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Application of Factor Analytic Mixed Model for Multi-environment Trial of Bread Wheat (*Triticum aestivum* L.) Genotypes in Ethiopia

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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

This study was carried out using dataset consisted of 15 multi-environment trials (MET) in Alpha lattice design with two replications arranged in plot arrays of rows and columns conducted in Ethiopia during 2021 and 2022 main seasons. The objective of this study was to identify promising

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wheat genotypes that might suite diverse agro-ecology of the country through analysis of multi-environment trials (MET) data using factor analytic mixed models. The result of the study revealed that estimates for genetic variance components ranged from 0.049 to 1.036 and 0.33 to 1.915 for error variance. By ranking average best linear unbiased prediction (BLUPs) within clusters, the fifteen bread wheat environments were clustered into five mega environments (C1, C2, C3, C4 and C5) for grain yield. Thus, factor analytic linear mixed model can be fitted to large and complex MET datasets using a large and highly unbalanced MET dataset where there is a factorial treatment structure. This method is used as a selection indicator, assisting in screening superior and adaptable genotypes. The predicted performance of genotypes based on BLUP values averaged across correlated trails after eliminating C4 and C5 due to low genetic correlation with the other trials and low genetic variation. In addition, the results of the factor analysis for considering relationships among measured traits were confirmed through the cluster analysis. Based on these clusters, the genotypes EBW202104, EBW202058, EBW202057 and EBW202088 were identified as potential genotypes in Bread wheat improvement programs. Moreover, about 58.33% of the genotypes had average grain yield above grand mean; accordingly these genotypes might be selected for subsequent study in bread wheat breeding activities. The examined FA models have also better data fitting, which significantly improves heritability. Therefore, increasing the application of this efficient analysis method will improve the selection of superior bread wheat genotypes. Our study also supports the usefulness of this statistical tool to interpret MET data results and assist decision-making for its routine use in Bread wheat breeding programs.

Keywords: Cluster; factor analysis; linear mixed model; multi-environment trials (MET).

1. INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the world's major food crops and has great economic importance. In Ethiopia Bread wheat is the most important food security crops which is cultivated on a total area of 2.1 million(1.7 million ha rain fed and 0.4 million ha irrigated) hectares annually with a total production of 6.7 million tons of grain at an average productivity of 3.0 and 4.0 t/ha under rain-fed and irrigated conditions, respectively during 2021/22(CSA, 2022), relatively lower than the attainable yield of the crop, which is reaching up to 5 t /ha (Zegeye F. *et al*., 2020). The yield gap observed could be due to lack of high yielding and stable varieties well adapted to diverse agro-ecologies; biotic stresses (Olivera *et al*., 2015; Singh *et al*., 2015; Tolemariam *et al.,* 2018) and abiotic stresses (Hodson *et al*., 2020; Negash *et al.,* 2022; Abate, 2023). Thus, development of wheat varieties with higher grain yield potential and adapted to different environmental conditions is a major priority in enhancing grain yield and yield stability of bread wheat across different areas of Ethiopia. Better performing genotypes should be evaluated based on multi-environment trials (MET) to ensure that the selected genotypes have higher performance in diverse environments of the target areas. Based on this, MET are carried out all over the world for major crops each year where various traits are mostly recorded (Yan and Rajcan, 2002).

Multi-environment trials (METs) are used to determine sites representing the target environment and can identify superior cultivars for recommendation to farmers in which data collected from METs are required for precise estimation of genotypic value and yield stability (Yan and Hunt, 2001). Hence, efficient approaches that account for more complex environmental variation require complementing experimental designs with appropriate models of analysis (Qiao CG, *et. al* (2000) and Smith A, *et. al* (2002)). The analysis of MET data is significantly improved by the FA models developed by Smith et al. (2001a), which were used to model genetic effects. More importantly, modeling genetic effects using FA models in conjunction with spatial models for non-genetic effects significantly improves the analysis of the MET data set. This was also demonstrated in related studies by Cullis *et al*. (2010) and Kelly *et al*. (2007). The FA models have been found to be useful not only for accurately estimating/predicting genetic effects, but also for estimating their variance and performing graphical analysis. Correlated environments can be identified using estimated genetic variance, and breeders can select genotypes using BLUPs averaged across correlated environments. Its significance for the estimate of the related variance structure for GxE effects is a crucial component of the factor analytic (FA) model for multi-environment trials (MET). Thus this study aimed to improve selection strategies in bread

wheat breeding through data analysis of multi-environment trials using linear mixed models (FA model) frame work. Therefore, the present study was conducted to evaluate the performance of Bread wheat genotypes that might suite diverse agro-ecology of the country through analysis of MET data using more efficient statistical methods.

2. MATERIALS AND METHODS

2.1 Used Materials and Experimental Design

A total of 60 bread wheat genotypes including five controls (Boru, Deka, Lemu, Danda'a, Dursa,) were evaluated under MET across eight locations (Kulumsa, Bekoji, Asassa, Debrezeit, Sinana, Goro (only in 2021 data), Holleta and Adet) in 2021 and 2022 main cropping seasons. In this study, fifteen MET datasets trials were conducted using Alpha lattice design with two replications laid out in row x column array of plots. All crop management practices such as land preparation as well as rates of fertilizers, fungicides, herbicides and Insecticides were applied as recommended for specific testing sites. These eight locations represent the different wheat growing agro-ecologies of Ethiopia and detailed descriptions of the study locations are presented in Table 1.

2.2 Data Collection

Data were collected on the following traits: days to heading, plant height, thousand kernel weight and grain yield. The description of the collected data/traits has been shown as follows:

1. **Days to Heading (DTH): r**ecorded as the number of days from sowing to the stage where 75% of spikes have fully emerged.
2. **Plant height(cm)(PHT):** The average height of five plants from ground level to the tip of spike excluding the awns.
3. **Thousand Kernel Weight (g)(TKW):** Weight of 1000 seeds in gram
4. **Grain Yield (t/ha):** Grain yield in gram was obtained from the central four rows of each plot and converted to tone per hectare at 12.5% moisture content.

2.3 Statistical Analysis

The factor analytic linear mixed model can be fitted to large and complex MET datasets using a large and highly unbalanced MET dataset where there is a factorial treatment structure. 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 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 (Smith AB, *et. al.* 2018). 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 selection cycle.

Table 1. Detailed Agro-ecological and Weather descriptions of the study locations

Location	Code	Soil type	Altitude (m)	Latitude	Longitude	Annual average Temp.(^{0}C)		Average Rainfall (mm)
						Min.	Max.	
Kulumsa	KU	Luvisol	2200	08°01'10"N	39°09'11"E	10.5	22.8	820
Bekoji	BE	Nitosol	2780	07°32'629"N	39°15'360"E	7.9	18.6	1010
Asasa	AA	Gleysol	2360	07°07'228"N	39°11'932"E	5.8	23.6	620
Debre Zeit	DZ	NA	2050	08°38'08"N	38°30'15"E	NA	NA	900
Sinana	SN	NA	2450	7˚7'N	39˚49'E	10˚C	22˚C	791
Goro	GR	NA	1650	09°11′0"N	38°43′0"E	NA	NA	829.5
Holleta	HL	Nitosol	2400	09°03'414"N	38°30'436"E	6.1	22.4	976
Adet	AD	NA	2216	11°16' N	37° 29' E	9.2	25.5	1250

Table 2. Summary of trial parameters and Average trait measurements across trials

Trials	Reps	Row	Column	Entry	Average Measurement			
					GYD	DTH	PHT	TKW
21AAP	2	10	6	60	7.00	69.4	87.17	37.2
21ADP	2	10	6	60	4.04	63.4	81.73	37.6
21BEP	2	10	6	60	5.41	83.1	89.67	21.9
21DZP	2	10	6	60	6.07	63.8	84.15	40.1
21GRP	2	10	6	60	2.20	72.6	56.77	29.9
21HLP	2	10	6	60	5.72	73.0	94.22	45.0
21KUP	2	10	6	60	8.46	73.0	91.35	44.2
21SNP	2	10	6	60	6.26	75.6	102.0	42.9
22AAP	2	10	6	60	8.83	62.5	96.17	38.8
22ADP	2	10	6	60	5.69	84.3	80.4	39.7
22BEP	2	10	6	60	7.51	66.0	94.4	48.2
22DZP	2	10	6	60	7.32	71.9	89.83	40.3
22HLP	2	10	6	60	8.81	66.6	92.73	47.9
22KUP	2	10	6	60	6.41	68.4	93.87	41.9
22SNP	2	10	6	60	5.95	69.4	97.22	36.0

GYD= grain yield, DTH= Days to heading, PHT=Plant height, TKW=Thousand kernel weight

3. RESULTS AND DISCUSSION

This study identified the relative genetic merits of different genotypes where trials were correlated. According to the summarized data (Table 3), the average performance of all genotypes at the 22AAP environment was greater (8.83t/ha) than other trials. In contrast, the potential of the 21GRP environment trial was the lowest (2.2t/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 various environments is used to decide genotype selection for the next trial. The predicted GxE variance may be used to identify correlated environments, and breeders can choose genotypes using BLUPs averaged over associated environments (Tesfaye K *et. al*. 2023).

3.1 Variance Components

The genetic variance and error variances for each trial from FA model are presented in Table 3. The estimates for variance component parameters ranged from 0.049 to 1.036 for genetic variance and from 0.33 to 1.915 for error variance. A higher genetic variance for yield was observed for 22AAP trials. Seven trails (22AAP, 22ADP, 22HLP, 22BEP, 21KUP, 21ADP and 22KUP) of the fifteen trials had higher genetic variance for yield. This indicated that relatively high genotypes discrimination power of these testing locations. On other hand, the trials 22DZP, 22GRP, 21BEP and 22SNP were poor trials with little genetic variation, which might be due to unfavorable weather condition during the evaluation season in these environments. As a result, while averaging across trials for picking better genotypes, we excluded the BLUPs from these trials. In general, using FA model to analyze MET data improved precision and accuracy of genotype evaluation by capturing non-genetic variation associated with agricultural field experiments and appropriately exploiting the information stored in the MET dataset (Smith AB, *et al.* 2005).

Heritability for days to Heading ranged from 77.08% to 99.25% with an average of 95.15% over all testing environments and this indicates that days to heading is one of the highly heritable traits. Similarly, plant height had heritability value ranged from 34.58% to 93.39%. Similarly, 84.53% to 97.71% heritability range for thousand kernel weight and 26.45% to 88.79% for grain yield. Hence, according to this experiment output days to heading and thousand kernel weight were found to be highly heritable traits (Table 3) and those most of trail environments are highly correlated which indicated that the genotypes were evaluated in ideal testing environments and selection made for a given environment could be

compliment for another location (Fig. 2) for these traits. This indicates that taking more samples to measure days to heading and thousand kernel weight may not give significant result deviate from the result obtained from single observation of correlated trial environments. Similar finding was reported for experiment across environments and over season following similar fashion of this study (Tajalifar M, *et al*. 2022).

3.2 Factor Analysis

Robust statistical techniques offer a theoretically sound and intuitively appealing framework for getting around some of the limitations of traditional analysis, most notably its limitation in the analysis of incomplete and correlated MET data. Thus, learning more about the genetic components that contribute to significant character variations is of primary interest to plant breeders. Additionally, having a precise and accurate understanding of heritability is essential for the plant breeding program to be successful. Due to this, it is essential from the perspective of plant breeding programs to quantify various genetic variances and make decisions regarding their inheritance based on estimates of various genetic characteristics acquired by using reputable statistical techniques like FA mixed model statistics which demonstrates how applying FA analysis strengthens heredity. Factor analysis is applied to the matrix whose elements consist of the sum of the BLUPs of the genotypic effects and the BLUPs of the effects of the interaction (G+GE), which were obtained from multi-environment analysis. Thus, properly utilizing the data recorded in the MET dataset, processing this dataset with factor analytic model often increases genotype generation precision and accuracy (Smith & Cullis, 2018; Cullis et al., 2010).

The FA models were considered for genotype by environment (GxE) analysis while keeping the spatial models provided in the individual trial analysis. The adequacy of the FA models of several orders was formally assessed as it was fitted within a mixed model framework based on the percentage of GxE variance explained by the factor components. The findings of the factor analysis are shown in Table 4. 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 most trials well and the two-factor components well described the genetic variation. Overall, the factor analytic models accounted for >50% of the genetic variance, with the first FA term accounting for about 80.24 percent. The inadequate fit of 21BEP and 22ADP trials with the FA model implies that the trials are not as well correlated as some of the other trials (Cullis BR*, et al,* 2010, Gadisa A *et al.* 2024).

Factor analysis also produces another important summary of statistics when cluster analysis is performed using a dendrogram. The cluster analysis using the dendrogram was used to group trials based on genetic similarity. The cluster analysis grouped the trials according to how environmentally related they were using the dendrogram in Fig. 1. Based on Cullis *et al*. (2010) suggestion on the dissimilarity cut-off (approximately below 0.5) that clusters are formed, the dendrogram (Fig. 1) suggests possibly two clusters of trials for DTH, where one cluster is comprised of at most two trials and only one cluster was identified for TKW. This shows that the genotype ranking is almost similar for all trials found within these formed clusters and a different ranking of genotype for the trials found in different clusters. However, we can find about five clusters of trials for YLD, and four clusters for PHT which implies that we would have different genotype rankings for a range of clusters of trials for these particular traits. In this regard, yield is a complex trait, which could potentially have high GEI effects. Genotype selection, therefore, was performed for each cluster using average BLUPs as a selection index, provided that the formed clusters are reasonably justified for making genotype selection independently for each of the clusters (Tadese D. *et al*. 2021, Alemu G. *et al*.; 2024). This demonstrates that, whereas genotype rankings differ for trials located in different clusters, they are substantially the same for trials located inside these established clusters. Given that the produced clusters are logically reasonable for doing genotype selection independently for every one of the clusters, genotype selection was performed for each cluster individually utilizing average BLUPs as a selection index.

Table 3. Variance components and heritability results in MET analysis FA models

Trial	DTH			PHT			TKW			GYLD			
	Gvar	Evar	H^2	Gvar	Evar	H^2	Gvar	Evar	H^2	Mean	Gvar	Evar	H^2
21AAP	2.84	1.04	89.82	18.19	36.48	89.32	8.85	5.48	85.52	7.00	0.20	0.33	72.63
21ADP	21.25	0.41	**99.25**	12.84	7.02	89.72	7.39	1.57	92.09	4.04	0.45	1.90	63.70
21BEP	0.06	8.62	99.23	1.14	39.64	63.63	2.69	7.98	96.81	5.41	0.05	0.75	**26.45**
21DZP	16.45	1.01	97.98	3.13	18.06	92.60	3.93	4.83	**84.53**	6.07	0.17	0.46	70.87
21GRP	25.53	1.37	98.33	13.20	54.99	77.94	11.37	1.26	**97.71**	2.20	0.06	0.85	68.07
21HLP	15.25	1.24	97.46	17.51	10.67	**93.39**	11.03	4.61	91.23	5.72	0.15	0.42	81.19
21KUP	11.23	1.23	96.53	26.21	10.48	92.48	5.76	6.55	96.84	8.46	0.46	0.34	82.51
21SNP	13.39	4.43	94.19	2.27	30.87	34.58	12.74	7.70	89.88	6.26	0.16	0.37	63.64
22AAP	21.68	0.73	99.00	13.41	20.37	92.60	6.02	2.46	91.74	**8.83**	0.14	0.85	83.23
22ADP	4.20	0.42	95.69	11.45	13.15	91.76	7.53	5.09	91.64	5.69	1.04	1.92	59.94
22BEP	37.03	1.78	98.20	21.33	22.43	80.50	4.59	5.81	97.12	7.51	0.52	0.61	74.70
22DZP	23.55	1.83	97.41	18.04	23.73	81.70	12.53	2.40	96.61	7.32	0.06	1.47	78.61
22HLP	17.08	2.37	96.70	9.98	18.75	90.16	8.83	6.61	88.11	8.81	0.92	0.54	**88.79**
22KUP	0.90	0.88	77.64	13.55	19.37	93.07	8.25	5.30	90.32	6.41	0.40	0.47	79.45
22SNP	2.84	1.04	89.82	1.34	20.49	66.79	8.85	5.48	85.52	5.95	0.05	0.61	56.75

GYD= grain yield, DTH= Days to heading, PHT=Plant height, TKW=Thousand kernel weight, Gvar= Genetic variance, Evar= Error variance, H^2 = heritability

Table 4. Results from fitting the factor analytic model

Environments	Factor_1	Factor_2	Factor_3	Factor_4	Total
21AAP	44.22	19.46	3.1	0.65	67.43
21ADP	37.5	57.7	1.68	3.13	100
21BEP	7.85	0.08	8.58	8.94	25.45
21DZP	48.94	0	6.33	21.31	76.57
21GRP	4.98	1.86	2.18	90.98	100
21HLP	77.56	2.54	6.36	13.54	100
21KUP	58.05	4.66	18.74	18.55	100
21SNP	3.68	17.26	29.53	49.54	100
22AAP	86.8	1.66	5.64	5.89	100
22ADP	18.01	31.4	5.72	0.75	55.89
22BEP	52.9	0.14	17.12	0.01	70.17
22DZP	40.28	18.23	2.56	38.92	100
22HLP	80.24	5.56	7.82	6.38	100
22KUP	37.69	30.99	28.7	2.62	100
22SNP	34.98	9.07	1.44	22.13	67.62

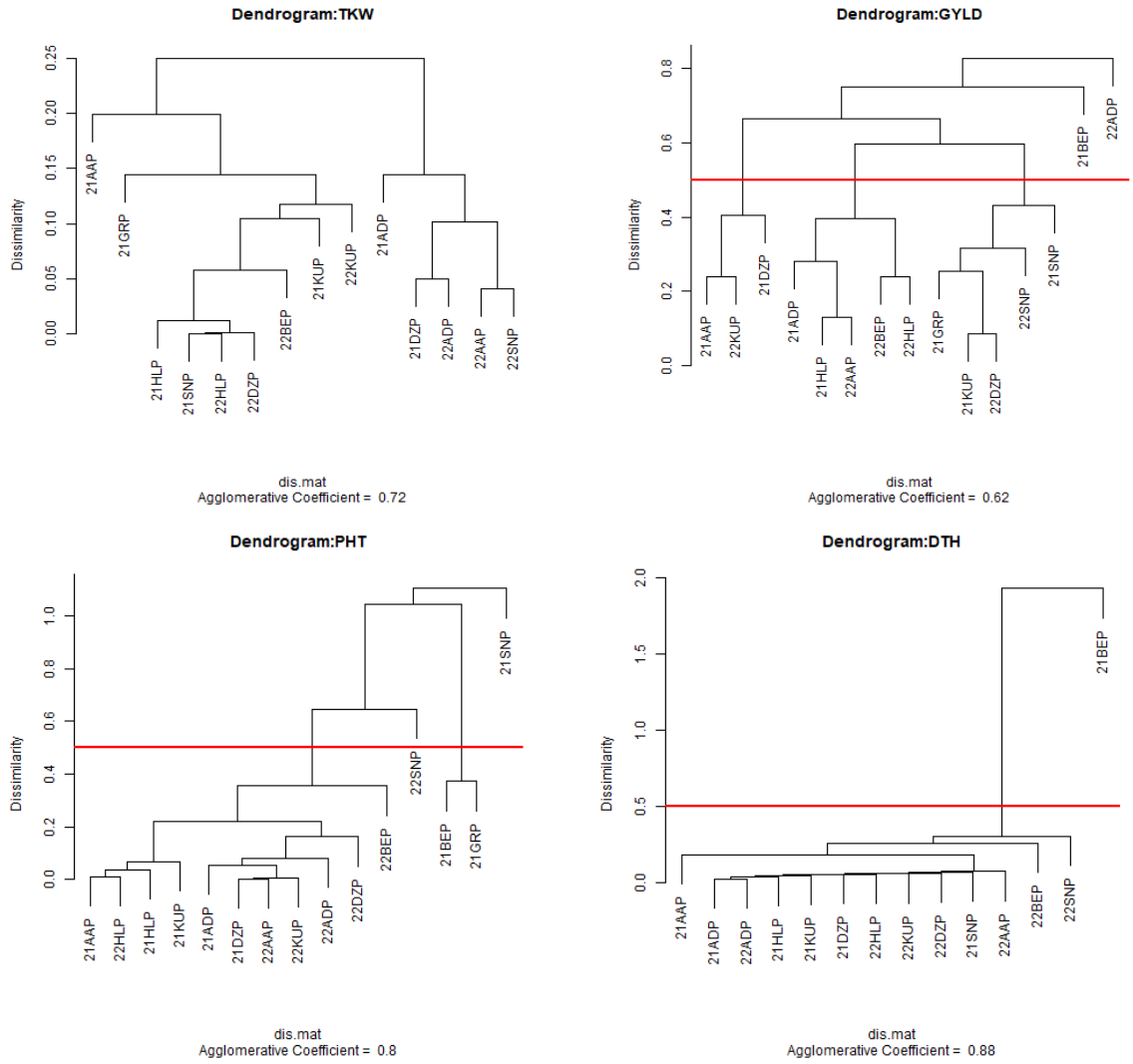

Fig. 1. Dendrogram of the dissimilarity matrix from the final FA models fitted to the Yield (YLD), Plant Height (PHT), Day to Heading (DTH) and Thousand Kernel weight (TKW)

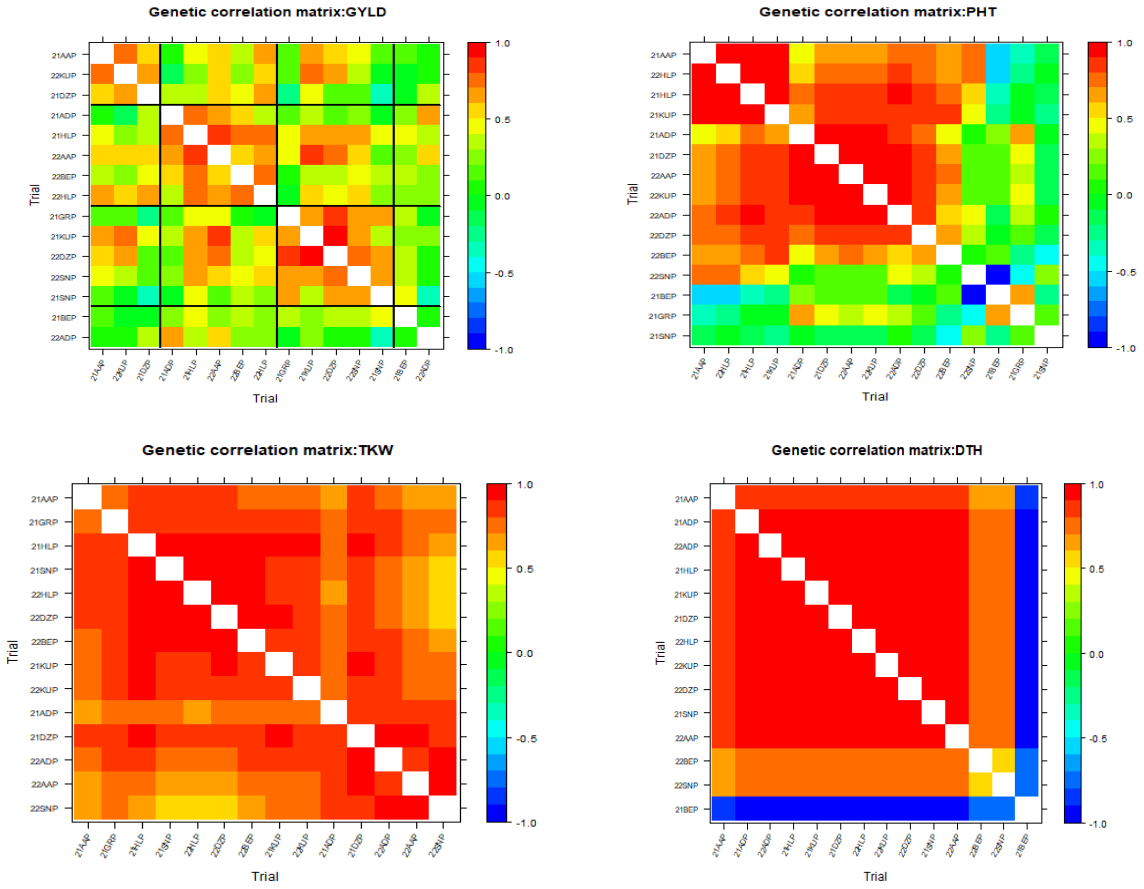

Fig. 2. Heat map representation of the genetic correlation matrix

In addition to the dendrogram, other typical summaries from the MET analysis include a heat map of the genetic correlations between all trials for each trait. A heatmap depicting the genetic links among all trials is another popular component of factor analysis reports. These are presented in Fig. 2, which shows the different correlation patterns for each trait. Only a few of the trials had a poor correlation, as evidenced by the heatmap, which reveals that the majority of the trials are highly connected. This suggests that almost all of the trials in the first cluster with the red hue can be used to average genotype means for genotype selection. Additionally, there are trials with a negative genetic association, such as the one between 21SNP and 22ADP (Table 6), which suggests that genotype rankings may have reversed in these trials.

From the heat map, we can see most of the trials are highly correlated for the DTH, TKW, and PHT, and have a weak correlation for the GYLD. This indicates that it is possible to carry out genotype selection through averaging of genotype means over nearly all trials for all traits except grain yield. However, for yield, BLUPs for genotype means should be averaged over trials for C1, C2 and C3, not for C4 and C5 since the genetic correlation is weak between trails for C4 and C5. Therefore, based on the dendrogram and heat-map (Figs 1 and 2) and the genetic variance as well from Table 3, we considered five clusters of trials (C1, C2. . .C5) for YLD, where 22ADP was in C5; 22BEP in C4; 21GRP, 21KUP, 22SNP, 21SNP in C3; 21ADP,21HLP, 22AAP, 22BEP,22HLP, In C2 and 21AAP, 22KUP AND 21DZP in C1. Similarly, two clusters were considered for DTH, where only one cluster for TKW, PHT (4 clusters) C4; 21SNP, C3; 21BEP AND 2GRP; C2; 22SNP and C1**;** with 11 Trials**.** Thus**,** Application of factor analytic mixed models and BLUP, both of which are well-suited for analysing genotype-by-environment interactions and predicting performance which ensure unbiased, accurate assessments critical for selecting stable, high-yield genotypes.

Table 5. BLUPs for genotype means across cluster of correlated environments

Genotype	21AAP	21ADP	21BEP	21DZP	21GRP	21HLP	21KUP	21SNP	22AAP	22ADP	22BEP	22DZP	22HLP	22KUP	22SNP
EBW202004	5.73	3.81	5.20	5.13	2.08	5.03	6.80	6.07	8.01	5.40	6.17	6.74	6.30	4.58	5.55
EBW202005	7.14	3.53	5.45	5.90	2.35	5.57	8.63	6.42	8.78	4.85	7.14	7.41	8.35	6.57	6.04
EBW202006	6.88	4.28	5.33	6.17	2.22	5.66	8.49	6.02	8.91	6.36	7.17	7.23	8.32	6.30	5.90
EBW202014	6.35	4.12	5.37	5.81	2.25	5.54	8.12	6.16	8.69	5.89	6.77	7.16	7.78	5.84	5.81
EBW202018	7.00	5.03	5.52	6.33	2.19	6.20	8.55	6.35	9.18	6.07	8.42	7.30	9.63	6.12	6.01
EBW202019	7.39	3.99	5.42	6.34	2.23	5.83	8.82	6.29	9.04	5.51	7.46	7.41	9.31	6.85	6.00
EBW202020	7.56	3.48	5.38	6.06	2.35	5.59	8.85	6.35	8.88	4.57	7.42	7.46	8.58	6.88	6.01
EBW202021	7.49	3.50	5.46	5.96	2.58	5.79	9.40	6.64	9.07	4.77	7.55	7.70	8.73	7.16	6.17
EBW202025	6.80	4.40	5.36	6.26	2.40	5.84	9.10	6.12	9.17	6.53	7.34	7.44	8.49	6.69	6.02
EBW202035	6.98	3.62	5.23	6.03	2.19	5.40	8.44	5.98	8.75	6.24	6.79	7.24	8.12	6.59	5.82
EBW202036	7.18	3.87	5.44	6.11	2.22	5.62	8.59	6.14	8.88	5.50	7.14	7.31	8.61	6.62	5.94
EBW202043	6.39	2.89	5.37	5.18	2.33	5.03	7.72	6.43	8.17	4.11	5.66	7.16	6.74	5.70	5.80
EBW202045	6.38	3.89	5.39	5.48	2.26	5.38	7.68	6.32	8.42	4.94	7.18	7.07	7.25	5.35	5.79
EBW202047	6.60	4.32	5.36	6.43	1.98	5.66	8.24	5.83	8.90	6.34	7.19	7.10	8.98	6.41	5.77
EBW202049	6.41	3.50	5.35	5.49	2.20	5.14	7.63	6.10	8.31	4.83	6.78	7.02	6.95	5.58	5.62
EBW202057	7.29	4.91	5.44	6.70	1.99	6.22	8.55	6.19	9.24	6.87	8.70	7.26	10.50	6.56	6.08
EBW202058	7.12	5.18	5.42	6.68	2.07	6.26	8.78	6.08	9.36	6.97	8.59	7.30	10.23	6.58	6.02
EBW202061	6.88	4.49	5.48	5.95	2.50	5.99	8.87	6.57	9.07	6.31	7.40	7.48	8.53	6.18	6.07
EBW202062	7.31	3.59	5.47	6.00	2.28	5.57	8.76	6.21	8.88	5.00	7.33	7.39	8.61	6.85	5.96
EBW202067	7.17	3.83	5.49	6.25	2.31	5.80	8.74	6.49	8.94	5.49	7.34	7.45	9.08	6.67	6.03
EBW202071	6.97	4.26	5.56	5.69	2.32	5.90	8.08	6.76	8.73	5.61	8.02	7.29	8.72	5.62	6.02
EBW202072	7.34	3.37	5.15	6.32	2.30	5.66	9.00	6.38	8.96	4.99	7.10	7.52	9.16	7.22	6.06
EBW202073	7.33	3.51	5.51	6.09	2.27	5.89	8.82	6.73	8.95	5.04	7.89	7.54	9.89	7.00	6.12
EBW202074	6.91	3.57	5.42	5.95	2.05	5.56	7.84	6.43	8.54	4.20	7.71	7.16	8.96	6.11	5.87
EBW202075	7.65	3.34	5.37	6.22	2.15	5.74	8.77	6.48	8.92	5.10	7.68	7.47	9.88	7.22	6.06
EBW202077	7.26	3.31	5.43	6.27	2.20	5.65	8.63	6.47	8.81	4.46	7.76	7.43	9.36	6.97	6.06
EBW202079	7.32	3.76	5.37	6.48	1.97	5.79	8.26	6.34	8.84	5.19	8.24	7.26	10.04	6.73	5.97
EBW202080	7.00	3.36	5.40	6.38	1.91	5.36	8.10	5.92	8.64	5.29	6.94	7.12	9.00	6.78	5.84
EBW202081	6.99	4.21	5.45	6.03	2.13	5.76	8.41	6.16	8.92	6.76	7.88	7.25	9.01	6.40	5.94
EBW202082	7.05	4.13	5.51	6.43	2.13	5.74	8.46	6.15	8.92	5.64	7.84	7.26	9.08	6.51	5.95
EBW202084	7.06	3.63	5.36	5.92	2.09	5.47	8.01	6.20	8.60	5.41	7.42	7.16	8.52	6.23	5.91
EBW202085	6.71	3.43	5.30	5.93	2.13	5.26	8.11	5.99	8.56	5.28	6.50	7.14	7.84	6.34	5.77
EBW202086	7.38	4.12	5.42	6.36	2.17	5.91	8.74	6.30	9.06	5.90	8.12	7.39	9.64	6.81	5.98
EBW202087	6.81	3.92	5.40	5.85	1.96	5.41	7.51	6.05	8.47	5.14	7.21	6.95	8.26	5.69	5.72
EBW202088	7.17	4.80	5.51	6.25	2.34	6.09	9.02	6.25	9.27	7.01	7.56	7.43	9.16	6.53	6.01
EBW202099	6.37	3.66	5.48	5.58	2.26	5.46	7.76	6.53	8.43	4.51	6.91	7.16	7.79	5.57	5.86

Genotype	21AAP	21ADP	21BEP	21DZP	21GRP	21HLP	21KUP	21SNP	22AAP	22ADP	22BEP	22DZP	22HLP	22KUP	22SNP
EBW202102	6.60	2.99	4.91	5.99	1.82	4.63	7.57	5.17	8.25	5.49	5.93	6.79	6.82	6.39	5.44
EBW202104	7.72	3.92	5.58	6.26	2.58	6.15	9.77	6.76	9.38	5.42	7.89	7.83	9.77	7.46	6.26
EBW202105	7.45	3.99	5.48	6.42	2.10	5.86	8.59	6.30	8.99	5.79	7.64	7.34	9.74	6.79	5.97
EBW202106	6.89	5.06	5.63	5.97	2.56	6.35	8.89	6.85	9.22	5.77	8.30	7.53	9.08	5.86	6.18
EBW202107	6.93	4.28	5.51	6.20	1.96	5.79	7.86	6.25	8.75	5.35	7.87	7.09	9.40	5.99	5.86
EBW202108	6.64	3.64	5.35	5.73	2.29	5.48	8.18	6.39	8.60	5.11	6.86	7.25	7.94	6.04	5.88
EBW202109	6.94	4.02	5.23	6.52	1.68	5.39	7.59	5.56	8.62	6.12	7.59	6.85	9.01	6.25	5.62
EBW202110	7.48	4.59	5.52	6.24	2.62	6.19	9.82	6.44	9.51	6.38	7.94	7.74	9.14	7.15	6.30
EBW202111	7.49	4.14	5.37	6.50	2.07	5.78	8.80	5.94	9.11	6.27	7.51	7.31	9.51	7.04	6.05
EBW202112	7.14	4.03	5.34	6.17	2.13	5.53	8.40	5.91	8.84	6.33	7.23	7.19	8.37	6.46	6.25
EBW202113	6.60	4.22	5.32	6.13	1.87	5.38	7.61	5.65	8.59	6.72	7.21	6.87	8.18	5.85	6.53
EBW202114	6.78	4.81	5.59	5.64	2.52	6.23	8.79	6.82	9.13	6.13	7.94	7.50	9.00	5.92	5.17
EBW202115	6.70	3.64	5.35	5.46	2.33	5.42	7.88	6.50	8.44	5.31	7.01	7.19	7.46	5.58	6.76
EBW202116	7.03	4.82	5.32	6.39	2.18	5.88	8.91	5.76	9.25	7.30	7.68	7.28	8.88	6.67	6.30
EBW202117	7.46	4.34	5.35	6.48	2.31	6.01	9.32	6.19	9.32	5.94	7.81	7.53	9.55	7.18	6.85
EBW202118	7.23	5.04	5.57	6.42	2.59	6.33	9.69	6.43	9.56	7.55	7.79	7.68	9.25	6.83	6.25
EBW202119	7.34	4.60	5.41	6.43	2.03	6.00	8.47	6.15	9.09	6.27	8.07	7.24	9.87	6.51	6.39
EBW202120	7.69	4.52	5.47	6.63	2.20	6.12	9.18	6.20	9.36	6.33	8.14	7.48	10.12	7.15	5.56
EBW202121	7.20	3.66	5.34	6.48	2.22	5.56	8.91	6.00	8.98	5.79	7.14	7.39	8.74	7.12	6.30
Boru	7.09	4.30	5.45	6.00	2.20	5.85	8.48	6.29	8.95	6.62	7.81	7.29	9.04	6.32	5.98
Danda'a	6.97	3.83	5.59	5.87	2.12	5.96	8.03	6.90	8.71	4.46	8.41	7.32	9.98	6.12	6.11
Deka	7.13	4.50	5.51	6.00	2.43	6.24	8.95	6.82	9.18	4.87	8.65	7.57	9.68	6.43	6.20
Dursa	7.08	4.71	5.50	6.05	2.38	6.00	8.79	6.34	9.12	6.17	7.89	7.39	8.72	6.21	5.99
Lemu	6.68	3.94	5.42	5.71	1.95	5.50	7.34	6.27	8.41	5.40	7.80	6.95	8.50	5.48	5.19

Table 6. Genetic correlation between environments

Trial	21AAP	21ADP	21BEP	21DZP	21GRP	21HLP	21KUP	21SNP	22AAP	22ADP	22BEP	22DZP	22HLP	22KUP
21AAP	1													
21ADP	0.035	1												
21BEP	0.123	0.241	1											
21DZP	0.549	0.31	**-0.016**	1										
21GRP	0.157	0.182	0.308	**-0.246**	1									
21HLP	0.441	0.758	0.426	0.382	0.489	1								
21KUP	0.643	0.323	0.221	0.444	0.674	0.686	1							
21SNP	0.158	**-0.003**	0.435	**-0.325**	0.691	0.499	0.304	1						
22AAP	0.585	0.681	0.26	0.599	0.457	0.871	**0.889**	0.167	1					
22ADP	0.084	0.639	0.007	0.394	**-0.029**	0.371	0.269	**-0.342**	0.503	1				
22BEP	0.395	0.526	0.321	0.408	0.088	0.748	0.363	0.343	0.582	0.231	1			
22DZP	0.588	0.154	0.329	0.199	0.819	0.68	**0.914**	0.651	0.726	0.014	0.374	1		
22HLP	0.671	0.361	0.264	0.674	**-0.05**	0.729	0.503	0.244	0.676	0.203	0.76	0.467	1	
22KUP	0.761	**-0.145**	**-0.018**	0.642	0.138	0.257	0.75	**-0.056**	0.588	0.091	0.205	0.612	0.572	1
22SNP	0.467	0.232	0.35	0.168	0.604	0.676	0.666	0.635	0.598	0.013	0.465	0.778	0.515	0.39

3.3 BLUPs for Genotypes across Trials

In this study, an average of BLUPs was used as a selection index to choose superior and stable genotypes through ranking average BLUPs within clusters and assessing the stability for all the traits across clusters of trials. Hence, the performance of genotypes was graded using BLUP values averaged across correlated settings of the first three clusters (C1, C2 and C3), eliminating C4 and C5 due to low genetic correlation with the other trials and low genetic variation. More than *58.33%* of genotypes exhibited average grain yields of more than grand mean. Hence, these candidate genotypes with higher mean grain yield could be advanced for further testing in breeding program and release as new variety after subsequent yield trails.

Furthermore, BLUP analysis revealed that 22AAP, 22HLP, 21KUP, 22BEP and 22DZP 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. The genotypic BLUPs for grain yield over the 15 trials for EBW02104, EBW2202058, EBW202057 and EBW202088 genotypes with highest overall average grain yield (Table 5). These genotypes were found ideal for further utilization in bread wheat breeding program. Genotype performance can be graded based on the averaged values of BLUPs across the correlated environments of the first cluster (C1), excluding 21BEP and 22ADP because they are in distinct clusters. According to the enhanced method of analysis we used here, cluster one (C1) would be the basis for genotype selection, and thus the genotypes with higher yield performance over correlated trials and can potentially be used as stable genotypes with broad adaptability (Cullis BR *et .al.(*2010).

3.4 Interrelationship among Environments

Correlation coefficients among the 15 environments are presented in Table 6 with bold characters indicating values that are statistically different from zero (P 0.05). This study identified the relative genetic merits of different genotypes where trials are correlated with the corresponding environments of the experiments. When trials are correlated (similar response of genotypes at testing environment) selecting best genotypes in a given environment is the same as selecting best material in another environment. Most of the trials were strongly positively correlated for DTH and TKW which are important trait to get good genotype for grain yield purpose. Then, information from one of the correlated environments is the same as selecting from the other site and can be combined to improve genetic gains. In this case, MET data analysis can help the breeder to understand the broad and specific adaptation of genotypes over a range of target environments. The correlations between testing environments for grain yield performance of testing genotypes in respect to testing environments ranged from 0.91(22DZP and 21KUP) to-0.342(21SNP and 22ADP). Hence, negative correlations indicate that the performance of the genotypes at that specific testing environment falls in opposite direction, implying that the best performing genotypes in one environment were the lowest performing genotypes in the other environment (Argaw T *et. al*. 2024). The cause this low correlation among the location could due to year differences or spatial variation. On the other hand, correlation of positive values (approximate to +1) is an indication of perfect similarity between the environments, hence selection of superior genotypes in one environment is the same as selection for another environment (Fig. 2 and Table 6) (Piepho et al. 2021, Rut et al. 2024).

4. CONCLUSION

Efficient statistical methods must be employed for the evaluation of Bread wheat genotypes to accurately select superior varieties that contribute to agricultural productivity. The Factor Analytic (FA) model is superior in achieving the most common aim of METs which is the selection of superior genotypes for future use and release as a variety. Hence, FA model is a parsimonious form used to approximate the fully unstructured form of the genetic variance-covariance matrix in the model for MET data. The linear mixed model with the FA models showed to be an effective data analysis technique for this investigation. EBW02104, EBW2202058, EBW202057 and EBW202088 were found to be potentially useful as stable genotypes with a wide range of adaptability because they demonstrated good yield performance over correlated locations. This is due to the fact that the enhanced method of analysis we employed here revealed that correlated locations served as the base for genotype selection. Moreover, the factor analytic linear mixed model can be fitted to large and

complex MET datasets using a large and highly unbalanced MET dataset where there is a factorial treatment structure. Hence, further application of such an efficient analysis method is very important for enhancing the selection of superior genotypes in breeding program.

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 the writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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