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Multi-environment Evaluation of Bread Wheat (*Triticum aestivum* L.) Genotypes in Mid-altitude of Ethiopia using Advanced Mixed Models

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ABSTRACT

The experiment was conducted during May to December, 2024–2025 main seasons at mid-altitude bread wheat growing agro-ecologies of Ethiopia to study the agronomic performance, genotype-by-environment (G×E) interactions, heritability, cluster and correlation of bread wheat breeding genotypes across 11 multi-environment trials (METs).Utilizing an alpha lattice and partially replicated design, the study employed Factor Analytic Mixed Models (FAMM) and GGE biplot analysis to partition variance, GxE and identify drivers of yield stability. Grain yield ranged significantly from 1.60 to 6.50 t ha^{-1}, underscoring substantial phenotypic plasticity across the environments. Results indicated that 55.80% of genotypes exceeded the grand mean yield, 77% yielded above 4.5 t ha^{-1}, and 20% outperformed the standard check "Melka." While grain yield exhibited high heritability (H^2) ranged 16·48%–92.19%), traits like days to heading (DTH) and plant height (PHT) remained genetically stable (H^2 > 85%). GGE biplot analysis partitioned testing sites into distinct mega-environments, identifying locations 25BWOPNMKU, 24BWPNMAB and 25BWOPNMAA as the most discriminative testing sites for selection. Although genotype EBW190004 achieved the highest mean yield (5.52 t ha^{-1}), it showed high environmental sensitivity. Conversely, EBW190128 and EBW190063 were the most stable genotypes. Notably, EBW222059 appeared as the promising candidate for regional release, balancing high productivity (5.44 t ha^{-1}) with exceptional resilience in moisture-constrained environments. Furthermore, the study confirmed high potential for genetic gain and demonstrated that the FAMM-based MET analysis provided a robust framework for identifying superior genotypes in bread wheat breeding programs across the mid-altitude regions of Ethiopia.

KEYWORDS: Cluster, factor analysis, genetic variance, heritability, mixed model

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Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, author have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is a hexaploid (2n=6x=42; AABBDD) cereal and the world's most widely grown crop. It accounts for approximately 95% of global wheat production and provides nearly 20% of the total calories and protein consumed by humans (Anonymous, 2023, Shewry, 2009). In Ethiopia, bread wheat is a top-priority strategic crop for national food security and rural livelihoods. It currently occupies over 90% of the country's wheat-growing area, surpassing traditional durum wheat due to the introduction of improved varieties with higher yield potential and superior disease resistance (Hodson et al., 2020; Jaleta et al., 2018). Beyond its role as a vital source of protein, dietary fiber, vitamins, and minerals (Shewry et al., 2015), bread wheat is indispensable for traditional Ethiopian foods such as bread, porridge, local beer, roasted grain, boiled grain and *injera* (Mullualem et al., 2024). Additionally, wheat straw is a critical resource for roofing and livestock feed, highlighting its socio-economic value in mixed farming systems (Anteneh et al., 2020). In Ethiopia, bread wheat cultivation is extensive and pivotal for food security, being the most important crop in the country and well-suited to various agro-ecological zones. Thus, total production in the 2021/22 season reached 6.7 million tons, with average yields of 3 tons per hectare (rain-fed) and 4 tons per hectare (irrigated). Recently, Ethiopia achieved 100% wheat self-sufficiency with a surplus for export, driven by a transformational irrigated wheat initiative (Abate et al., 2023). The government continues to boost production through land expansion, farmer agro-clustering, and the expansion of irrigation into lowland areas (Mekonen et al., 2025). Despite these achievements, national productivity remains lower than the attainable yield potential of 5 tons per hectare (Belachew et al., 2022). This yield gap is largely attributed to a shortage of high-yielding, stable varieties adapted to diverse agro-ecological conditions and resilient against biotic stresses (Olivera et al., 2015; Valdez-Rodríguez et al., 2025) and abiotic stresses (Hodson et al., 2020; Belete et al., 2022; Abate, 2023; Mekonen, 2025)). Consequently, developing varieties with higher yield potential and broad environmental adaptation is a primary goal for enhancing regional productivity (Alemayehu et al., 2025). Achieving this requires evaluating genotype through multi-environment trials (METs) to ensure superior performance across target environments (Yan et al., 2007). METs also help identify representative testing sites and the best genotypes for farmer recommendations. Efficient analysis of these trials requires advanced statistical approaches that account for complex environmental variations by combining experimental designs with appropriate analytical models (Basford et al., 2004; Qiao et al., 2000). The analysis of MET data has been significantly improved by factor analytic (FA) models, which effectively model genetic effects (Smith et al., 2001). Combining FA models with spatial models for non-genetic effects further enhances the accuracy of MET datasets **(**Smith et al., 2018**;** Kelly et al., 2007). FA models are valuable for estimating and predicting genetic effects, calculating variance, and conducting graphical analyses. By utilizing estimated genetic variance, breeders can identify correlated environments and select genotypes based on Best Linear Unbiased Predictions (BLUPs) averaged across these environments (Argaw et al., 2024). The core strength of the FA model lies in its ability to estimate the related variance structure for genotype-by-environment effects. Generally, this study aimed to improve selection strategies in bread wheat breeding through analysis of multi-environment trials data using advanced mixed models (FA model) frame work. Therefore, the present study was undertaken to evaluate the performance and stability of bread wheat genotype across diverse agro-ecologies of Ethiopia using MET data analysis within a linear mixed model framework.

2. MATERIALS AND METHODS

2.1. Experimental sites, materials and design

This study is part of the METs program conducted across six locations-Asasa (AA), Adet (AD), Ambo (AM), DebreZeit (DZ), Kulumsa (KU), and Sinana (SN)-representing the diverse mid-altitude bread wheat growing agro-ecologies of Ethiopia. Detailed descriptions of the study locations are presented in Table 1. The unique MET dataset presented in this study combines 11 environments (unbalanced combinations among two years and six locations) and 699 genotypes (including 3 released varieties) with detailed phenotyping of 5 traits of bread wheat genotypes. The standard check varieties used in the trials included Melka, Boru, and Deka. Hence, the METs were conducted using alpha lattice and partially replicated (P-reps) designs arranged in a rectangular array of plots during the 2024 to 2025 cropping seasons. All crop management practices were applied as recommended for specific testing sites.

2.2. Dataset

The MET data were aggregated from two trial series: Observation-Preliminary-National Variety Trials (OPN) and Preliminary-National Variety Trials (PN). These trials were conducted across diverse locations representing major bread wheat growing regions in mid highland of Ethiopia, with the NVT series providing broader geographical coverage (Table 2). The final curated dataset included 11 trials and 699 unique genotypes, three of which are check varieties. Before data analysis, the genotype connectivity was conducted to examine the overlap in genotypes across trials. The matrix (Table 3) shows high-level genotype connectivity among trials. This level of connectivity

Table 1: Detailed descriptions of the study locations

Location	Code	Altitude (m)	Latitude	Longitude	Annual average temp.		Average rainfall (mm)
					Min.	Max.	
Adet	AD	2216	11°16' N	37° 29' E	9.20	25.50	1250
Ambo	AB	2223	8° 57' N	38° 07' E	10.30	26.40	1,036
Asasa	AA	2360	07°07'228"N	39°11'932"E	7.80	23.60	620
DebraZeit	DZ	2050	08°38'08"N	38°30'15"E	NA	NA	900
Kulumsa	KU	2200	08°01'10"N	39°09'11"E	10.50	22.80	820
Sinana	SN	2450	7°7'N	39°49'E	10.00	22.00	791

Table 2: Summary of trial design and average trait measurements across trials

Trials	No. of reps	No. of rows	No. of columns	No. of genotypes	Average trait measurement				
					GYLD	DTH	TKW	PHT	HLW
24BWOPNMAA	3	33	20	378	4.53	68.82	29.94	106.50	59.10
24BWOPNMKU	3	33	20	378	4.68	73.64	34.99	97.95	65.20
24BWPNMAB	3	20	9	60	5.66	63.95	36.16	93.66	75.82
24BWPNMAD	3	20	9	60	4.89	59.89	41.54	90.81	76.64
24BWPNMDZ	3	20	9	60	4.09	61.64	30.42	95.28	80.30
24BWPNMSN	3	20	9	60	3.16	68.26	38.88	103.28	66.13
25BWOPNMAA	3	44	12	332	5.53	68.49	26.67	83.85	79.00
25BWOPNMAB	3	10	9	30	5.31	90.16	36.66	83.91	71.37
25BWOPNMAD	3	10	9	30	5.12	59.11	NA	71.67	71.62
25BWOPNMDZ	3	10	9	30	1.60	66.48	NA	95.91	NA
25BWOPNMKU	3	44	12	332	6.50	63.27	NA	NA	NA

GYLD: Grain yield; DTH: Days to heading; PHT: Plant height; TKW: Thousand kernel weight; HLW: Hectoliter weight

between trial pairs ensures that MET analysis is attainable while preserving diversity across test environments and seasons (Smith et al., 2015). High connectivity values, such as the 378 and 332 scores within the 24BWOPNM and 25BWOPNM groups indicated strong overlap of genotypes across those specific environmental sets. While the 24BWPNM subgroup showed moderate and uniform connectivity (60), the significantly lower values (6 to 11) recorded between the 2024 and 2025 environmental series suggest limited overlap that differentiates these cycles. Overall, the matrix highlights that while certain genotypes are highly integrated within their specific year-groups, there is a clear drop in connectivity when moving across different temporal or environmental blocks.

2.3. Data collection

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

2.3.1. Grain yield (t ha^{-1})

Grain yield in gram was obtained from the entire plots harvested after physiological maturity, weighed, and converted to tons per hectare at 12.5% moisture content

2.3.2. Thousand kernel weight (g)

Determined by counting the seeds with a seed counter and weighing them on a sensitive balance at 12.5% moisture content.

2.3.3. Hectoliter weight (kg hl^{-1})

Measured as the flour density (kg hl^{-1}) produced from a hectoliter of seed after harvest using a specialized grain analyzer.

2.3.4. *Days to heading (DTH)*

Obtained by recording days from the sowing date to when 75%of spikes have fully emerged.

2.3.5. Plant height (cm)

Measured by averaging the height of five random

Table 3: Genotype connectivity across environments

Site	24BWOPNMAA	24BWOPNMKU	24BWPNMAB	24BWPNMAD	24BWPNMDZ
24BWOPNMAA	378	378	60	60	60
24BWOPNMKU	378	378	60	60	60
24BWPNMAB	60	60	60	60	60
24BWPNMAD	60	60	60	60	60
24BWPNMDZ	60	60	60	60	60
24BWPNMSN	60	60	60	60	60
25BWOPNMAA	11	11	6	6	6
25BWOPNMAB	11	11	6	6	6
25BWOPNMAD	11	11	6	6	6
25BWOPNMDZ	11	11	6	6	6
25BWOPNMKU	11	11	6	6	6

Table 3: Continue...

Site	24BW-PNMSN	25BWOP-NMAA	25BWO-PNMAB	25BWOPN-MAD	25BWOPNMDZ	25BWOPNMKU
24BWOPNMAA	60	11	11	11	11	11
24BWOPNMKU	60	11	11	11	11	11
24BWPNMAB	60	6	6	6	6	6
24BWPNMAD	60	6	6	6	6	6
24BWPNMDZ	60	6	6	6	6	6
24BWPNMSN	60	6	6	6	6	6
25BWOPNMAA	6	332	30	30	30	332
25BWOPNMAB	6	30	30	19	19	30
25BWOPNMAD	6	30	19	30	21	30
25BWOPNMDZ	6	30	19	21	30	30
25BWOPNMKU	6	332	30	30	30	332

plants from the ground to the spike tip (excluding awns) after physiological maturity.

2.4. Statistical analysis

The Multi-Environment Trial (MET) analysis was performed for trials evaluated at mid-altitude areas of Ethiopia during the 2024 to 2025 cropping seasons. Genetic variance, error variance, heritability and clustering across trials were analyzed using more enhanced Statistical approached such as Factor analytic mixed model and Genotype-by-Environment interaction through ASReml and the Metan R package (Olivoto et al., 2020). The ASReml-R statistical software package was used to fit all models analyzed in this study (Galili, 2015; Butler, 2009). 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. This methodology allowed comparing free genetic values of environmental effects and not the phenotypic means to improve genetic gain in the subsequent selection cycle (Smith et al., 2001).

3. RESULTS AND DISCUSSION

3.1. Mean performances of trials

The evaluation of mean performances across eleven distinct environments revealed significant environmental influence on grain yield and agronomic performance (Table 2). Grain Yield (GYLD) varied substantially by site, with the environment at 25BWOPNMDZ producing a minimum of 1.60 t ha^{-1}, while site 25BWOPNMKU yielded a peak of 6.50 t ha^{-1}. To quantify these variations, an Environmental Index (Ij) was calculated by subtracting the grand mean (4.64 t/ha) from the mean yield of each site (Table 4). This index identified 25BWOPNMKU (Ij=+1.86) and 24BWPNMAB (Ij=+1.02)) as highly favorable environments, whereas

Table 4: Environmental index ranking

Trial site	Yield (t ha^{-1})	Environmental index (Ij)	Classification
25BWOPNMKU	6.50	1.86	Highly favorable
24BWPNMAB	5.66	1.02	Favorable
25BWOPNMAA	5.53	0.89	Favorable
25BWOPNMAB	5.31	0.67	Favorable
25BWOPNMAD	5.12	0.48	Favorable
24BWPNMAD	4.89	0.25	Average
24BWOPNMKU	4.68	0.04	Average
24BWOPNMAA	4.53	-0.11	Marginal
24BWPNMDZ	4.09	-0.55	Marginal
24BWPNMSN	3.16	-1.48	unfavorable
25BWOPNMDZ	1.60	-3.04	Highly unfavorable

25BWOPNMDZ (Ij=-3.04) and 24BWPNMSN (Ij= -1.48) were classified as unfavorable. As noted by Tadesse et al. (2019), understanding such site-specific favorability is essential for identifying stable breeding genotypes, as environmental factors like soil properties and moisture availability dictate the realization of genetic yield potential. Environmental adaptation, reflected in Days to Heading (DTH), ranged from 59.11 to 90.16 days across trials. The environment at 25BWOPNMAD enabled the earliest heading (59.11 days), suggesting conditions-such as higher temperatures or specific photoperiods-that accelerated phenological development. According to Abdelghany et al. (2024), such environments often imposed a "drought-escape" condition on the crop. However, environments that compress the vegetative phase often realize a reduction in total biomass; Sukumaran et al. (2015) emphasized that while early heading avoids terminal stress, it can limit the duration of grain filling, which may explain the moderate yield (5.12 t ha^{-1}) at the 25BWOPNMAD site compared to the high-index environment of 25BWOPNMKU. Moreover, mean Plant Height (PHT) across environments varied from 71.67 cm at site 25BWOPNMAD to 106.50 cm at 24BWOPNMAA. The significant reduction in height at certain 2025 series sites, particularly those with lower environmental indices, likely reflects environmental influences such as moisture deficit during the stem elongation phase. Abdelghany et al. (2024) explained that plant height is an elastic trait highly responsive to environmental variation. Environments that support moderate height (80–90 cm) were generally more conducive to high-input management without the risk of lodging, which is critical for maintaining the high yield levels realized in favorable environments like 24BWPNMAB.

Furthermore, grain quality parameters also showed strong environmental dependency. Thus, thousand kernel weight (TKW) reached its peak (41.54 g) at the 24BWPNMAD site, while hectoliter weight (HLW) was highest (80.30 kg hl^{-1}) at 24BWPNMDZ. These metrics are vital for determining the commercial value of the harvest from different regions. Wang et al. (2020) demonstrated that the inter-relationship between kernel weight and Hectoliter weight is a primary indicator of grain-filling efficiency, which is often hindered in environments with negative indices where heat or moisture stress occurs during the milk-ripe stage. The missing data (NA) in several 2025 environments, especially at site 25BWOPNMKU, highlighted that even in highly favorable environments for yield, logistical or environmental constraints can impede the collection of secondary quality traits, necessitating multi-year validation.

3.2. Variance components and heritability

The analysis of genetic and error variances, alongside heritability estimates for the eleven trials, revealed a refined relationship between the genetic architecture of bread wheat and the specific agro-ecology of the mid-altitude wheat belt of Ethiopia (Table 5). According to the results of the study, grain yield (GYLD) exhibited the most significant fluctuations in heritability (H^2), ranging from 16.48% in trial 24BWOPNMAA to 92.19% in 24BWPNMAB. The exceptionally low heritability in 24BWOPNMAA was driven by an extremely high error variance (Evar=1.89) relative to genetic variance (Gvar=0.05), indicating that non-genetic factors accounted for nearly 84% of the variation. Conversely, trials such as 25BWOPNMKU, 24BWPNMAB, 24BWPNMAD, 25BWOPNMAA, and 25BWPNMAD served as high-potential selection environments by minimizing (Evar) to values between 0.16 and 0.35, allowing the genetic signal for yield to be clearly captured. These findings aligned with Tadesse et al. (2019), who emphasized that wheat breeding in Ethiopia must account for sharp environmental gradients where yield stability is as critical as potential.

Across all eleven trials, days to heading (DTH) appeared as the most genetically stable trait, with heritability consistently exceeding 90% and peaking at 98.99% in 24BWPNMAD. Genetic variance for DTH was substantial, reaching 67.45, while error variance remained negligible, suggesting control by major-effect loci. This high H^2 offered a breeding advantage for selecting early-heading genotypes to avoid late-season moisture stress, a strategy supported by Gahlot et al. (2020). Similarly, plant height (PHT) demonstrated

Table 5: Genetic and error variances and heritability for yield and other traits for each trial

Trials	GYLD			DTH			TKW			PHT			HLW		
	Gvar	Evar	H^2	Gvar	Evar	H^2	Gvar	Evar	H^2	Gvar	Evar	H^2	Gvar	Evar	H^2
24BWO-PNMAA	0.05	1.89	16.48	23.27	1.88	96.80	15.39	7.52	75.46	48.66	18.76	86.45	22.77	8.51	84.18
24BWO-PNMKU	0.89	0.30	80.18	67.45	2.55	97.99	9.82	1.62	95.90	63.70	25.23	85.69	8.74	3.33	79.90
24BWP-NMAB	0.99	0.31	92.19	33.02	4.34	98.77	10.35	9.03	86.88	24.82	9.34	90.70	3.00	1.14	90.98
24BWP-NMAD	0.22	0.16	82.69	17.00	0.67	98.99	9.03	4.50	89.16	60.59	11.95	95.88	1.97	2.11	82.63
24BWP-NMDZ	0.38	0.35	86.87	20.60	3.39	95.96	15.53	12.09	71.10	64.46	11.44	95.58	1.67	1.13	85.10
24BWP-NMSN	0.11	0.25	74.36	12.45	2.87	95.70	5.96	1.84	91.26	51.95	18.96	87.55	12.99	5.18	83.83
25BWO-PNMAA	1.04	0.49	79.86	15.82	2.52	93.94	1.97	7.58	64.45	77.83	21.42	97.53	1.99	0.52	92.39
25BWO-PNMAB	0.22	0.72	79.87	6.07	2.91	92.20	9.54	7.97	66.34	55.96	7.86	97.85	2.45	4.49	84.66
25BWO-PNMAD	0.03	0.18	69.86	11.16	0.40	98.93	NA	NA	NA	2.74	20.49	70.93	2.12	0.74	81.17
25BWO-PNMDZ	0.10	0.13	83.24	9.41	1.18	97.60	NA	NA	NA	36.95	19.53	86.23	NA	NA	NA
25BWO-PNMKU	0.48	0.40	67.63	8.09	2.23	90.38	NA	NA	NA	NA	NA	NA	NA	NA	NA

robust genetic control with heritability between 85% and 97%. The highest Gvar (77.83) and H^2 (97.53%) for PHT obtained in 25BWOPNMAA, confirming that semi-dwarf genes were well-integrated and protected against environmental masking, as noted by Kumar et al. (2021). Moreover, thousand kernel weight (TKW) and Hectoliter weight (HLW) also exhibited high heritability, generally exceeding 70%, with TKW reaching 95.90% in 24BWOPNMKU. Generally, because TKW and HLW, with H^2 reached 92.39% (in 25BWOPNMAA), were more likely genetically fixed than yield, they could be identified as reliable alternatives for selecting superior genotypes in erratic environments. Mwadzingeni et al. (2016) previously argued that selecting for such stable kernel traits leads to more consistent genetic gains. Overall, the "PNM" trials captured genetic variation more effectively than the "OPN" series. In low-heritability sites like 24BWOPNMAA, the results suggested that direct phenotypic selection for yield would likely fail, necessitating the use of selection indices that prioritized highly heritable traits like DTH and TKW. Overall, the implementation of the Factor Analytic Mixed Model (FAMM) across eleven mid-altitude wheat trials in Ethiopia (2024–2025) provided a high-resolution partitioning of phenotypic variance, outperforming traditional models by accounting for spatial heterogeneity and multi-trait correlations.

3.3. Cluster analysis and correlation patterns across trials

The hierarchical cluster analysis (AC), performed across five distinct phenotypic traits, revealed a nuanced structural background, with Agglomerative Coefficients (AC) ranging from 0.57 to 0.91 (Figure 1). This variation in AC values reflected differing levels of trait-specific sensitivity to environmental and temporal factors. The structural consistency of the clades across most traits suggested that the underlying biological drivers are robust, while the specific branching patterns within each dendrogram provided critical insights into the relationship between individual samples and their respective cohorts (Märzinger et al., 2021). The dendrogram for grain yield exhibited a moderately strong clustering structure, grouping into four primary clusters at a dissimilarity threshold of 0.6. A significant feature of this trait was the isolation of sample 24BWOPNMAA as a significant outlier, joining the primary hierarchy only at a dissimilarity height exceeding 1.0. This suggested that for GYLD, this specific site possessed a highly divergent profile compared to the rest of the group. The remaining trails demonstrated varying degrees of interrelation, with the

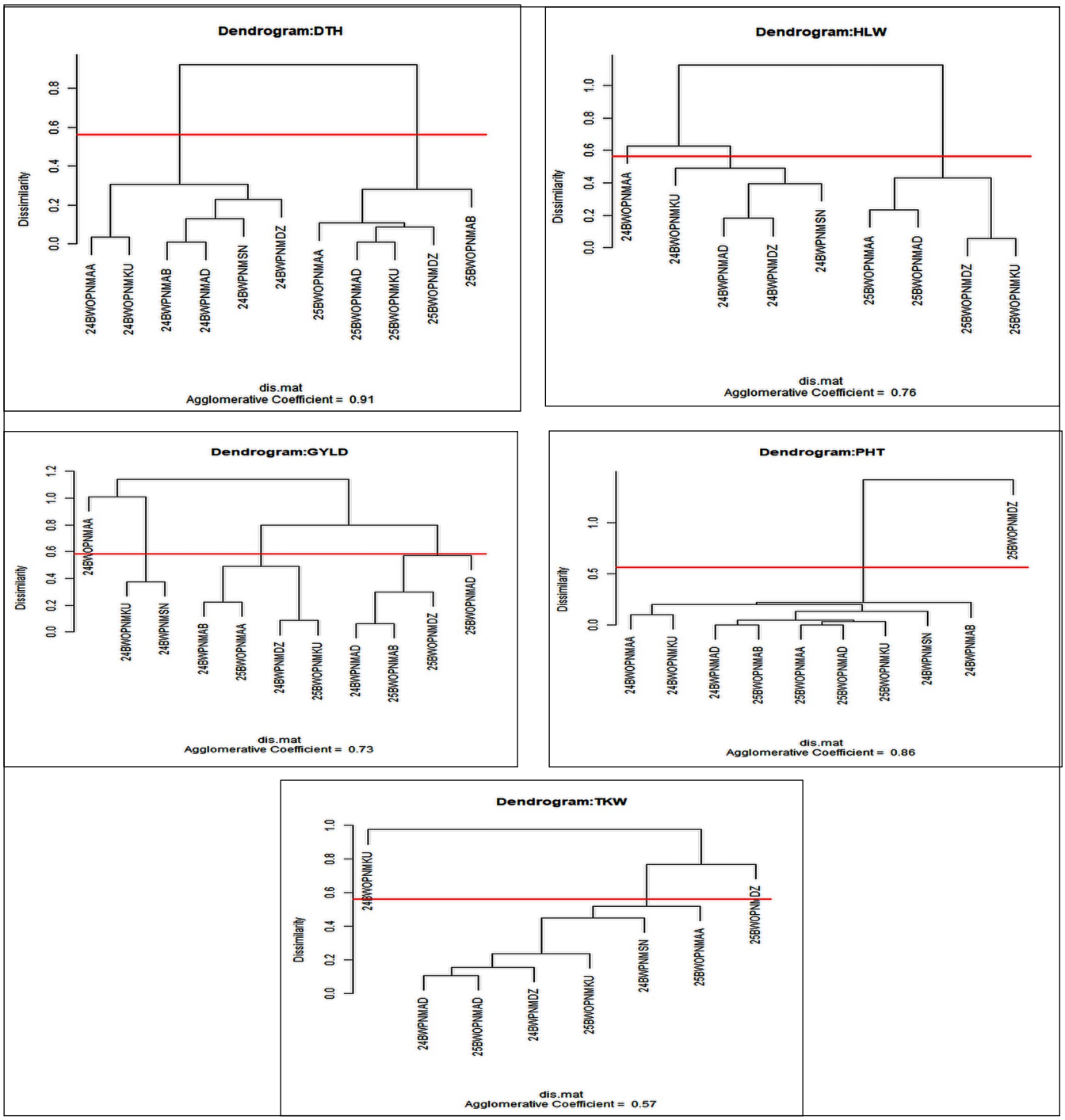


Figure 1: Dendrogram of the dissimilarity matrix from the final FA models fitted to different traits

pairing of 24BWOPNMKU and 24BWPNMSN showing the highest interrelationship. The broad distribution across the red partition line indicated that GYLD captured substantial variation, likely reflecting a high degree of phenotypic plasticity within the population (López-Oriona et al., 2025).

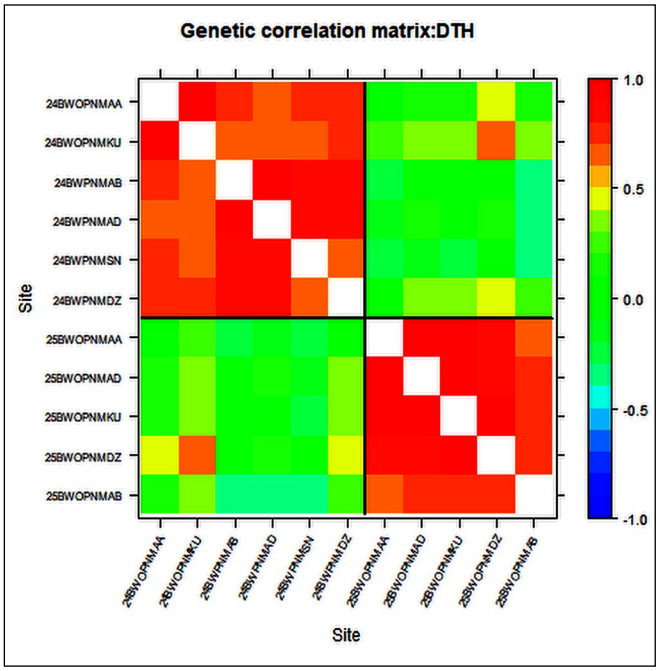
Based on the dendrogram, the TKW dataset produced the lowest AC, indicating a more unsolidified and less stratified clustering structure. Despite this, the dendrogram successfully identified a major outlier of site 24BWOPNMKU. The very low dissimilarity merging of 24BWPNMAD and 25BWOPNMAD suggested that TKW trait for these trials were remarkably stable across years. However, the overall moderate AC of 0.57 implied that TKW may be subject to higher levels of stochastic noise or minor environmental fluctuations that distorted

the boundaries between functional groups (Murtagh et al., 2012). Similarly, the HLW dendrogram demonstrated a robust clustering structure, dominated by a primary chronological split. At a height of 1.1, the clusters separated into two major groups that align almost perfectly with the 2024 (left) and 2025 (right) groups. This sharp division indicated that HLW is highly sensitive to year-on-year variations, creating a distinct "batch effect" that dominated individual trials similarities. Within the 2025 group, the formation of two very tight sub-pairs (merging below 0.2) highlights a high degree of trait preservation within that specific year. According to Mohammadi et al. (2003), such strong partitioning is essential for identifying year-specific biomarkers and suggested that HLW is a highly reliable trait for temporal classification.

Moreover, the DTH trait exhibited the most definitive clustering structure of the entire study. The cluster splits symmetrically at a height of 0.95 into 2024 and 2025 cohorts, with virtually no overlap between the years. This indicated that DTH is the most sensitive indicator of temporal or experimental divergence in the study. The internal branching within each year's clade is also highly structured, with sample pairs like 24BWPNMAB and 24BWPNMAD showing near-zero dissimilarity. This high resolution suggested that DTH measurements were exceptionally precise, providing a "clean" dataset for high-confidence multivariate modeling (Greenacre et al., 2021). On the other hand, hierarchical clustering of plant height (PHT) among trails of bread wheat genotypes revealed a highly structured population, as evidenced by a robust agglomerative coefficient of 0.86 (Kaufman et al., 1990). At a dissimilarity threshold of 0.55, the trials were partitioned into two distinct clusters. Thus, Cluster I comprised 90% of the population, exhibiting high phenotypic uniformity with internal dissimilarity levels below 0.25. This indicated a high degree of architectural similarity, likely reflecting selection for stable, lodging-resistant semi-dwarf genotypes required for high-yield mid-altitude environments (Tadesse et al., 2019). The most significant finding was the isolation of trail 25BWOPNMDZ as a standalone outlier in Cluster II. This site displayed extreme divergence, with a dissimilarity index exceeding 1.0, making it a unique environment for height variation within the trials. Such distinctiveness is a key result for breeders, identifying 25BWOPNMDZ as the best site for improving biomass or adjusting harvest index among diverse agro-ecologies (de Lima et al., 2021).

In summary, the transition from the low clustering in TKW to the firm, highly structured partitioning in DTH highlighted the varying sensitivity of these different traits. The high AC values across HLW, DTH, and PHT provide strong statistical support for the validity of these hierarchical groupings (Everitt et al., 2011). The consistent appearance of specific outliers across multiple traits suggested that these individuals' locations possessed unique biological characteristics that warrant deeper investigation. Ultimately, the hierarchical cluster analysis (AC) of dendrograms provided a robust foundational framework for defining operational groups, allowing for a reduction in data complexity while preserving the core evolutionary and environmental relationships within the dataset (Murtagh et al., 2012; Greenacre et al., 2021).

Figure 2 displayed a heatmap that visually represents the genetic correlations between environments for each trait. The resulting genetic correlation matrices demonstrated that environmental similarity was highly dependent on the specific trait being measured, shaped by both geographical



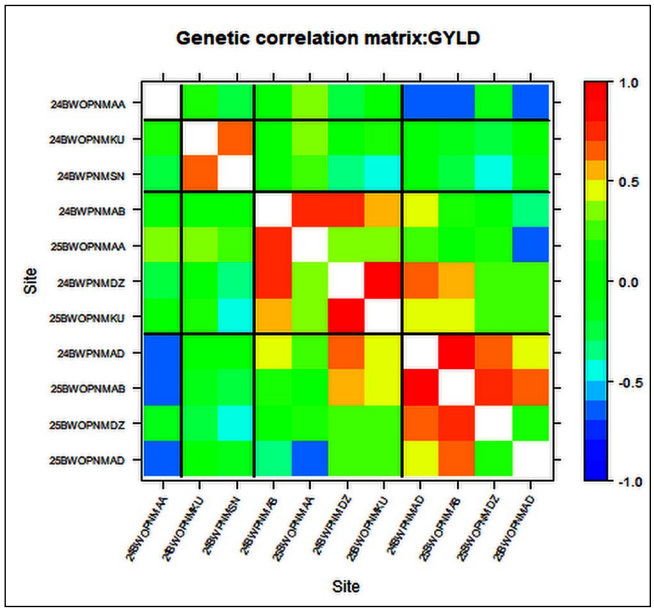


Figure 2: Continue...

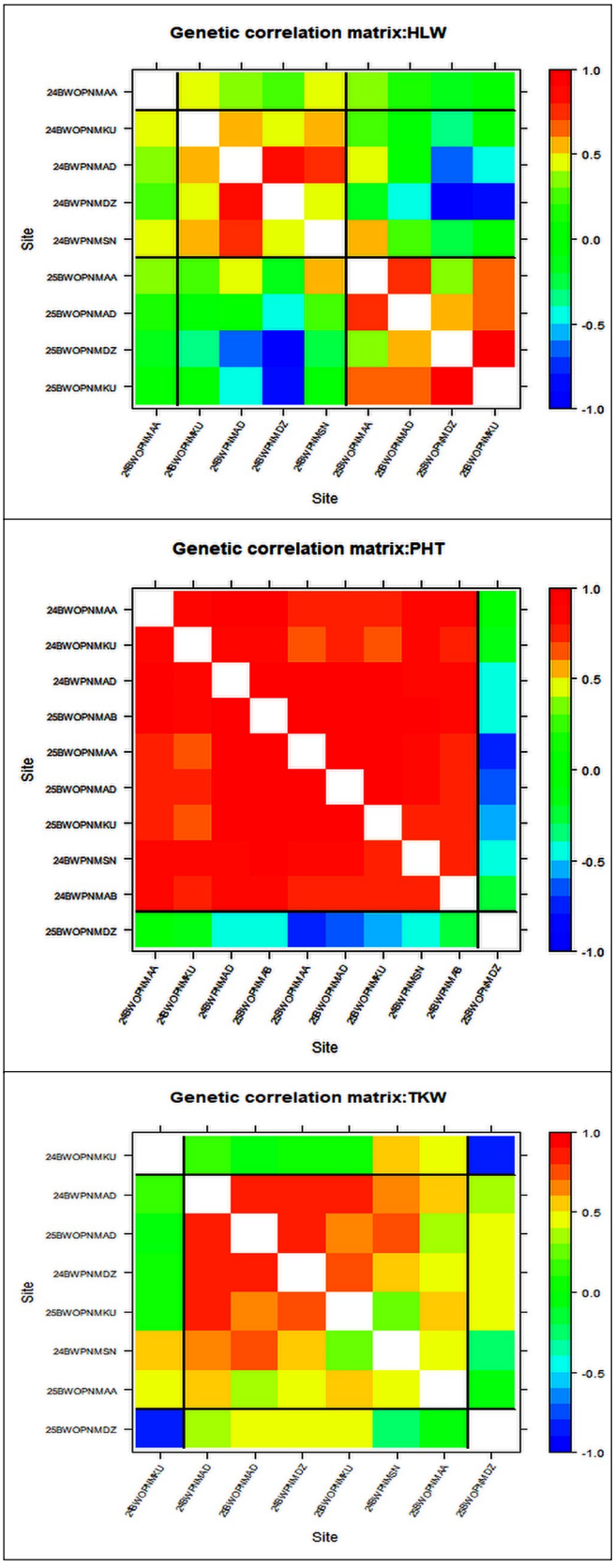


Figure 2: Heat map representation of the genetic correlation matrix from the final FA models fitted to different traits

coordinates and inter-annual climatic shifts. For grain yield (GYLD), the analysis identified a complex network of correlations that indicated substantial G×E interaction. Notably, a major cluster of strong positive genetic correlations (r_g >0.65) was found between specific testing sites, such as 24BWPNMAD and 25BWOPNMAB. These findings suggested the presence of a stable "mega-environment" where genotype rankings remained consistent. However, distinct negative correlations at sites like 24BWOPNMAA highlighted significant crossover interactions driven by localized differences in soil pH and moisture availability typical of Rift Valley transition zones ((Dinsa et al., 2024, Gahlot et al., 2020). Regarding grain physical quality, thousand kernel weight (TKW) showed relatively high stability within central environmental clusters, indicating consistent genetic control over grain sink-filling efficiency. Conversely, hectoliter weight (HLW) emerged as the most unstable trait evaluated, where sharp negative correlations occurred between successive trial years at the same locations, such as the transition from 24BWPNMDZ to 25BWOPNMDZ. According to Asefa et al. (2026), this indicated that physical grain quality was exceptionally sensitive to terminal environmental shocks, specifically seasonal fluctuations in heat and moisture stress that drastically reduced flour extraction potential in vulnerable genotypes.

On the other hand, phenological and morphological traits displayed the most distinct partitioning in their correlation structures. Days to heading (DTH) exhibited high stability within a single year but showed almost zero correlation between seasons. This suggested that while genotypes responded uniformly to a specific year's climate, their relative heading dates were unpredictable across different years due to erratic rainfall onset (Dinsa et al., 2024). In contrast, plant height (PHT) was identified as the most genetically stable trait overall, maintaining near-universal positive correlations across approximately 90% of the testing sites. As highlighted, only one outlier, 25BWOPNMDZ, served as a "stress hotspot" in which growth was stunted, confirming that the genetic architecture of stem elongation was highly predictable and facilitated reliable selection for stature and lodging resistance (Feyisa et al. (2023). The synthesis of these matrices established a clear hierarchy of trait stability for variety selection. Thus, plant height (PHT) was the most predictable, followed by thousand kernel weight (TKW) and grain yield (GYLD). While GYLD required extensive multi-site testing to manage crossover interactions, the presence of strong correlation blocks allowed for the potential streamlining of testing networks by identifying representative sites (Messele et al., 2023). On the other hand, days to heading (DTH) and hectoliter weight (HLW) demonstrated the lowest predictability. The extreme inter-

annual rank reversals for HLW indicated that grain density was the most vulnerable trait to the erratic terminal stressors of the Ethiopian mid-altitudes, necessitating a targeted selection approach to maintain grain quality standards across fluctuating seasons (Eskezia et al., 2026). The findings confirmed that while morphological traits offered high predictability, economically vital traits such as grain yield and quality were subject to limited variability. Therefore, by identifying mega-environments, genotypes showing stability within specific clusters could be fast-tracked for sub-regional release rather than being delayed by poor performance in divergent outlier sites. Furthermore, breeding programs were encouraged to prioritize phenological plasticity and dynamic stability in grain quality to ensure that new varieties could better synchronize with the unpredictable rainfall patterns and withstand terminal stress.

3.4. *Genotype×environment (g×e) interaction and stability analysis*

The GGE biplot analysis explained 92% of the total variation, with PC1 and PC2 accounting for 75.5% and 16.5%, respectively (Figure 3). This high level of explained variance confirmed a robust evaluation of genotype (G) and genotype-by-environment (GE) effects (Eskezia et al., 2026). According to the grain yield and stability rankings (Table 6), EBW190004 achieved the highest mean yield of 5.52 t ha^{-1}, which represented a 15.20% advantage over the check variety, Melka. This superior performance was attributed to its high-yield potential and specific adaptation to favorable environments. However, its moderate stability indicated that its productivity was sensitive to environmental shifts, a trait often observed in germplasm optimized for high-potential sites (Abdelghany et al., 2024).

The analysis also identified EBW222059 (5.44 t ha^{-1}) as a superior candidate genotype, characterized by high stability and broad adaptation with a 13.50% advantage over Melka. The ability of this genotype to maintain high productivity across diverse environments suggested a robust physiological resilience. Furthermore, EBW190128 and EBW190063 (5.41 t ha^{-1}) exhibited very high stability, which was essential for ensuring reliable yields in regions prone to unpredictable climatic shifts. As noted by Sukumaran et al. (2015), selecting for such high stability was vital to ensure that phenotypic differences reflected true genetic merit rather than environmental noise.

On the other hand, environmental discriminative power was highest at sites such as 25KU and 24KU, which displayed the longest vectors from the biplot origin (Figure 3). These sites were considered ideal for selection because they provided the greatest resolution for differentiating genotypes (Dinsa et al., 2024). Conversely, the "which-won-where" pattern indicated that certain genotypes, such as EBW222895 (5.36 t ha^{-1}) and EBW232928 (5.24 t ha^{-1}), exhibited environment-specific adaptation to sites like 24KU and 24AA, respectively. This environment-dependency supported the findings of Wang et al., 2020 who highlighted

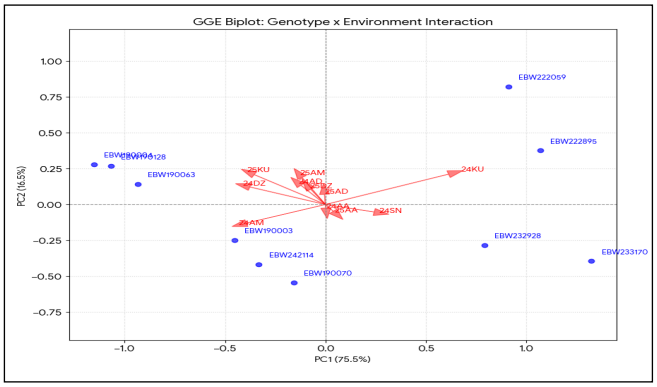


Figure 3: GGE biplot illustrating genotype performance and stability across environments

Table 6: Stability and yield ranking of top performing genotypes

Rank	Genotype	Mean yield (t ha^{-1})	Stability level	Performance profile	Advantage over melka (%)
1	EBW190004	5.52	Moderate	High-yield potential/Specific adaptation	15.20%
2	EBW222059	5.44	High	Stable/Broad adaptation	13.50%
3	EBW190063	5.41	Very high	Highly stable/Reliable across sites	12.90%
4	EBW190128	5.41	Very high	Highly stable/Reliable across sites	12.90%
5	EBW222895	5.36	Moderate	Environment-specific (24KU)	11.80%
6	EBW242114	5.35	High	Consistent performer	11.60%
7	EBW190070	5.28	High	Consistent performer	10.20%
8	EBW190003	5.27	Moderate	Average performance	9.90%
9	EBW232928	5.24	Low	Variable specific adaptation (24AA)	9.30%
10	EBW233170	5.24	Low	Variable/Specific adaptation (24SN)	9.30%

those specific environmental stresses during critical growth stages hindered grain-filling efficiency and altered genotype rankings (Mullualem et al., 2024).

The "which-won-where" polygon view of the GGE biplot effectively partitioned the 11 trial sites into distinct mega-environments. The clustering of environments such as 25KU, 24DZ, and 24AM suggested the existence of a high-yielding mega-environment where EBW190004 was the winning genotype. Meanwhile, site 24KU formed a separate niche dominated by EBW222895, and 25DZ represented a mid-to-low potential mega-environment where EBW222059 excelled. This partitioning demonstrated that the mid-altitude areas of Ethiopia were not environmentally homogenous, requiring the deployment of specific germplasm to targeted ecological niches to maximize productivity (Tadesse et al., 2019).

Furthermore, consistently performing genotypes like EBW242114 (5.35 t ha^{-1}) and EBW190070 (5.28 t ha^{-1}) also maintained high stability levels. The capacity of these genotypes to out yield the check by over 10% while remaining stable suggested they possessed the necessary adaptive traits for regional food security (Kelly, et al., 2007). The identification of these stable mega-environments and genotypes provided a clear framework for maximizing genetic gain through specialized adaptation, as recommended by Tadesse et al. (2019). Generally, the study demonstrated that achieving a balance between high-yielding potential and environmental resilience was essential for the sustainable agriculture. Overall, EBW222059 appeared as the most promising candidate for regional release in the mid-altitude areas of Ethiopia, as it uniquely combined a high mean yield (5.44 t ha^{-1}) with superior stability across diverse environments. While EBW190004 achieved the maximum productivity, its moderate stability indicated a higher risk for farmers in regions with high climatic variability. Ultimately, the integration of GGE biplot metrics and stability rankings provided a definitive framework for advancing germplasm that could withstand unpredictable shifts while ensuring consistent food security in the mid-altitude agro-ecologies of Ethiopia.

3.5. BLUPs for genotypes across trials

To identify superior and stable bread wheat genotypes, this study utilized average Best Linear Unbiased Predictions (BLUPs) as a refined selection index. Following the methodology of Tajalifar et al. (2022), genotypes were ranked based on mean performance within clusters of correlated environments, ensuring consistency across various trials. The assessment of 699 genotypes across 11 trial environments revealed substantial genetic potential within the evaluated genotypes. Hence, a significant majority of the genotypes (77%) achieved a mean yield exceeding 4.5 t ha^{-1} and 55.80% performed above the experimental grand mean. Notably, 20% of the genotypes gave yield above the Melka variety, a recently released high-yielding standard check variety. This subset of superior genotypes represented considerable progress in genetic gain and provided a robust selection pool for future variety development. The high frequency of genotypes outperforming Melka variety underscored the success of contemporary selection strategies in identifying superior performing genotypes with a better genetic background.

The application of BLUP is critical in this context, as it provided a more accurate estimation of breeding values than simple arithmetic means (Yan et al., 2024). As demonstrated by Crespo-Herrera et al. (2017), the BLUP method effectively accounts for the unbalanced nature of multi-environment trials and reduces phenotypic noise. This ensured that the selected top 20% of genotypes possessed true genetic superiority rather than localized environmental advantages. Furthermore, the broad distribution of high-yielding genotypes suggested a successful accumulation of yield-enhancing genetic materials. According to Watson et al. (2018) and Jaleta et al. (2018), such a high proportion of elite genotypes indicated intensive selection for physiological efficiency and environmental plasticity, confirming that the breeding program is effectively raising the regional yield ceiling. The identification of these top-tier genotypes also aligns with modern genomic selection frameworks. As noted by Crossa et al. (2017) and Yan et al. (2024), BLUP-based phenotypic values serve as the gold standard for training populations in genomic prediction models because they maximize trait heritability. Consequently, the genotypes identified as superior to the best regional check represent both immediate candidates for release and foundational parents for the next cycle of recurrent selection. Elite lines such as EBW190004 and EBW222059 stood out as top performers, with the latter demonstrating an exceptional balance of high yield and stability according to GGE biplot analysis (Yan et al., 2007). These superior genotypes could be recommended for advanced multi-environment trials and national performance tests to confirm their resilience across wider agro-ecological zones of Ethiopia.

4. CONCLUSION

The study demonstrated that FAMM and GGE biplots effectively partitioned G×E interactions across Ethiopia's mid-altitude environments. EBW222059 emerged as the premier candidate, successfully balancing high grain yield (5.44 t ha^{-1}) with outstanding stability. While EBW190004 achieved maximum yield, it exhibited high environmental sensitivity. Results indicated that while direct yield selection was effective in high-potential sites, selection indices weighted toward highly heritable traits like

DTH and TKW were more robust in stressed environments, offering a framework for climate-resilient wheat breeding.

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6. REFERENCES

Anonymous, 2023. The State of Food Security and Nutrition in the World 2023. Urbanization, agrifood systems transformation and healthy diets across the rural–urban continuum. Rome, FAO. DOI: https://doi.org/10.4060/cc3017en. Accessed on 19th March 2026.

Abate, F.S., Walelign, W., 2023. Ethiopia's wheat production pathways to self-sufficiency through land area expansion, irrigation advance, and yield gap closure. Heliyon 9(10), e20736. DOI: 10.1016/j.heliyon.2023.e20736.

Abdelghany, A.M., Zhang, S., Zhang, Y., Gao, J., 2024. Exploring the relationship between plant height and yield-contributing attributes of wheat in drought conditions. Frontiers in Plant Science, 15. DOI: 10.54112/bcsrj.v2024i1.854.

Alemayehu, S., Getaneh, F., Fufa, H., 2025. Review on opportunities and challenges of low land irrigated wheat production in Ethiopia: In the case of Afar region. International Journal of Agricultural Science and Food Technology 11(1), 045–053. DOI: 10.11648/j.sf.20250601.11.

Anteneh, A., Asrat, S., 2020. Wheat production and marketing in Ethiopia: Review study. Cogent Food and Agriculture 6(1), 1778893. DOI: 10.1080/23311932.2020.1778893.

Argaw, T., Fenta, B.A., Assefa, E., 2024. Application of factor analytic and spatial mixed models for the analysis of multi-environment trials in common bean (*Phaseolus vulgaris* L.) in Ethiopia. PLoS ONE 19(4), e0301534. DOI: 10.1371/journal.pone.0301534.

Asefa, B., Sime, B., Geleta, N., Solomon, T., Dabi, A., Alemu, G., Zegeye, H., Dhuga, R., Delesa, A., Asneke, D., Zewdu, D., Getamesay, A., 2026. Evaluation of bread wheat (*Triticum aestivum* L.) genotypes in multi-environment trials using linear mixed models. Ecological Genetics and Genomics 39, 100459. DOI: 10.1016/j.egg.2026.100459.

Basford, K.E., Federer, W.T., DeLacy, I.H., 2004. Mixed Model Formulations for Multi-Environment Trials. Agronomy Journal 96, 143–147. DOI: 10.2134/agronj2004.1430.

Belachew, K.Y., Maina, N.H., Dersseh, W.M., Zeleke, B., Stoddard, F.L., 2022. Yield gaps of major cereal and grain legume crops in Ethiopia: A review. Agronomy 12(10), 2528. DOI: 10.3390/agronomy12102528.

Belete, Y., Shimelis, H., Laing, M., 2022. Wheat production in drought-prone agro-ecologies in Ethiopia: diagnostic assessment of farmers' practices and sustainable coping mechanisms and the role of improved cultivars. Sustainability 14(13), 7579. DOI: https://doi.org/10.3390/su14137579.

Butler, D.G., 2009. ASReml-R reference manual. queensland department of primary industries and fisheries. Available from: https://asreml.kb.vsni.co.uk/wp-content/uploads/sites/3/ASReml-R-3-Reference-Manual.pdf.

Crespo-Herrera, L.A., Crossa, J., Huerta-Espino, J., Autrique, E., Mondal, S., Velu, G., Vargas, M., Braun, H.J., Singh, R.P., 2017. Genetic yield gains in CIMMYT's international elite spring wheat yield trials by modeling the genotype×environment interaction. Crop Science 57(2), 789–801. DOI: 10.2135/cropsci2016.06.0553.

Crossa, J., Pérez-Rodríguez, P., Cuevas, J., Montesinos-López, O., Jarquín, D., de los Campos, G., Varshney, R.K., 2017. Genomic selection in plant breeding: Methods, models, and perspectives. Trends in Plant Science 22(11), 961–975. DOI: 10.1016/j.tplants.2017.08.011.

de Lima, V.J., Gracia-Romero, A., Rezzouk, F.Z., Diez-Fraile, M.C., Araus-Gonzalez, I., Kamphorst, S.H., do Amaral Júnior, A.T., Kefauver, S.C., Aparicio, N., Araus, J.L. 2021. Comparative performance of high-yielding european wheat cultivars under contrasting mediterranean conditions. Frontier Plant Science 12, 687622. DOI: 10.3389/fpls.2021.687622.

Dinsa, T., Balcha, U., 2024. Evaluation of agronomic performance and grain yield stability of bread wheat (*Triticum aestivum*) genotypes in East Shewa zone, Oromia. Advances in Agriculture and Biology 7(1). DOI: 10.63072/aab.24007.

Eskezia, A., Ayenew, A., Azene, Y., Aytenew, M., Nakachew, K., 2026. Genotype by environment interaction and yield stability analysis of durum wheat (*Triticum turgidum* var. *durum*) varieties using AMMI and GGE biplot analysis in Amahara region, Northwest Ethiopia. PLoS ONE 21(3), e0342401. DOI: 10.1371/journal.pone.0342401.

Everitt, B.S., Landau, S., Leese, M., Stahl, D., 2011. Cluster Analysis (5th ed.). Wiley. DOI: 10.1002/9780470977811.

Feyisa, H., Mengistu, G., Biri, A., Chimdessa, T., 2023. Grain yield and yield related traits of bread wheat as influenced by n and seeding rates and their interaction effects in 2020 under Irrigation at Western and North of Oromia, Ethiopia. International Journal of Agronomy 2023, 8666699, 13. DOI: https://doi.org/10.1155/2023/8666699.

Gahlot, S., Lin, T.S., Jain, A.K., Roy, S.B., Sehgal, V.K., Dhakar, R., 2020. Impact of environmental changes and land-management practices on wheat production in India. Earth System Dynamics 11(3), 641–652. DOI: 10.5194/esd-11-641-2020.

Galili, T., 2015. dendextend: an R package for visualizing, adjusting and comparing trees of hierarchical clustering. Bioinformatics 31(22), 3718–3720. DOI: 10.1093/bioinformatics/btv428.

Greenacre, M., 2021. Compositional data analysis. Annual Review of Statistics and its Application 8, 271–299. DOI: 10.1146/annurev-statistics-042720-124436.

Hodson, D.P., Jaleta, M., Tesfaye, K., Yirga, C., Beyene, H., Kilian, A., Carling, J., Disasa, T., Alemu, S.K., Daba, T., Misganaw, A., Negisho, K., Alemayehu, Y., Badebo, A., Abeyo, B., Erenstein, O., 2020. Ethiopia's transforming wheat landscape: Tracking variety use through DNA fingerprinting. Scientific Reports, 10(1), Article 18532. DOI: 10.1038/s41598-020-75181-8. https://doi.org/10.3390/su14137579.

Jaleta, M., Kassie, M., Marenya, P., Yirga, C., Erenstein, O., 2018. Impact of improved maize adoption on household food security of maize producing smallholder farmers in Ethiopia. Food Security 10(1), 81–93. DOI: 10.1007/s12571-017-0759-y.

Kaufman, L., Rousseeuw, P.J., 1990. Finding groups in data: an introduction to cluster analysis. John Wiley and Sons. DOI: 10.1002/9780470316801.

Kelly, A.M., Smith, A.B., Eccleston, J.A., Cullis, B.R., 2007. The accuracy of varietal selection using factor analytic models for multi-environment plant breeding trials. Crop Science 47(3), 1063–1070. DOI: 10.2135/cropsci2006.08.0540.

Kumar, N., Rana, M., Mehta, B., Chand, S., Shiv, A., Wani, S.H., Kumar, S., 2021. Genomic selection for wheat improvement. In: Wani, S.H. (Ed.) Physiological, molecular, and genetic perspectives of wheat improvement. Switzerland: Springer Nature Switzerland AG, 175–194. DOI: 10.1007/978-3-030-59577-7_9.

Lopez-Oriona, A., Sun, Y., Vilar, J.A., 2025. Improving the prediction accuracy of statistical models: A new hierarchical clustering approach. Statistics and Computing 35(6). DOI: 10.1007/s11222-025-10683-x.

Mekonen, G.S., 2025. Progress and limitations in Ethiopian irrigated wheat (*Triticum aestivum* L.) production: A review. Research and Development 6(2), 35–38. DOI: 10.11648/j.rd.20250602.12.

Messele, M.T., Zewotir, T., Derese, S.A., Belay, D.B., Shimelis, H., 2023. Linear mixed model to identify the relationship between grain yield and other yield related traits and genotype selection for sorghum. Heliyon 9(7), e17825. DOI: 10.1016/j.heliyon.2023.e17825.

Mohammadi, S.A., Prasanna, B.M., 2003. Analysis of genetic diversity in crop plants-salient statistical tools and considerations. Crop Science 43(4), 1235–1248. DOI: 10.2135/cropsci2003.1235.

Mullualem, D., Tsega, A., Mengie, T., Fentie, D., Kassa, Z., Fassil, A., Wondaferew, D., Gelaw, T.A., Astatkie, T., 2024. Genotype-by-environment interaction and stability analysis of grain yield of bread wheat (*Triticum aestivum* L.) genotypes using AMMI and GGE biplot analyses. Heliyon 10(12), e32918. DOI: 10.1016/j.heliyon.2024.e32918.

Murtagh, F., Contreras, P., 2012. Algorithms for hierarchical clustering: an overview. WIREs Data Mining and Knowledge Discovery 2, 86–97. DOI: 10.1002/widm.53.

Murtagh, F., Contreras, P., 2017. Algorithms for hierarchical clustering: An overview, II. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery 7(6), e1219. DOI: 10.1002/widm.1219.

Mwadzingeni, L., Shimelis, H., Dube, E., Laing, M.D., Tsilo, T.J., 2016. Breeding wheat for drought tolerance: Progress and technologies. Journal of Integrative Agriculture 15(5), 935–943. DOI: 10.1016/S2095-3119(15)61102-9.

Marzinger, T., Kotik, J., Pfeifer, C., 2021. Application of hierarchical agglomerative clustering (HAC) for systemic classification of pop-up housing (PUH) environments. Applied Sciences 11(23), 11122. DOI: 10.3390/app112311122.

Olivera, P.D., Newcomb, M., Szabo, L.J., Rouse, M., Johnson, J., Gale, S., Luster, D.G., Hodson, D.P., Cox, T.S., Jin, Y., 2015. Phenotypic and genotypic characterization of race TKTTF of *Puccinia graminis* f. sp. tritici that caused a wheat stem rust epidemic in Ethiopia in 2013–14. Phytopathology 105(7), 917–928. DOI: 10.1094/PHYTO-11-14-0302-FI.

Olivoto, T., Lucio, A.D., 2020. metan: An R package for multi-environment trial analysis. Methods in Ecology and Evolution 11(6), 783–789. DOI: 10.1111/2041-210X.13384.

Qiao, C.G., Basford, K.E., DeLacy, I.H., Cooper, M., 2000. Evaluation of experimental designs and spatial analyses in wheat breeding trials. Theoretical and

Applied Genetics 100(1), 9–16. DOI: 10.1007/s001220050002.

Shewry, P.R., Hey, S.J., 2015. The contribution of wheat to human diet and health. Food and Energy Security 4(3), 178–202. DOI: 10.1002/fes3.64.

Shewry, P.R., 2009. Wheat. Journal of Experimental Botany 60(6), 1537–1553. DOI: 10.1093/jxb/erp058.

Smith, A., Cullen, B., Thompson, R., 2001. Analyzing variety by environment data using multiplicative mixed models and adjustments for spatial field trend. Biometrics 57(4), 1138–1147. DOI: 10.1111/j.0006-341x.2001.01138.x.

Smith, A.B., Cullis, B.R., 2018. Plant breeding selection tools built on factor analytic mixed models for multi-environment trial data. Euphytica 214, 143. DOI: 10.1007/s10681-018-2220-5.

Sukumaran, S., Dreisigacker, S., Lopes, M., Chavez, P., Reynolds, M.P., 2015. Genome-wide association study for grain yield and related traits in an elite spring wheat population grown in temperate irrigated environments. Theoretical and Applied Genetics 128, 353–363. DOI: 10.1007/s00122-014-2435-3.

Tadesse, W., Sanchez-Garcia, M., Assefa, S., Amri, A., Bishaw, Z., Ogbonnaya, F.C., 2019. Genetic gains in wheat breeding and its role in feeding the world. Crop Breeding, Genetics and Genomics 1(1), e190005. DOI: 10.20900/cbgg20190005.

Tajalifar, M., Rasooli, M., 2022. Importance of BLUP method in plant breeding. Journal of Plant Science and Phytopathology 6, 040–042. DOI: 10.29328/journal.jpsp.1001072.

Valdez-Rodriguez, Y.R., Huerta-Espino, J., Benítez-Riquelme, I., Dreisigacker, S., Santacruz-Varela, A., Mendoza-Castillo, M.C., 2025. Genetic analysis of resistance to Puccinia triticina Erikss. in *Triticum spelta* L. Frontiers in Bioscience-Scholar 17(3), 39712. DOI: 10.31083/FBS39712.

Wang, K., Fu, B.X., 2020. Inter-relationships between test weight, thousand kernel weight, kernel size distribution and their effects on durum wheat milling, semolina composition and pasta processing quality. Foods 9(9), 1308. DOI: 10.3390/foods9091308.

Watson, A., Ghosh, S., Williams, M.J., Cuddy, W.S., Simmonds, J., Rey, M.D., Md Hatta, M.A., Hinchliffe, A., Steed, A., Reynolds, D., Adamski, N.M., Breakspear, A., Korolev, A., Rayner, T., Dixon, L.E., Riaz, A., Martin, W., Ryan, M., Edwards, D., Batley, J., Raman, H., Carter, J., Rogers, C., Domoney, C., Moore, G., Harwood, W., Nicholson, P., Dieters, M.J., DeLacy, I.H., Zhou, J., Uauy, C., Boden, S.A., Park, R.F., Wulff, B.B.H., Hickey, L.T., 2018. Speed breeding is a powerful tool to accelerate crop research and breeding. Nature Plants 4, 23–29. DOI: 10.1038/s41477-017-0083-8.

Yan, J., Zhao, Y., Zhang, X., Wang, H., 2024. Comparative study of single-trait and multi-trait genomic best linear unbiased prediction models in plant breeding. Animals 14(20), 2961. DOI: 10.3390/ani14202961.

Yan, W., Kang, M.S., Ma, B., Woods, S., Cornelius, P.L., 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Science 47(2), 641–653. DOI: 10.2135/cropsci2006.0374.