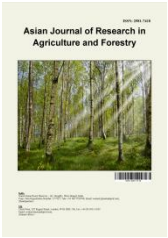

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Evaluation of Bread Wheat (*Tritium aestivum* L.) Genotype in Multi-environment Trials Using Enhanced Statistical Models

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

In varietal selection field trials, spatial variation and genotype by environment (GxE) interaction are frequent and present a major challenge to plant breeders comparing the genetic potential of several cultivars. To consistently select superior cultivars that increase agricultural production, bread wheat breeding studies must be evaluated using efficient statistical techniques. By modeling the interactions of geographical field trends and genotypes by environment interaction, this work aimed to forecast the genetic potential of bread wheat varieties across settings and improve selection tactics. The dataset utilized in this investigation consisted of sixteen multi-environment trials (MET) that were carried out using a randomized complete block design (RCBD), with two replications arranged in plot arrays of rows and columns. The findings showed that the factor analytical and spatial models were effective ways to analyze the data for this study under the linear mixed model. By ranking average Best Linear Unbiased Predictions (BLUPs) within clusters, the 16 bread wheat environments were grouped into three mega environments (C1, C2, and C3) based on yield. This served as a selection indicator. Ranking average BLUPs helped in the selection of superior and stable genotypes. The first cluster (C1)'s mean BLUP values were used to score the genotypes' performance; C2 and C3 were excluded because of their limited genetic variety and low genetic connection with the other trials. The genotypes with the highest potential based on this cluster were EBW192346 and EBW192347, chosen for a subsequent verification study to release a variety. The estimates for variance component parameters ranged from 0.013 to 3.024 for genetic variance and from 0.072 to 0.37 for error variance. Hence, scaling up the use of this efficient analysis method will improve the selection of superior bread wheat varieties.

Keywords: Average yield; BLUPs; cluster; factor analytic; genetic variation; spatial; target environment.

1. INTRODUCTION

Wheat (*Triticum aestivum* L.) is grown in an extensive range of agroecosystems, and Ethiopia has enormous potential and ideal agroecosystems for growth [1]. The majority of Ethiopia's wheat-growing regions are located between mid-altitude (1900-2300 m a.s.l) and high altitude (2300-2700 m.a.s.l), where rainfall is ample and consistent [2]. Both studies, like Abebe et al. [3], and Gadisa et al. [4] found that Ethiopia's highlands and mid-altitudes are key wheat producers. Wheat provides more nutrition globally [5,6], and is used as a key source of calories [7]. Wheat's popularity is due to the wide variety of culinary products that can be made from it, which helps to explain why it is now being grown in places where it was not previously grown [5,8].

Global yield per unit area has increased significantly as a result of new wheat varieties [9]. Researchers are now working on crop breeding that combines stability with yield to develop stable and high-yield genotypes in which both yield and stability traits are examined concurrently in addition to lowering genotype interaction [10]. High-yield genotypes should be chosen in the environment [11]. Because the production of new cultivars and the endorsement of newly released varieties necessitate a greater variety of Candidate genotypes, evaluating genotypic values is crucial to every breeding endeavor [10].

Plant breeders face a great deal of difficulty in assessing the genetic potential of various cultivars because of the prevalence of spatial variation and GxE interaction in varietal selection field trials. Efficient techniques that account for more complicated environmental variation necessitate the use of appropriate models of analysis [12,13]. Spatial analysis is a type of analysis in which the variance of each trial is investigated and a suitable structure is utilized to estimate the effects of the trial. This method, rather than eliminating the requirement for proper experimental design, increases it because once a treatment effect is confused with an ambient effect, the two cannot be separated [14]. Smith et al. [15,16] extended the GGE analysis using factor-analytic multiplicative mixed models. Its importance in estimating the related variance structure for GxE effects is an important component of the factor analytic model for multi-environment trial data, because it provides a good and sparse approximation to the unstructured form and is generally more computationally robust [17].

The breeding values of genotypes evaluated across multiple environments, estimated by best linear unbiased prediction (BLUPs) from mixed models can be employed in the selection process [18]. Bernardo [19] stated the two advantages of BLUPs: they allow the comparison of genotypes evaluated in different sets of environments and they allow the use of information on relatives. The environment in which a breeding line completes its life cycle determines whether it can realize the full potential of its genotype [20]. The application of efficient statistical models to provide accurate and enlightening findings has enhanced MET data analysis, which has a long history with older statistical approaches like as the analysis of variance [16,21,22]. As a result, it's critical to assess bread wheat genotypes using more efficient statistical methods and mixed model approaches. The primary goal of this work was to predict bread wheat genetic potential across environments and enhance selection strategies by modeling the interactions of spatial field trends and GEI.

2. MATERIALS AND METHODS

2.1 Description of Eco-Location and Genotypes

A study was undertaken by using germplasm of different genetic backgrounds to determine their level of GE in their biological yield responses. 90 bread wheat advanced breeding genotypes including check varieties were evaluated each over two seasons between 2020 and 2021 at 8 (Adet, Asasa, Bekoji, Holeta, Sinana, Robe Arsi, Dabra Markos, and Dabra Zeit) locations resulting in 16 environments (environment was considered as the combination of years and locations). The test genotypes were derived from the National Variety Trial (NVT) tested at potential environments. The trial was carried out by randomized complete block design (RCBD) laid out in a rectangular (row x column) array of plots with two replications. In row-column designs the experimental units were grouped in two directions, i.e., two blocking factors were used with one factor representing the rows of the design and the other factor representing columns. Each genotype was planted on six rows of 2.5m long in 20cm between row spacing. The trial was included in this study with their respective row, column, and genotypes in each trial (Table 1). Production was all under rain-fed conditions. The geographic information of testing sites is presented in Table 1.

2.2 Statistical Analysis

For the statistical analysis, the matrix structure of the mixed linear model was applied using the R software. In multi-environment trial (MET) data analysis, there are many possible forms of genetic variance matrix structures while using a linear mixed model and the standard structure. While fitting a linear mixed model in this study, spatial field trend fitted first for each environment and tested for the potential existence of field trend between the neighbor plots. 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 mean [23]. The BLUP pair grain yields were ordered in descending order to identify the genotypes or

Table 1. List of test environments, number of genotypes used, and their respective geographic information

Site	Environment	No Genotype	Row	Column	No Rep	Latitude	Longitude	Altitude
Arsi Robe	20BWNL1RA	90	18	10	2	07º53'02"N	39º37'40"E	2420
Arsi Robe	20BWNL2RA	90	18	10	2	07º53'02"N	39º37'40"E	2420
Asasa	20BWNL1AA	90	18	10	2	07º07'09"N	39º11'50"E	2340
Asasa	20BWNL2AA	90	18	10	2	07º07'09"N	39º11'50"E	2340
Bekoji	20BWNL2BE	90	18	10	2	07º32'37"N	39º15'21"E	2780
Bekoji	20BWNL1BE	90	18	10	2	07º32'37"N	39º15'21"E	2780
Dabra Markos	20BWNL1DM	90	18	10	2	10° 19′59″N	37°44′53″E	2450
Dabra Markos	20BWNL2DM	90	18	10	2	10° 19′59″N	37°44′53″E	2450
Dabra Zeit	20BWNL1DZ	90	18	10	2	08°38'N	38°30'E	1900
Dabra Zeit	20BWNL2DZ	90	18	10	2	08°38'N	38°30'E	1900
Holeta	20BWNL1HL	90	18	10	2	09°03′41″N	38°30′44″E	2400
Holeta	20BWNL2HL	90	18	10	2	09°03′41″N	38°30′44″E	2400
Kulumsa	20BWNL1KU	90	18	10	2	08º01'10"N	39º09'11"E	2200
Kulumsa	20BWNL2KU	90	18	10	2	08º01'10"N	39º09'11"E	2200
Sinana	20BWNL1SN	90	18	10	2	7°7’N	39°49'E	2450
Sinana	20BWNL2SN	90	18	10	2	7°7’N	39°49'E	2450

superior lines. This methodology allowed comparing free genetic values of environmental effects and not the phenotypic means to improve genetic gain in the subsequent selection cycle.

3. RESULTS AND DISCUSSION

This study identified the relative genetic merits of different lines or genotypes where trials were correlated. According to the summarized data (Table 4), the average performance of all genotypes at the 20BWNL1AA environment was greater (5.64 t/ha) than in all other trials. In contrast, the potential of the 20BWNL2BE environment trial was the lowest (1.28 t/ha). Looking at the performance of each genotype and the rank change across testing conditions is critical for selecting 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 narrow adaptation of genotypes across a variety of target environments. 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 [24].

3.1 Factor Analysis

MET data analysis revealed that modeling GE interactions with FA models in conjunction with models for geographical variations resulted in a considerable increase in genetic parameter estimations. Not only the FA models were effective for estimating and forecasting GEI effects, but they also were beneficial for calculating GEI variance and doing bi-plot analysis. The findings of the factor analysis are shown in Table 2. It comprises the total percentage of (GEI) variance explained by the model's factor components for each trial as well as the overall percentage of variance explained by the model's factor components for all trials. The FA models fit virtually all trials well, apart from 20BWNL1DZ, 20BWNL2DZ, 20BWNL1SN, 20BWNL2DM, and 20BWNL2AA, and the two-factor components well described the genetic variation. Overall, the factor analytic models' two multiplicative factors accounted for over 70% of the GxE variance, with the first multiplicative term accounting for about 72.79 percent. The inadequate fit of 20BWNL1DZ, 20BWNL2DZ, 20BWNL1SN, 20BWNL2DM, and 20BWNL2AA with the FA model implies that the trial is not as well correlated as some of the other trials [25].

A cluster analysis using a dendrogram, as shown in Fig. 1, was another important conclusion of component analysis, clustering trials based on genetic correlation. The dendrogram revealed that genotype rating was virtually the same for all trials detected inside these established clusters, but that trials discovered in other clusters had a separate genotype ranking [24]. As Diriba and Mekuria [26] reported when trials are correlated, the ranking of genotypes is similar so that the one best-performing genotype/s in a specific environment has similar performance with the one highly correlated environment. Using the dendrogram generated at the dissimilarity matrix we discovered three groups of correlated environments, which contributed to the selection of excellent bread wheat genotypes within each cluster. 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. This is also reported by Tesfaye et al. [24] on finger millet and Diriba and mekuria [26] on durum wheat. 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.

Aside from the dendrogram, additional popular factor analysis summaries a heatmap of the genetic relationships between all trials. The correlations between environments varied from -1 to 1. Correlations of -1 show that the performance of the environments falls in the opposite direction (the angle between the two environments is more than 90 degrees), meaning that the top-performing genotypes in one environment were the lowest-performing genotypes in the other. A correlation of +1 indicates a full correlation between two environments; hence, selecting superior genotypes based on one environment is the same as selecting another. This is seen in Fig. 2, which depicts the various correlation patterns

between trials. The heatmap shows that most of the trials were highly correlated. This showed that genotype selection may be achieved by averaging genotype means over almost all trials in the first red cluster. There were also some trials with negative genetic correlations, such as 20BWN1HL having a negative correlation with 20BWN2AR and 20BWN2SN and 20BWN1DM having a negative correlation with 20BWNL2BE (Table 3), suggesting that there may have been a reversal effect in genotype ranks among these negatively associated trials. Generally, correlations ranged from negative to positive on both sides. Based on the closeness in terms of discriminating the genotypes, the 16-bread wheat environments were clustered into three mega environments (C1, C2 and C3) for yield, where 20BWNL1AA, 20BWNL2KU, 20BWNL1RA, 20BWNL2RA, 20BWNL2SN, 20BWNL1BE, 20BWNL2BE, 20BWNL1SN, 20BWNL1KU, 20BWNL2HL, 20BWNL2DM, 20BWNL2AA and 20BWNL1DZ were in C1; 20BWNL1DM in C2; and 20BWNL1HL and 20BWNL2DZ were in C3 using a dendrogram (Fig. 1) and heat-map (Fig. 2) as well as the genetic correlation from Table 3. To choose superior and stable types, an average of BLUPs was utilized as a selection indicator by ranking average BLUPs within clusters.

Table 2. Results from fitting the FA model

Environments	Factor1	Factor2	Factor3	Factor4	Factor5	Total
20BWNL1AA	97.78	0.01	0.03	2.15	0.03	100
20BWNL1BE	86.51	1.6	10.73	0.16	1	100
20BWNL1DM	4.21	75.43	13.68	0.64	6.03	100
20BWNL1DZ	35.34	0.5	3.35	14.45	2.63	56.27
20BWNL1HL	0.11	80.06	1.05	1.46	0.34	83.03
20BWNL1KU	69.61	24.48	0.49	5	0.42	100
20BWNL1RA	80.87	0.1	0.74	1.08	4.45	87.24
20BWNL1SN	65.59	0.41	1.16	0	1.32	68.48
20BWNL2AA	69.07	0.64	19.23	4.36	6.71	100
20BWNL2BE	70.57	2.22	11.1	4.53	0.71	89.13
20BWNL2DM	50.37	14.24	16.46	1.03	3.13	85.23
20BWNL2DZ	4.99	2.71	2.01	32.51	15.22	57.43
20BWNL2HL	66.43	30.63	0.01	2.63	0.3	100
20BWNL2KU	85.95	0.54	0.01	0.47	0.47	87.43
20BWNL2RA	85.99	4.31	0.55	2.99	6.17	100
20BWNL2SN	67.44	10.92	1.82	0.96	1.49	82.63

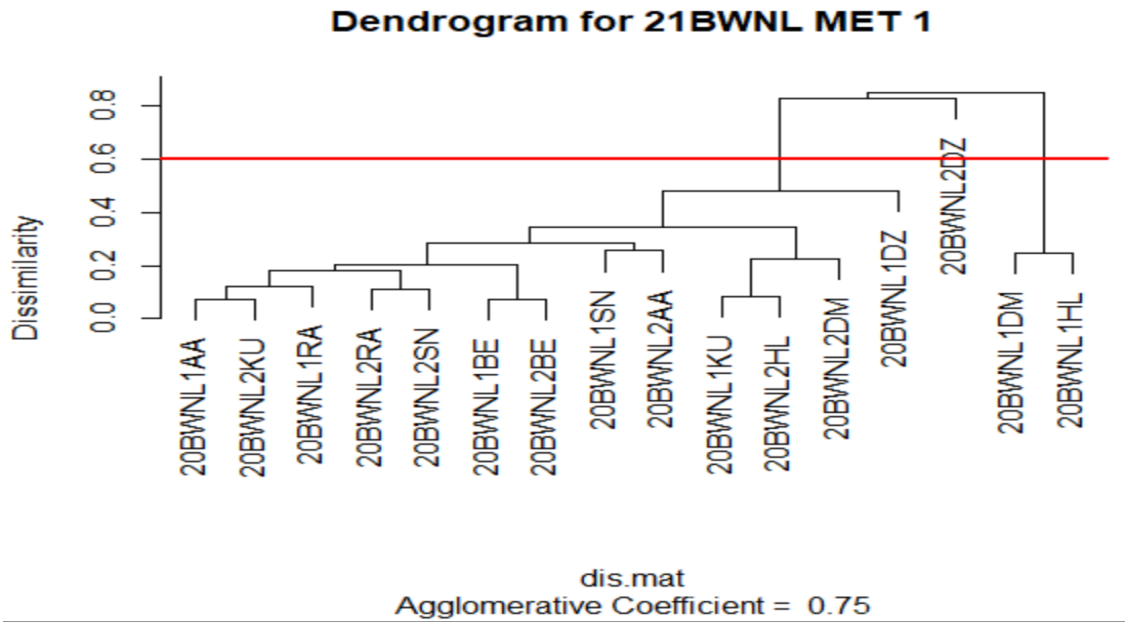

Fig. 1. Dendrogram of the dissimilarity matrix

Table 3. Genetic Correlation Between Environments

	20 AA	20 BE	20DM	20 DZ	20 HL	20 KU	20 RA	20 SN	21 AA	21 BE	21 DM	21 DZ	21 HL	21 KU	21 RA	21 SN
20AA																
20BE	0.91															
20DM	0.22	-0.07														
20DZ	0.54	0.53	0.06													
20HL	0.02	-0.05	0.75	-0.03												
20KU	0.86	0.72	0.61	0.35	0.45											
20RA	0.90	0.84	0.19	0.45	0.01	0.78										
20SN	0.81	0.74	0.12	0.52	-0.05	0.63	0.70									
21AA	0.80	0.65	0.32	0.69	0.06	0.64	0.63	0.74								
21BE	0.79	0.93	-0.12	0.54	-0.05	0.60	0.75	0.66	0.61							
21DM	0.72	0.46	0.68	0.40	0.32	0.78	0.64	0.58	0.73	0.37						
21DZ	0.32	0.16	0.19	-0.01	0.05	0.36	0.16	0.23	0.24	0.03	0.27					
21HL	0.79	0.70	0.62	0.52	0.54	0.91	0.69	0.63	0.77	0.64	0.76	0.20				
21KU	0.93	0.84	0.28	0.51	0.09	0.83	0.85	0.74	0.75	0.74	0.71	0.23	0.78			
21RA	0.89	0.85	0.08	0.61	-0.13	0.64	0.87	0.74	0.76	0.80	0.64	-0.01	0.66	0.85		
21SN	0.80	0.75	-0.05	0.55	-0.26	0.50	0.75	0.69	0.70	0.71	0.53	0.05	0.50	0.74	0.89	

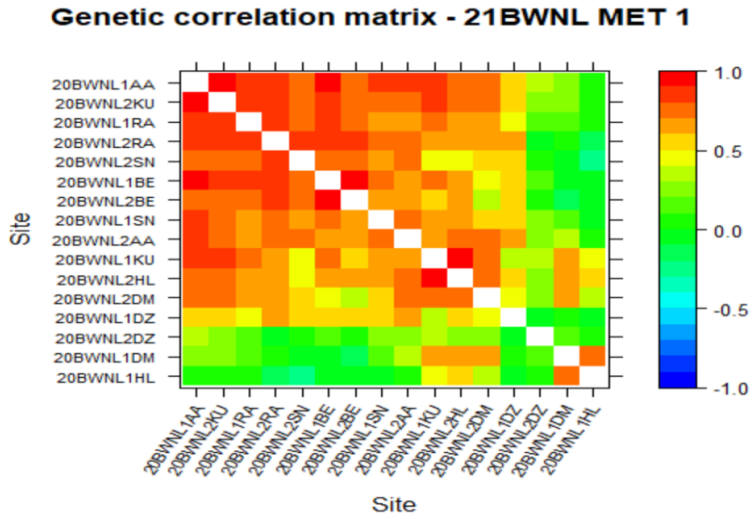

Fig. 2. Heat map representation of the genetic correlation matrix

Table 4. Variance component results in MET analysis using spatial and FA models

Environments	Mean GYLD	Genetic Variance	Error Variance
20BWNL1AA	5.64	3.024	0.294
20BWNL1BE	2.131	1.327	0.266
20BWNL1DM	2.77	0.133	0.37
20BWNL1DZ	1.58	0.013	0.109
20BWNL1HL	2.541	1.057	0.167
20BWNL1KU	3.176	0.502	0.213
20BWNL1RA	1.557	0.299	0.105
20BWNL1SN	1.768	0.783	0.118
20BWNL2AA	3.424	0.811	0.122
20BWNL2BE	1.268	0.801	0.072
20BWNL2DM	5.16	0.116	0.223
20BWNL2DZ	2.187	0.127	0.175
20BWNL2HL	2.4	0.772	0.11
20BWNL2KU	4.76	1.493	0.186
20BWNL2RA	3.006	0.848	0.245
20BWNL2SN	3.411	1.322	0.173

3.2 Variance Components

The genetic variance and error variance for each trial from the final fitted Spatial +FA models are presented in Table 4. The estimates for variance component parameters ranged from 0.013 to 3.024 for genetic variance and from 0.072 to 0.37 for error variance. except for five trials, all trials had a higher genetic variance for yield. This indicated that these testing locations had relatively high discriminating power for genotypes. Five of the sixteen trials had higher genetic variance for yield (20BWNL1AA, 20BWNL1BE, 20BWNL1HL, 20BWNL2SN, and 20BWNL2KU). This might be related to much greater rainfall levels and dispersion for Asasa, Bekoji, and Holeta in 2020, and Kulumsa and Sinana in 2021. This also highlighted the need to use meteorological data from a certain cropping season when proposing the optimal genotype for a given cropping season, as well as its wider use throughout the country's diverse agroecologies. Furthermore, the trials 20BWNL1KU, 20BWNL1RA, 20BWNL1DM, 20BWNL2DZ, and 20BWNL2DM were determined to be poor trials with little genetic variation, which might be related to low rainfall or drought in these environments. As a result, while averaging across trials for picking better genotypes, we excluded the BLUPs from these trials. 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 [25,27].

Table 5. BLUPs for genotype means across cluster 1 (C1) of correlated environments

Genotype	20AA	20BE	20DZ	20KU	20RA	20SN	21AA	21BE	21DM	21HL	21KU	21RA	21SN	Mean
Danda'a	5.36	2.27	1.59	2.96	1.61	1.06	3.04	1.09	4.93	2.12	4.87	3.09	3.47	2.88
EBW120002	5.60	1.89	1.49	3.92	1.53	1.41	3.31	1.16	5.34	3.36	5.08	2.63	2.35	3.01
EBW120004	5.19	1.60	1.46	3.49	1.32	1.84	3.05	0.65	5.26	2.69	4.31	2.64	2.27	2.75
EBW120011	3.97	1.23	1.58	2.75	1.06	1.53	3.14	1.02	5.13	2.38	3.53	2.50	2.36	2.48
EBW120014	5.38	1.57	1.55	3.23	1.53	1.93	3.49	0.59	5.34	2.49	4.83	3.02	3.10	2.93
EBW120039	4.31	1.25	1.54	2.43	1.18	1.30	3.37	0.55	4.92	1.74	3.38	2.48	2.90	2.41
EBW120041	1.93	0.29	1.40	2.20	0.43	0.47	1.74	0.25	4.50	1.40	1.89	0.78	0.73	1.39
EBW120042	4.05	1.70	1.54	3.21	1.01	1.37	3.13	1.03	4.92	3.05	3.50	1.70	1.44	2.43
EBW120044	2.50	0.90	1.48	2.21	0.76	0.52	1.65	0.76	4.63	1.41	2.83	1.81	2.19	1.82
EBW120052	1.25	0.02	1.43	1.36	0.23	0.33	1.54	-0.02	4.29	0.39	1.26	0.87	1.22	1.09
EBW120053	6.51	2.44	1.59	4.04	1.70	1.47	3.88	1.38	5.51	3.56	5.80	3.21	3.31	3.42
EBW120054	6.19	2.81	1.59	4.07	1.81	1.29	3.51	1.65	5.32	3.75	5.25	3.08	2.89	3.32
EBW120056	1.22	0.26	1.41	1.63	0.31	-0.11	0.90	0.21	4.23	0.53	2.12	0.89	1.26	1.14
EBW120060	4.56	1.20	1.50	3.24	1.35	1.62	2.71	0.71	5.13	2.37	4.43	2.44	3.14	2.65
EBW120063	5.26	2.09	1.55	2.74	1.49	1.66	3.06	1.33	4.96	1.80	4.32	3.21	3.66	2.86
EBW172056	3.97	0.98	1.43	2.49	1.29	0.84	2.26	0.27	4.82	1.11	3.03	1.87	1.95	2.02
EBW172082	5.14	1.52	1.55	2.62	1.45	1.40	3.56	0.93	5.17	1.77	4.05	3.14	4.58	2.84
EBW172088	8.19	3.72	1.66	4.25	2.57	3.38	4.21	2.63	5.69	3.70	6.65	4.83	5.53	4.39
EBW172093	8.37	4.09	1.58	4.07	2.85	2.30	3.72	2.89	5.41	2.99	6.14	4.40	4.41	4.09
EBW172105	7.22	2.58	1.64	3.92	1.85	2.24	4.31	1.35	5.66	3.25	5.90	3.73	3.96	3.66
EBW172319	5.60	1.33	1.41	3.71	1.65	1.50	2.76	0.47	5.38	2.36	4.74	2.46	3.10	2.81
EBW172393	3.74	0.46	1.62	2.14	0.93	1.12	3.72	0.29	5.19	1.63	3.62	2.55	3.34	2.33
EBW172440	6.41	2.83	1.57	3.38	1.72	1.59	3.52	1.96	5.20	2.53	5.58	3.34	3.64	3.33
EBW172474	7.57	3.93	1.62	4.06	2.22	1.94	3.41	2.39	5.12	3.14	5.67	3.53	4.15	3.75
EBW172862	7.74	3.76	1.63	3.51	2.55	2.59	4.14	2.57	5.35	2.84	6.50	4.73	6.02	4.15
EBW172864	7.98	4.54	1.72	3.69	2.00	2.17	4.42	3.62	5.20	3.41	6.72	4.53	4.68	4.21
EBW172872	5.31	1.97	1.51	3.04	1.43	1.36	2.97	0.95	5.03	1.99	4.36	2.67	2.65	2.71
EBW172936	6.92	3.26	1.61	3.27	2.15	2.77	3.56	2.07	5.07	2.18	5.34	3.44	4.28	3.53
EBW172996	2.15	0.17	1.50	1.73	0.84	0.07	2.16	0.28	4.74	1.01	2.04	2.04	2.58	1.64
EBW173001	6.37	2.09	1.54	3.38	1.70	2.12	3.86	1.05	5.32	2.40	5.57	3.05	4.04	3.27
EBW173004	3.20	0.75	1.54	1.84	0.79	0.50	3.02	1.15	4.77	1.24	3.86	2.45	2.62	2.13
EBW173006	2.42	0.22	1.46	1.73	0.68	0.53	2.12	0.18	4.70	0.69	2.61	1.70	1.94	1.61
EBW173031	6.17	2.73	1.59	3.15	1.90	0.73	3.10	1.54	5.08	2.08	4.95	3.49	4.22	3.13
EBW173207	5.92	2.34	1.56	3.11	1.75	2.26	3.55	1.19	5.10	2.23	4.68	3.01	3.77	3.11
EBW173261	3.05	0.47	1.56	1.75	0.74	0.98	3.01	0.30	4.75	0.98	2.67	2.00	3.20	1.96
EBW173263	4.91	1.26	1.58	2.48	1.25	1.62	3.69	0.67	5.09	1.66	4.43	2.99	4.55	2.78

Genotype	20AA	20BE	20DZ	20KU	20RA	20SN	21AA	21BE	21DM	21HL	21KU	21RA	21SN	Mean
EBW173270	5.55	1.78	1.63	3.19	1.33	2.35	3.82	0.96	5.26	2.56	4.79	2.83	3.63	3.05
EBW173288	6.74	2.44	1.55	4.32	2.03	1.10	3.57	1.42	5.59	3.59	6.04	3.13	3.04	3.43
EBW173292	7.44	3.24	1.63	4.20	1.93	1.84	4.46	2.14	5.52	3.95	6.34	3.85	4.45	3.92
EBW173332	5.66	2.80	1.60	2.72	1.92	1.27	3.31	2.31	5.08	2.13	4.63	4.07	4.53	3.23
EBW173353	8.67	4.61	1.71	4.45	2.59	4.39	4.39	3.82	5.55	4.17	7.39	4.92	4.66	4.72
EBW173366	5.71	1.95	1.53	4.13	1.74	1.95	3.18	0.97	5.44	3.57	5.09	2.79	3.15	3.17
EBW173378	5.97	2.89	1.57	3.25	1.62	1.58	3.10	1.86	5.00	2.42	4.87	3.20	3.32	3.13
EBW173380	6.80	1.89	1.55	4.11	2.09	1.47	3.75	0.80	5.78	3.20	5.50	3.60	3.56	3.39
EBW174116	7.23	3.55	1.57	3.58	1.79	2.63	3.46	2.16	5.10	2.41	5.54	3.11	3.16	3.48
EBW174170	2.61	0.70	1.36	1.97	0.78	0.56	1.71	0.33	4.43	0.77	2.13	1.40	1.27	1.54
EBW174187	4.80	2.03	1.49	2.74	1.15	1.97	2.86	0.99	4.83	1.85	3.96	2.50	2.75	2.61
EBW174456	4.00	0.94	1.45	2.61	1.11	0.84	2.12	0.33	4.82	1.18	3.98	1.95	2.04	2.11
EBW182052	7.57	3.56	1.49	3.61	2.24	3.12	3.39	1.93	5.21	2.36	5.81	3.96	5.54	3.83
EBW182122	4.93	1.45	1.56	2.66	1.47	1.77	3.31	0.84	5.11	1.81	4.02	3.14	4.05	2.78
EBW182146	5.77	2.75	1.61	2.77	1.82	0.92	2.91	1.84	4.94	1.76	5.18	3.79	3.73	3.06
EBW192318	6.46	2.56	1.61	3.12	1.77	1.93	3.58	1.51	5.22	2.03	5.46	3.45	3.79	3.27
EBW192319	6.72	2.92	1.62	3.69	1.75	1.92	4.14	1.94	5.40	3.29	5.59	3.52	3.98	3.58
EBW192320	6.99	2.23	1.70	3.75	1.73	2.65	5.16	1.21	5.72	3.56	5.73	3.63	3.74	3.68
EBW192321	6.44	2.33	1.58	3.46	1.57	2.12	4.08	1.30	5.25	2.74	5.39	3.13	3.48	3.30
EBW192322	6.47	2.25	1.68	3.66	1.73	3.04	4.42	1.51	5.49	3.35	5.50	3.58	3.89	3.58
EBW192323	6.61	2.85	1.69	3.30	1.69	2.51	4.37	1.72	5.28	2.90	5.57	3.67	4.23	3.57
EBW192324	5.71	2.17	1.67	2.88	1.37	1.97	4.39	1.74	5.19	2.55	4.75	3.15	3.04	3.12
EBW192325	5.50	2.24	1.64	2.69	1.29	1.95	3.88	1.56	4.99	2.15	4.73	3.24	3.83	3.05
EBW192326	5.75	2.23	1.63	2.91	1.56	2.00	3.81	1.25	5.12	2.21	4.37	3.13	3.75	3.06
EBW192327	6.27	3.06	1.59	2.83	1.62	2.53	3.54	1.87	4.88	1.93	5.03	3.50	4.97	3.36
EBW192328	6.40	2.45	1.58	3.09	1.67	2.24	3.90	1.18	5.10	2.16	5.00	3.29	4.21	3.25
EBW192330	6.51	2.52	1.66	3.88	1.78	2.10	4.44	1.43	5.44	3.69	5.29	3.10	3.38	3.48
EBW192331	6.38	2.70	1.68	3.16	1.41	2.01	4.41	1.45	5.18	2.75	5.38	3.35	4.50	3.41
EBW192332	6.28	2.14	1.64	3.21	1.51	1.93	4.59	1.27	5.41	2.77	5.33	3.24	4.02	3.33
EBW192333	5.77	1.98	1.66	3.02	1.48	2.18	4.25	0.99	5.23	2.58	4.95	3.25	3.85	3.17
EBW192335	4.41	0.94	1.53	2.62	1.28	1.07	3.16	0.34	5.04	1.58	3.83	2.12	2.07	2.31
EBW192336	5.66	1.50	1.50	3.75	1.30	0.92	3.90	0.46	5.41	3.05	4.25	1.90	1.72	2.72
EBW192337	5.12	1.06	1.49	3.69	1.15	0.88	3.32	0.52	5.41	2.83	4.00	1.93	2.38	2.60
EBW192339	3.44	0.52	1.45	2.47	0.83	0.69	2.36	0.10	4.98	1.33	2.87	1.71	1.75	1.88
EBW192341	5.12	1.75	1.56	3.12	1.25	1.75	3.58	0.95	5.03	2.54	4.38	2.49	2.65	2.78
EBW192343	8.07	3.84	1.65	3.70	2.61	2.66	4.24	2.49	5.44	2.91	5.88	4.51	5.23	4.09
EBW192346	9.20	5.07	1.80	4.12	2.51	3.75	5.71	4.25	5.41	4.26	6.87	4.81	5.40	4.86
EBW192347	9.16	5.13	1.71	4.30	2.39	3.25	5.05	3.85	5.35	4.01	6.65	4.25	5.25	4.64

Genotype	20AA	20BE	20DZ	20KU	20RA	20SN	21AA	21BE	21DM	21HL	21KU	21RA	21SN	Mean
EBW192348	6.04	1.39	1.58	3.23	1.28	2.79	4.37	0.67	5.58	2.46	5.05	3.09	4.31	3.22
EBW192991	6.78	2.18	1.61	3.50	1.96	2.55	4.25	0.96	5.47	2.75	5.76	3.85	4.56	3.55
EBW192992	6.93	2.73	1.53	3.86	1.97	2.36	3.36	1.37	5.37	2.66	5.46	3.05	3.66	3.41
ETBW9077	7.78	3.45	1.50	3.44	1.91	3.09	3.43	1.67	5.18	1.87	5.89	3.91	5.06	3.71
ETBW9080	7.15	2.63	1.71	3.76	1.82	2.99	4.95	1.40	5.57	3.43	5.34	3.47	3.89	3.70
ETBW9128	4.91	1.72	1.58	2.80	1.33	1.53	3.15	0.70	5.09	2.03	4.41	2.98	3.18	2.72
ETBW9136	7.48	3.16	1.63	3.83	2.14	2.05	4.14	1.84	5.47	3.11	6.09	4.01	4.46	3.80
ETBW9396	7.03	3.49	1.64	3.62	1.58	2.44	3.67	2.79	5.12	2.75	5.68	3.09	3.72	3.59
ETBW9452	5.41	1.60	1.56	3.01	1.10	2.23	3.74	0.67	5.25	2.25	4.91	2.78	2.48	2.85
ETBW9642	4.80	1.04	1.52	3.22	1.39	0.90	3.28	0.38	5.41	2.47	4.95	2.54	2.38	2.64
ETBW9647	5.08	1.65	1.54	2.93	1.53	1.04	2.93	0.76	5.06	1.89	4.97	2.91	3.06	2.72
ETBW9648	1.85	0.18	1.31	2.21	0.43	-0.04	0.86	-0.05	4.47	0.79	3.92	0.54	0.63	1.32
ETBW9650	5.92	2.34	1.54	3.19	1.86	1.35	3.36	1.31	5.17	2.28	5.14	3.23	3.34	3.08
ETBW9654	5.25	1.94	1.46	2.94	1.61	1.29	2.35	1.03	4.99	1.52	4.33	2.92	2.89	2.66
Lemu	**4.08**	**1.46**	**1.46**	**3.21**	**1.27**	**0.99**	**2.51**	**0.71**	**4.99**	**2.66**	**3.66**	**2.34**	**2.66**	**2.46**
Wane	**5.62**	**1.70**	**1.46**	**3.28**	**1.71**	**2.24**	**3.03**	**0.47**	**5.17**	**2.02**	**4.81**	**2.54**	**3.08**	**2.86**
Mean	**5.64**	**2.14**	**1.56**	**3.17**	**1.55**	**1.75**	**3.44**	**1.28**	**5.16**	**2.40**	**4.77**	**3.00**	**3.41**	**3.02**
G. Variance	**3.02**	**1.33**	**0.01**	**0.50**	**0.30**	**0.78**	**0.81**	**0.80**	**0.12**	**0.77**	**1.5**	**0.85**	**1.32**	
E. Variance	**0.29**	**0.27**	**0.11**	**0.21**	**0.11**	**0.12**	**0.12**	**0.7**	**0.22**	**0.11**	**0.19**	**0.25**	**0.17**	

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. The performance of genotypes may be graded using BLUP values averaged across correlated settings of the first cluster (C1), eliminating C2 and C3 due to low genetic correlation with the other trials and low genetic variation. More than 55.56% (50) of the 90 genotypes exhibited average grain yields of more than 3.02 t/ha, according to Table 5. The estimated mean grain yield, on the other hand, indicated eight candidate genotypes with mean yields of more than 4 t/ha: two of these candidate genotypes (EBW192346 and EBW192347) are advanced to variety verification trials for further testing and release as new variety (Table 5). Furthermore, BLUP analysis revealed that 20BWNL1AA trials in 2020, 20BWNL2DM trials in 2021, and 20BWNL2KU trials in 2021 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.

4. CONCLUSION

To develop stable and high-yielding genotypes where both yield and stability qualities are assessed concurrently in addition to low genotype by environment interaction, researchers are currently focusing on crop breeding that combines stability and yield. High-yielding genotypes should be chosen in the environment. Both the production of new cultivars and the endorsement of newly released varieties necessitate a selection from a larger range of candidate genotypes, therefore evaluating genotypic values is crucial to every breeding effort. Combining MET with spatial and FA models improved knowledge of the genetic influence and increased the precision and accuracy of genotype evolution by allowing the breeder to account for the GEI effect. Depending on the purpose, this allows for the isolation of the genetic influence or a deeper investigation of the GEI effect. Using the fitted data, the genotypes with the highest potential for future verification and release as a variety may be identified. As a result, the ETW192346 and ETW192347 genotypes outperform other genotypes and were chosen for variety verification testing.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

The authors have declared that no competing interests exist.

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