

Research Article

# Multi Environment Trials and Adaption of Advanced Bread Wheat (*Triticum aestivum* L.) Genotypes in Low Moisture Stress Areas of Ethiopia

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## Abstract

To predict bread wheat genetic potential across environments and adaption in low moisture stress wheat growing areas of Ethiopia. Multi-location trials were conducted in Ethiopia from 2020 to 2021 in main seasons. A total of advanced genotypes including the checks were arranged in randomized complete block design in a rectangular (row x column) array of plots with two replications. The results showed that, under the linear mixed model, the spatial and factor analytic models were efficient methods of data analysis for this study. By ranking average best linear unbiased prediction (BLUPs) within clusters, the 13 bread wheat environments were clustered into three mega environments (C1, C2, and C3) for the trait grain yield. This method used as a selection indicator, assisting in the selection of superior and adaptable types. The predicted performance of genotypes based on BLUP values averaged across correlated settings of C1 and C2, eliminating C3 due to low genetic correlation with the other trials and low genetic variation. Based on these clusters, the genotypes with the highest potential EBW192350 and EBW192369 were selected for a subsequent verification study that might potentially use them as a released variety. For genetic variance, the estimates for variance component parameters ranged from 0.069 to 2.896 and error variance, they ranged from 0.175 to 1.002. Therefore, increasing the application of this efficient analysis method will improve the selection of superior bread wheat varieties. The two genotypes can be further verified using national performance trials/ or verified in farmers' fields for registration and commercialization.

## Keywords

Average Yield, BLUPs, Cluster, Factor Analytic, Genetic Variation, Spatial, Target Environment

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## 1. Introduction

The global wheat (*Triticum species*) production during 2022 was 2019 MHa while its total production was 808 MT with average productivity of 3.69 t/ha [9]. In the same year in Ethiopia it was produced on 2.30 MHa with total production of 7.0 MT with average productivity of 3.0 t/ha. Wheat is an essential component of the human diet, providing 20% of daily calories and protein. An estimated 80 million peasants depend on for survival making it the second most important food crop in developing nations behind rice in terms of ensuring food security [11]. Wheat is the sources of starch, protein, vitamins, minerals, dietary fiber, and phytochemicals [13, 17].

Due to natural and human selection, wheat is adapted to wide environments as compared to other cereal crops [7, 9, 20] and the modern wheat varieties have high yield potential despite their susceptibility to biotic and abiotic stresses as compared to the landraces and wild relatives [3]. The modern varieties have good yield potential, food making qualities; efficient use of nutrients due to human selection. Over 95% of the wheat grown in the world is common wheat, which is mostly used as whole flour and refined flour to produce a wide variety of flat and fermented breads and for the manufacture of a wide variety of other bakery products. The remaining 5% is mostly durum wheat used to produce semolina (coarse flour), the main raw material for the manufacture of a wide variety of different baking products [8, 14].

G×E interaction reduces the efficiency of selection and accuracy of varietal recommendation. Due to it is necessary to test genotypes in the target environments before introducing new high-yielding varieties [12, 16]. Combining traits for adaptability and high-yielding in the genotypes are and with minimum G×E interaction is important [19]. A genotype is stable if its performance is constant across diverse environments and its contribution to G×E interaction is small [2, 4, 10]. Therefore, estimating genotypic values is breeding efforts is paramount important [19].

About 43% of the arable land for wheat cultivation lay in the low moisture stress areas in Ethiopia (ref??). Therefore, low moisture adaptable varieties are important for the areas.

Plant breeders use information from the analysis of multi-environment trial (MET) data to select superior varieties and an advanced and broadly used method of analysis for multi-environment trial data involves a linear mixed model with factor analytic (FA) variance structures for a variety of environmental effects [1]. According to the same authors; the model can accommodate unbalanced data, that is, not all varieties in all environments, it allows the use of pedigree information and appropriate accommodation of individual trial experimental designs, and most importantly the FA structure for the variety by environment effects is parsimonious and regularly results in a good fit to the data. It provides accurate predictions of the variety effects for every environment in the data set but this constitutes a large and unwieldy amount of information to process for variety selection. Both the development of new cultivars as well as the recommendation of newly released varieties requires a selection to be made among a larger set of candidate genotypes, so the estimation of genotypic values is at the heart of any breeding effort [15]. The primary goal of this study was to estimate bread wheat genetic potential across environments and improve selection strategies by modeling the interactions of spatial field trends and GEI.

## 2. Materials and Methods

### 2.1. Description of Eco-location and Genotypes

In the present study 75 bread wheat advanced genotypes including check varieties (Table 2) were evaluated for two seasons (2020 and 2021) at different locations (Asasa, Alem Tena, Ambo, Dhera, Kulumsa, Melkasa, Goro, and Sirinka) and at 13 environments. The genotypes arranged in randomized complete block design (RCBD) in a rectangular (row x column) array of plots with two replications. Each genotype was planted on plot size of 6 rows of 2.5m long in 20cm between row spacing. The trials were conducted under rain-fed conditions.

**Table 1.** Descriptions of test locations.

Locations	Latitude	Longitude	Altitude
Asasa	07°07'09"N	39°11'50"E	2340
Alem Tena	08°18'N	38°57'E	1611
Dhera	08°19'10"N	39°19'13"E	1650
Kulumsa	08°01'10"N	39°09'11"E	2200
Melkasa	08°24'N	39°21'E	1550
Sirinka	12°15'N	39°12'E	1468

Locations	Latitude	Longitude	Altitude
Ambo	08°59'N	37°51'E	2101
Goro	09°11'0"N	38°43'0"E	1650

**Table 2.** List of advanced bread wheat genotypes evaluated in 13 environments and their pedigrees.

No	Genotype	Pedigree
1	Atlas	Atlas
2	Balcha	Balcha
3	EBW120086	DASHEN/HW5216#6
4	EBW120101	KAKABA/HD3075
5	EBW120104	KAKABA/HW5216#6
6	EBW120105	KAKABA/HW5216#6
7	EBW120106	KAKABA/HW5216#6
8	EBW120109	KAKABA/HW5216#6
9	EBW120110	KAKABA/HW5216#6
10	EBW120111	KAKABA/HW5216#6
11	EBW120115	KAKABA/HW5216#6
12	EBW120116	DANDA'A/JEFFERSON
13	EBW120118	DANDA'A/JEFFERSON
14	EBW120125	SHORIMA/KWS CHAMSIN
15	EBW120126	SHORIMA/KWS CHAMSIN
16	EBW120135	SHORIMA/HW5216#6
17	EBW120137	SHORIMA/HW5216#6
18	EBW120149	KAKABA/HW5216#6
19	EBW120152	SHORIMA/KERN1552
20	EBW172060	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBL1*2/6/WBL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP//KAUZ/5/KACHU #1
21	EBW172600	FRANCOLIN #1/YANAC/5/KIRITATI/4/2*BAV92//IRENA/KAUZ/3/HUITES
22	EBW172604	KFA/2*KACHU/4/WBL1*2/KURUKU//KRONSTAD F2004/3/WBL1*2/BRAMBLING
23	EBW172608	WHEAR//2*PRL/2*PASTOR/5/UP2338*2/SHAMA/3/MILAN/KAUZ//CHIL/CHUM18/4/UP2338*2/SHAMA/6/UP2338*2/KKTS*2//YANAC
24	EBW172619	WBL1*2/KKTS//PASTOR/KUKUNA/3/KINGBIRD #1//INQALAB 91*2/TUKURU/5/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/SAUAL
25	EBW172620	WBL1*2/KKTS//PASTOR/KUKUNA/3/KINGBIRD #1//INQALAB 91*2/TUKURU/5/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/SAUAL
26	EBW172627	FRET2*2/SHAMA//PARUS/3/FRET2*2/KUKUNA*2/4/KINGBIRD #1//INQALAB 91*2/TUKURU
27	EBW172709	NADI/3/ATTILA*2/PBW65//MURGA
28	EBW172713	MUCUY//MUTUS*2/TECUE #1
29	EBW172714	MUCUY//MUTUS*2/TECUE #1
30	EBW172771	PARUS/FRANCOLIN #1/3/PBW343*2/KUKUNA*2//FRTL/PIFED/4/PAURAQ/SUP152

No	Genotype	Pedigree
31	EBW172779	BECARD/AKURI/3/KINGBIRD #1//INQALAB 91*2/TUKURU/4/BECARD/AKURI
32	EBW172797	KFA/2*KACHU*2//QUELEA
33	EBW172803	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN/4/2*SOKOLL//SUNCO/2*PASTOR
34	EBW172827	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1/5/GK ARON/AG SECO 7846//2180/4/2*MILAN/KAUZ//PRINIA/3/BAV92
35	EBW172828	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN/5/CHRZ//BOW/CROW/3/WBLL1/4/CROC_1/AE.SQUARRO SA (213)//PGO
36	EBW172831	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN/5/GK ARON/AG SECO 7846//2180/4/2*MILAN/KAUZ//PRINIA/3/BAV92
37	EBW174102	HUBARA-1/5/CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/VEE#7/BOW/4/PASTOR
38	EBW174116	CHAM-4/MUBASHIIR-9
39	EBW174302	ATTILA*2/CROW/3/VEE#5/SARA//DUCULA
40	EBW174334	HUBARA-16/4/PASTOR/3/KAUZ*2/OPATA//KAUZ
41	EBW174371	SERI 82/SHUHA'S//GRU90-204782/3/MUNIA/CHTO//MILAN
40	EBW174374	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/HUBARA-13
43	EBW174388	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/SHIHAB-7
44	EBW174389	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/SHIHAB-7
45	EBW174413	SERI.1B//KAUZ/HEVO/3/AMAD/4/ESDA/SHWA//BCN
46	EBW174425	SERI.1B//KAUZ/HEVO/3/AMAD/4/TNMU/MILAN/5/WATAN-12
47	Deka	Deka
48	EBW192349	ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE*2/5/KACHU/DANPHE
49	EBW192350	MUTUS*2/HARIL #1/3/SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU/4/MUTUS*2/HARIL #1
50	EBW192351	MUTUS*2/HARIL #1/3/SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU/4/MUTUS*2/HARIL #1
51	EBW192352	FRNCLN/3/KIRITATI//HUW234+LR34/PRINIA/4/FRANCOLIN #1*2/5/KACHU*2/3/ND643//2*PRL/2*PASTOR
52	EBW192353	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1*2/4/KENYA SUN- BIRD*2/5/ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE
53	EBW192357	SUP152*2/TINKIO #1/4/FRET2*2/SHAMA//KIRITATI/2*TRCH/3/BAJ #1/5/SUP152*2/TINKIO #1
54	EBW192360	KACHU*2/3/ND643//2*PRL/2*PASTOR/4/2*KACHU/DANPHE
55	EBW192361	KACHU*2/3/ND643//2*PRL/2*PASTOR/4/2*KACHU/DANPHE
56	EBW192363	FRNCLN/NIINI #1//FRANCOLIN #1/3/BORL14
57	EBW192364	PAURAQ/NELOKI/3/WBLL1*2/BRAMBLING*2//BAVIS
58	EBW192369	MUCUY/3/SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
59	EBW192370	KACHU/DANPHE/3/KACHU//KIRITATI/2*TRCH
60	EBW192371	KACHU/DANPHE/3/KACHU//KIRITATI/2*TRCH
61	EBW192375	KACHU/DANPHE/3/KACHU//KIRITATI/2*TRCH
62	EBW192377	KACHU/DANPHE/3/KACHU//KIRITATI/2*TRCH
63	EBW192380	KACHU/DANPHE/3/KACHU//KIRITATI/2*TRCH
64	EBW192382	KACHU/DANPHE/3/KACHU//KIRITATI/2*TRCH
65	ETBW9080	KACHU//WHEAR/SOKOLL

No	Genotype	Pedigree
66	ETBW9172	ND643/2*WBLL1//KACHU
67	ETBW9396	BOUSHODA-1/4/CROC-1/AE.SQUARROSA (205)//KAUZ/3/SASIA
68	ETBW9452	REBWAH-19/HAAMA-14
69	ETBW9578	NAVJ07/SHORTENED SR26 TRANSLOCATION/3/ATTILA/BAV92//PASTOR
70	ETBW9581	KSW/SAUAL//SAUAL/3/REEDLING #1= KASUKO
71	Hawi	Hawi
72	Kakaba	Kakaba
73	Kingbird	Kingbird
74	Ogolcho	Ogolcho
75	Tesfa	Tesfa

## 2.2. Statistical Analysis

The mixed linear model's matrix structure was used for the statistical analysis with R software. When utilizing a linear mixed model and the standard structure to analyze multi-environment trial (MET) data analysis, there are many possible forms of genetic variance matrix structures. This implies that all environments have constant genetic variance and all pairs of environments have the same genetic covariance. In this scenario, due to inefficient estimation, consider using an alternative variance structure model which is known as the Factor Analytic model which is analogous to the AMMI model. Furthermore, this model explains the nature of heterogeneous variance-covariance structures. To build a linear mixed model in this study, spatial field trend was first fitted for each environment and tested for the potential existence of field trend between the neighbor plots. Moreover, global variability and extraneous variation have been checked and included in the standard linear mixed model. Finally, trials across environments are combined keeping their specific trial information like spatial field trends, and included in a linear mixed model through a factor analytic model. The comparison of means was carried out using the BLUP predictors (best linear unbiased prediction) that represent the predicted value for each genotype concerning the general means [5]. The BLUP pair grain yields were ordered in descending order to identify the genotypes or superior lines. This methodology allowed comparing free genetic values of environmental effects and not the phenotypic means to improve genetic gain in the subsequent election cycle.

## 3. Results and Discussion

Multi-location trial analysis of this study identified the relative genetic merits of different genotypes where trials are

correlated. According to the summary data (Table 6), the average performance of all genotypes at 20BWNE1DR is greater (5.93 t/ha) than in other trials, whereas the potential of the 21BWNE2GR trial is lower (1.88 t/ha). Looking at the performance of each genotype and the rank change across testing conditions is critical for selection in a multi-environmental breeding program. When trials are correlated (similar response of genotypes in one environment), choosing the best material in one environment is the same as choosing the best material in another. The information from numerous environments may then be integrated to increase the accuracy of genetic gains in specific experiments. In this scenario, MET analysis can also aid in comprehending the wide and particular adaptation of genotypes across a variety of target populations. As a result, the reaction of these genotypes in their various environments is used to decide genotype selection for the next trial or release. The predicted GxE variance may be used to identify correlated environments, and breeders can choose genotypes using BLUPs averaged over associated environments.

### 3.1. Factor Analysis

Genetic parameter estimates increased significantly when GE interactions were modeled using FA models in combination with models accounting for regional differences, according to MET data. Not only were the FA models effective for estimating and forecasting GEI effects, but they were also beneficial for calculating GEI variance and doing bi-plot analysis. Table 2 displays the factor analysis's results. It comprises the total percentage of (GEI) variance explained by the model's factor components for each environment. FA model implies that the trial is not as well correlated as some of the other trials [6]. The environment 20BWNE1SK poorly contributed to the GEI variance and poorly correlated with the rest of the environments.

These groupings helped pick superior bread wheat varieties

within each cluster. These groupings helped pick superior bread wheat varieties within each cluster. Utilizing average BLUPs as a selection indicator, assuming that the formed clusters were sufficiently justified for carrying out genotype selection separately for each of the clusters, genotype selection was carried out independently for each of the clusters using average BLUPs as a selection indicator. Because it formed with a relatively high correlation and covered more environments, just one cluster was chosen for the complete

variety selection. The second and third clusters, on the other hand, have been found with fewer environments.

The largest clusters for the 12 environments are clustering one and two (Figure 1). Utilizing average BLUPs as a selection indicator, assuming that the formed clusters were sufficiently justified for carrying out genotype selection separately for each of the clusters. Because it formed with a relatively high correlation and covered more environments, just one cluster was chosen for the complete variety selection.

Table 3. Results from fitting the FA model.

SN	Environments	Factor1	Factor2	Factor3	Factor4	Total
1	20BWNE1AA	89.28	0.64	1.64	0.02	91.58
2	20BWNE1AT	24.02	38.4	1.24	0.63	64.28
3	20BWNE1DR	33.87	65.70	0	0.43	100
4	20BWNE1KU	62.68	4.25	0.87	2.04	69.85
5	20BWNE1MK	16.76	66.21	0.14	0.49	83.6
6	20BWNE1SK	0.18	0.47	0.01	5.24	5.90
7	20BWNE2AA	82.80	5.60	7.84	3.76	100
8	20BWNE2AB	3.42	43.85	6.13	46.6	100
9	20BWNE2AT	31.77	15.98	43.84	8.40	100
10	20BWNE2DR	37.19	1.04	47.87	1.32	87.42
11	20BWNE2GR	0.28	50.03	0.83	48.86	100
12	20BWNE2KU	99.69	0.14	0.07	0.10	100
13	20BWNE2MK	38.74	43.35	13.03	4.89	100

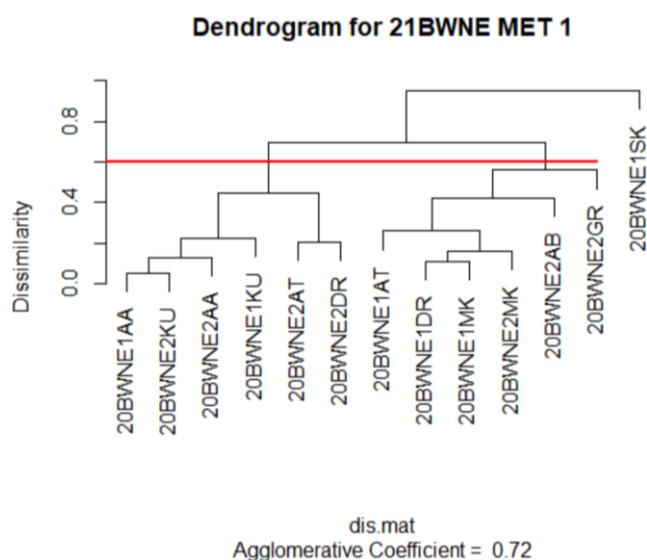


Figure 1. Dendrogram of the dissimilarity matrix.

Genetic correlation matrix - 21BWNE MET 1

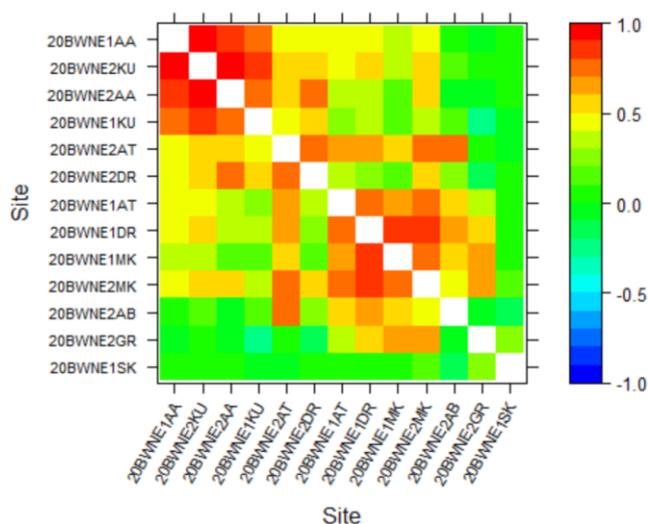


Figure 2. Heat map representation of the genetic correlation matrix.

In addition to the dendrogram, a heat map showing the genetic relationship among all trials was another popular feature analysis summary. The correlations between environments varied from -1 to 1. **Figure 2** indicates the various correlation patterns between environments. The heat map shows that there were some trials with positive genetic correlations, such as 20BWNE1AA having a positive correlation with 20BWNE2AA and 20BWNE2KU and also 20BWNE2KU has a positive correlation with 20BWNE1KU and 20BWNE2AA. This showed that genotype selection may be achieved by averaging genotype means in the first two trials in the first red cluster. There were also some trials with negative genetic correlations, such as 20BWNE2GR, having a negative correlation with 20BWNE1KU and 20BWNE2DH and 20BWNE1SK having a negative correlation with 20BWNE2AB. These suggest that there may have been a reversal effect in genotype ranks among these negatively associated trials. Based on the closeness in terms of discriminating the genotypes, the 13-bread wheat environments were clustered into three mega environments (C1, C2, and C3) for trait yield, where 20BWNE2KU, 20BWNE1AA, 20BWNE2AA, 20BWNE1KU, 20BWNE2AT and 20BWNE2DR were in C1;

20BWNE1AT, 20BWNE1DRH, 20BWNE1MK, 20BWNE2MK, 20BWNE2AB and 20BWNE2GR in C2; 20BWNE1SK in C3.

### 3.2. Variance Components

**Table 5** displays the genetic variance and error variance for each environment from the final fitted Spatial +FA models. For genetic variance, the estimates for variance component parameters ranged from 0.069 to 2.896 and error variance ranged from 0.175 to 1.002. Except one trial, all trials had a larger genetic variance for yield. This suggested that the genotype discriminating capacity of 20BWNE2GR was not lower. This environment highly low moisture stress area and all genotypes performed poorly or equally. Thus, we removed the BLUPs from this environment when averaged over others to choose superior genotypes. In general, using spatial and FA models to analyze MET data improved genotype evolution precision and accuracy by capturing non-genetic variation associated with agricultural field experiments and appropriately exploiting the information stored in the MET dataset [6, 18].

**Table 4.** Genetic correlation between environments.

	20AA	20AT	20DR	20KU	20MK	20SK	21AA	21AB	21AT	21DR	21GR	21KU	21MK
20AA													
20AT	0.40												
20DH	0.49	0.79											
20KU	0.76	0.28	0.30										
20MK	0.33	0.70	0.89	0.14									
20SK	0.03	0.05	0.07	-0.01	0.09								
21AA	0.84	0.32	0.33	0.77	0.18	0.07							
21AB	0.10	0.58	0.69	0.13	0.56	-0.10	-0.05						
21AT	0.42	0.62	0.67	0.47	0.51	-0.01	0.55	0.73					
21DR	0.50	0.32	0.28	0.59	0.13	0.00	0.75	0.30	0.79				
21GR	0.00	0.40	0.56	-0.21	0.65	0.21	-0.01	-0.02	0.05	-0.18			
21KU	0.95	0.47	0.55	0.80	0.38	0.03	0.90	0.18	0.54	0.60	0.01		
21MK	0.49	0.74	0.88	0.36	0.79	0.13	0.56	0.49	0.79	0.54	0.62	0.58	

**Table 5.** Variance component results in MET analysis using spatial and FA models.

SN	Environments	Mean GYD (t/ha)	Genetic Variance	Error Variance
1	20BWNE1AA	4.726	2.896	0.743
2	20BWNE1AT	3.101	0.206	0.257
3	20BWNE1DR	5.92	0.417	0.379
4	20BWNE1KU	2.212	0.239	0.189

SN	Environments	Mean GYD (t/ha)	Genetic Variance	Error Variance
5	20BWNE1MK	2.929	0.599	0.305
6	20BWNE1SK	3.786	0.088	0.19
7	20BWNE2AA	4.089	0.875	0.175
8	20BWNE2AB	3.925	0.095	0.305
9	20BWNE2AT	2.891	0.069	1.002
10	20BWNE2DR	3.178	0.254	0.556
11	20BWNE2GR	1.82	0.114	0.838
12	20BWNE2KU	4.175	1.987	0.237
13	20BWNE2MK	2.282	0.11	0.924

Where GYD: Grain Yield

### 3.3. BLUPs for Genotypes Mean Values Across Environments

Best linear unbiased prediction (BLUP) is a typical approach for estimating random effects in a mixed model that has the feature of least mean square error of prediction and can produce a more accurate assessment of the underlying effects. In a plant breeding environment where genotype ranking accuracy is critical for the selection of superior genotypes, genotype effects are generally fitted as random variables. This is especially important in the early phases of genotyping trials with a high number of entries. BLUP values of averaged across correlated environments graded C1 and C2 can be used to score genotype performance; C3 is eliminated

due to low genetic variation and genetic correlation with the other environments. Table 5 shows that among the 75 genotypes, more than 57.33% (43) had average grain yields more than 3.44 t/ha (grand mean). Eight candidate genotypes with mean grain yields of more than 4 t/ha were identified by the predicted mean grain yield, however two of these, genotypes (EBW192350 and EBW192369) have been advanced to variety verification trials for further testing before release as new variety (Table 6). Additionally, 20BWNE1DR and 20BWNE1AA environments and 20BWNE2KU and 20BWNE2AA environments produced high grain yields, according to BLUP analysis. This implies 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.

**Table 6.** BLUPs for genotype means across two clusters (C1 and C2) of correlated environments.

Genotype	20AA	20AT	20DR	20KU	20MK	21AA	21AB	21AT	21DR	21GR	21KU	21MK	Mean
Atlas	3.98	3.06	6.32	1.79	3.63	3.24	4.16	2.88	2.99	2.15	3.09	2.36	3.30
Balcha	8.00	2.87	5.84	3.11	2.35	6.00	3.87	3.04	4.02	1.37	6.89	2.25	4.13
EBW120086	4.68	2.91	5.59	2.33	2.64	4.31	3.61	2.66	3.09	1.96	4.15	2.13	3.34
EBW120104	2.59	3.07	5.45	2.01	2.46	3.65	3.69	2.74	3.15	2.07	2.61	2.17	2.97
EBW120105	2.15	3.00	5.20	1.79	2.03	3.26	3.76	2.68	2.95	1.79	2.28	1.94	2.74
Deka	7.09	2.83	5.81	2.52	2.58	5.05	3.59	2.71	3.25	1.92	5.47	2.22	3.75
EBW120101	4.21	2.43	5.04	2.04	1.77	2.84	3.48	2.12	1.82	1.64	3.15	1.45	2.67
EBW120106	3.31	2.70	4.95	2.00	1.83	3.78	3.66	2.71	3.29	1.61	2.78	1.89	2.88
EBW120109	2.34	2.80	5.67	1.71	2.82	2.52	4.00	2.66	2.71	1.97	1.84	2.01	2.75
EBW120110	5.75	3.15	5.82	2.75	2.39	5.00	3.82	2.95	3.69	1.79	5.04	2.31	3.71
EBW120111	6.23	3.21	6.05	2.72	3.23	4.71	3.82	2.81	3.27	1.90	5.22	2.27	3.79
EBW120115	3.48	2.53	5.43	1.70	2.37	2.48	3.85	2.38	2.12	1.69	2.58	1.66	2.69

Genotype	20AA	20AT	20DR	20KU	20MK	21AA	21AB	21AT	21DR	21GR	21KU	21MK	Mean
EBW120116	1.45	2.52	4.67	1.59	1.41	2.54	3.74	2.53	2.85	1.51	1.23	1.60	2.30
EBW120118	2.26	3.28	5.79	1.82	2.59	2.72	4.28	2.93	3.21	1.75	2.01	2.10	2.90
EBW120125	1.89	2.62	5.11	1.56	2.15	2.89	3.88	2.67	3.00	1.62	1.93	1.82	2.60
EBW120126	2.58	2.88	5.43	2.14	2.34	3.11	4.16	2.87	3.24	1.45	2.59	1.91	2.89
EBW120135	4.89	3.18	6.41	2.49	3.57	3.68	4.03	2.72	2.74	2.09	4.39	2.26	3.54
EBW120137	2.43	2.80	5.30	1.87	2.19	2.96	3.91	2.65	2.92	1.64	2.37	1.84	2.74
EBW120149	2.07	2.68	5.27	1.67	2.45	2.59	3.86	2.52	2.55	1.71	2.04	1.76	2.60
EBW120152	3.59	2.56	4.77	1.98	1.17	2.89	3.90	2.51	2.79	1.04	2.73	1.40	2.61
EBW172060	5.64	3.25	6.16	2.15	2.83	4.15	4.07	2.94	3.40	1.88	4.35	2.32	3.60
EBW172600	6.46	3.37	6.64	2.32	3.80	3.95	4.11	2.79	2.78	2.08	5.00	2.34	3.80
EBW172604	5.48	3.06	6.05	2.07	3.60	4.02	3.79	2.65	2.95	2.06	4.43	2.19	3.53
EBW172608	6.70	4.06	7.23	2.25	4.60	4.67	4.25	3.11	3.49	2.39	5.67	2.81	4.27
EBW172619	5.71	3.40	6.35	2.39	3.41	4.25	3.97	2.83	3.08	2.06	4.81	2.36	3.72
EBW172620	5.92	3.29	6.32	2.57	3.00	4.35	4.17	2.96	3.29	1.74	5.10	2.29	3.75
EBW172627	5.52	3.13	5.97	2.18	2.69	4.36	3.83	2.83	3.36	2.00	4.37	2.30	3.55
EBW172709	5.37	2.98	6.08	2.30	3.09	4.09	3.75	2.62	2.67	2.08	4.62	2.19	3.49
EBW172713	4.97	2.68	5.48	1.93	2.39	3.97	3.60	2.57	2.82	1.90	3.83	2.00	3.18
EBW172714	5.09	3.09	5.79	2.02	2.78	4.46	3.70	2.75	3.21	2.00	4.41	2.24	3.46
EBW172771	5.85	3.61	6.31	2.13	3.47	4.09	3.88	2.73	2.88	2.15	4.62	2.32	3.67
EBW172779	5.87	3.84	6.98	2.31	3.90	4.62	4.43	3.27	3.67	2.05	5.32	2.73	4.08
EBW172797	5.23	3.32	6.57	1.95	3.62	4.57	4.00	2.99	3.43	2.28	4.84	2.61	3.78
EBW172803	5.52	3.55	6.95	2.74	4.06	3.83	4.41	3.00	3.03	2.02	4.94	2.47	3.88
EBW172827	6.10	3.65	6.61	2.27	3.76	4.45	4.22	3.07	3.52	1.98	5.07	2.51	3.93
EBW172828	5.58	3.18	6.47	2.58	3.62	4.59	4.17	3.06	3.50	1.90	5.17	2.46	3.86
EBW172831	6.68	3.52	6.47	2.67	3.28	4.31	4.09	2.81	3.00	1.85	5.51	2.26	3.87
EBW174102	5.07	3.65	6.53	2.26	3.21	3.88	4.30	3.03	3.27	1.96	4.30	2.43	3.66
EBW174116	7.04	3.85	7.12	2.33	4.39	4.29	4.13	2.89	2.92	2.42	5.47	2.65	4.13
EBW174302	3.63	3.30	6.27	1.99	3.13	3.10	4.40	2.97	3.15	1.77	3.23	2.22	3.26
EBW174334	4.49	3.42	6.43	1.72	3.10	4.68	4.13	3.10	3.50	1.98	4.96	2.54	3.67
EBW174371	3.51	3.05	5.97	2.04	2.99	3.28	4.00	2.74	2.81	2.00	3.15	2.16	3.14
EBW174374	2.56	2.75	6.04	1.55	3.31	2.79	4.05	2.76	2.79	2.20	2.23	2.24	2.94
EBW174388	3.19	2.60	5.90	1.76	2.76	3.15	3.96	2.73	2.84	2.06	2.78	2.16	2.99
EBW174389	4.62	3.06	5.63	2.12	2.48	3.84	3.81	2.72	3.03	1.82	3.68	2.07	3.24
EBW174413	3.84	3.00	5.61	1.93	2.71	3.54	3.95	2.81	3.16	1.79	3.08	2.08	3.13
EBW174425	2.20	3.06	6.39	1.61	3.84	3.01	3.90	2.75	2.59	2.71	2.27	2.53	3.07
EBW192349	5.55	3.44	6.68	2.37	3.88	5.10	4.04	3.17	3.64	2.30	5.26	2.79	4.02
EBW192350	7.54	3.37	6.52	2.86	3.55	6.08	3.91	3.17	4.00	2.02	6.78	2.71	4.38
EBW192351	6.06	3.04	6.10	2.94	3.01	5.29	3.84	2.98	3.65	1.88	5.69	2.42	3.91
EBW192352	5.44	3.24	6.14	2.52	2.99	4.86	4.02	3.07	3.73	1.86	4.99	2.44	3.78

Genotype	20AA	20AT	20DR	20KU	20MK	21AA	21AB	21AT	21DR	21GR	21KU	21MK	Mean
EBW192353	7.26	3.09	6.04	2.73	2.71	4.81	3.87	2.78	3.27	1.70	5.78	2.16	3.85
EBW192357	5.01	2.38	5.00	2.67	1.86	4.86	3.56	2.75	3.64	1.45	4.50	1.92	3.30
EBW192360	6.65	2.91	5.46	3.04	2.28	5.15	3.75	2.84	3.61	1.40	5.56	2.02	3.72
EBW192361	5.55	2.94	5.54	2.13	2.25	4.61	3.63	2.71	3.23	1.79	4.65	2.09	3.43
EBW192363	3.91	3.56	6.37	2.42	3.31	3.70	4.30	3.08	3.40	1.97	3.60	2.44	3.51
EBW192364	5.53	3.03	6.09	2.62	2.76	4.70	4.14	3.13	3.84	1.71	4.80	2.39	3.73
EBW192369	6.08	3.72	6.47	3.12	3.32	5.75	3.98	3.21	4.00	2.02	6.11	2.72	4.21
EBW192370	6.26	2.73	5.51	2.72	2.20	5.02	3.64	2.85	3.64	1.77	4.81	2.21	3.61
EBW192371	5.77	2.46	5.34	2.70	1.68	4.70	3.82	2.82	3.50	1.33	4.89	1.94	3.41
EBW192375	5.81	2.85	5.36	2.48	2.10	4.95	3.61	2.80	3.55	1.66	4.77	2.10	3.50
EBW192377	5.81	2.50	4.88	2.54	1.47	4.90	3.50	2.69	3.52	1.37	4.64	1.83	3.30
EBW192380	5.65	2.90	5.62	2.31	2.45	4.94	3.71	2.89	3.69	1.81	4.71	2.26	3.58
EBW192382	6.07	2.69	5.28	2.65	1.79	5.05	3.57	2.74	3.39	1.56	5.09	2.01	3.49
ETBW9080	6.33	3.52	6.47	3.02	3.33	5.26	4.26	3.30	4.04	1.77	5.69	2.61	4.13
ETBW9172	5.74	3.15	6.39	2.83	3.27	4.72	4.07	3.02	3.58	1.96	5.18	2.47	3.87
ETBW9396	6.76	3.50	6.47	2.16	3.04	4.46	4.01	2.86	3.24	2.02	5.31	2.38	3.85
ETBW9452	5.85	3.80	6.57	2.29	3.48	4.35	4.02	2.92	3.02	2.21	4.85	2.51	3.82
ETBW9578	6.38	3.12	6.53	2.98	3.71	4.68	4.14	2.97	3.33	1.85	5.70	2.40	3.98
ETBW9581	5.91	3.38	6.05	2.66	3.56	4.99	3.74	2.88	3.54	2.08	5.10	2.43	3.86
Hawi	1.48	2.89	5.57	1.50	2.95	2.93	3.86	2.79	3.09	2.20	1.50	2.22	2.75
Kakaba	3.25	3.39	6.18	1.66	3.46	3.17	4.24	2.94	3.13	2.00	2.86	2.30	3.22
Kingbird	4.81	3.05	5.61	2.26	2.51	4.10	3.76	2.75	3.34	1.85	3.85	2.12	3.33
Ogolcho	0.65	1.86	4.13	0.92	1.45	2.15	2.89	1.88	1.72	2.16	0.29	1.40	1.79
Tesfa	3.34	2.90	5.97	1.73	3.26	3.04	4.11	2.78	2.85	1.91	2.90	2.12	3.08
Mean	4.84	3.08	5.93	2.25	2.87	4.09	3.92	2.83	3.20	1.88	4.15	2.22	3.44

Where 20AA: 2020 Asasa, 20AT: 2020 Alemtena, 20DR: 2020 Dhera, 20KU: 2020 Kulumsa, 20MK: 2020 Melkasa, 21AA: 2021 Asasa, 21AB: 2021 Ambo, 21AT: 2021 Alemtena, 21DR: 2021 Dhera, 21GR: 2021 Goro, 21KU: 2021 Kulumsa, 21MK: 2021 melkasa.

## 4. Conclusion

Multi-location trials of genotype  $\times$  environmental interaction are an important consideration for crop breeding that combines both yield and stability attributes. High-yielding genotypes should be chosen in the environment. The production of newly released varieties requires a selection from a larger range of candidate genotypes, therefore evaluating genotypic values is crucial to every breeding effort. Depending on the purpose, this allows for the isolation of the genetic influence or a deeper investigation of the GEI effect. From 75 tested genotypes, 43 (57.33%) genotypes average grain yields showed more than grand mean (3.44 t/ha). The genotypes with the highest poten-

tial for future verification and release as a variety may be identified. As a result, the ETW192350 and ETW192369 genotypes were superior yielding and stable from the others. Thus, these two genotypes are advanced to variety verification trials for further testing and release as new varieties.

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## Conflicts of Interest

The authors declare no conflicts of interest.

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