9149, ETBW9543, ETBW9545, ETBW9650, ETBW9651 and Ogolcho were unstable and undesirable as they were associated with high CV and produced relatively medium yield that ranged from 4.0 to 5.3 t ha^{-1}. Contrary to the present results, Bantayehu (2009) and Yaghotipoor, et al. (2017) reported association of lowest CV to lowest yield and vice versa.

3.4. Eberhart and rusell's model

Finlay and Wilkinson (1963) and Eberhart and Russell (1966) considered genotypes with high mean grain yield and regression coefficient equal to unity (bi=1) and deviation from regression as small as possible (S^2di=0) to be stable. Therefore, the genotypes ETBW9172, ETBW9396, ETBW9452 and ETBW9646 were the most stable genotypes. These genotypes produced grain yield that ranged from 5.4 to 5.8 t ha^{-1} (Table 4). Similarly, Gadisa et al. (2021) identified four stable and desirable bread wheat varieties by evaluating 15 commercial varieties across 21 diverse environments of Ethiopia. Likewise, Ahmed et al. (2016) identified eight stable and high yielding bread wheat genotypes by evaluating 14 bread wheat genotypes across 12 environments. In contrast, genotypes such as ETBW9545, ETBW9650 and ETBW9128, with regression coefficient greater than unity, were unstable, and they had specific adaptability to favorable environments. On the other hand, ETBW9116, ETBW9119 and Ogolcho whose bi values were less than unity were unstable and had specific adaptability to poor environments. Considering both bi and S^2di parameters bread wheat genotypes namely ETBW9172, ETBW9396, ETBW9452, ETBW9641 and ETBW9646 recorded bi values of unity and S^2di values of closer to zero and were therefore showed wide adaptability. Likewise, these genotypes showed superior performance as they produced a grain yield that ranged from 5.4 to 5.8 t ha^{-1}. Similar findings have been reported by several authors (Abera et al., 2004, Akcura et al., 2006, Mulusew et al., 2008, Bantayehu, 2009, Syukur et al., 2011, Changizi et al., 2014, Mulusew et al., 2014, Fentaw et al., 2015, Satoto and Widyastuti, 2016, Yaghotipoor et al., 2017, Solomon

Table 4: Stability analysis of advanced bread wheat genotypes across nine environments using different stability models

Gen Id.	Gen	Mean	Francis	Eberhart & Russell			Shuckla	Perkins & Jinks		WE	SM	Non parametric Nassar & Huehn	
			CV (%)	Bi	S^2di	R^2	ri^2	Bi	DJi	Wi	Pi	Si(1)	Si^2
1	DAKA	5.1	47.47	1.067	0.142	0.952	0.305	0.067	0.318	2.399	1.016	1.88	42.81
2	ETBW 9116	5.0	40.19	0.868	0.275	0.903	0.501	-0.132	0.451	3.837	1.184	1.19	59.12
3	ETBW 9119	4.8	41.95	0.855	0.481	0.861	0.716	-0.145	0.658	5.417	1.506	1.71	77.25
4	ETBW 9128	4.8	51.67	1.107	0.041	0.969	0.247	0.107	0.217	1.969	1.384	1.29	32.91
5	ETBW 9136	5.7	38.55	0.972	0.186	0.935	0.328	-0.028	0.362	2.564	0.318	2.11	39.41
6	ETBW 9139	5.8	41.28	1.070	0.132	0.954	0.298	0.070	0.308	2.343	0.267	1.79	36.03
7	ETBW 9149	5.0	46.65	1.030	0.280	0.928	0.418	0.030	0.456	3.228	1.062	2.47	49.75
8	ETBW 9065	5.4	46.17	1.066	0.614	0.889	0.754	0.066	0.791	5.702	0.741	3.44	93.44
9	ETBW 9077	5.1	40.73	0.916	0.194	0.926	0.369	-0.084	0.370	2.866	0.955	1.44	52.28
10	ETBW 9078	5.0	42.68	0.927	0.223	0.923	0.387	-0.073	0.399	2.999	1.243	2.08	43.56
11	ETBW 9080	5.5	41.15	0.974	0.511	0.885	0.636	-0.026	0.687	4.835	0.593	1.69	49.31
12	ETBW 9172	5.6	39.27	0.988	-0.009	0.970	0.139	-0.012	0.167	1.174	0.361	1.12	27.22
13	ETBW 9396	5.5	41.98	1.030	-0.032	0.976	0.121	0.030	0.144	1.044	0.490	1.28	24.22
14	ETBW 9452	5.4	41.66	0.999	0.013	0.967	0.159	-0.001	0.189	1.325	0.631	2.07	40.25
15	ETBW 9543	5.2	46.65	1.073	0.151	0.951	0.319	0.073	0.327	2.499	0.864	1.60	43.50
16	ETBW 9545	5.2	50.60	1.173	0.153	0.959	0.451	0.173	0.330	3.470	0.935	2.07	60.19
17	ETBW 9641	5.6	39.70	0.980	0.058	0.958	0.204	-0.020	0.234	1.654	0.444	1.50	26.81
18	ETBW 9642	5.4	45.52	1.101	-0.051	0.982	0.152	0.101	0.125	1.271	0.612	1.08	20.19
19	ETBW 9646	5.8	38.37	0.989	-0.033	0.974	0.117	-0.011	0.144	1.011	0.287	0.94	20.06
20	ETBW 9647	5.4	42.19	0.974	0.476	0.890	0.603	-0.026	0.652	4.591	0.779	2.50	58.53
21	ETBW 9648	5.7	36.84	0.928	0.105	0.945	0.274	-0.072	0.281	2.168	0.354	1.50	47.00
22	ETBW 9650	5.3	47.82	1.125	0.196	0.950	0.416	0.125	0.373	3.215	0.783	1.43	47.78
23	ETBW 9651	4.9	47.98	1.032	0.103	0.955	0.251	0.032	0.280	1.997	1.246	1.53	27.28
24	ETBW 9652	5.1	45.11	1.045	-0.138	0.994	0.027	0.045	0.038	0.349	0.827	0.71	8.56
25	OGOLCHO	4.0	57.87	0.711	3.203	0.453	3.635	-0.289	3.379	26.906	4.300	1.64	45.03

Where; GEN: Genotype; WE: Wricke's Ecovalence; SM: Superiority Measure; CV: Coefficient of variation; bi: regression coefficient; S^2di: deviation from regression; R^2: Coefficient of determination; r^2i: stability variance; Bi: adjusted linear regression coefficient and deviation; Wi: genotypic eccovalence; Pi: Superiority Index measure; Si(1) and Si^2: nonparametric stability statistics

et al., 2018, Gadisa et al., 2021, Abebe et al., 2022).

3.5. Wricke ecovalence model (Wi)

According to Wricke (1962) the GE interaction effect for genotype i, squared and summed across environments is the stability measure for genotype i. Low ecovalence (Wi) value indicates high relative stability, greatest stability is when Wi=0. Genotypes with a low Wi value have smaller deviations from the mean across environments and are therefore, more stable (Purchase, 1997, Fasahat et al., 2015). According to Wricke's stability parameter the genotypes ETBW9172, ETBW9396, ETBW9452, ETBW9641, ETBW9642, ETBW9646 and ETBW9652 with lower ecovalence were stable. These stable genotypes also produced high yield that ranged from 5.4–5.8 t ha^{-1} except ETBW9652 which produced grain yield of 5.1 t ha^{-1} (Table 4). Gadisa et al. (2021) identified four stable and four unstable bread wheat varieties by using Wi as stability parameter. Similarly, Yaghotipoor, et al. (2017) identified three stable and four unstable bread wheat genotypes by evaluating 20 bread wheat genotypes across 12 environments. Likewise, Bantayehu (2009) identified three stable and two unstable malt barley genotypes by evaluating 20 advanced malt barley genotypes across 12 environments. Moreover, Mohammadi and Mohmoodi (2008) identified five stable and five unstable barley genotypes by evaluating 13 barley genotypes across 18 environments. Furthermore, Akcura et al. (2006) identified seven stable and promising durum wheat genotypes by evaluating 15 durum wheat genotypes across eight environments. On the other hand, genotypes ETBW9116, ETBW9119, ETBW9065, ETBW9080, ETBW9545, ETBW9647 and Ogolcho with high ecovalence values were unstable. These unstable genotypes were relatively low yielders. However, Mulusew et al. (2014) and Fentaw et al. (2015) reported that highest yielding field pea and durum wheat genotypes were unstable by using ecovalence method of Wricke.

3.6. Lin and Binns model (Pi)

Lin and Binns (1988) introduced superiority measure of cultivar performance (Pi) and defined it as the mean square distance between the genotypes response and the maximum response at all locations (Mohammadi et al., 2012). A genotype is stable if it has a low Pi. In this case, genotypes ETBW9136, ETBW9139, ETBW9172, ETBW9641, ETBW9646 and ETBW9648 were stable and superior yielder as they produced a grain yield that ranged from 5.6 to 5.8 t ha^{-1}. Similar results have been reported by several authors (Mohammadi and Mohmoodi, 2008, Bantayehu, 2009, Syukur, et al., 2011, Changizi, et al., 2014, Ahmed et al., 2016, Gadisa, et al., 2021, Abebe et al., 2022). In contrary, genotypes ETBW9116, ETBW9119, ETBW9128, ETBW9149, ETBW9078, ETBW9651 and Ogolcho with high Pi were unstable and inferior yielders. Thus, their contribution to the total variation due to GEI is high. Similarly, Gadisa et al. (2021) identified four stable and four unstable bread wheat varieties by using Lin and Binns stability methods. Likewise, Fentaw et al. (2015) identified five stable and four unstable durum wheat varieties by evaluating 13 durum wheat varieties in North Western Ethiopia.

3.7. Pinthus stability model

Based on Pinthus coefficient of determination (R^2), the stability parameter values are the predictability of variation response estimates (Kilic et al., 2010) and the variation of mean yield is explained by the genotype response across different environments' and ranged from 0.86–0.98 except for Ogolcho which recorded the lowest R^2 value of 0.453. Hence, Ogolcho was exceptionally unstable and the lowest yielder by using Pinthus stability parameter. Similar to the present studies Changizi et al. (2014) evaluated 16 corn hybrids in 24 environments and identified all hybrids as stable by using coefficient of determination as stability parameter. Likewise, Mulusew et al. (2014) evaluated 16 field pea genotypes in 12 environments in South Eastern Ethiopia and identified all genotypes as stable. Moreover, Akcura et al. (2006) reported that all of genotypes were considered as stable for grain yield regarding this stability parameter. Furthermore, Yaghotipoor, et al. (2017) reported similar results by evaluating 20 bread wheat genotypes across 12 environments. On the other hand, Karimizadeh et al. (2012) identified only five stable durum wheat genotypes by evaluating 20 durum wheat genotypes across 15 environments.

3.8. Shuckla stability variance (ri2)

Shuckla (1972) proposed the variance component of each genotype across environments as relevant measure of phenotypic stability. GxE sum of square is partitioned into components, one corresponding to each genotype (Shuckla, 1972, Fasahat et al., 2015). If the stability variance of a genotype was equal to environmental variance (ri2=0), then the genotypes is identified as stable. A slightly large value of ri2 will therefore, illustrate more instability of the ith genotype. Accordingly, genotypes ETBW9128, ETBW9172, ETBW9396, ETBW9452, ETBW9641, ETBW9642, ETBW9646 and ETBW9652 were stable for their ri2 values were nearly zero. Besides, listed genotypes produced highest yield that ranged from 5.4–5.8 t ha^{-1}except ETBW9128 and ETBW9652 (Table 4). Similar to the present findings, Abebe et al. (2022) identified six stable and highest yielding advanced bread wheat genotypes by using Shuckla stability model. Likewise, Ahmed et al. (2016) identified five stable and four unstable bread wheat genotypes by evaluating 14 bread wheat genotypes across 12 environments. On the other hand, ETBW9116, ETBW9119, ETBW9065, ETBW9080, ETBW9545, ETBW9647 and Ogolcho were unstable. Similar results were reported by several authors (Akcura et al., 2006, Akcura and Kaya, 2008, Bantayehu, 2009, Fentaw et al., 2015, Yaghotipoor, et al., 2017, Gadisa et al., 2021).

3.9. Perkins and Jinks

Perkins and Jinks proposed statistical analysis whereby the GE interaction effects are regressed on the environmental effect (Purchase, 1997). Based on Perkins and Jinks (1968) methods of stability analysis ETBW9136, ETBW9149, ETBW9080, ETBW9172, ETBW9396, ETBW9452, ETBW9641, ETBW9646, ETBW9647, ETBW9651 and ETBW9652 were the most stable genotypes. All listed genotypes produced superior grain yield that ranged from 5.4–5.8 t ha^{-1} except ETBW9149, ETBW9651 and ETBW9652 that produced less than or equal to 5.1 t ha^{-1} (Table 4). On the other hand, ETBW9116, ETBW9119, ETBW9128, ETBW9545, ETBW9650 and Ogolcho were unstable and relatively low yielding genotypes. Similar findings were reported by Syukur et al. (2011).

3.10. Nassar and Huehn stability model

According to Nassar and Huehn (1987) two rank stability measures Si1 and Si2 were proposed and based on the ranks of the genotypes across the environments and they gave equal weight to each environment. For a genotype with a maximum stability (Si1=0) Si2 gives the variance among the ranks across environments. Zero variance is an indication of maximum stability (Akcura and Kaya, 2008). These two statistics usually ranked genotypes similarly for stability. Accordingly, ETBW9128, ETBW9136, ETBW9139, ETBW9172, ETBW9396, ETBW9641, ETBW9642, ETBW9646, ETBW9651 and ETBW9652 gave smaller values, thus they were considered as the most stable (Table 4). Besides, these stable genotypes produced the highest grain yield that ranged from 5.4 to 5.8 t ha^{-1} except ETBW9128, ETBW9651 and ETBW9652 that produced grain yield of 5.1 t ha^{-1} or less. Similarly, Abdipour et al. (2017) identified four the most stable and three unstable barley genotypes by evaluating 20 advanced barley genotypes across nine environments. On the contrary, ETBW 9119, ETBW 9149, ETBW 9065, ETBW 9080, ETBW 9545, ETBW 9647, ETBW 9648 and Ogolcho were unstable genotypes. Similar findings have been reported by Sabaghnia et al. (2006), Akcura and Kaya (2008), Fentaw et al. (2015), Ahmed et al. (2016) and Yaghotipoor et al. (2017).

3.11. Reaction of promising and advanced bread wheat genotypes to wheat yellow and stem rusts

Wheat rusts (*Puccinia* spp.) control remain a continuous challenge on the globe because wheat rusts have high ability to generate new races through mutation and recombination, have ability to disseminate their spores over thousand kilometers, have ability to tolerate climate change and overwinter and have alternate hosts like barberry (*Berberis holstii)* coupled with mono-cropping, continuous cultivation of susceptible and genetically uniform mega varieties, weak extension and seed system. Currently, stem and yellow rusts are number one production and productivity constraints of wheat in Ethiopia specially in wheat belt zones namely Arsi, West Arsi and Bale (Meyer et al., 2021). Stem and yellow rusts severe epidemics have frequently occurred in Ethiopia. For instance, in 2009-10 yellow rust epidemic devastated very popular, highly productive and widely adaptable varieties namely *'Kubsa'* and *'Galama'*. Similarly, stem rust epidemic devastated another popular variety *'Digalu'* in 2013-14 (Hodson et al., 2020). Hence, incessant breeding for high yielding, durable rust resistance and appropriate end use quality are of paramount importance and environmentally and economically feasible control measures. Identified high yielding, stable and rusts resistant advanced bread wheat genotypes (Table 5) could serve as an option for millions Ethiopian wheat farmers in lowland to mid altitude areas. These genotypes can also be incorporated

Table 5: Reaction of promising bread wheat genotypes to SR and YR diseases

Gen Id	GEN	YLD (t ha^{-1})	YR (S %) mean	YRR	YR (S %) Range	SR (S %) mean	SRR	SR (S %) range
1	DEKA	5.1	8	MRMS	0–15	8	MSMR	0–20
5	ETBW 9136	5.7	2	MRMS	0–5	11	MRMSS	0–30
6	ETBW 9139	5.8	7	MSMR	0–15	11	MRMSS	0–30
8	ETBW 9065	5.4	16	MRMSS	0–60	4	MSMR	0–10
11	ETBW 9080	5.5	2	MR	0–5	4	MSMR	0–10
12	ETBW 9172	5.6	2	MRMS	0–5	9	MRMSS	0–30
13	ETBW 9396	5.5	1	MR	Tr	6	MRMSS	0–30
14	ETBW 9452	5.4	3	MRMS	0–10	7	MRMSS	0–40
17	ETBW 9641	5.6	9	MSS	0–40	24	SMS	0–80
18	ETBW 9642	5.4	2	MR	0–5	26	SMS	0–70
19	ETBW 9646	5.8	2	MR	0–5	20	SMS	0–70
20	ETBW 9647	5.4	5	MRMSS	0–15	32	S	0–60
21	ETBW 9648	5.7	22	MSS	0–60	4	MRMS	0–10
25	OGOLCHO	4.0	26	S	0–90	26	SMS	0–40

Gen Id: Genotype ID; GEN: Genotype; YLD (t ha^{-1}): Grain Yield in tons per hectare; YR: Yellow rust; SR: Stem rust; S%: severity percent; R: Disease reaction or field response; MR: Moderately resistant; MS: Moderately susceptible; S: Susceptible; Tr: trace in bread wheat multi-purpose crossing blocks in order to further improve commercial and elite lines.

4. CONCLUSION

Twelve advanced bread wheat genotypes produced seed yield that ranged from 5.4 to 5.8 t ha^{-1}, indicating their superior yielding potential. ETBW 9136, ETBW 9139, ETBW 9172, ETBW 9396, ETBW 9452, ETBW 9641, ETBW 9642 and ETBW 9646 were the most stable genotypes as confirmed by five to ten stability models. ETBW 9136, ETBW 9139, ETBW 9172 and ETBW 9396 were superior yielding, stable, resistant and moderately resistant to prevailing rusts. Thus, these four genotypes shall be verified and released.

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6. REFERENCES

Abdipour, M., Vaezi, B., Hamzekhanlu, M.Y., Ramazani, S.H., 2017. Nonparametric phenotypic stability analysis in advanced barley (*Hordeum vulgare* L.) Genotypes. Journal of Crop Science and Biotechnology 20(4), 305–314.

Abebe, D., Gadisa, A., Negash, G., Alemu, D., Habtemariyam, Z., Tafesse, S., Rut, D., Dawit, A., Zerihun, T., Bayisa, A., Abebe, G., 2022. Stability and performance evaluation of advanced bread wheat (*Triticum aestivum* L.) genotypes in optimum areas of Ethiopia. International Journal of Bio-resource and Stress Management 13(1), 69–80.

Abera, W., Rensburg, J.B.J., Labuschagne, M.T., Maartens, H., 2004. Genotype-environment interactions and yield stability analyses of maize in Ethiopia. South African Journal of Plant and Soil 21(4), 251–254.

Adane, C.C., Abebe, D.A., 2018. AMMI AND GGE biplot analysis of linseed (L*inum usitatissimum* L.) Genotypes in Central and South-eastern Highlands of Ethiopia. Journal of Plant Breeding and Genetics 6(3), 117–127.

Adugnaw, A., Dagninet, A., 2020. Wheat production and marketing in Ethiopia: Review study. Cognet Food and Agriculture 6(1) https://doi.org/10.1080/23311932.2020.1778893.

Ahmadi, J., Mohammadi, A., Najafi, M.T., 2012. Targeting promising bread wheat (*Triticum aestivum* L.) lines for cold climate growing environments using AMMI and SREG GGE biplot analyses. Journal of Agricultural Sciences and Technology 14(3), 645–657.

Ahmed, M.A., ElSayed, K.M., Sharshar, M.S.E., EL-Fanah, A.M.S., 2016. Stability analysis of yield and solvent retention capacity (SRC) measures for bread wheat genotypes in Egypt. Egypt Journal of Plant Breeding 20(4), 677–699.

Aina, O.O., Dixon, A.G.O., Paul, I., Akinrinde, E.A., 2009. G×E interaction effects on yield and yield components of cassava (landraces and improved) genotypes in the savanna regions of Nigeria. African Journal of Biotechnology 8(19), 4933–4945.

Akcura, M., Kaya, Y., Taner, S., Ayranci, R., 2006. Parametric stability analyses for grain yield of durum wheat. Plant, Soil & Environment 52(6), 254–261.

Akcura, M., Kaya, Y., 2008. Nonparametric stability methods for interpreting genotype by environment interaction of bread wheat genotypes (*Triticum aestivum* L.). Genetics and Molecular Biology 31(4), 906–913.

Annicchiarico, P., 2002. Defining adaptation strategies and yield stability targets in breeding programs. In: Kang, M.S. (Ed.), Quantitative genetics, genomics, and plant breeding. CABI, Wallingford, UK, 365–383.

Ashrei, A.A.M., Ghareeb, Z.E., 2015. Genotype-environment Interaction for Yield in Lupin (*Lupinus albus* L.). Egypt Journal of Plant Breeding 19(5), 239–256.

Asfaw, A., Alemayehu, F., Gurum, F., Atnaf, M., 2009. AMMI and SREG GGE biplot analysis for matching varieties onto soybean production environments in Ethiopia. Scientific Research and Essay 4(11), 1322–1330.

Asrat, A., Fistum, A., Fekadu, G., Mulugeta, A., 2009. AMMI and SREG GGE biplot analysis for matching varieties onto soybean production environments in Ethiopia. Scientific Research and Essay 4(11), 1322–1330.

Assefa, F., Megersa, T., Million, E, Asnake, F., Lijalem, K., Nigussie, G., Dagnachew, B., Ridwan, M., Zewdie, B., Ganga, R. N., Moses, S., Emmanuel, M., Pooran, G., Chris, O., 2017. Genotype by environment interaction on yield stability of desi type chickpea (*Cicer arietinum* L.) at major chickpea producing areas of Ethiopia. Australian Journal of Crop Sciences 11(02), 212–219.

Assefa, A., Firew, M., Wuletaw, T., Kindie, T., 2020. Genotype×environment interaction and stability of drought tolerant bread wheat (*Triticum aestivum* L.) genotypes in Ethiopia. International Journal of Research Studies in Agricultural Sciences 6(3), 26–35.

Bantayehu, M., 2009. Analysis and correlation of stability parameters in malting Barley. African Crop Science Journal 17(3), 145–153.

Becker, H.C., Leon, J., 1988. Stability analysis in plant breeding. Plant Breeding 101(1), 1–23.

Boakye, P.B., Kwadwo, O., Isaac, A., Parkes, E.Y., 2013. Performance of nine cassava (*Manihot esculanta* Crantz) clones across three environments. Journal of Plant Breeding and Crop Science 5(4), 48–53.

Brasesco, F., Asgedom, D., Sommacal, V., Casari, G., 2019. Strategic analysis and intervention plan for wheat and wheat products in the agro-commodities procurement zone of the pilot integrated agro-industrial park in central-eastern Oromia, Ethiopia. Addis Ababa. FAO. 104 pp.

Changizi, M., Choukan, R., Heravan, E. M., Bihamta, M. R., Darvish, F., 2014. Evaluation of genotype-environment interaction and stability of corn hybrids and relationship among univariate parametric methods. Canadian Journal of Plant Sciences 94, 1255−1267.

Cockx, L., Colen, L., De Weerdt, J., Gomez, Y., Paloma, S., 2019. Urbanization as a driver of changing food demand in Africa: Evidence from rural-urban migration in Tanzania, EUR 28756 EN, Publications Office of the European Union, Luxembourg, 2019, ISBN 978-92-79-73182-2, doi:10.2760/515064, JRC107918.

CSA (Central Statistics Agency for Ethiopia), 2022. Agricultural sample survey of area and production of major crops. Available from: https://www.statsethiopia.gov.et/. Accessed on September 2022.

Ebdon, J.S., Gauch, H.G., 2002. Additive main effect and multiplicative interaction analysis of national turfgrass performance trials: I. Interpretation of genotype×environment interaction. Crop Science 42, 489–496.

Eberhart, S.A., Russel, A.W., 1966. Stability parameters for comparing varieties. Crop Science 6, 36–40.

Farshadfar, E., Sadeghi, M., 2014. GGE biplot analysis of genotype×environment interaction in wheat-agropyron disomic addition lines. Agricultural Communications 2(3), 1–7.

Fasahat, P., Rajabi, A., Mahmoudi, S.B., 2015. An overview on the use of stability parameters in plant breeding. Biometrics and Biostatistics International Journal 2(5), 149–159.

Fentaw, A., Firew, M., Yigzaw, D., 2015. Association of different parametric and non-parametric stability models in durum wheat (*Triticum turgidum* Desf.) genotypes. International Journal of Plant & Soil Science 7(4), 192–201.

Finlay, K.W., Wilkinson, G.N., 1963. The analysis of adaptation in a plant-breeding programme. Australian Journal of Agricultural Research 14, 742–754.

Fransis, T.R., Kannenberg, L.W., 1978. Yield stability studies in short-season maize. I. A descriptive method for grouping genotypes. Canadian Journal of Plant Sciences 58, 1029–1034.

Gadisa, A., Alemu, D., Negash, G., Tafesse, S., Abebe, D., Rut, D., Habtemariam, Z, Dawit, A., Abebe, G., Bayisa, A., Demeke, Z., Bekele, G.A., Ayele, B., Bedada, G., 2020. Development of bread wheat (*Triticum aestivum* L.) varieties for high moisture areas of Ethiopia: A G×E Interaction and stability analysis for grain yield. Ethiopian Journal of Crop Sciences 8(1), 87–104.

Gadisa, A., Negash, G., Alemu, D., Abebe, D., Tefasse, S., Rut, D., 2021. Stability models for selecting adaptable and stable bread wheat (*Tritium aestivum* L.) varieties for grain yield in Ethiopia. Journal of Agricultural Science and Engineering 7(1), 14–22.

Gauch, H.G., 2006. Statistical analysis of yield trials by AMMI and GGE. Crop Science 46, 1488–1500.

Golkari, S., Haghparast, R., Roohi, E., Mobasser, S., Ahmadi, M.M., Soleimani, K., Khalilzadeh, G., Abedi-Asl, G., Babaei, T., 2016. Multi-environment evaluation of winter bread wheat genotypes under rainfed conditions of Iran-using AMMI model. Crop Breeding Journal 4, 5 and 6(2, 1 and 2), 17–31.

Habte, D., Tadesse, K., Admasu, W., Desalegn, T., Mekonen, A. 2014. Agronomic and economic evaluation of the N and P response of bread wheat growing in the moist and humid midhighland vertisols areas of Arsi zone, Ethiopia. African Journal of Agricultural Research 10, 89–99

Haruna, A., Gloria, B.A., Samuel, S.B., 2017. Analysis of genotype by environment interaction for grain yield of intermediate maturing drought tolerant top-cross maize hybrids under rain-fed conditions. Cogent Food & Agriculture 3, 1–13.

Hassan, K., Ali, A.A., Mohtasham, M., Hassan, G., Tahmasb, H., Mohammad, A., 2017. Evaluation of adaptability in bread wheat genotypes under dryland conditions in tropical and subtropical locations. Journal of Research in Ecology 5(2), 948–957.

Hei, N.B., Tesfaye, T., Woldeab, G., Hailu, E., Hundie, B., Kassa, D., Yirga, F., Anbessa, F., Alemu, W., Abebe, T., Legesse, M., Seid, A., Gebrekirstos, T., 2018.

Distribution and frequency of wheat stem rust races (*Puccinia graminis* f. *sp. tritici*) in Ethiopia. Journal of Agriculture and Crop Research 6(5), 88–96.

Hodson, D.P., Jaleta, M., Tesfaye, K., Yirga, C., Beyene, H., Kilian, A., Carling, J., Disasa, T., Alemu, S.K., Daba, T., Alemayehu, Y., Badebo, A., Abeyo, B., Erenstein, O., 2020. Ethiopia's transforming wheat landscape: tracking variety use through DNA fingerprinting. Scientific Reports, 10, 18532, https://doi.org/10.1038/s41598-020-75181-8.

Jeberson, M.S., Kant, L., Kishore, N., Rana, V., Walia, D.P., Singh, D., 2017. AMMI and GGE biplot analysis of yield stability and adaptability of elite genotypes of bread wheat (*Triticum aestivum* L.) for Northern hill zone of India. International Journal of Bio-resource and Stress Management 8(5), 635–641.

Karimizadeh, R., Mohammadi, M., Sabaghnia, N., Shefazadeh, M.K., Pouralhossini, J., 2012. Univariate stability analysis methods for determining genotype×environment interaction of durum wheat grain yield. African Journal of Biotechnology 11(10), 2563–2573.

Kaya, Y., Palta, C., Taner, S., 2002. Additive main effects and multiplicative interactions analysis of yield performances in bread wheat genotypes across environments. Turkish Journal of Agriculture and Forestry 26, 275–279.

Kaya, Y., Akcura, M., Taner, S., 2006. GGE-biplot analysis of multi- environment yield trials in bread wheat. Turkish Journal of Agriculture and Forestry 30, 325–337.

Kilic, H., Akura, M., Aktas, H., 2010. Assessment of parametric and non-parametric methods for selecting stable and adapted durum wheat genotypes in multi-environments. Notulae Botanicae Horti Agrobotanici Cluj-Napoca 38(3), 271–279.

Kumar, P., Yadava, R.K., Gollen, B., Kumar, S., Verma, R.K., Yadav, S., 2011. Nutritional contents and medicinal properties of wheat: A Review. Life Sciences and Medicine Research 22, 1–11.

Lin, C.S., Binns, M.R., 1988. A superiority measure of cultivar performance for cultivar×location data. Canadian Journal of Plant Sciences 68, 193–198.

Meyer, M., Bacha, N., Tesfaye, T., Alemayehu, Y., Abera, E., Hunde, B., Woldeab, G., Girma, B., Gemechu, A., Negash, T., Mideksa, T., Smith, J., Jelata, M., Hodson, D., Gilligan, C.A., 2021. Wheat rust epidemics damage Ethiopian wheat production: a decade of field disease surveillance reveals national-scale trends in past outbreaks. Plos One, https://doi.org/10.1371/journal.pone.0245697.

Mitrovic, B., Stanisavljevi, D., Treski, S., Stojakovic, M., Ivanovic, M., Bekavac, G., Rajkovic, M., 2012. Evaluation of experimental maize hybrids tested in multi-location trials using AMMI and GGE biplot analysis. Turkish Journal of Field Crops 17(1), 35–40.

MoANR (Ministry of Agriculture and Natural Resource), 2021. Plant variety release, protection and quality control directorate. Crop Variety Register. Issue No. 24. Addis Ababa, Ethiopia.

Mohammadi, M., Karimzadeh, R., Sabaghnia, N., Shefazadeh, M.K., 2012. Genotype-environment interaction and yield stability analysis of new improved bread wheat genotypes. Turkish Journal of Field Crops 17, 67–73.

Mohammadi, R., Mahmoodi, K.N., 2008. Stability analysis of grain yield in Barley (*Hordeum vulgare* L.). International Journal of Plant Breeding 2(2), 74–78.

Mohammadi, R., Armion, M., Shabani, A., Daryaei, A., 2007. Identification of stability and adaptability in advanced durum genotypes using AMMI analysis. Asian Journal of Plant Sciences 6(8), 1261–1268.

Mohebodini, M., Behghani, H., Sabaghpour, S.H., 2006. Stability of performance in lentil (*Lens culinaris* Medik) genotypes in Iran. Euphytica 149(3), 343–352.

Mortazavian, S.M.M., Nikkhah, H.R., Hassani, F.A., Sharif-al-Hosseini, M., Taheri, M., Mahlooji, M., 2014. GGE piplot and AMMI analysis of yield performance of barley genotypes across different environments in Iran. Journal of Agricultural Science and Technology 16, 609–622.

Mulusew, F., Bing, D.J., Tadele, T., Amsalu, A., 2014. Comparison of biometrical methods to describe yield stability in field pea (*Pisum sativum* L.) under south eastern Ethiopian conditions. African Journal of Agricultural Research 9(33), 2574–2583.

Mulusew, F., Tadele, T., Tesfaye, L., 2008. Genotype-environment interactions and stability parameters for grain yield of faba bean (*Vacia faba* L.) genotypes grown in south eastern Ethiopia. International Journal of Sustainable Crop Production 3(6), 80–87.

Nassar, R., Huehn, M., 1987. Studies on estimation of phenotypic stability: Tests of significance for nonparametric measures of phenotypic stability. Biometrics 43, 45–53.

Pacheco, A., Vargas, M., Alvarado, G., Rodriguez, F., Crossa, J., Burgueno, J., 2016. GEA-R (Genotype×environment analysis with r for windows) Version 4.0, CIMMYT Research Data and Software Repository Network.

Perkins, J.M., Jinks, L.J., 1968. Environmental and genotype environmental components of variability. III. Multiple lines and crosses. Heredity 23, 339–356.

Pinthus, M.J., 1973. Estimate of genotypic value: A proposed method. Euphytica 22, 345–351.

Purchase, J.L., 1997. Parametric analysis to describe genotype by environment interaction and yield stability in winter wheat. PhD Thesis, Department of Agronomy at the University of Orange Free State, Bloemfontein.

Purchase, J.L., Hating, H., Van Deventer, C.S., 2000. Genotype-environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. South African Journal of Plant and Soil 17, 101–107.

Rakshit, S., Ganapathy, K.N., Gomashe, S.S., Rathore, A., Ghorade, R.B., Nagesh Kumar, M.V., Ganesmurthy, K., Jain, S.K., Kamtar, M.Y., Sachan, J.S., Ambekar, S.S., Ranwa, B.R., Kanawade, D.G., Balusamy, M., Kadam, D., Sarkar, A., Tonapi, V.A., Patil, J.V., 2012. GGE biplot analysis to evaluate genotype, environment and their interactions in sorghum multi-location data. Euphytica 185, 465–479.

Sabaghnia, N., Dehghani, H., Sabaghpour, S.H., 2006. Nonparametric methods for interpreting genotype by environment interaction of lentil genotypes. Crop Science 46, 1100–1106.

Sajid, M., Mohammad, F., 2018. Identifying stable bread wheat derived lines across environments through GGE biplot analysis. Sarhad Journal of Agriculture 34(1), 63–69.

Satoto, I., Rumanti, A., Widyastuti, Y., 2016. Yield stability of new hybrid rice across locations. AGRIVITA 38(1), 33–39.

Shewry, P.R., Hey, S.J., 2015. The contribution of wheat to human diet and health. Food and Energy Security 4(3), 178–202.

Shiferaw, B., Negassa, A., Koo, J., Wood, J., Sonder, K., Braun, J.A., Payne, T., 2011. Future of wheat production in sub-saharan Africa: analyses of the expanding gap between supply and demand and economic profitability of domestic production. Paper presented at Increasing Agricultural Productivity & Enhancing Food Security in Africa: New Challenges and Opportunities 1-3 November 2011, Africa Hall, UNECA, Addis Ababa, Ethiopia

Shiferaw, B., Kassie, M., Jaleta, M., Yirga, C., 2014. Adoption of improved wheat varieties and impacts on household food security in Ethiopia. Food Policy 44, 272–284.

Shukla, G.K., 1972. Some statistical aspects of partitioning genotype-environmental components of variability. Heredity 29, 237–245.

Singh, C., Gupta, A., Gupta, V., Kumar, P., Sendhi, R., Tyagi, B.S., Singh, G., Chatrath, R., Singh, G.P., 2019. Genotype×environment interaction analysis of multi-environment wheat trials in India using AMMI and GGE biplot models. Crop Breeding and Applied Biotechnology 3, 309–318.

Singh, R.P., Hodson, D.P., Jin, Y., Lagudah, E.S., Ayliffe, M.A., Bhavani, S., Mathew, N., Zacharias, R., Pretorius, A., Les, J., 2015. Emergence and spread of new races of wheat stem rust fungus: Continued threat to food security and prospects of genetic control. Phytopathology 105, 872–884.

Solh, M., Nazari, K., Tadesse, W. Wellings, C.R., 2012. "The growing threat of stripe rust worldwide", Borlaug Global Rust Initiative (BGRI) Technical Workshop, Beijing, China.

Solomon, T., Shewaye, Y., Zegeye, H., Asnake, D., Tadesse, Z., Girma, B., 2018. Performance evaluation of advanced bread wheat genotypes for yield stability using the AMMI stability model. Journal of Agricultural Research 3(4), 1–7.

Syukur, M., Sriani, S., Rahmi, Y., Darmawan, A.K., 2011. Parametric stability analysis for yield of chili pepper (*Capsicum annuum* L.). Indonesian Journal of Agronomy 39 (1), 31–37.

Tadesse, W., Bishaw, Z., Assefa, S., 2018. Wheat production and breeding in Sub-Saharan Africa challenges and opportunities in the face of climate change. International Journal of Climate Change Strategies and Management 11(5), 696–715.

Tadesse, W., Zegeye, H., Debele, T., Kassa, D., 2022. Wheat production and breeding in ethiopia: retrospect and prospects. Crop Breeding, Genetics and Genomics 4(3), e220003. https://doi.org/10.20900/cbgg20220003

Tamene, T.T., Gemechu, K., Musa, J., Yeneneh, B., 2013. Genotype-environment interaction and performance stability for grain yield in field pea (*Pisum sativum* L.) genotypes. International Journal of Plant Breeding 7(2), 116–123.

Tariku, S., 2018. Adaptability Performances of Cowpea [*Vigna unguiculata* (L.) Walp] genotypes in Ethiopia. Food Science and Quality Management 72, 43–47.

Thangavel, P., Anandan, A., Eswaran, R., 2011. AMMI analysis to comprehend genotype-by-environment (G×E) interactions in rainfed grown mungbean (*Vigna radiata* L.). Australian Journal of Crop Science 5(13), 1767–1775.

Tolemariam, A., Jaleta, M., Hodson, D., Alemayehu, Y., Yirga, C., Abeyo, B., 2018. Wheat varietal change and adoption of rust resistant wheat varieties in Ethiopia from 2009/10 to 2013/14. Socioeconomics Program Working Paper 12. Mexico, CDMX: CIMMYT.

Wricke, G., 1962. On a method of understanding the biological diversity in field research. Z. Pflanzenzucht

47, 92–96.

Yaghotipoor, A., Farshadfar, E., Saeidi, M., 2017. Evaluation of phenotypic stability in bread wheat accessions using parametric and non-parametric methods. The Journal of Animal & Plant Sciences 27(4), 1269–1275.

Yan, W., 2011. GGE Biplot vs AMMI graphs for genotype by environment data analysis. Journal of the Indian Society of Agricultural Statistics 65(2), 181–193.

Yan, W.K., Sheng, Q.L., Hu, Y.G., 2001. GGE biplot-an ideal tool for studying genotype by environment interaction of regional yield trial data. Acta Agronomica Sinica 27, 21–28.

Yan, W., Tinker, N.A., 2006. Bi-plot analysis of multi-environment trial data: Principles and Applications. Canadian Journal of Plant Science 86, 623–645.

Yayis, R., Agdew, B., Yasin, G., 2014. GGE AND AMMI biplot analysis for field pea yield stability in SNNPR state, Ethiopia. International Journal of Sustainable Agricultural Research 1(1), 28–38.

Zerihun, J., 2012. Evaluation of ICARDA Barley genotypes for yield stability and lodging resistance in southeastern Ethiopia highlands. Electronic Journal of Plant Breeding 3(2), 722–732.