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Genotype and Environment Interaction and Yield Stability Analysis of Hexaploid Wheat (Triticum aestivum L.) Using AMMI and GGE Biplot Models under Contrasting Agro-Climatic Conditions

Syed Asad Abbas
Student, College of Agriculture, University of Sargodha
syedasadabbas2012@gmail.com

Dr. Naeem Akhtar
Associate Professor, Department of Plant breeding and Genetics, University of Sargodha
naeem.siraj@uos.edu.pk

Tanzila Aslam
Senior Scientific Assistant (Pakistan Navy) and Government College Women University, Faisalabad
tanzilaaslam@gcwuf.edu.pk

Syed Asghar Hussain Shah
, Principal Scientist (SF) Soil and Water Testing Laboratory for Research Sargodha.
asghar2626@gmail.com

Iffat Naseem
Entomologist, Lahore
Iffatnaseem533@gmail.com

Aftab Ahmad Sheikh
Chief Scientist (Rtd) Agriculture Department, Punjab, Lahore.
aftabas@yahoo.com

Dr Najma Parveen
Senior scientist, Maize Research Station, AARI, Faisalabad
najma.awais@yahoo.com

Shoaib Anwar Kohli
Scientific Officer, Fodder Research Institute, Sargodha
shoaibkohli2@gmail.com

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ABSTRACT

Bread wheat (Triticum aestivum L.) is a strategic cereal crop for global food security, yet its productivity is increasingly threatened by climate variability and environmental heterogeneity. This study evaluated genotype × environment (G × E) interaction and yield stability of hexaploid wheat genotypes under contrasting agro-climatic conditions using combined ANOVA, AMMI, GGE biplot, and correlation analyses. The combined ANOVA revealed highly significant ($p \leq 0.01$) effects of genotypes, environments, and G × E interaction, indicating substantial genetic variability and differential genotype responses across testing sites. AMMI analysis partitioned the interaction variance into significant principal components, identifying stable genotypes with near-zero IPCA scores and specifically adapted genotypes with large interaction effects. GGE biplot analysis further illustrated the “which-won-where” pattern and delineated mega-environments, enabling identification of superior and widely adapted genotypes. Correlation analysis revealed positive associations between grain yield and key agronomic traits, suggesting the potential for indirect selection to enhance breeding efficiency. The integration of parametric and multivariate stability models improved the precision of genotype evaluation and selection. Overall, the study identified high-yielding and stable genotypes suitable for broad adaptation and highlighted the importance of multi-environment testing in wheat breeding programs aimed at enhancing productivity and resilience under climate variability.

Keywords; AMMI; Genotype × environment interaction; GGE biplot; Stability analysis; Wheat yield

Introduction

Wheat (Triticum aestivum L.) is regarded as one of the most significant staple cereal crops in the world and has a major role in world food security. It plays a significant role in the total caloric and protein intake in the daily and especially in the developing states as population growth has remained a strain in the food production systems (FAO, 2021) . Climatic variability, the amalgamations of soils and the practices of cultivating crops serve to have a great effect on wheat productivity in different countries with different agro-ecological regions, and as a result, they establish contrasting production environments. To maintain and even elevate the yield of wheat under such fluctuating conditions is an ultimate goal of breeding schemes in modern times.

Wheat grain yield is a quantitative complex trait which is regulated by several genes and to a large extent by the environmental factors. These genotype x environment (G x E) interaction is conferred by the differentiality of genotypes to the environment, making it difficult to detect better cultivars (Allard and Bradshaw, 1964) . Genotype rankings are likely to shift between environments when there is a significant G x E interaction which lowers the extent by which one can use the mean yield performance as a determinant of selection. Thus, it is vital to know the character and the intensity of the interaction between G x E to be able to develop cultivars and recommend them effectively.

Multi-environment trials (METs) are commonly implemented to test the performance of genotypes within a variety of different environments and to isolate the total variation into genotype, environment, and G x E interaction factors. Nevertheless, the existence of considerable G x E interaction tends to weaken the normal analysis of variance in detecting steady and commonality adapted genotypes (Zobel et al., 1988) . As a result, a number of statistical methods have been invented to determine adaptability and provide stability with greater accuracy.

The initial stability tests were based on regressions. The linear regression model suggested by Finlay and Wilkinson (1963) takes into account the response of genotypes to the environmental index but the model by Eberhart and Russell (1966) includes both the regression coefficient and regression deviation as an expression of adaptability and stability. These models make a difference between the genotypes that are general in their adaptability and those that are specialized in their adaptation to the environment. Subsequently, other parameters of stability were proposed but in the form of non parametric and variance based stability parameters, the stability variance of Shukla (Shukla, 1972) and the rank sum approach chosen by Kang (Kang, 1993) are parameters that allow yield and stability to be selected simultaneously. Becker and

Leon (1988) also categorized concepts of stability and emphasized on the fact that they had to choose the genotypes not only in terms of their performance but also in terms of consistency.

Most traditional methods though convenient tend to have linear responses and trying to explain complex patterns of interaction may not be able to serve the purpose. In order to eliminate these shortcomings, there are multivariate statistical models that have been created. Additive Main Effects and Multiplicative Interaction (AMMI) model combines analysis of variance of the main effects which are additive; and principal component analysis of the interactive effects which is multiplicative (Gauch, 1992) . This method not only increases the comprehension of the structure of interaction, but also increases the accuracy of the evaluation of genotypes. It was proven by Gauch and Zobel (1997) that by dividing noise and real interaction signals, AMMI analysis is more predictive.

The Genotype plus Genotype x Environment (GGE) biplot methodology is also another powerful graphical methodology. In contrast with AMMI, dividing the genotype and environment and interaction effects, the biplot of GGE is centered on the most important genotype and G x E interaction effects (Yan et al., 2000) to evaluate a genotype. The technique gives visual aids like which-won-where, identification of mega- environment and ratings of genotypes by mean performance and stability (Yan and Kang, 2003) . Such graphical representations can help breeders to find broadly and specially adapted genotypes.

As stated in the work by Annicchiarico (2002), the cultivar adaptation should be considered in the framework of the target environment, especially in the areas where the degree of climatic variation is high. Hence a combination of parametric stability statistics and more multivariate models like AMMI and GGE biplot ensure a complete analytical scheme of interpreting G x E interaction and being able to come up with better genotypes.

Considering the significance of production of wheat species with different agro-climatic features and considering the presence of high G x E interaction, the current experiment seeks to compare hexaploid wheat genotypes with AMMI and GGE biplot models. This study aims at solving the problem by combining the old stability parameters with the new multivariate to come up with high yielding and stable genotypes in a variety of environmental conditions and thus help in the implementation of the sustainable wheat improvement programs.

Research Methdology

Statistical Analysis

All the statistical tests were done to measure the strength of genotype x environment (G x E) interaction and to select high yielding and stable hexaploid wheat genotype in the varying agro-climatic ambiance. Data on the yield of grains obtained in any of the environments were initially analyzed done separately per environment to determine the experiment precision and then again as a whole across the environments to measure the major components of total variation. The statistical processes were found at the recognized stability analytical models and multi-variable models, which were mentioned in the thesis and that bring about methodological rigor and comparability with the past wheat improvement study.

Combined Analysis of Variance

An analysis of variance (ANOVA) in all the test environments was used to establish the significance of the effect of genotype (G), environment (E) and genotype x environment (G x E) on the yield of grain. The model concerned genotypes as fixed effects and environments as random effects so as to be able to infer on genotype performance in varied agro-climatic environments. The overall amount of squares was decomposed into those components which could be attributed to genotypes, environments, G x E interaction and experimental error.

The environment effect showed the differentiation between sites because of a rise in the climatic and edaphic variability whereas the genotype effect showed the genetic variation that exists between the wheat entries. G x E interaction component involved the study of the dissimilar genotype reactions in the different environments. An interaction of significant value meant that there was a lack of consistency in the ranking of genotypes and an indication of additional consistency analysis. This analysis scheme adheres to the principles outlined on multi-environment trials in crop research enhancement studies.

AMMI Analysis

Additive Main Effects and Multiplicative Interaction (AMMI) model was also used to investigate even more the nature of G x E interaction. The AMMI method combines additive main effects analysis of variance (genotype and environment) and multiplicative interaction effects analysis (principal component analysis (PCA)).

Here, the G x E interaction sum of squares derived as a result of ANOVA was broken down into Interaction Principal Component Axes (IPCAs). The components of IPCA were tested to identify which percentage of axes of interaction were meaningful and thus to keep. Genotypes that had low IPCA were termed as stable since they had little to do with interactive effects, yet those with very large values of negative or positive outcome were thought to be adjusted to specific environments.

AMMI biplots were produced to show how the relationship between genotypes and the environment looks like. The graphical form helped in the recognition of the stable genotypes which were adapted genotypes and interaction patterns. This type of predictive accuracy is improved by isolating the signal of real interaction and the noise.

GGE Biplot Analysis

Multi-environment trial data were analyzed by the Genotype plus Genotype x Environment (GGE) biplot analysis to produce a graphical representation of the data. As compared to AMMI where the main effects of genotype and environment are separated, GGE is based on G, G x E interaction effects that are most pertinent with regard to cultivar evaluation.

GGE biplot was built on the basis of the first two principal components as a result of the single value decomposition on the basis of the environment-centered yield data. The winning genotypes in various sectors and the definition of possible mega-environment was determined using the so-called which-won-where polygon view. The average environment coordination (AEC) technique was used to rank the genotypes by the average performance and stability.

In addition, there was use of a standard of ideal genotype to distinguish between entries that have high mean yield and the maximum stability. In the same way, the "ideal environment" was decided on account of the discriminating ability and representativeness. This carried out genotype adaptability on bases of different agro-climatic situations with the help of the graphical interpretation, providing the global understanding.

RESULTS AND DISCUSSION

Analysis of Variance and Mean Comparison

Plant Height (cm)

The ANOVA of the plant height showed that the environments, genotype and the interaction been significant at $p = 0.05$, suggesting that the growing conditions were strong and the genetic variation of the tested genotypes were significant on the height of the plants (Alemayehu et al., 2025). The magnitude of the genotype effect (Table 4.1.1) implies that there is sufficiently large variation in the genotype regarding height of plant, which implies that there are possibilities to selectively enhance such phenotype among genotypes as previously noted by Ashkar et al. (2023). Equally, there was also a genotype × environment interaction with $p < 0.05$ value implying that all genotypes themselves were not similarly expressed in all environments nor did all of them vary equally in some traits such as height in the presence of new environmental conditions (Eskezia et al., 2025). The replication effects were not found to be significant ($p > 0.05$) to show that the experimental error was kept to a minimum, and it had no bearing on the overall line of results (Gomez & Gomez, 1984). In addition, a fairly small error in the data indicated the consistency of the treatment impacts and the data could be utilized in the further analysis (Montgomery, 2017). Clearly differing heights of the plants precipitated by the environment were observed.

The mean values of plant height revealed that the highest mean value of plant height (97.70 cm) was obtained at Sargodha but the lowest (84.82 cm) was obtained at Layyah. Gujranwala (88.20 cm) and Chakwal (87.00 cm) measured at moderate level were statistically similar to each other (Figure 4.1.1 A). There was also genotypic variation in that Akbar-2019 had a mean height of 95.46 cm slägt which is followed by G-7 (94.38 cm) and Dilkash-2021 (93.55 cm) which places these genotypes as some of the taller responses (Figure 4.1.1 B). The variations between the genotypes suggest not only the practical genotypic variability but also the presence of the genetic determination of the height of plants (Bubuche et al., 2025). The genotype x environment interaction pattern showed reduction in height expression across sites. Genotype G-7 and G-4 were greater than 105 cm in Sargodha with same genotypes being shorter in other places (Figure 4.1.1 C; Dabi et al., 2021). These changes have shown that the height of the plant depends on the genetic composition besides the environmental factors and predetermines the sensitivity of this characteristic to this environment (Khare et al., 2024).

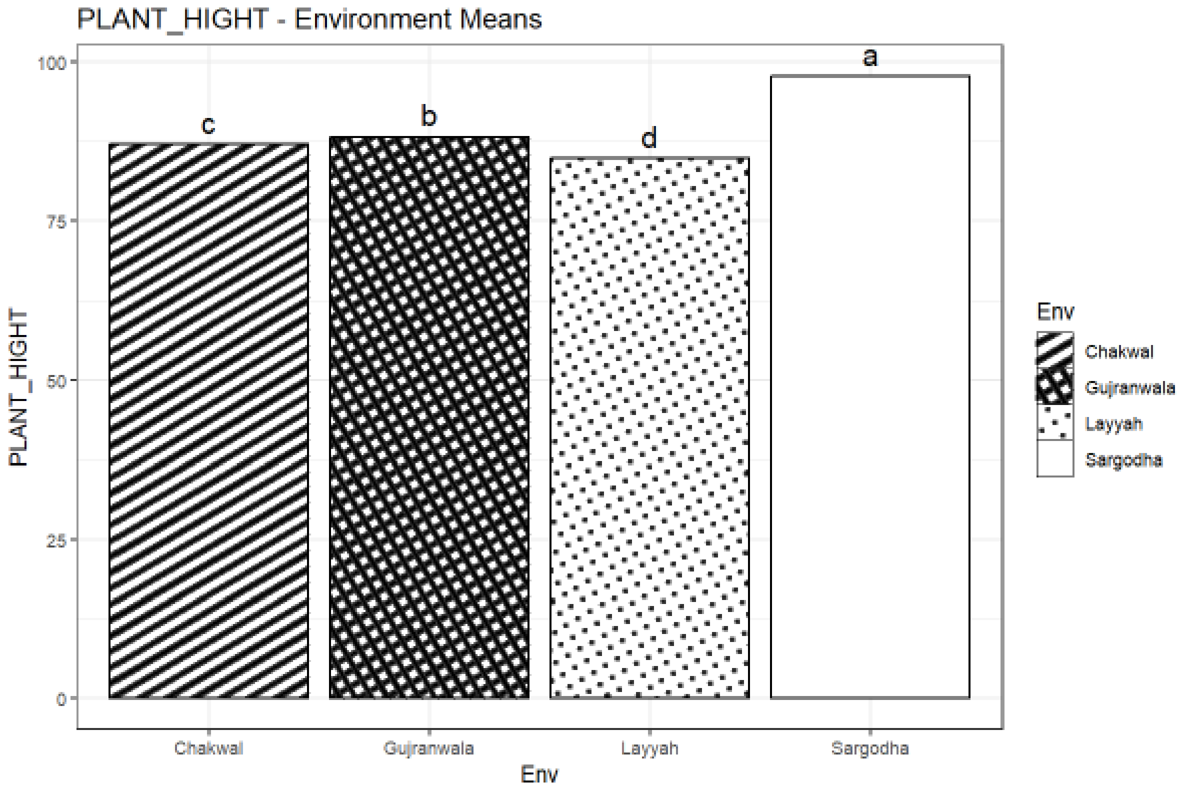

Figure 1 (A): Means comparison of plant height (cm) across multi-environments

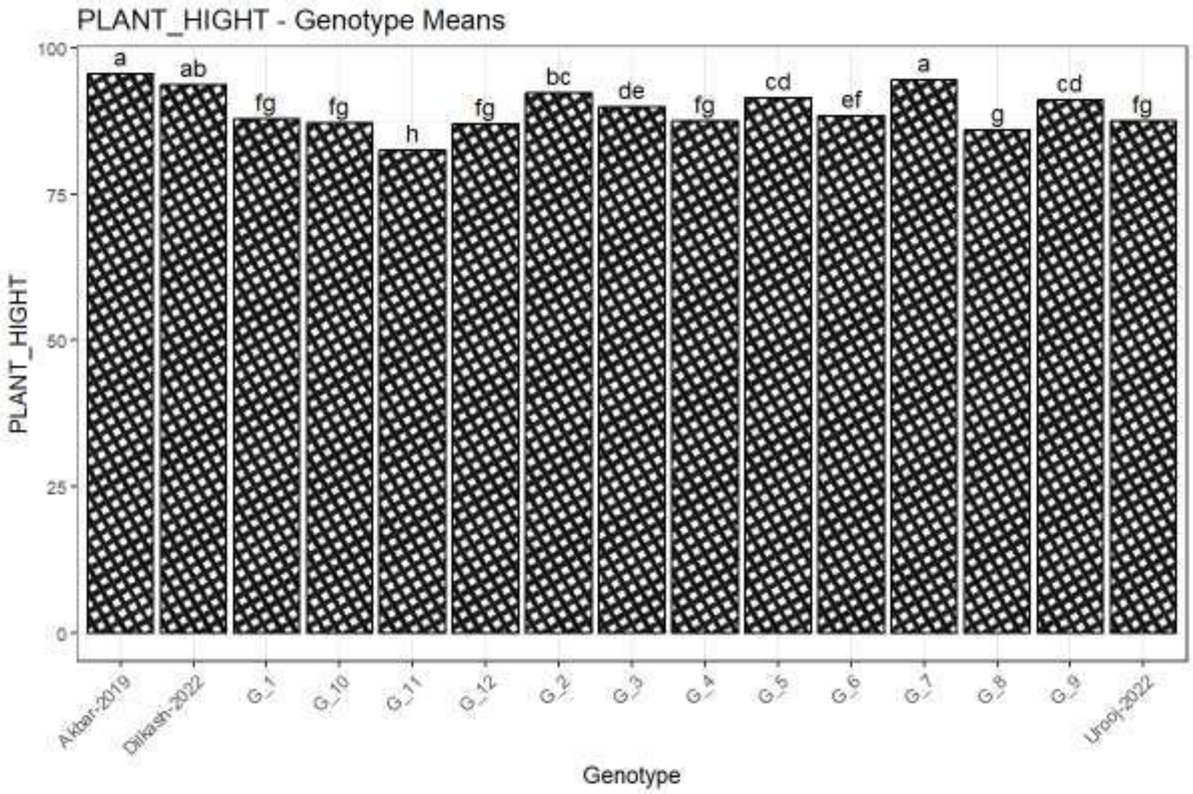

Figure 1 (B): Means comparison of plant height (cm) among studied genotypes

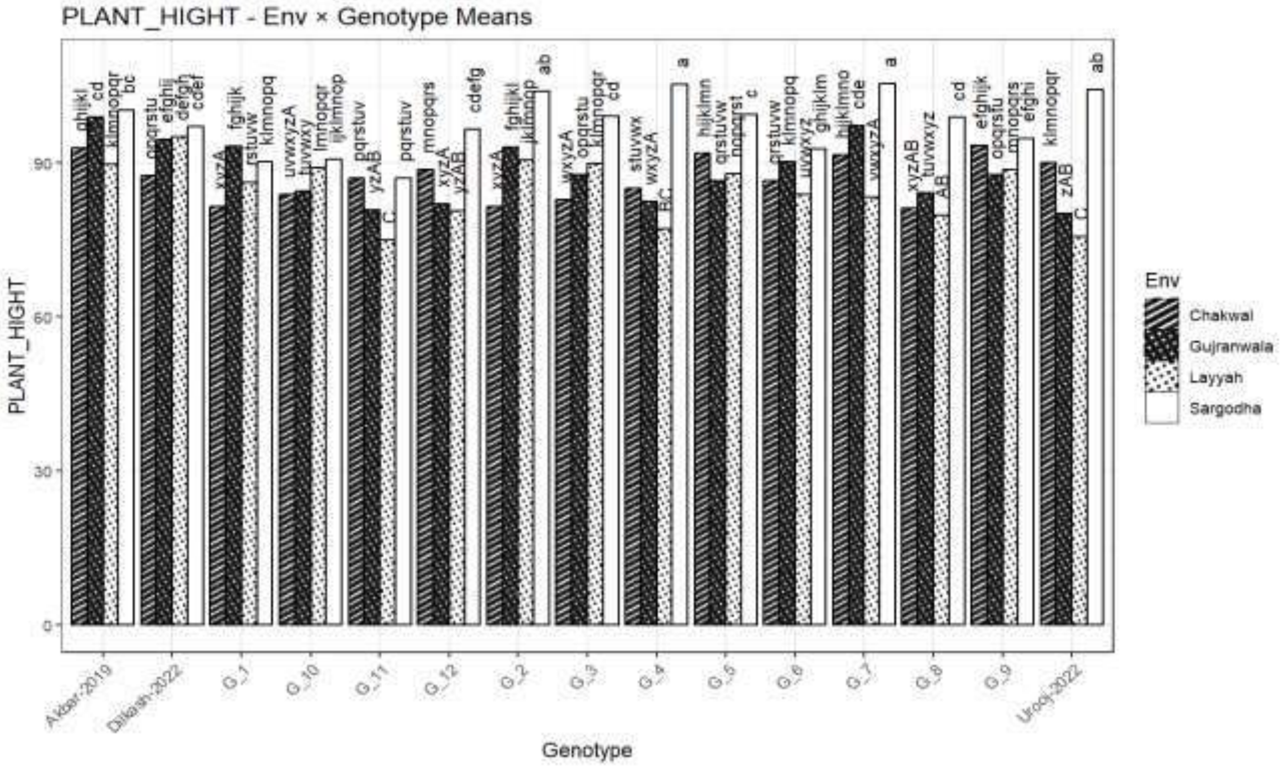

Figure 1 (C): Means comparison of plant height (cm) for G × E interaction across multi-environments

Number of Tillers per Plant

The ANOVA findings regarding the number of tillers per plant revealed that all environment, genotype, and their or interaction were significant at p 56 -1 signifying the presence of genetic disparity along with differences between environments in the formation of tillers (Dong et al., 2023). The genotype effect shown in Table 4.1.2 was significant ($p \leq 0.05$), which implied that genetic variation among genotypes was satisfactory in relation to tillering establishment ability and their preferred traits to selection (Bubuche et al., 2025). The massive interaction of genotypes and the environment ($p = 0.05$) also meant that even in time different genotypes did not react in a similar way to the environmental conditions because some entries reacted with higher or lower levels of tiller numbers to microclimate conditions of experimental field (Eskezia et al., 2025). The replicate effects were non-significant ($p > 0.05$) which meant that experimental error was also not out of hand and did not play a role in the treatment differences observed (Gomez & Gomez, 1984). The fact that the residual variation was low also pointed to the reliability of the data that may then be further analyzed, statistically (Montgomery, 2017).

There was apparent variation in tiller number in every environment. Gujranwala (11.26) and Sargodha (11.06) had maximum mean tillers number with Chakwal (10.43) coming second with about 2 extra tillers than Layyah (8.67) (Aqib et al., Trumpet, 2017) (Figure 4.1.2 A). Genotypic means also were highly diverse, G -7 topped in the number of tillers per plant (13.78) and G -9 (12.41) and G -5 (11.79), respectively. However, the number of tillers per plant was found moderate in Akbar-2019 (10.84) and G-3 (10.64) displaying a beneficial genetic diversity of this characteristic (Figure 4.1.2 B). The genotype by environment interaction pattern further indicated that the production of the tiller varied in different locations since certain genotypes were more successful at producing more tillers in one location than the other (Dabi et al., 2021). Such results are congruent with environmentally sensitive traits that show a high genetic by environment interaction in trait expression (Khare et al., 2024) and the joint effect of early season management choices.

Table 1. Analysis of variance for number of tillers per plant in studied wheat genotypes under multi-environments.

SOV	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Environments	3	187.44	62.48	131.66	0
Replications	2	2.37	1.19	2.5	0.09
Genotypes	14	318.84	22.77	47.99	0
E × G	42	73.27	1.74	3.68	0
Residuals	118	56	0.47		

$P \leq 0.05$ = significant; $P \leq 0.01$ = highly significant; $P > 0.05$ = non-significant

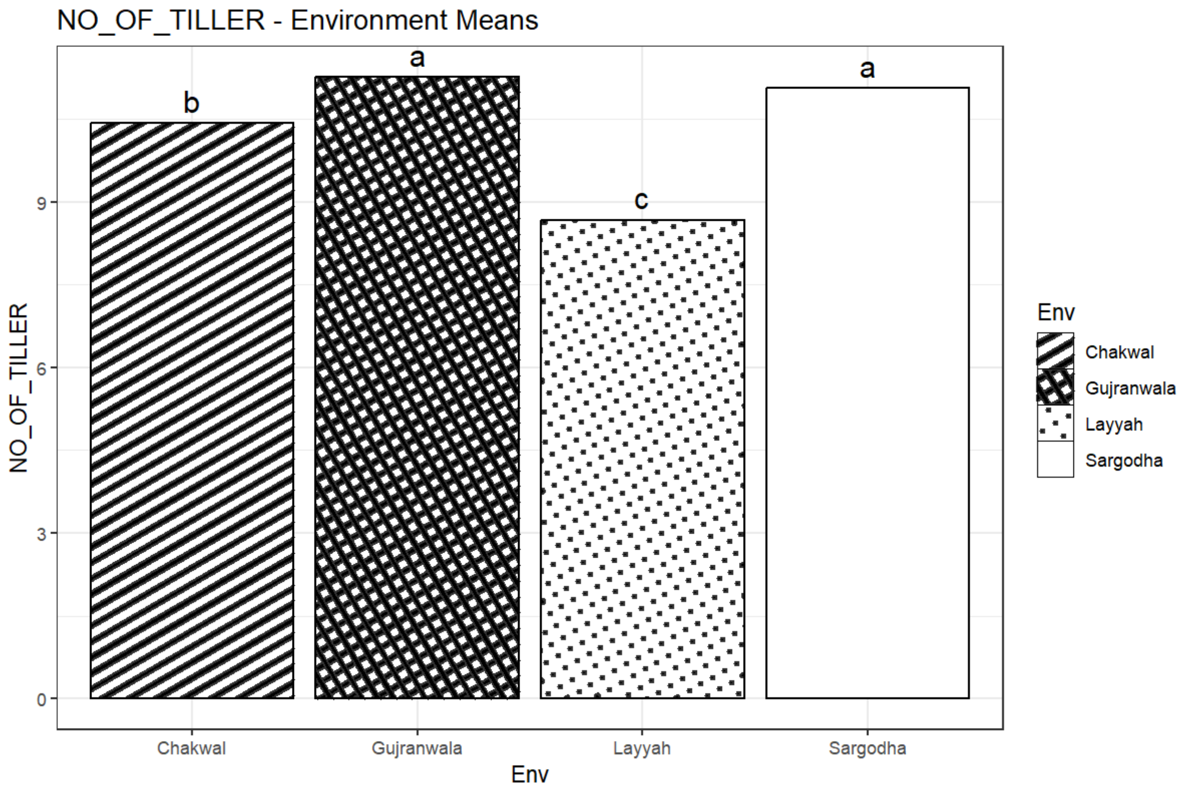

Figure 2 (A). Means comparison of number of tillers per plant of multi-environments

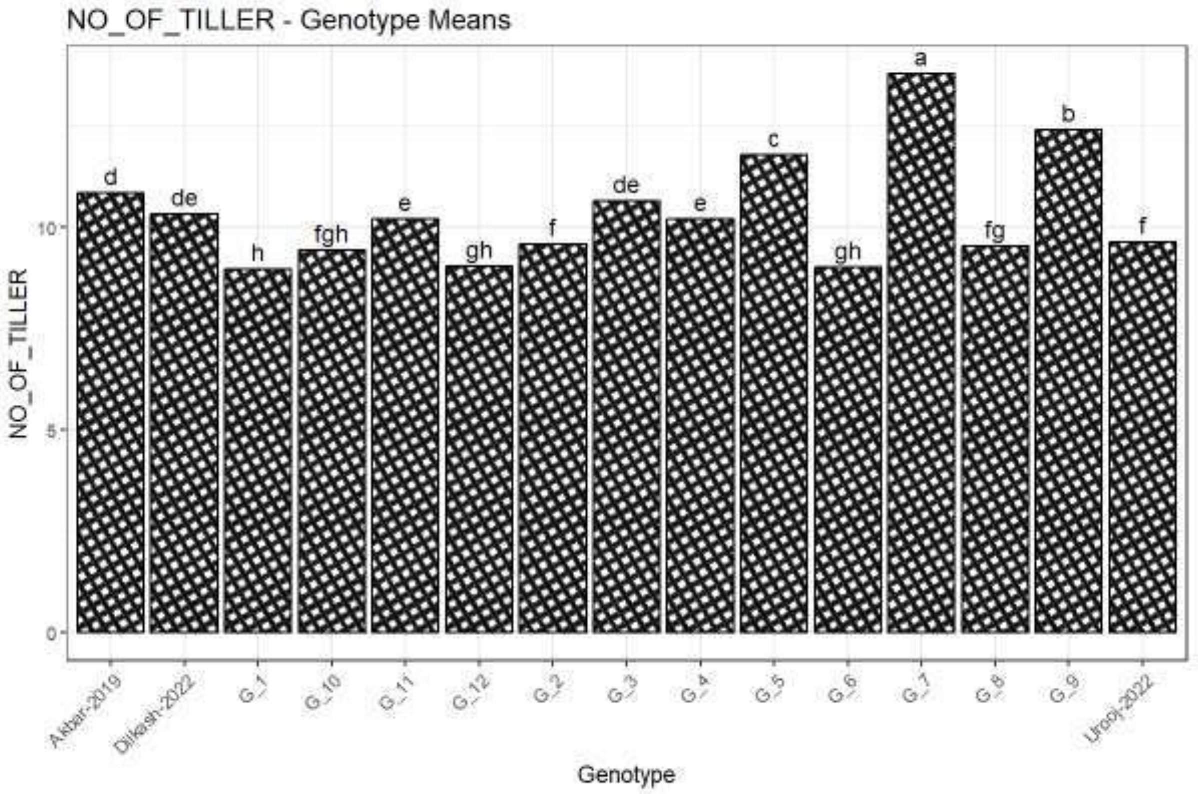

Figure 2 (B) Means comparison of number of tillers per plant in studied genotypes

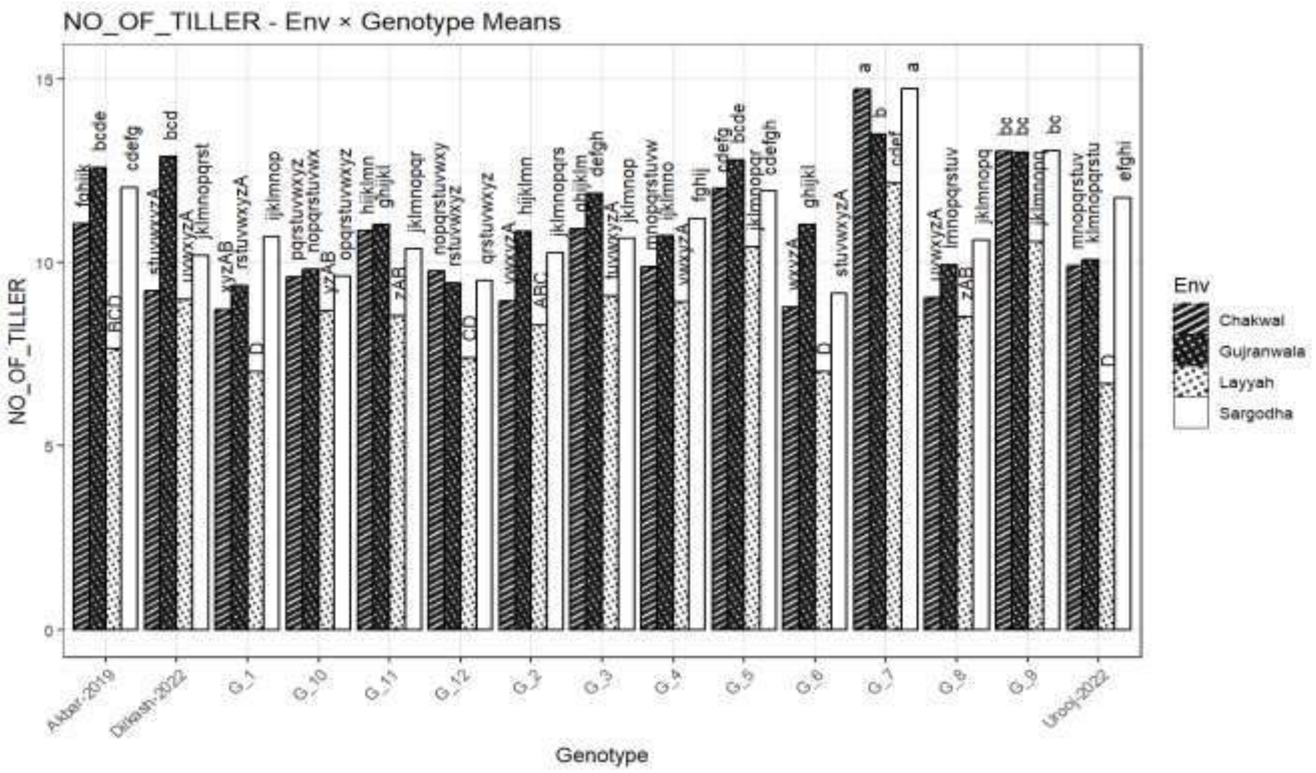

Figure 2 ©. Means comparison of number of tillers per plant for G x E interaction in multi-environments

Peduncle Length (cm)

The analysis by variance of peduncle length showed that there were significant effects in environments (E), genotypes (G) and interaction of genotypes and environments (G x E) at p [?] 0.05 (Table 4.1.3).This indicates that variability in the trait is explained by the presence of variation in the environment, or the genotype (Alemayehu et al., 2025). The genotype effects are significant (p [?] 0.05) which means that peduncle length has an appropriate amount of variability that can be subjected to selection and gains (Ashkar et al., 2023). The fact that the interaction of G x E was significant (p [?] 0.05) also indicated that the peduncle length did not correlate uniformly at the different locations, and certain genotypes experienced dramatic change upon altering the same environment (Eskezia et al., 2025). The effects of replication too were not significant (p > 0.05) which implied that there was a maintenance of the accuracy of the experiment and that random error did not conceal the treatment differences (Gomez &

Gomez, 1984). Besides, the little left deviation is the sign of a high stability of the data and the trust in the interpretation of these findings (Montgomery, 2017).

The average peduncle length of various environments indicated that the various environment had important impacts on the manifestation of peduncle length. Records of the tallest length of peduncles were recorded at Sargodha (33.10 cm) and Gujranwala locations followed by Chakwal (29.92 cm) and Dilkash-2021 with the last one being the lowest and genotypic performance at Akbar-2019 (33.68 cm), then G-2, and Dilkash-2021 following Akbar-2019 because it is in the upper range relative to the other entries recorded in the Figure 4.1. This diversity implies that there is a genetic variation on peduncle length subject to exploitation (Bubuche et al., 2025). The phenotypic information on the peduncle length at the jointing stage also revealed that the environment had a bearing on the phenotypic expression of this trait as certain genotypes were doing better in one site compared to the other (Figure 4.1.3 C; Dabi et al., 2021). Such variability suggests the polygenic tendencies of the variation in the length of the peduncle and the interplay of the environment (Khare et at., 2024).

Table 2. Analysis of variance for peduncle length (cm) in studied wheat genotypes under multi-environments.

SOV	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Environments	3	469.44	156.48	123.77	0
Replications	2	4.33	2.16	1.71	0.19
Genotypes	14	540.08	38.58	30.51	0
E × G	42	1008.46	24.01	18.99	0
Residuals	118	149.19	1.26		

$P \leq 0.05$ = significant; $P \leq 0.01$ = highly significant; $P > 0.05$ = non-significant

Spike Length (cm)

Another grain yield giving attribute of wheat plant is spike length. The results of ANOVA represented that the environment, genotypes, and their interaction had significant effects on the spike length at p 0.05 or less (Table (4.1.4). This trend showed the variation in spike length was controlled by genetic (Alemayehu et al., 2025) as well as environmental condition in the field. In addition, the large genotype effects at ($p \leq 0.05$) showed that enough variation existed in the genotypes of wheat under study. Therefore, the character of spike length is not so devoid of hereditability to be chosen in wheat as proclaimed by Ashkar et al. 2023). Nonetheless, the significant interaction in genotype and environment ($p \leq 0.05$) showed that there was no homogeneity in the spike length expression across reported locations and certain genotypes responded better to changes in the environment (Eskezia et al., 2025). Replicating effects ($p > 0.05$) did not result in significant which was to denote variability was minimal due to experiment error and did not disperse general outcomes of treatment to the target responses (Gomez and Gomez, 1984). A small residual variation would have gave us a stronger belief on the clarity and reliability of the observed responses (Montgomery, 2017). A spike length difference with high significance indicating its potential significance was revealed by an environmental manner.

Table 3. Analysis of variance for spike length (cm) in studied wheat genotypes under multi-environments.

SOV	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Environments	3	22.18	7.39	33.14	0
Replications	2	0.49	0.24	1.09	0.34
Genotypes	14	87.04	6.22	27.87	0
E × G	42	63.96	1.52	6.83	0
Residuals	118	26.32	0.22		

$P \leq 0.05$ = significant; $P \leq 0.01$ = highly significant; $P > 0.05$ = non-significant

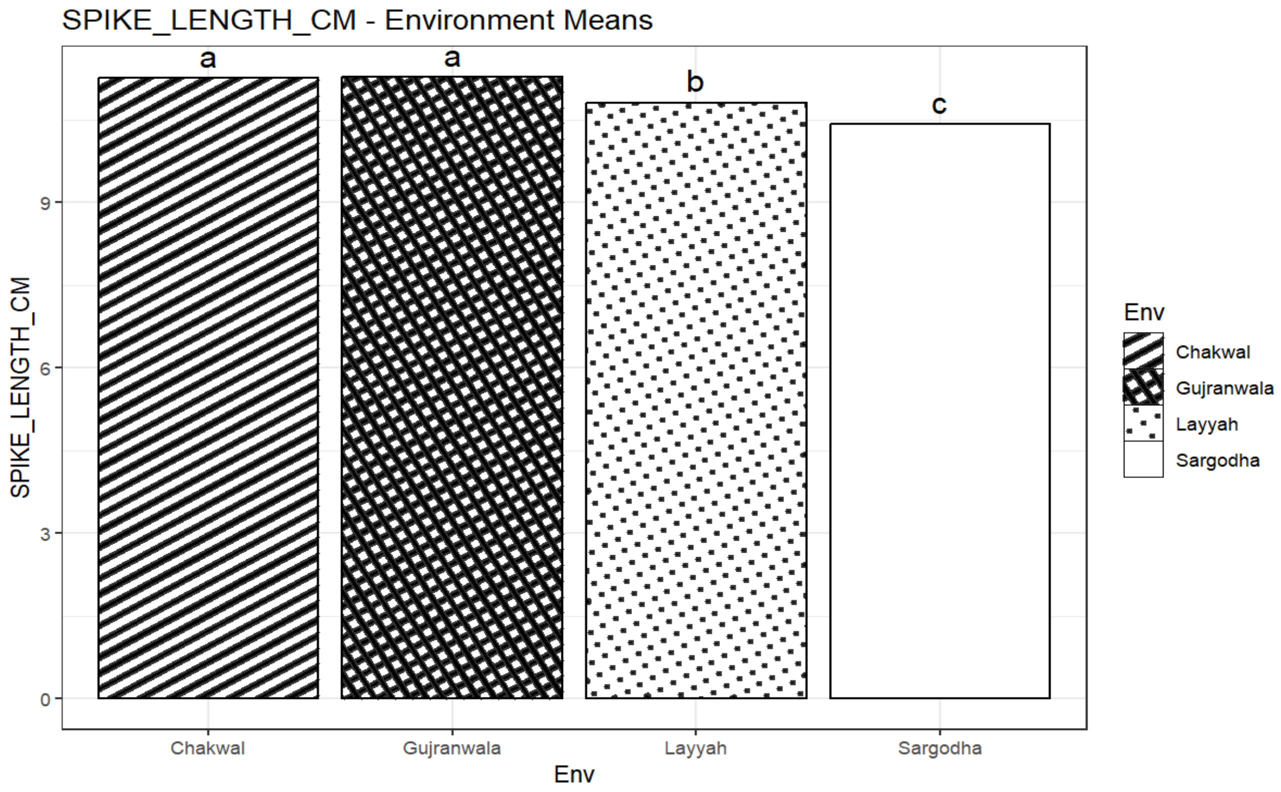

Figure 3 (A) Means comparison of spike length (cm) across multi-environments

Number of Spikelets per Spike

The number of spikelets per spike ANOVA results indicated that the environments, genotypes and their interaction both had a significant effect at the p 0.05 level (Table 4.1.5). It is possible to read it: this trait was subject to both the influence of the genetic composition of the material and to the differences between the environmental conditions of the test places (Al-Sayaydeh et al., 2023). There was significant genotype effect ($p \leq 0.05$) which indicated that spikelet was highly varied between genotypes, which indicated that trait heritable potential is good and is capable of responding to selection (Mullualem et al., 2024). Interaction between the genotypes and the environment was also significant ($p \leq 0.05$), that is, genotypes did not behave equally across the environment. Not all the entries responded equally to the change of the conditions (Andradeet al., 2025). Replication effects, however, were insignificant ($p > 0.05$) and it indicated that the accuracy of the experiment was fairly responsible and did not pertain much on the treatment means due to random error (Finlay & Wilkinson, 1963). The small residual variation further proves how good and consistent the data was so that it could be interpreted (Wricke, 1962).

Table 4. Analysis of variance for number of spikelets per spike in studied wheat genotypes under multi-environments.

SOV	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Environments	3	22.18	7.39	33.14	0
Replications	2	0.49	0.24	1.09	0.34
Genotypes	14	87.04	6.22	27.87	0
E × G	42	63.96	1.52	6.83	0
Residuals	118	26.32	0.22		

$P \leq 0.05$ = significant; $P \leq 0.01$ = highly significant; $P > 0.05$ = non-significant

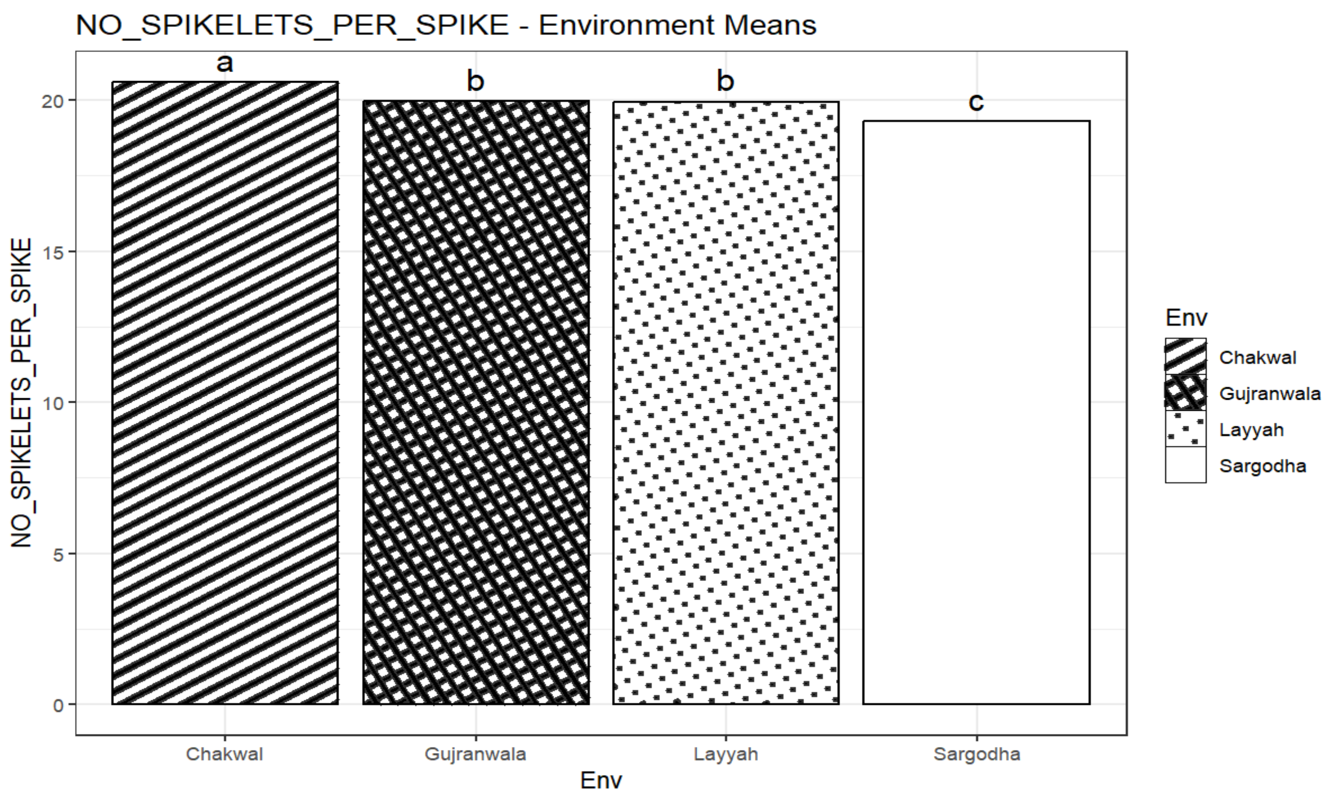

Figure 4. (A) Means comparison of number of spikelets per spike across multi-environments

Grain Yield per Spike (g)

The grain yield per spike table of the ANOVA showed that all or all of environments, genotypes and their interaction were significant ($p \leq 0.05$), i.e. yield per spike changed based on the conditions in the field, also because the genotypes that were used differed in their genetic background (Bishwas et al., 2021). Based on Table 4.1.6, the genotypes effect ($p \leq 0.05$) showed that sufficient variation was found to allow those genotypes to be selected to increase the yield per spike (Krishnappa et al., 2022). Interaction section ($p \leq 0.05$) revealed that yield per spike failed to be constant across all conditions and there were also entries that altered in response to a shift in environmental conditions (Saeidnia et al., 2023). Reproduction remained insignificant ($p > 0.05$), hence the error side turned out to be rather stable and did not interfere with the principal findings (Shukla, 1972).

Table 5. Analysis of variance for grain yield per spike (g) in studied wheat genotypes under multi-environments.

SOV	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Environments	3	1.13	0.38	17.27	0
Replications	2	0.13	0.06	2.97	0.05
Genotypes	14	6.56	0.47	21.53	0
E × G	42	15.69	0.37	17.17	0
Residuals	118	2.57	0.02		

P ≤ 0.05 = significant; P ≤ 0.01 = highly significant; P > 0.05 = non-significant

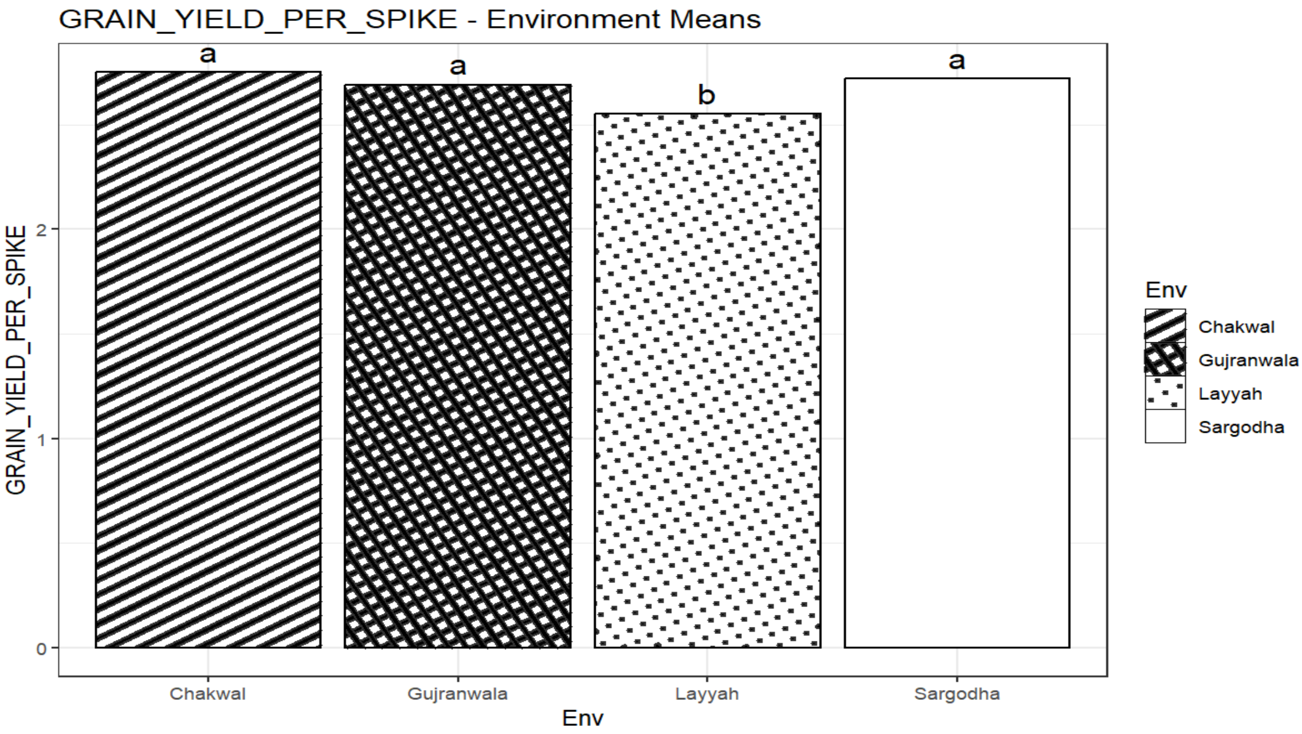

Figure 5. Means comparison of grain yield per spike (g) across multi-environments

Number of Grains per Spike

The result of ANOVA on the number of grains per spike of the spores revealed that the environment, the genotype, and their interaction were all significant ($p \leq 0.05$), which implies that there was variation in number of grains per spike under changing field conditions and also exists between the genotypes due to genetic variation among the entries (Pretini et al., 2021). The genotypes effect was found to be significant ($p \leq 0.05$) as in Table 4.1.7, indicating that there was good genetic variation in grains per spike and it could be selected (Sakuma and Schnurbusch, 2020). The interaction aspect ($p \leq 0.05$) further revealed that the number of grains per spike was not consistently the same at different locations, and there were entries where the performance of the animal was more likely to shift when the environmental conditions were altered depending on the location (Wolde et al., 2021).

Table 6. Analysis of variance for number of grains per spike in studied wheat genotypes under multi-environments.

SOV	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Environments	3	309.44	103.15	41.39	0
Replications	2	18.75	9.38	3.76	0.03
Genotypes	14	1358.53	97.04	38.94	0
E × G	42	3687.53	87.8	35.23	0
Residuals	118	294.03	2.49		

$P \leq 0.05$ = significant; $P \leq 0.01$ = highly significant; $P > 0.05$ = non-significant

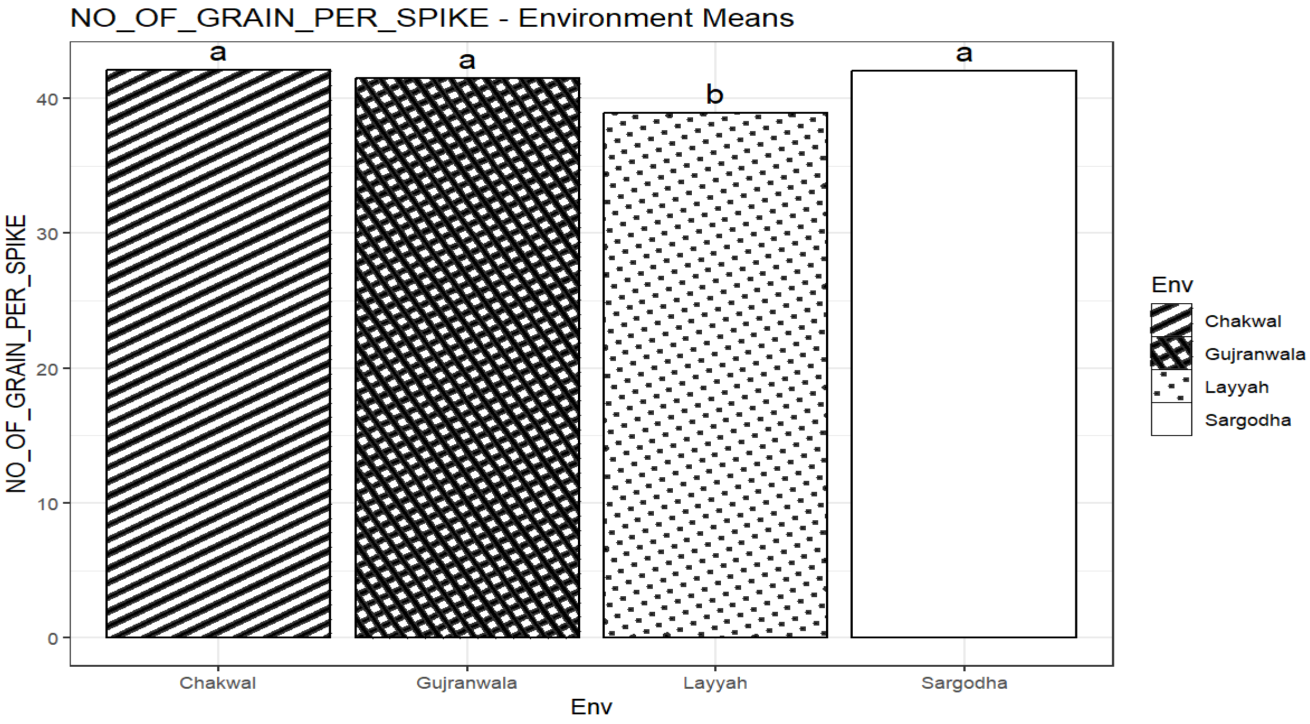

Figure 6 A. Means comparison of number of grains per spike across multi-environments

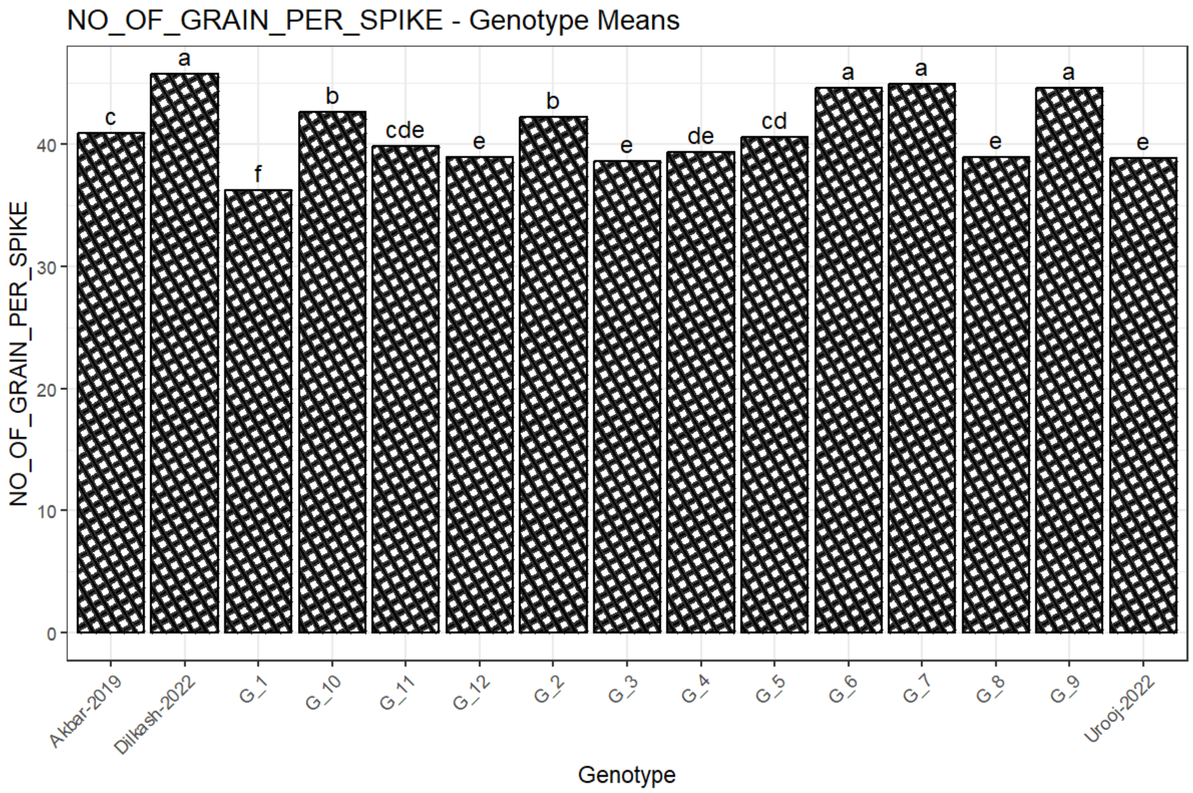

Figure 6 (B). Means comparison of number of grains per spike among studied genotypes

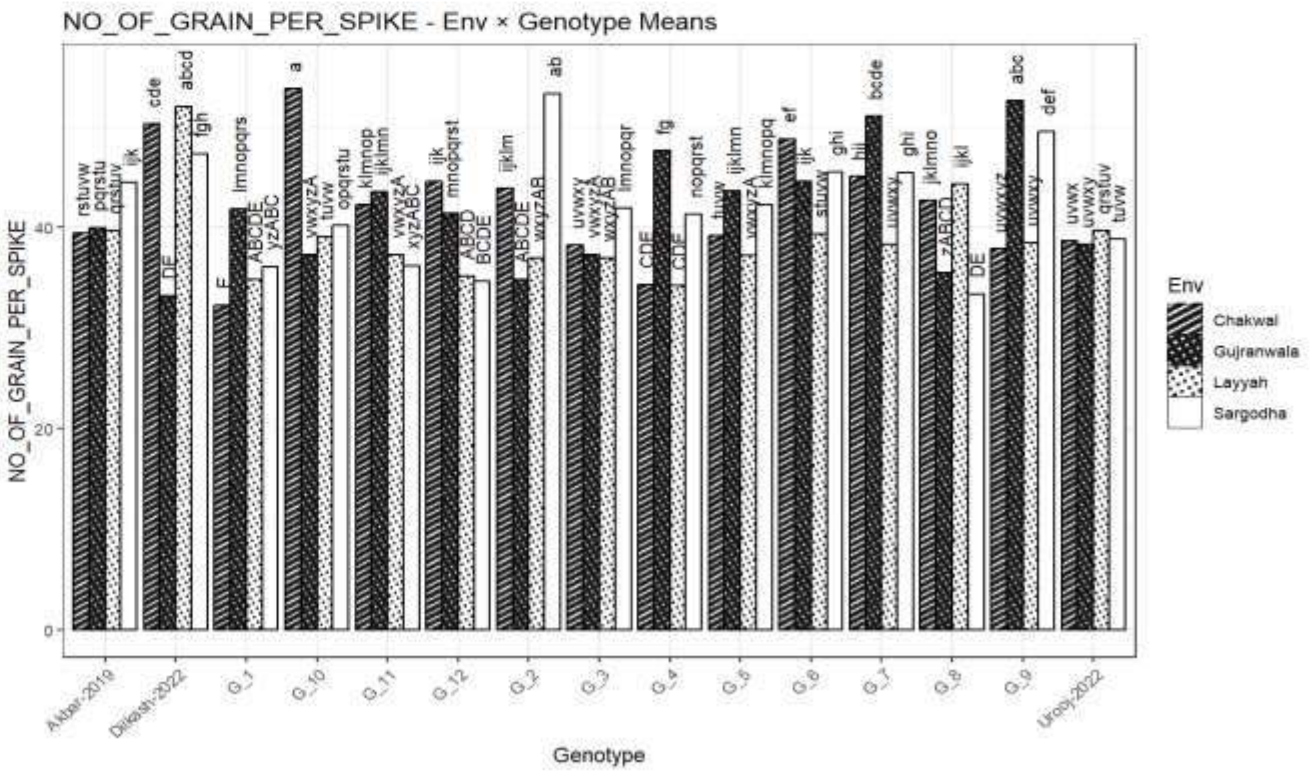

Figure 6 (C) Means comparison of number of grains per spike for G × E interaction across multi-environments

Grain Yield per Plant (g)

Grain yield per plant exhibited highly significant G × E interaction, indicating that genotype ranking changed across locations.

Table 7. Analysis of variance for grain yield per plant (g) in studied wheat genotypes under multi-environments.

SOV	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Environments	3	105.58	35.19	98.42	0
Replications	2	2.6	1.3	3.63	0.03
Genotypes	14	114.94	8.21	22.96	0

E × G	42	346.12	8.24	23.05	0
Residuals	118	42.2	0.36		

P ≤ 0.05 = significant; P ≤ 0.01 = highly significant; P > 0.05 = non-significant

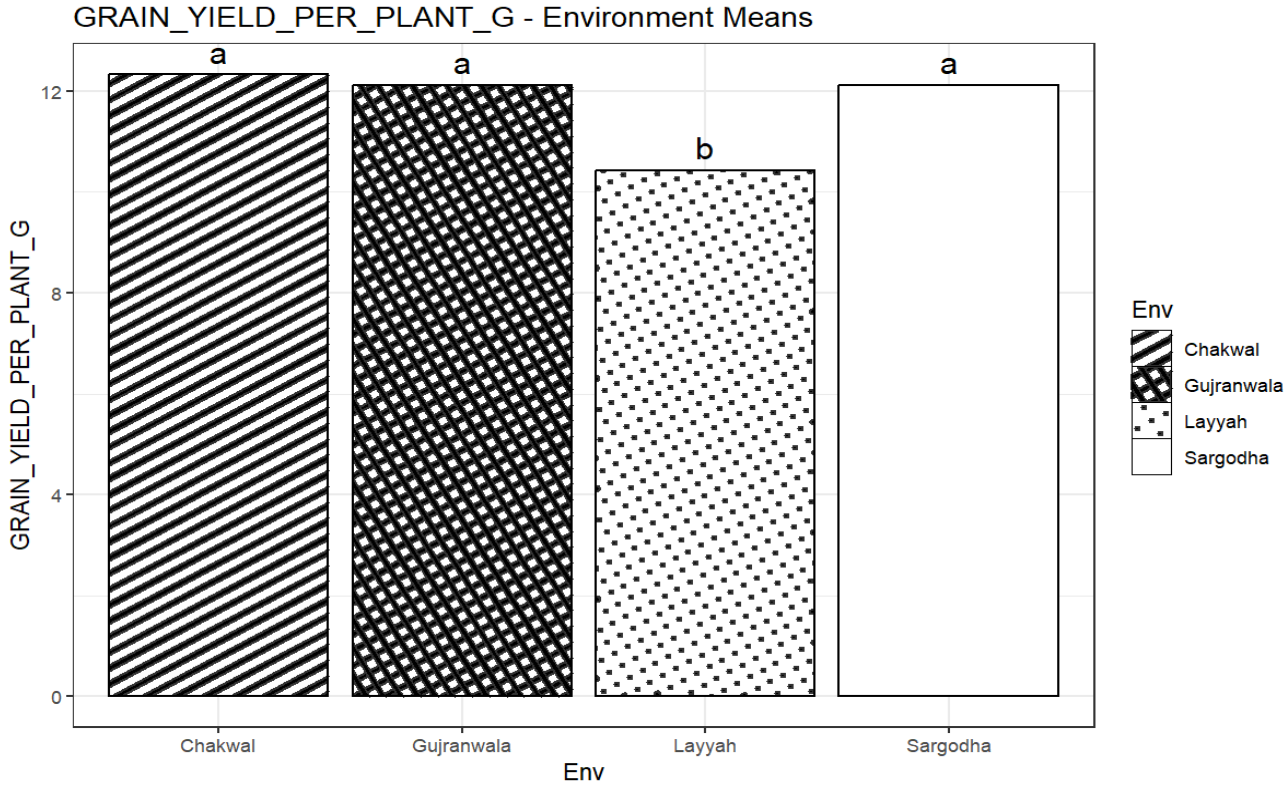

Figure 7. Means comparison of grain yield per plant (g) across multi-environments

Correlation Matrix

In all of the environments, there were evident positive correlations between grain yield per plot (Ypplo) and a variety of yield-contributing traits, suggesting consistency in the relationships with data pooled (Figure 4.2.1E). GrYpS (r = 0.50) and NoGpS (r = 0.46) positive relationships with Ypplo differentiated that spike productivity was an influential factor in determining plot yield between locations. The same positive correlation was found between Ypplo and number of spikelets on spike (NoSPIK; r = 0.39), which implies that the bigger the spike sink size, the higher the yield. There was also a moderate positive relationship between a thousand-grain weight (TGwH) and Ypplo (r = 0.38), such that the heavier the grain, the positively related to yield was. The association between plant biomass (PIB) and Ypplo (r = 0.29) was positive, which indicates the supportive role of total production of assimilates in promoting grain yield. The positive correlation with Ypplo was found with structural features including plant height or plant index (PIH; r = 0.51) and peduncle length (PeL; r = 0.36), indicating that favorable plant structure and capacity of assimilates transport are associated with the formation of yield. Element NoT also had a positive connection with Ypplo (r = 0.27), but the relationship was less strong than between spike-related characteristics. A high positive correlation with Ypplo was observed only in the case of harvest index (HI) (r = 0.14) which showed that biomass partitioning efficiency did not meaningfully contribute at average values across environments. Such patterns of correlation are in line with previous reports they very much rely on the joint effect of spike fertility and grain weight together with plant architecture on wheat yield in various environments (Slafer et al., 2021; Sukumaran et al., 2018; Mullualem et al., 2024).

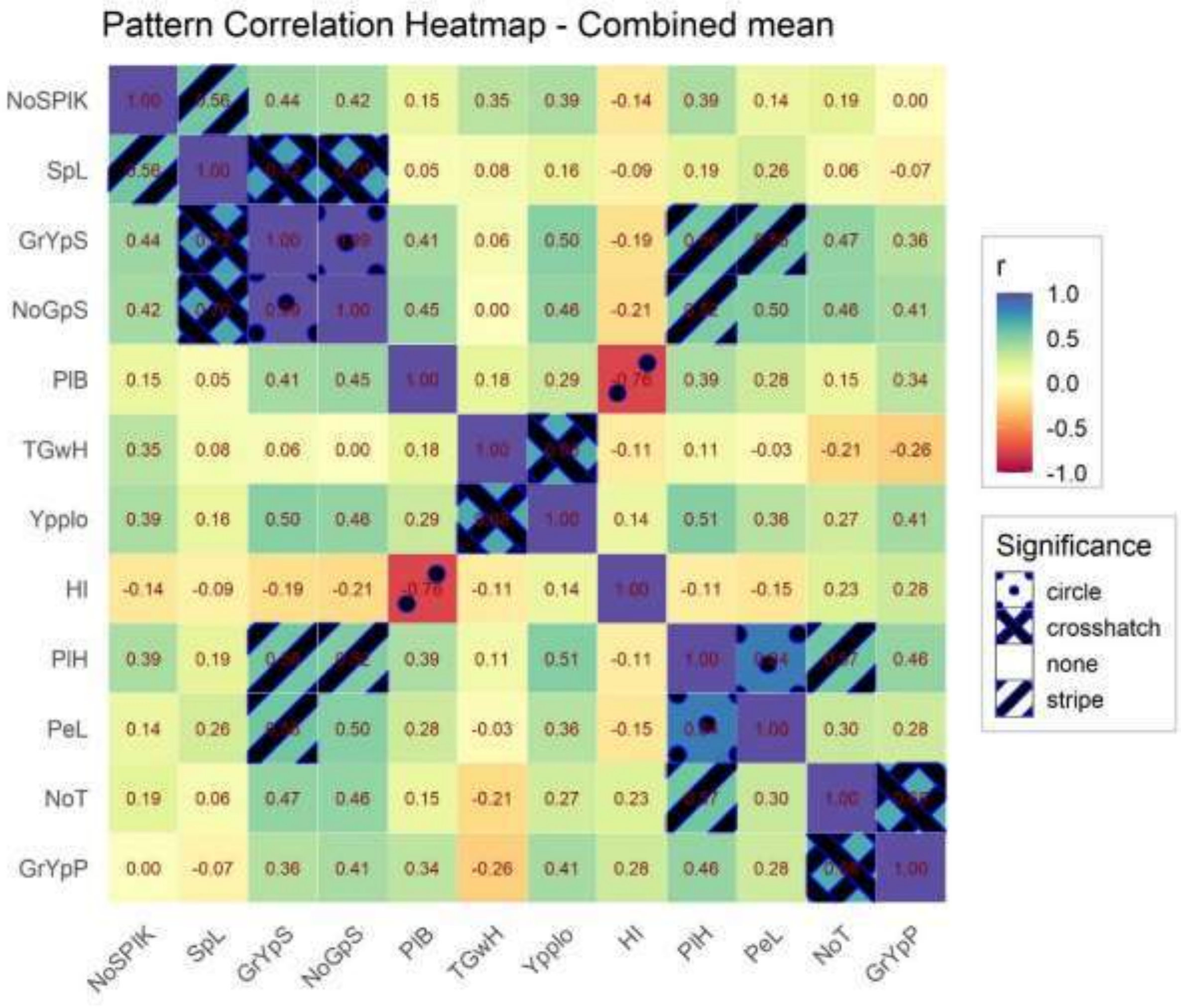

Figure 8. Correlation coefficients of studied traits in wheat genotypes across all environments

DISCUSSION

Significance of Genotype, Environment and G × E Interaction

The ANOVA, in combination, in this analysis, indicated extremely significant effects of both the genotypes (G), the environments (E), and the genotype by environment (G x E) on the total of the grain yield. This implies that the tested hexaploid wheat genotypes have a high-level of genetic variation and the environment has a strong influence in contrasting agro-climatic conditions. This has been reported many times in the multi-environment tests in wheat, where the effects of environment for the most part of the total variation (Mohammadi et al., 2012; Khazratkulova et al., 2015; Mullualem et al., 2024).

Simultaneously, the high level of environmental impact, which is revealed in the current research, is aligned with the world insights that the formation of the yield of wheat products is extremely depending on the climatic variability, especially the temperature, rainfall distribution, and water supply (Ahmed et al., 2019; Mahmood et al., 2019; Amdneh, 2025). The variability of the wheat yield under different climate conditions will also grow and it will support the necessity to consider the genotypes in different environments (Hossain et al., 2021; Kaium et al., 2025).

The huge G × E interaction that was observed in this experiment implies consistent environmental environments of varying genotype response. This suggests that genotype ranking differed between one place and the other and stability analysis was an important analysis that should have been followed to choose correctly. Dabi et al. (2021), Eskezia et al. (2025), and Andrade et al. (2025) came to similar conclusions that the neglect of the existence of G × E interaction can result in false varietal recommendations. Also, in the study conducted by Raffo and Jensen (2023), the uttermost role in wheat breeding programs is the degree of genotype x environment interaction, which is supposed to improve adaptation and resilience.

Analysis and Stability Interpretation, AMMI

The AMMI analysis separated the G × E interaction into interaction principal component axes (IPCA) to allow a better understanding of the stability and adaptability of genotypes. The large IPCA values meant that the first several principal components explained much of the variance of interaction, which was a validation of the appropriateness of the AMMI model to this data. AMMI has been shown to be the most effective in the dissection of such complex G × E patterns (Mohammadi et al., 2012; Bishwas et al., 2021; Alemayehu et al., 2025). AMMI offers a compromise between additive and multiplicative factors, which enhance the precision of prediction models in contrast with the conventional linear regression methods (Eberhart and Russell, 1966; Finlay and Wilkinson, 1963).

Genotypes that had IPCA scores near to zero were said to be more stable in the diverse environment whereas those with a large positive or negative changes had a certain adaptation. Alemu et al. (2021), Kumar et al. (2022), and Meena et al. (2025) reported similar interpretations and also showed that it was in the form of stable wheat genotypes where interaction effects were minimal and yield performance was consistent.

The fact that the visions of the breeding goal in the current study are associated with identifying stable genotypes underlines that the literature yields the results expected by the breeding goal (i.e., the development of cultivars that remain productive within the framework of varied agro-climatic conditions). The fact of stability is more relevant in the conditions of climate variability, and droughts and heat stresses are becoming more and more frequent in the wheat field (Ayed et al., 2021; Khare et al., 2024).

GGE Biplot Analysis and Mega-Environment Delineation

GGE biplot analysis also gave a graphical description of the stability and the genotype performance. The which-won-where pattern was used to show that there were clear mega-environment, and it is in the environments ones specific genotypes could outperform others. This validates cross over effects of genotypes in testing locations. Mega-environmental similar patterns have also been established in wheat and were observed under opposing climatic conditions (Bishwas et al., 2021; Al-Sayaydeh et al., 2023; Mullualem et al., 2024). Recent discoveries of the mega-environments are necessary to enable the region-specific recommendation of cultivars and breeding objectives (Yan and Kang structure demonstrated by Mohammadi et al., 2012).

High-yielding and stable genotypes were also identified through the average environment coordination (AEC) view, which also enabled the recognition of good, even compassionate genotype. All AEC abscissa projections were assessed and genotypes that had projections closer were viewed as ideal that were characterized by high mean yield and stability. Similar interpretations have been reported by Fouad et al. (2024) and Bubuche et al. (2025) who validated the superiority of GGE biplot in the selection of widely adapted genotypes of wheat. The definition of mega-environments is gaining more and more significance in the framework of climate change, in which analysis of patterns of variability in climatic conditions of regions affects the productivity of wheat (Ahmed et al., 2019; Babadjanova, 2024).

Correlation ANOVA of Yield and Agronomic Traits

The correlation analysis showed that there were strong positive relationships between grain yield and agronomic important characteristics. This implies that indirect selection of correlated traits may increase the breeding efficiency. Organizational correlations between yield and yield components have received extensive reports in wheat (Pretini et al., 2021; Dong et al., 2023).

The number of tillers, spikes, grain filling period are some of the traits that have a significant effect on the formation of yield (Farooq et al., 2021; Li et al., 2021). The increase in the ability to tiller and the effective growth of spikes leads to the increase in the number of grains and final yield (Dong et al., 2023; Bastos et al., 2020). The observed high correlations within the study show that both traits can be selected together to achieve an improvement in the yield. This is evidenced by Mulugeta et al. (2022) and Kyratzis et al. (2022) who highlighted the significance of using multivariate methods in the process of breeding wheat.

Conclusions in the Breeding of Wheat in Climate variances

The overall findings of ANOVA, AMMI, GGE biplot and the correlation analysis indicate the complexity of the genotype performance in the field. The overwhelming effect of environmental factors and considerable G x E interaction provide the importance of multi-location experiments before varietal introduction (Montgomery, 2017; Gomez & Gomez, 1984). Considering that the production of wheat is prone to climate change (Hossain, 2012; Hossain et al, 2021) and due to the rising global demand of wheat (Mottaleb and Ray, 2023;

Islam, 2023), it is important to find permanent and high yielding genotypes that will improve Food security (Majumdar, 2023; Erenstein, 2022).

The promising candidates to grow in the same agro-climatic areas and parental material in breeding programs to increase resilience and yield can be identified as stable genotypes which are identified in this study (Alipour et al., 2021; Guan et al., 2018). Combining ANOVA, AMMI, GGE biplot, and correlation analyses were found to be efficient in selecting the genotypes that have high yield performance and stability. These integrated solutions are highly advised in the next-generation wheat enhancement programs with the agro-climatic settings that are contrasting (Ashkar et al., 2023; Mekonnen et al., 2023; Andrade et al., 2025).

CONCLUSION

The present study demonstrated that grain yield performance of hexaploid wheat is strongly influenced by environmental variability and genotype × environment (G × E) interaction. The highly significant effects of genotype, environment, and their interaction confirmed the necessity of multi-environment trials for reliable selection. The AMMI model effectively partitioned interaction effects and identified stable genotypes with consistent performance across environments, while the GGE biplot provided a clear graphical interpretation of mega-environment patterns and genotype superiority.

The integration of ANOVA, AMMI, GGE biplot, and correlation analyses enhanced the understanding of genotype adaptability and yield stability under contrasting agro-climatic conditions. Stable and high-yielding genotypes identified in this study can be recommended for cultivation in similar environments and utilized as valuable parental materials in breeding programs. The study highlights that combining statistical stability models with multi-location testing is essential for developing resilient wheat cultivars capable of sustaining productivity under climate variability and changing agro-ecological conditions.

REFERENCES

Ahmed, M. J., Choi, K.-S., Cho, G.-H., & Kim, S.-H. (2019). Future wheat yield variabilities and water footprints based on the yield sensitivity to past climate conditions. *Agronomy, 9*(11), 744–760. https://doi.org/10.3390/agronomy9110744

Alemayehu, L., Kebede, M., & Wada, E. (2025). AMMI analysis of elite bread wheat (Triticum aestivum L.) selections for genotype by environment interaction and stability of grain yield in Southern Ethiopia. *PLOS One, 20*(1), e0318559. https://doi.org/10.1371/journal.pone.0318559

Allard, R. W., & Bradshaw, A. D. (1964). Implications of genotype–environmental interactions in applied plant breeding. *Crop Science, 4*(5), 503–508. https://doi.org/10.2135/cropsci1964.0011183X000400050021x

Al-Sayaydeh, R., Shtaya, M., Qubbaj, T., Al-Rifaee, M., Alabdallah, M., Migdadi, O., Gammoh, I., & Al-Abdallat, A. (2023). Performance and stability analysis of selected durum wheat genotypes differing in their kernel characteristics. *Plants, 12*(14), 2664. https://doi.org/10.3390/plants12142664

Andrade, A. P., Torres, M. E., Cántaro-Segura, H., Díaz-Morales, L., & Matsusaka, D. (2025). Stability and yield performance of durum wheat genotypes across environments in Southern Peru. *International Journal of Plant Biology, 16*(4), 127–139. https://doi.org/10.3390/ijpb16040127

Annicchiarico, P. (2002). *Genotype × environment interactions: Challenges and opportunities for plant breeding and cultivar recommendations*. FAO Plant Production and Protection Paper No. 174. Food and Agriculture Organization of the United Nations. https://www.fao.org/3/y4391e/y4391e00.htm

Ashkar, I., Sallam, M., Almutairi, K. F., Shady, M., Ibrahim, A., & Alghamdi, S. S. (2023). Detection of high-performance wheat genotypes and genetic stability to determine complex interplay between genotypes and environments. *Agronomy, 13*(2), 585. https://doi.org/10.3390/agronomy13020585

Becker, H. C., & Léon, J. (1988). Stability analysis in plant breeding. *Plant Breeding, 101*(1), 1–23. https://doi.org/10.1111/j.1439-0523.1988.tb00261.x

Bishwas, K., Poudel, M. R., & Regmi, D. (2021). AMMI and GGE biplot analysis of yield of different elite wheat lines under terminal heat stress and irrigated environments. *Heliyon, 7*(6), e07112. https://doi.org/10.1016/j.heliyon.2021.e07112

Crossa, J. (1990). Statistical analyses of multilocation trials. *Advances in Agronomy, 44*, 55–85. https://doi.org/10.1016/S0065-2113(08)60818-4

Dabi, A., Alemu, G., Geleta, N., Delessa, A., Solomon, T., Zegaye, H., Asnake, D., Asefa, B., Duga, R., & Getamesay, A. (2021). Genotype × environment interaction and stability analysis for grain yield of bread wheat (Triticum aestivum) under low moisture stress areas of Ethiopia. *American Journal of Plant Biology*, *6*(3), 44–62. https://doi.org/10.11648/j.ajpb.20210603.11

Eberhart, S. A., & Russell, W. A. (1966). Stability parameters for comparing varieties. *Crop Science*, *6*(1), 36–40. https://doi.org/10.2135/cropsci1966.0011183X000600010011x

Eberhart, S. A., & Russell, W. A. (1966). Stability parameters for comparing varieties. *Crop Science*, *6*(1), 36–40. https://doi.org/10.2135/cropsci1966.0011183X000600010011x

FAO. (2021). *FAOSTAT statistical database*. Food and Agriculture Organization of the United Nations. https://www.fao.org/faostat/

Finlay, K. W., & Wilkinson, G. N. (1963). The analysis of adaptation in a plant-breeding programme. *Australian Journal of Agricultural Research*, *14*(6), 742–754. https://doi.org/10.1071/AR9630742

Finlay, K. W., & Wilkinson, G. N. (1963). The analysis of adaptation in a plant-breeding programme. *Australian Journal of Agricultural Research*, *14*(6), 742–754. https://doi.org/10.1071/AR9630742

Fouad, H., El-Karamity, A., Salim, M., Naguib, S., & Ibrahim, S. M. (2024). Uni and multivariate methods to estimate stability of some bread wheat genotypes. *Journal of Plant Production*, *15*(6), 303–320. https://doi.org/10.21608/jpp.2024.000000

Gauch, H. G. (1992). *Statistical analysis of regional yield trials: AMMI analysis of factorial designs*. Elsevier. https://doi.org/10.1016/C2013-0-03706-2

Gauch, H. G., & Zobel, R. W. (1997). Identifying mega-environments and targeting genotypes. *Crop Science*, *37*(2), 311–326. https://doi.org/10.2135/cropsci1997.0011183X003700020002x

Gomez, K. A., & Gomez, A. A. (1984). *Statistical procedures for agricultural research* (2nd ed.). John Wiley & Sons.

Hossain, A., Skalicky, M., Brestic, M., Maitra, S., Ashraful Alam, M., Syed, M. A., Hossain, J., Sarkar, S., Saha, S., & Bhadra, P. (2021). Consequences and mitigation strategies of abiotic stresses in wheat (Triticum aestivum L.) under the changing climate. *Agronomy*, *11*(2), 241. https://doi.org/10.3390/agronomy11020241

Kang, M. S. (1993). Simultaneous selection for yield and stability in crop performance trials: Consequences for growers. *Agronomy Journal*, *85*(3), 754–757. https://doi.org/10.2134/agronj1993.00021962008500030042x

Mohammadi, M., Karimizadeh, R., Sabaghnia, N., & Shefazadeh, M. (2012). Genotype × environment interaction and yield stability analysis of new improved bread wheat genotypes. *Turkish Journal of Field Crops*, *17*(1), 67–73.

Mottaleb, K. A., & Ray, S. (2023). Projecting wheat demand in China and India for 2030 and 2050. *Frontiers in Nutrition*, *10*, 1077443. https://doi.org/10.3389/fnut.2022.1077443

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 using AMMI and GGE biplot analyses. *Heliyon*, *10*(12), e162711. https://doi.org/10.1016/j.heliyon.2024.e162711

Shukla, G. K. (1972). Some statistical aspects of partitioning genotype–environmental components of variability. *Heredity*, *29*(2), 237–245. https://doi.org/10.1038/hdy.1972.87

Yan, W., & Kang, M. S. (2003). *GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists*. CRC Press. https://doi.org/10.1201/9781420040371

Yan, W., Hunt, L. A., Sheng, Q., & Szlavnics, Z. (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Science*, *40*(3), 597–605. https://doi.org/10.2135/cropsci2000.403597x

Zobel, R. W., Wright, M. J., & Gauch, H. G. (1988). Statistical analysis of a yield trial. *Agronomy Journal*, *80*(3), 388–393. https://doi.org/10.2134/agronj1988.00021962008000030002x