Identification of Climate-Smart Bread Wheat (*Triticum aestivum* L.) Germplasm for Optimum Moisture Areas of Ethiopia.

Abstract

Ethiopia's Bread Wheat Breeding Program conducts annual multi-environment yield trials to develop advanced wheat genotypes for Ethiopian wheat cultivation, ensuring a steady supply of new and improved varieties to meet production and marketing challenges.The objective of this research was to assess the potential yield and the interactions between genotype and environment in wheat through many environments since every cultivar has a distinct response to soil and climate. The BLUP analysis reveals that 22AA and 22KU trials in 2022 and 21KU trials in 2021 yielded high grain, indicating optimal testing locations for distinguishing bread wheat genotypes and agroecologies.The study found that seven out of sixteen trials had a higher genetic variance for yield, indicating high genotype discriminating power, with estimates ranging from 0.043 to 0.989 for genetic variance, 0.084 to 1.147 for error variance, and 72.7 to 96.4 for heritability.EBW202471 and EBW202473 are stable genotypes with good yield performance over correlated locations, with EBW202471 showing the highest yield (4.98 t/ha) and Deka having a lower yield (4.07 t/ha).Three wheat genotypes, EBW202471, EBW202472, and EBW202473, were found to be moderately resistant to moderately susceptible to stem and yellow rust among 20 wheat genotypes. Finally, two genotypes EBW202471 and EBW202473, were advanced to National Performance Trials to evaluate their performance alongside top genotypes from regional federal research centers and be released as new varieties.

Keywords: BLUP, National performance trials, Wheat genotype, Variance, Varieties

Introduction

Wheat (Triticum aestivum L., 2n = 6x = 42, AABBDD), is the world's most widely cultivated cereal [1, 2], and is crucial for global food security [3,4,5]. Wheat is a staple source of nutrients for around 40% of the world’s population [6missingin reference,7]. Bread wheat contributes to the human diet and supplies 20% of dietary calories[8,9,10]. Wheat is a highly nutritious cereal food that surpasses all other food sources in terms of human nutrition.Rapid population growth, urbanization, and changing food preferences have made wheat an important food crop globally. It is a mandatory crop and a staple food in various regions [11]. With over 720 million people worldwide suffering from hunger and three billion with nutrient-deficient diets [12], wheat availability, accessibility, and production are crucial for food security [13]. By 2050, with 9.4 billion people, the demand for wheat is expected to rise by 60% due to increased wealth and consumption[14]. Ethiopia's wheat is a vital component of the people's social and economic life, consumed in various forms like bread, porridge, beer, roasted grain, boiled grain, pasta, macaroni, and various confectionary products[15, 16].

Wheat is grown in a diverse climate.It plays a crucial role in agriculture[17, 18]. Wheat, the second-largest grain globally in terms of grain acreage and total production volume, reached a global production volume of nearly 784.91 million metric tons in 2023/24 [19].Ethiopia is the largest wheat producer in Sub-Saharan Africa. Ethiopia's wheat production reached 8.2 million tons in 2022, achieving 100% self-sufficiency [20]. The Ethiopian government is enhancing wheat production through land expansion, agro-clustering, and irrigation expansion to lowlands and dry seasons [21, 22]. Since the 1980s, wheat demand has doubled, with developing countries harvesting 50% of global wheat production annually [6].

Wheat production globally, including in Ethiopia, is significantly impacted by abiotic and biotic stresses, with phytopathogenic diseases being the most significant contributors, causing substantial yield and quality loss. Potential threats to worldwide wheat production include biotic challenges like insects, nematodes, and diseases, as well as abiotic stresses like heat, drought, cold, and salinity[23]. Climate change and socioeconomic factors also impact wheat production and productivity. The main biotic factor affecting Ethiopia's wheat yield is rust. Both biotic and abiotic stresses, along with socioeconomic factors, significantly influence Ethiopia's wheat production and productivity [24]. It accounts for a 30–40% loss of wheat globally [25, 26].

The growing global population and climate change are major concerns in agriculture. Food production and security are crucial issues, as food output may double by 2050, andinnovative approaches are needed to increase agricultural productivity and meet the rising demand for food, as food output may need to double by 2050[27]. Global wheat production increased by 4% in the first decade post-revolution, with 8% growth in South Asia, East Asia, Mexico, and Central America [6]. Climate change and related stresses necessitate efforts to include resilience while improving production and quality to secure food security for the fast-rising global population. Bread wheat germplasm has wide genetic diversity, which means it can withstand a lot of biotic and abiotic stresses [28]. New crop cultivars, particularly those resistant to biotic and abiotic factors and adaptable to climatic variations, are crucial for addressing climate change.

Genotype-environment interactions significantly influence quantitative traits like yield, and stability analysis helps identify varieties with superior performance and yield stability in various environments.Germplasm offers the best opportunity to develop varieties with a small G × E interaction. Climate-smart varieties tolerate the negative effects of climate change better and produce a higher yield and better quality in stressful environments. Ethiopia's wheat breeding aims to produce high-yield, resilient material with superior end-use quality, requiring multi-environment testing, specific screening for biotic and abiotic stresses, and favorable gene accumulation.This study aimed to evaluate the yield potential and genotype-environment interactions of bread wheat genotypes in Ethiopian wheat growing areas through yield trials.

Materials and methods

Bread wheat genotypes are evaluated in multistage, multilocation field trials by gradually reducing the number of genotypes tested from a large number in a few locations to a smaller number in several locations (Table 1).The study assessed the high yield and superior agronomic performance of 18 advanced bread wheat genotypes and two checks in NVT, grown in Ethiopia during the 2021-2023 main wheat growing seasons in seven locations.Three replications were conducted in a row-column experiment design, consisting of 2.5 m long and 1.2 m wide plots with six plant rows, separated by 1.5 meters and 1 meter respectively.The study used 150 kg/ha of seed and collected data on parameters like days to heading, days to maturity, plant height, grain yield per plot, hectoliter weight, and thousand kernel weight.The notes on rust diseases were recorded using a 0-9 scale.

Table 1: List of Testing locations, altitude, and respective Geographic information

Geographic position and altitude	Testing site						
	Asasa	Debre Zeit	Kulumsa	Sinana	Adet	Ambo	Areka
Latitude	07^{o}07'09"N	08°38'N	08^{o}01'10"N	7°7’N	7°7’	08°59′N	7°3′25" N
Longitude	39^{o}11'50"E	38°30'E	39^{o}09'11"E	39°49'E	39°49'	37°51′E	37°40'52" E
Altitude (m)	2340	1900	2200	2450	2450	2101	2230

Table 2: The list of 18 advanced bread wheat genotypes and two newly released varieties that were assessed during the main cropping season of 2021-2023.

Genotypes	Pedigree
Boru	SAUAL/MUTUS/6/CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/ FH6-1-7/7/CNO79//PF. 70354/MUS/3/PASTOR/4/BAV92*2/5/FH6-1-7
Deka	ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE
EBW202038	KACHU/DANPHE*2//KENYA SUNBIRD/KACHU

EBW202040	KACHU/DANPHE*2//KENYA SUNBIRD/KACHU
EBW202056	WBLL1*2/BRAMBLING//NIINI #1/3/VILLA JUAREZ F2009*2/4/KFA/2*KACHU
EBW202207	SUP152/2*DANPHE #1//BORL14
EBW202239	BAVIS #1//ND643/2*WBLL1*2/3/BORL14
EBW202341	KACHU/DANPHE*2//KENYA SUNBIRD/KACHU
EBW202362	PBW343*2/KUKUNA//PBW343*2/KUKUNA*2/6/C80.1/3*BATAVIA//2*WBLL1/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213) //PGO/4/HUITES/7/BORL14
EBW202414	ALTAR 84/AE.SQUARROSA (221)//3*BORL95/3/URES/JUN//KAUZ/4/WBLL1/5/MUTUS*2/6/DANPHE #1/KENYA SUNBIRD//DANPHE
EBW202434	BAVIS/VORB/5/CROC_1/AE.SQUARROSA (205) //BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/6/BABAX/LR42//BABAX*2/3/SHAMA/4/WAXWING*2/KRONSTAD F2004/7/BABAX/LR42//BABAX/3/ER2000/4/2*MUNAL
EBW202460	VILLA JUAREZ F2009//KIRITATI/2*TRCH/3/WBLL1*2/BRAMBLING/4/KFA/2*KACHU
EBW202466	TRCH*2//ND643/2*WBLL1/3/BORL14
EBW202471	KENYA SUNBIRD/2*KACHU/3/SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
EBW202472	PFAU/MILAN/5/CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/VEE#7/BOW/4/PASTOR/6/2*BAVIS #1/7/BORL14
EBW202473	PFAU/MILAN/5/CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/VEE#7/BOW/4/PASTOR/6/2*BAVIS #1/7/BORL14
EBW202475	BECARD//ND643/2*WBLL1/3/KACHU/DANPHE
EBW202487	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1*2/4/KENYA SUNBIRD*2/5/ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE
EBW202501	KACHU/DANPHE*2//KENYA SUNBIRD/KACHU
EBW212081	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/PBW343*2/TUKURU/5/C80.1/3*BATAVIA//2*WBLL1/6/CMH75A.66/SERI/7/MUNAL #1*2/8/TAM200/PASTOR//TOBA97/3/FRNCLN/4/WHEAR//2*PRL/2*PASTOR

Statistical analysis

The study used R software for statistical analysis, applying a mixed linear model to multi-environment trial data analysis. The factor analytic model, similar to the AMMI model, was used to capture heterogeneous variance-covariance structures. Spatial field trends were fitted first for each environment and tested for potential field trends between neighbor plots. Global variability and extraneous variation were checked and included in the standard linear mixed model. Trials across environments were combined with specific trial information, including spatial field trends. The BLUP predictors were used to compare the means of each genotype with the general mean, as described by Biasutti[29].The BLUP pair grain yields were ranked descending to identify genotypes or superior lines, allowing comparison of environmental effects' free genetic values for improved genetic gain in subsequent selection cycles.

Results and discussion

The study analyzed genotypes in correlated trials, finding all genotypes perform better at 22AA (7.79 t/ha), followed by 21KU (6.00 t/ha) and 22KU (5.59 t/ha), with the potential of the 21AD trial being lower (2.78 t/ha) (Table 3). In multi-environmental breeding programs, selection considers genotype performance and rank change between testing situations. MET analysis helps understand genotype adaptation across target populations. Breeders choose genotypes using BLUPs averaged over associated environments and predicted GxE variance to identify connected environments. This information is crucial for successful selection in multi-environmental breeding programs.

The study found high heritability for all traits, ranging from 72.7% for grain yield t/ha to 99.3% for days to heading. Heritability values above 80% were considered very high, while values between 60-79% were moderately high, 40-59% medium, and less than 40% low. All traits had a very high broad sense of heritability at all locations, except for plant height at 21SN, thousand kernel weight at 23KU, hectoliter weight at 23DZ, and grain yield at 23KU.The study found moderate broad sense heritability values for traits such as plant height (79% at 21SN), thousand kernel weights (69% at 23KU), hectoliter weight (75.3% at 23DZ), and grain yield (72.7%) (Table 3).Nine out of 20 tested genotypes in the 2021-23 crop season showed high mean grain yields. Genotype EBW202471 was the highest-performing genotype (4.98 t/ha), while genotype Deka had a lower yield (4.07 t/ha).Two genotypes, EBW 202471 and EBW 202473, were advanced to National Performance Trials to evaluate their performance alongside top genotypes from regional federal research centers and be released as new varieties (Table 5).

Table 3: Variation for individual environment variance components and grain yield means for grain yield and broad-sense heritability for all traits, in 16 environments

Environments	GRAIN YIELD			HERITABILITY				
	Trial Mean	Genetic Variance	Error Variance	GYLD	DTH	PHT	HLW	TKW
21AA	5.23	0.70	0.10	96.40	-	92.00	94.90	93.90

21AD	2.78	0.00	0.10	81.00	99.30	95.30	91.00	96.20
21AR	4.52	0.30	0.20	93.10	95.20	96.10	-	81.00
21DZ	4.18	0.40	0.50	83.70	98.80	87.50	91.50	95.90
21KU	6.00	0.80	0.40	96.10	97.50	92.60	96.20	95.80
21SN	4.71	0.60	0.20	92.40	85.90	79.00	83.70	96.40
22AA	7.79	0.70	0.20	95.00	97.60	92.10	95.80	92.40
22AD	4.81	0.20	0.60	78.70	99.10	92.30	87.80	95.10
22AR	4.40	0.20	0.50	88.60	93.50	91.50	-	79.30
22DZ	5.25	0.30	1.10	81.70	99.20	-	90.70	87.60
22KU	5.59	0.90	0.30	92.60	97.70	94.10	96.70	92.50
23AA	3.71	1.00	0.30	93.90	99.10	96.90	97.30	95.90
23AB	3.16	0.10	0.30	82.50	99.00	95.60	-	-
23DZ	2.93	0.30	0.50	88.10	99.20	92.70	75.20	89.70
23SN	4.20	0.70	0.60	87.80	95.00	-	96.20	95.10
23KU	3.73	0.40	0.30	72.70	95.40	80.60	82.40	69.00

Note: 21AA: 2021 Asasa, 21AD: 2021 Adet, 21AR: 2021 Areka, 21DZ: 2021 Debreziet, 21KU: 2021 Kulumsa, 21SN:2021 Sinana, 22AA: 2022Asasa, 22AD: 2022 Adet, 22AR: 2022 Areka, 22DZ: 2022 Debreziet, 22KU: 2022 Kulumsa, 23AA: 2023 Asasa, 23AB: 2023 Ambo, 23DZ: 2023 Debreziet, 23KU: 2023Kulumsa, 23SN:2023 Sinana,

Factor analytical model and Variance components

The factor analysis models (FA) were used for genotype by environment (GxE) analysis, maintaining spatial models from individual trial analysis. The adequacy of FA models was assessed within a mixed model framework, focusing on the percentage of GxE variance explained by factor components. The FA models fit almost all trials well, with the genetic variance well explained by the six-factor components, accounting for nearly 87.85% of GxE variance. Every trial had a good association with other trials since it was adequately fitted using the FA model. The study analyzed MET data and found that modeling GE interactions with FA models combined with spatial variations improved genetic parameter estimates, demonstrating heritability. This was also observed in sorghum [30], durum wheat [31], and maize [32]. The study also found that FA models were useful for estimating and predicting GxE interaction effects, estimating GxE variance, and performing bi-plot analysis. These findings suggest that FA models can be a valuable tool in genetic analysis.

The study revealed that seven out of sixteen trials had a higher genetic variance for yield, suggesting high discriminating power for genotypes. Estimates ranged from 0.043 to 0.989 for genetic variance, 0.084 to 1.147 for error variance, and 72.7 to 96.4 for heritability (Table 3).The study emphasizes the significance of meteorological data from a specific cropping season in recommending the best genotype for a given season and its wider application across various agroecologies due to higher rainfall distribution. In addition, the 21AD, 23AB, 22AD, and 22AR trials were found to be poor trials with low genetic variance (Table 3).

Table 4: Results from fitting the FA model

Site	fac_1	fac_2	fac_3	fac_4	fac_5	fac_6	all
21AA	59.14	5.94	31.14	1.07	0.22	2.49	100
21AD	28.9	3.32	0.03	67.24	0.33	0.17	99.99
21AR	81.78	6.82	0.67	0.34	7.36	3.02	99.99
21DZ	57.13	25.31	1.56	3.3	4.51	8.19	100
21KU	84.7	2.34	2.41	4.57	1.47	4.51	100
21SN	25.86	58.97	0.03	6.92	4.25	3.97	100
22AA	82.14	6.01	0.15	9.99	0	1.71	100
22AD	13.06	2.53	28.71	40.89	6.4	8.41	100
22AR	47.57	16.09	19.67	8.88	6.75	1.04	100
22DZ	14.84	2.64	31.83	27.96	2.31	20.42	100
22KU	80.95	1.12	0.08	1.03	3.7	0.97	87.85
23AA	3.91	66.44	15.1	13.25	0.72	0.58	100
23AB	47.44	0.74	0.91	21.57	21.03	0.32	92.01
23DZ	47.35	1.64	21.3	2.08	5.2	22.43	100
23SN	38.75	28.45	1.85	30.3	0.2	0.45	100
23KU	37.81	14.92	2.2	8.16	28.77	8.13	99.99

Note: 21AA: 2021 Asasa, 21AD: 2021 Adet, 21AR: 2021 Areka, 21DZ: 2021 Debreziet, 21KU: 2021 Kulumsa, 21SN:2021 Sinana, 22AA: 2022Asasa, 22AD: 2022 Adet, 22AR: 2022 Areka, 22DZ: 2022 Debreziet, 22KU: 2022Kulumsa, 23AA: 2023 Asasa, 23AB: 2023 Ambo, 23DZ: 2023Debreziet, 23KU: 2023Kulumsa, 23SN:2023Sinana,

BLUPs for genotypes mean values across environments

Best linear unbiased predictions(BLUPs) have a minimum mean square error of prediction, enabling more accurate estimation of underlying effects in plant breeding. Genotype effects are typically fitted as random factors and precise genotype ranking is crucial for selecting superior genotypes [33]. In plant breeding, genotype ranking accuracy is crucial for selecting superior genotypes. Genotype effects are typically fitted as random variables, especially during early genotyping trials with numerous entries.

The performance of genotypes may be graded using BLUP values averaged across correlated environments. More than 45.00% (9) of the 20 genotypes exhibited average grain yields of more than 4.56 t/ha, according to Table 5. The estimated mean grain yield, on the other hand, indicated nine candidate genotypes with mean yields more than standard check Boru: two of these candidate genotypes (EBW202471 and EBW202473) are advanced to National Performance trials for further testing and release as new variety (Table 5). Furthermore, BLUP analysis revealed that 22AA trials in 2022, 21KU trials in 2021, and 22KU trials in 2022 produced high grain yields, implying that these sites are the best testing locations for distinguishing between bread wheat genotypes and the best-suited agro-ecologies for bread wheat production in general. Genotype rankings differed across environments, justifying the evaluation of cross-environment yield stability. The BLUPs per genotype (Table 5) demonstrate overall variation in grain yield differences. The bread wheat genotypes EBW202471, EBW202472, EBW202056, EBW202472, EBW202341, EBW202434, EBW202466, EBW202475, EBW202501 and Boru had an overall grain yield of >4.56 ton /ha.The estimated GxE variance can be used to identify correlated environments, and breeders can select genotypes by calculating BLUPs averaged across these correlated environments.The superior varieties were selected based on average BLUPs to accurately predict their performance ranking [34, 35]. Anuradha et al.,[36] used BLUPs analysis using a simultaneous selection index, but our BLUP was enhanced by capturing spatial variations and modeling the genetic correlation structure between environments.

Table 5: BLUPs for genotypes mean values across environments

Genotypes	**21AA**	**21AD**	**21AR**	**21DZ**	**21KU**	**21SN**	**22AA**	**22AD**	**22AR**	**22DZ**	**22KU**	**23AA**	**23AB**	**23DZ**	**23SN**	**23KU**	**Mean**
Boru	5.71	2.80	4.83	3.90	6.10	5.68	7.88	4.80	4.62	4.95	5.76	2.94	3.25	2.63	3.47	3.60	4.56
Daka	4.32	2.53	4.27	3.65	4.97	4.42	7.24	4.70	4.08	4.57	4.75	2.86	2.84	2.35	4.00	3.61	4.07
EBW202038	4.87	2.83	4.47	4.13	5.65	4.74	7.26	5.03	4.11	5.14	5.02	3.77	3.12	2.67	3.78	3.95	4.41
EBW202040	5.12	2.81	4.28	3.83	6.16	4.48	7.63	4.81	4.24	5.77	5.38	3.54	3.18	3.28	3.73	3.54	4.49
EBW202056	6.15	2.99	5.22	4.51	6.70	6.10	8.23	5.11	4.76	5.15	6.17	3.52	3.63	2.81	3.76	4.08	4.93
EBW202207	5.15	2.73	4.31	3.92	5.72	4.61	7.55	4.65	4.36	5.16	5.29	3.57	3.04	2.81	3.91	3.45	4.39
EBW202239	4.02	2.68	4.37	3.85	5.88	3.94	7.64	5.16	3.79	5.68	5.00	3.05	3.12	3.34	4.39	4.23	4.39
EBW202341	5.68	2.89	4.76	3.91	6.53	4.63	7.88	4.95	4.31	5.72	5.48	3.64	3.59	3.35	3.95	4.14	4.71
EBW202362	4.73	2.54	4.25	3.56	5.78	4.51	7.97	4.52	4.39	5.23	5.43	2.51	2.91	3.04	4.12	3.21	4.29
EBW202414	5.67	2.71	4.35	3.75	5.37	5.31	7.33	4.39	4.65	4.56	5.15	3.37	3.08	2.20	3.29	2.99	4.26
EBW202434	5.41	2.77	4.52	3.95	6.77	5.49	8.55	4.72	4.74	5.81	6.43	2.60	3.08	3.45	3.77	3.06	4.69
EBW202460	5.59	2.66	4.40	4.03	5.72	4.75	7.86	4.37	4.69	4.82	5.64	3.62	3.01	2.65	4.26	3.23	4.46
EBW202466	5.71	2.66	4.71	4.28	5.94	3.61	8.09	4.49	4.48	4.93	5.56	4.42	3.32	3.04	5.55	4.27	4.69
EBW202471	5.81	2.88	4.84	5.13	6.30	4.33	8.22	4.84	4.61	5.09	6.25	5.20	3.28	3.01	5.56	4.37	4.98
EBW202472	5.46	2.73	4.79	5.03	6.38	4.45	8.70	4.72	4.75	5.08	6.63	4.37	3.08	3.15	5.82	4.02	4.95
EBW202473	5.31	2.87	4.84	4.97	6.09	4.99	8.03	5.06	4.50	4.96	6.04	4.40	3.12	2.74	4.88	4.21	4.81
EBW202475	4.72	3.03	4.45	4.55	6.12	4.74	7.27	5.40	3.95	5.78	5.33	4.38	3.29	3.08	3.77	4.21	4.63
EBW202487	5.07	2.80	4.24	4.50	5.61	4.52	7.46	4.73	4.37	5.07	5.52	4.45	2.96	2.67	4.31	3.52	4.49
EBW202501	5.04	2.90	4.29	3.90	6.49	4.47	7.67	5.00	4.13	6.20	5.50	3.62	3.31	3.59	3.62	3.68	4.59
EBW212081	5.15	2.80	4.12	4.30	5.68	4.52	7.44	4.64	4.40	5.24	5.50	4.30	2.97	2.79	4.05	3.29	4.45
Mean	5.23	2.78	4.52	4.18	6.00	4.71	7.79	4.81	4.40	5.25	5.59	3.71	3.16	2.93	4.20	3.73	4.56

Disease Resistance of the genotypes

The severity of yellow rust and stem rust was evaluated using the 0-9 scale at Merero and Debreziet hotspots respectively.The genotype's response to field infection was scored twice for stem rust and three times for yellow rust.Among 20 wheat genotypes, three wheat genotypes, EBW202471, EBW202472, and EBW202473, were found to be moderately resistant to moderately susceptible (MRMS) for stem rust based on average first and second scoring(Table 6).The final yellow rust severity levels were recorded for each genotype when the check was severely rusted and the disease rate reached its maximum level.Three genotypes EBW202471, EBW202472, and EBW202473 exhibited moderate resistance reactions according to Merero disease scoring.The other genotypes showed moderate resistance to moderately susceptible to susceptible for one of two rusts. Finally based on their response to yellow rust and stem rust two genotypes were selected for national performance trials in 2024.

Table 6: Selection based on Wheat Rust (Yellow and Stem Rust)

SN	Genotypes	stage	SrS1	SrS2	Sr average	Merero Yr3
1	Boru	CHECK	5.61	6.47	6.04	7.09
2	Daka	CHECK	5.80	6.75	6.27	5.94
3	EBW202038	NVT1	5.68	6.12	5.90	4.48
4	EBW202040	NVT1	5.48	5.94	5.71	5.90
5	EBW202056	NVT1	4.75	6.25	5.50	3.13
6	EBW202207	NVT1	5.18	6.46	5.82	4.26
7	EBW202239	NVT1	5.79	6.61	6.20	3.58
8	EBW202341	NVT1	5.38	6.19	5.79	6.62
9	EBW202362	NVT1	4.45	5.67	5.06	6.63
10	EBW202414	NVT1	5.11	5.94	5.53	6.43
11	EBW202434	NVT1	5.34	6.01	5.67	3.50
12	EBW202460	NVT1	5.60	6.59	6.10	7.04
13	EBW202466	NVT1	6.33	6.88	6.61	3.58
14	EBW202471	NVT1	3.81	4.95	4.38	3.58
15	EBW202472	NVT1	3.76	5.42	4.59	3.40
16	EBW202473	NVT1	3.12	4.85	3.99	3.70
17	EBW202475	NVT1	6.24	6.87	6.56	3.82
18	EBW202487	NVT1	4.98	6.38	5.68	6.62
19	EBW202501	NVT1	4.25	5.28	4.77	5.95
20	EBW212081	NVT1	5.60	6.53	6.06	6.94

NB: 0=Immune,1= resistance, 2= Resistant-Moderately-Resistant, 3=Moderately resistance,4=Moderately Resistant-Moderately Susceptible,5=Moderately Susceptible,6=Moderately Susceptible-Susceptible, 7= Susceptible, 8-9= very Susceptible

Quality traits of the genotypes

In addition to raising yield, improving quality attributes has always been a priority in wheat breeding [37]. Advanced wheat genotypes, developed by breeders, are evaluated based on various quality parameters such as grain starch, protein contents, gluten content, milling content, and zeleny. The genotypes showed significant differences in grain starch, protein content, gluten content, milling, and zeleny. The starch content in the grain varied from 63.84 to 68.15%, with an average of 65.59%, with EBW202472 having the highest content (68.15%), while EBW202434 had the lowest (63.84%).The protein content in the sample ranged from 12.29 to 14.48%,with an average of 12.89%, EBW202414 having the highest content (14.48%) and EBW202341 having the lowest (12.29%). Gluten content ranged from 25.43 to 33.27%, with an average of 26.40%. EBW202414 had the highest gluten content (33.27%), while EBW202341 had the lowest (25.43%). The milling content of the samples was in the range of 64.66% to 77.70% with an average of 68.64%.EBW202471 had the highest milling content (77.7%), while Deka had the lowest (64.66%). The zeleny content of the samples was in the range of 35.63 to 50. 33% with an average of 40.61%. EBW202414 had the highest milling content (50.33 %), while EBW202341 had the lowest (35.63%)(Table 7).

Table 7: Quality traits of the genotypes

SN	Genotypes	Gluten	Milling	Protein	Starch	Zeleny
1	Boru	26.37	69.75	12.76	66.42	40.60
2	Deka	28.54	64.66	13.30	66.27	42.59
3	EBW202038	28.44	74.02	13.12	66.20	41.12
4	EBW202040	26.18	67.76	12.66	65.41	38.30
5	EBW202056	27.75	74.43	12.87	67.11	41.11
6	EBW202207	27.94	74.44	13.05	67.33	42.89
7	EBW202239	29.13	73.36	13.35	66.91	45.11
8	EBW202341	25.43	72.46	12.29	67.27	35.63
9	EBW202362	28.70	69.90	13.54	65.64	46.71
10	EBW202414	33.27	76.57	14.48	64.71	50.33
11	EBW202434	27.93	70.11	13.29	63.84	41.07
12	EBW202460	30.33	73.00	13.54	66.52	47.10
13	EBW202466	27.29	71.10	12.56	67.05	38.88
14	EBW202471	30.45	77.70	13.55	67.17	47.40
15	EBW202472	28.85	73.15	13.01	68.15	43.50
16	EBW202473	30.73	74.28	13.62	67.09	48.20

17	EBW202475	27.60	71.33	12.73	67.30	39.83
18	EBW202487	30.89	73.12	13.73	66.75	44.51
19	EBW202501	26.75	69.66	12.83	66.22	39.92
20	EBW212081	30.89	74.54	13.65	65.62	44.33
	Mean	28.67	72.27	13.20	66.45	42.96

Conclusion and Recommendation

Ethiopian farmers need a steady supply of new and improved varieties to meet production and marketing challenges. Multi-environment trials (MET) are essential for varietal evaluation, as each cultivar responds differently to climatic and soil conditions. FA models have improved data fitting, resulting in significant improvements in heritability.Integrating MET with spatial and FA models improved the understanding of genetic effects and genotype evolution precision by considering the GxE interaction effect. This enabled breeders to isolate the genetic effect or explore the interaction effect, and the fitted information could identify genotypes with the highest potential for further verification studies. More than 45.00% (9) of the 20 genotypes exhibited average grain yields of more than 4.56 t/ha. Furthermore, BLUP analysis revealed that 22AA trials in 2022, 21KU trials in 2021, and 22KU trials in 2022 produced high grain yields, implying that these sites are the best testing locations for distinguishing between bread wheat genotypes and the best-suited agro-ecologies for bread wheat production in general. EBW202471 and EBW202473 are found to be useful as stable genotypes with a wide range of adaptability, demonstrating good yield performance over correlated locations. The estimated mean grain yield, on the other hand, indicated nine candidate genotypes with mean yields more than standard check Boru: two of these candidate genotypes (EBW202471 and EBW202473) are advanced to National Performance trials for further testing and release as new varieties.

Data availability

Available from the first author upon request

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