NARDI FUNDULEA, ROMANIA ROMANIAN AGRICULTURAL RESEARCH, NO. 42, 2025
www.incda-fundulea.ro; doi.org/10.59665/rar4233 First Online: March, 2025. DII 2067-5720 RAR 2025-78

Genotype Stability and Yield Performance of Wheat in Barani Areas: An AMMI and GGE Biplot Approach

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ABSTRACT

Wheat is a globally significant cereal crop, playing a vital role in ensuring food security. The cultivation of wheat under rain-fed (barani) conditions is practiced in many countries, achieving higher yields than in Pakistan due to the use of superior cultivars and advanced management practices. Enhancing wheat production in rain-fed regions requires the selection of appropriate cultivars, as varieties successful in other areas may not perform optimally under these conditions. Plant breeders are focused on increasing yield potential by developing stable and optimized genotypes. With Pakistan facing significant food security challenges due to rapid population growth, improving wheat yields in rain-fed areas is crucial. This study leverages yield data from systematically conducted annual multi-environment trials (MET) at the Barani Agriculture Research Institute (BARI) during 2021-22. The primary objective was to identify stable wheat genotypes through the analysis of this data. Fifteen wheat genotypes were evaluated using a RCB design across three diverse environments. The AMMI analysis was carried out in combination with other statistical methods for stability. The results identified genotypes 20C208, 20C206, 20C207, 20C209, and 20C205 as desirable wheat genotypes for higher yields in variable environments, due to their optimal combination of yield and stability. Among the areas studied, Attock area was found to be the best, followed by Chakwal area.

Keywords: AMMI, AMMI Stability Index (ASI), wheat, G×E, biplot, stability measures, multi-environment trials, Barani Areas, Rainfed Areas.

INTRODUCTION

The population of Pakistan is growing at an annual rate of 2.55%, highest in the region, according to the Housing and Population Census 2023 which means the country will double its population by 2050 to about 485 million. This rapid increase in population will pose a significant challenge of food security. To achieve food security in Pakistan, it is essential to prioritize wheat production, given its critical role as a staple crop. According to the Economic Survey of Pakistan 2023-24, wheat was cultivated on 9.0 million hectares, yielding an annual production of 31.4 million tons. As wheat constitutes a major part of the diet for millions, maintaining and expanding its production is vital to meet the nutritional demands of the country's growing population.

Agriculture forms a cornerstone of Pakistan's diversified economy, contributing 24% to the national GDP and employing 37.4% of the workforce. Due to its strong interconnections with other sectors, growth in agriculture is pivotal for driving overall economic development, generating employment opportunities, and reducing poverty across the country. The agricultural domain of Pakistan is categorized

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Received 1 December 2024; accepted 5 March 2025.

into principal crops such as cereals, secondary crops including fruits and vegetables, along with livestock, aquaculture, and forestry (Anwar et al., 2021; Li et al., 2023; Zhou et al., 2024). This domain is of paramount importance for the economic advancement of the nation, facilitating food security, generating employment prospects, and alleviating scarcity. Significantly, key crops are responsible for 20.67 percent to the value addition in Agriculture and 4.97 percent to the GDP. Other crops contribute 13.51 percent to the sector's growth and 3.25 percent to the GDP. Wheat (*Triticum aestivum*), with a global output of 785 million metric tonnes, is of considerable importance as one of the vital crops worldwide. Global demand for wheat is projected to rise to 858 million metric tonnes by 2050 (Alexandratos and Bruinsma, 2012; Yang et al., 2019; Liang et al., 2023).

Wheat productivity in Pakistan remains lower than that of other agricultural countries, which intensifies current and future food security concerns. As a result, both the government and agricultural scientists are persistently striving to achieve self-sufficiency in wheat production. Researchers and breeders are focusing on increasing wheat yields by developing new varieties which are more resilient through multi-environmental trials. The analysis of these trials highlights the importance of genotype-environment (G×E) interactions, as they are crucial in identifying genotypes that are both high-performing and stable. In plant performance experiments, researchers have long been invested in devising strategies for selecting superior genotypes (Yan *et al.*, 2000). Multilocation trials provide a structured approach to enhancing the yield stability of new crop varieties across various environments (Letta et al., 2008). In the context of agricultural applications, the AMMI model has been recognized as superior to other models (Gauch Jr et al., 2008; Ma et al., 2022).

Researchers have increasingly concentrated on the challenges associated with genotype-environment (G×E) interactions. This growing focus is primarily due to the considerable and variable nature of environmental conditions. Understanding G×E interactions allows to address key questions about the stability of different varieties across varied agro-ecologies, while also offering valuable insights into the characterization of genotypes based on their productivity levels (Yau, 1995; Ma and Liu, 2020). Methods that partition G×E interactions into genotype-specific components are particularly beneficial for breeders. Several parameters are now available to evaluate the stability of genotypes tested across diverse environments. Among these, AMMI analysis is particularly notable for its integration of ANOVA with PCA, effectively combining both additive and multiplicative parameters into a single framework (Gauch and Zobel, 1988; Zobel et al., 1988; Gauch Jr et al., 2008). In addition to the AMMI, other parameters for stability analysis have been proposed by (Finlay and Wilkinson, 1963) and (Eberhart and Russell, 1966).

These methods, which assess genotype stability by analyzing the regression of average yield on an environmental index and considering deviations from this regression as a secondary measure, have proven invaluable for breeders when evaluating genotype performance across various environments. Moreover, the ecovalence index for stability introduced by Wricke and the stability variance developed by (Shukla, 1972) have been employed to quantify each genotype's contribution to G×E interactions.

Given the importance of AMMI analysis in exploring G×E interactions, along with the utility of biplot analysis for identifying stable genotypes, researchers have concentrated their efforts on these techniques. Both AMMI analysis and G×E biplots are valuable statistical methods for assessing the stability and adaptability of genotypes across various environments. These methods are commonly used in plant breeding for selecting stable genotypes. Various researchers used AMMI analysis and G×E biplots to select stable genotypes for different crops like chickpea (Erdemci, 2018), cotton (Farias et al., 2016), okra (Alake and Ariyo, 2012), barley (Kendal and Dogan, 2015; Verma et al., 2016; Solonechnyi et al., 2018), peanut (de Oliveira and de Godoy, 2006), rice (Devi et al., 2020), wheat (Kashif et al., 2023), and rapeseed (Sara et al., 2019; Chen et al., 2024). These studies have found stable genotypes that consistently perform well for various environments and can be recommended for cultivation in targeted regions. AMMI analysis and G×E biplots have been found to be effective in selecting stable genotypes with high productivity and stability across different environments.

Out of the total 12.7 million hectares under cultivation, the Barani (rainfed) tract in Punjab covers 3.1 million hectares, constituting approximately 25% of the area. This Barani Tract encompasses the entire Attock, Rawalpindi, Jhelum, and Chakwal districts, along with parts of several other districts. Historically, agricultural research has predominantly focused on irrigated areas, leaving the Barani region, which constitutes about 30% of Punjab's agricultural land, relatively neglected. Given the significant portion of land under rainfed conditions, there is a compelling need to direct research efforts toward improving production of core crops like wheat in these areas. Enhancing productivity in the Barani tract will be crucial for optimizing land use and supporting efforts to achieve food security.

Cultivating wheat under rain-fed (barani) conditions is common in many countries, where higher yields are achieved due to superior cultivars and management practices. In Pakistan, improving wheat production in rain-fed areas requires selecting cultivars specifically suited to these conditions, as those successful elsewhere may not perform well here. With the country's growing population and escalating food security challenges, optimizing wheat yield is critical. This study aims to identify stable wheat genotypes at Rainfed areas in the Punjab. The study will utilize yield data from multi-environment trials (MET) conducted at the Barani Agriculture Research Institute (BARI) to identify stable, high-yielding wheat genotypes for rain-fed regions.

MATERIAL AND METHODS

To fulfill the study's objectives, multi-environmental data were collected from the Barani Agricultural Research Institute (BARI) Chakwal under Punjab Uniform Wheat Yield Trials (PUWYT). The experiments were conducted on three different locations using fifteen wheat genotypes.

Variance analysis was conducted both at individual locations and across multiple environments, utilizing various R software packages, with a focus on the metan package (Olivoto and Lúcio, 2020). A combined analysis of variance was also performed across the different environments. To visually assess the relationships between environments and genotypes, AMMI and GGE biplots were employed, offering graphical insights into genotype-environment interactions and patterns. The AMMI analysis was particularly useful in evaluating the stability and influence of different locations on the grain protein content in durum wheat genotypes, as demonstrated by (Haile et al., 2007).

To analyze genotype-environment interactions, the AMMI method combines analysis of variance technique with PCA making it an effective tool for exploring complex GEI dynamics.

The statistical model for AMMI is as follows

$$Y_{ijk} = \mu + g_i + e_j + b_k(e_j) + (ge)_{ij} + \varepsilon_{ijk} \quad (1)$$

where:

Y_{ijk} is the yield for i^{th} genotype,

j^{th} environment and k^{th} replicate,

μ is the overall mean,

g_i is the main effect for i^{th} genotype,

e_j is the main effect for j^{th} environment,

ge_{ij} is the effects for GE interaction,

$b_k\left(e_j\right)$ is the effect of the replication k within the j^{th} environment and

e_{ijk} are the random errors produced by the experiment which assumed to be to be independent having normal distribution as,

$$e_{ijk} \sim N\left(0, \frac{\sigma^2}{k}\right)$$

The AMMI model splits the GEI into further components:

$$(ge)_{ij} = \sum_{v=1}^{n} \lambda_v \alpha_{iv} \gamma_{jv} + \rho_{ij} \quad (2)$$

where:

λ_v representing eigenvalue for the PCI with v axis,

a_{iv} and γ_{jv} are the scores of principal components for i^{th} genotype and j^{th} environment with v axis,

ρ_{ij} denote the residuals including all multiplicative terms not part of the model,

n is the number of PC's kept by the model.

This approach is represented by the statistical function for the additive main effects and multiplicative interaction model, which is particularly relevant in the context of replicated experiments as noted by (Hongyu et al., 2014).

$$Y_{ijk} = \mu + g_i + e_j + b_k(e_j) + \sum_{v=1}^{n} \lambda_v \alpha_{iv} \gamma_{jv} + \rho_{ij} + \varepsilon_{ijk} \quad (3)$$

The model presented above along with the Genotype × Environment (GGE) biplot, has gained significant popularity among scientists for selecting elite genotypes across various crops, such as wheat, castor, and orange-fleshed sweet potatoes (Karuniawan et al., 2021; Omrani et al., 2022; Memon et al., 2023).

Statistical methods for stability, such as joint regression b_i and deviation from regression models Sd_i^2 introduced by (Finlay and Wilkinson, 1963) and further developed by (Eberhart and Russell, 1966), have been extensively utilized in agricultural research to evaluate genotype performance across varying environments (Horhocea et al., 2024). In addition to these methods, several other measures have been proposed and applied to assess genotype stability, including (Shukla, 1972) r_i^2, Wricke's ecovalence W_i, superiority index (P_i) by (Lin and Binns, 1988), the coefficient of variation (CV%) introduced by (Francis and Kannenberg, 1978), and the coefficient of determination by (Pinthus, 1973). These methodologies allow researchers to simultaneously analyze yield and stability components, facilitating the identification of genotypes that are both high-yielding and stable across different environmental conditions. The significance of these approaches has been highlighted by numerous researchers in their efforts to understand and improve genotype performance in diverse environments (Hernandez et al., 1993; Kang, 1993; Bajpai and Prabhakaran, 2000). The specific genotype codes and environments used in these analyses are detailed in Table 1.

Table 1. List of genotype codes and Locations with codes

Sr. No	Genotype code	Location/ code	Name of location
1.	20C197	CHKL	Chakwal
2.	20C198	FTJH	Fatehjhang
3.	20C199	ATOK	Attock
4.	20C200		
5.	20C201		
6.	20C202		
7.	20C203		
8.	20C204		
9.	20C205		
10.	20C206		
11.	20C207		
12.	20C208		
13.	20C209		
14.	20C210		
15.	Barani-17 (Check)		

RESULTS AND DISCUSSION

The combined analysis of variance (ANOVA) for 15 genotypes and three environments revealed highly significant effects of environment, genotype, and their interaction (Table 2). The presence of significant interaction of genotype-by-environment showed that the relative performance of genotypes varied by different environments, suggesting the need for further investigation using AMMI procedure. Furthermore, this significant GEI also indicated the existence of heterogeneous genetic variances among the environments, specifically in relation to wheat yield.

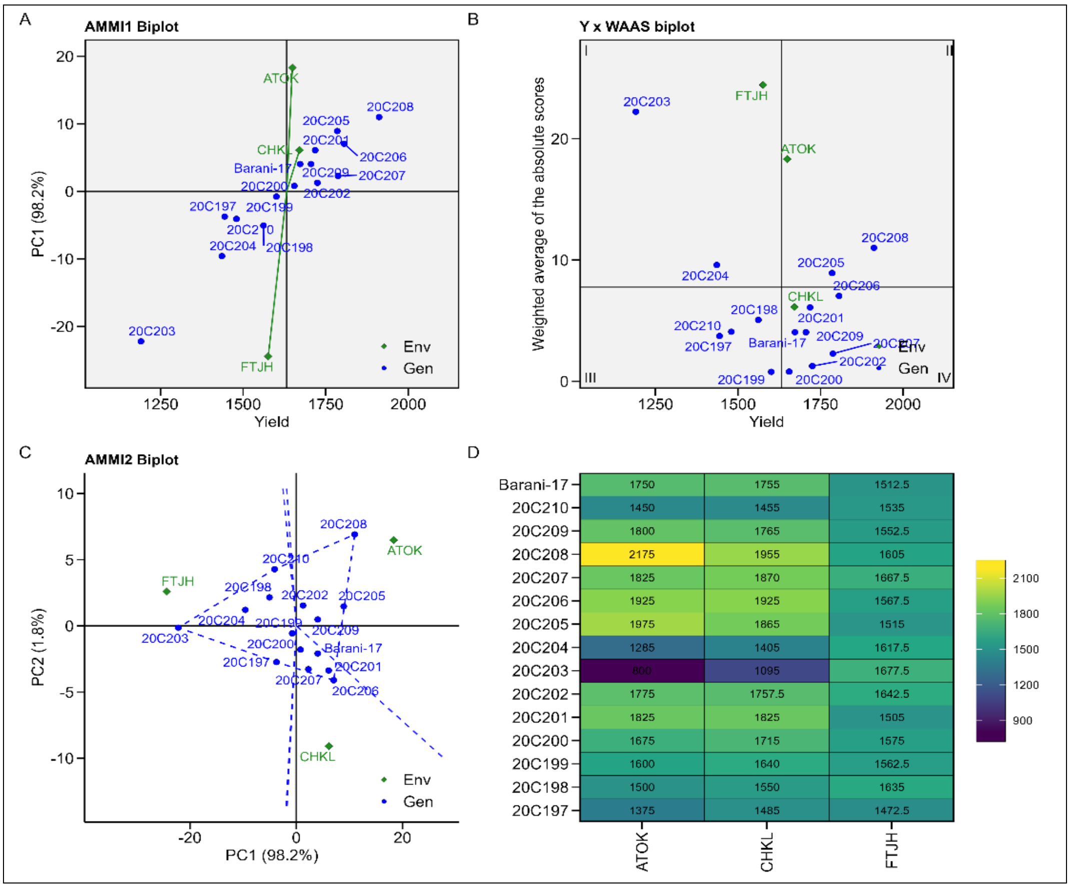
The AMMI model, integrating both ANOVA and PCA, was employed to get a complete understanding of the data. The first principal component (PC) exhibited significant variation ($p<0.0000$) and described 98.2% of the total variance observed (Table 2).

Table 2. Genotype (G), environment (E) and G×E mean squares for wheat yield
(Results of AMMI Model Using wheat Trials)

Source of Variation	Degrees of Freedom	Sums of Square	Mean Squares	F Statistic	P value	Proportion	Accumulated
Env	2	147432	73716	1.2	0.4217ns	-	-
Rep(Env)	3	189452	63151	6.9	0.0007**	-	-
Gen	14	2862940	204496	22.3	0.0000**	-	-
Gen:Env	28	1915393	68407	7.5	0.0000**	-	-
PC1	15	1880906	125394	13.7	0.0000**	98.2	98.2
PC2	13	34487	2653	0.3	0.9905ns	1.8	100.0
Residuals	42	384923	9165	-	-	-	-
Total	117	7415533	63381				

** significant at 0.01, * significant at 0.05, ns = not significant.

The extent of each genotype's and environment's interaction is explained by the IPCAI vs IPCA II biplot (Figure 1A). The worst genotypes and surroundings are those that are most remote from the origin and are more sensitive. When genotypes and environments in the same sector are in opposition to each other and the genotypes with the lowest interaction along both axes are located close to the origin, they interact both positively and negatively. AMMI2 Biplot for grain yield was constructed using interaction of IPCA2 against IPCA1 scores of 15 wheat genotypes (G) in 5 environments (Figure 1C). As a result, the Chakwal and Attock imposed considerable forces of interaction whereas the Fatehjhang did not. In the present study, the genotypes 20C199, 20C200, 20C202, and 20C209 were close to their point of origin, making them less susceptible to environmental factors, while 20C199 obtained a high mean yield with great stability. Genotypes 20C203 and 20C208 since they were further from the source and subject to environmental influences, they were more responsive. The heat map showed the high yielding genotypes in environments by lighter shade and the low yielding in darker shade (Figure 1D).



	ATOK	CHKL	FTJH
Barani-17	1750	1755	1512.5
20C210	1450	1455	1535
20C209	1800	1765	1552.5
20C208	2175	1955	1605
20C207	1825	1870	1667.5
20C206	1925	1925	1567.5
20C205	1975	1865	1515
20C204	1285	1405	1617.5
20C203	800	1095	1677.5
20C202	1775	1757.5	1642.5
20C201	1825	1825	1505
20C200	1675	1715	1575
20C199	1600	1640	1562.5
20C198	1500	1550	1635
20C197	1375	1485	1472.5

Figure 1. The AMMI1 and AMMI2 biplots illustrating genotype-by-environment (GE) interactions for 15 wheat genotypes across three environments (A and C), the biplot based on grain yield and the WAASB statistic is used for selecting stable and high yielding wheat genotypes (B), the variation in grain yield among the 15 wheat genotypes across three environments during the 2021-22 growing season (D)

Figure 2 showed that genotype 20C208 was observed as the highest yielding genotype in both Attock and Chakwal whereas genotype 20C203 is the lowest yielding in both environments. In Fatehjang environment only two genotypes 20C202 and 20C207 showed mean greater than the overall average all other genotypes are below average.

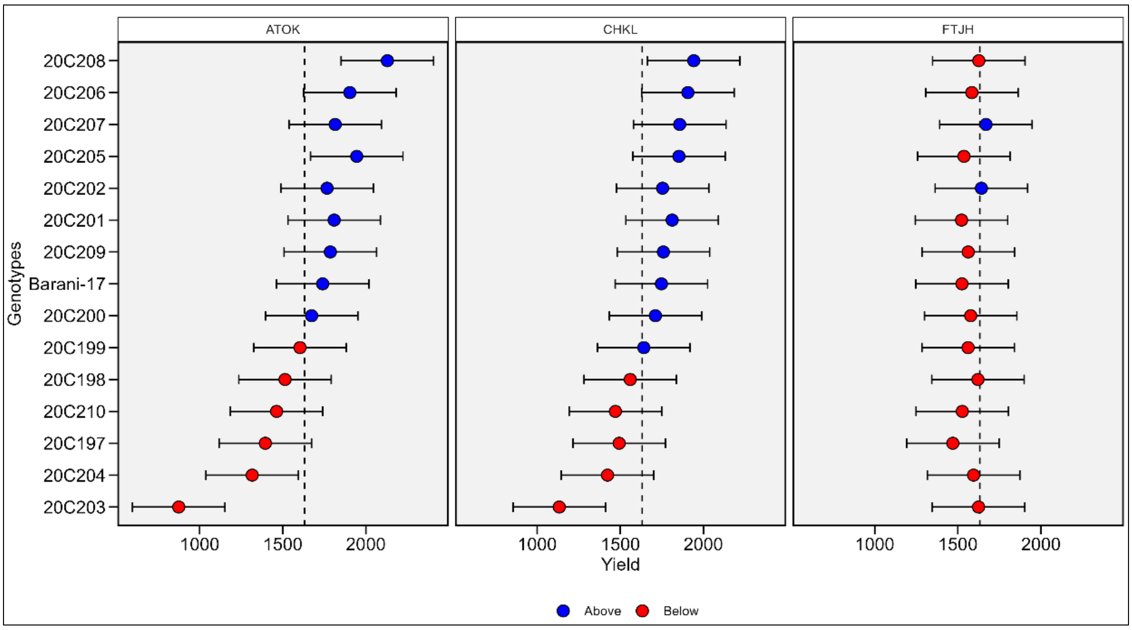


Figure 2. Mean yield of all genotypes with indication of above and below average by environments

The genotype 20C199 was categorized as the top performing by most of the stability models. Stability models such as coefficient of variation (CV%), Regression coefficient, σ_i^2 , and W_i. Hence, almost 4 models have declared it as the most stable (Table 3).

Table 3. Different stability analysis models of 15 wheat genotypes cultivated in three different environment in Punjab

Gen	Mean	R_i^2	CV(%)	b_i	σ_i^2	W_i	P_i	S_i^1	S_i^2	N_i^1	N_i^2
20C197	1444	0.04	4.17	-0.24	5742	29025	150488	1.33	16.00	2.67	0.21
20C198	1562	0.68	4.37	-1.14	12036	50845	103576	3.00	27.00	3.00	0.27
20C199	1601	0.90	2.42	0.74	-2271	1249	73846	1.33	5.33	1.33	0.13
20C200	1655	1.00	4.36	1.45	-2030	2082	53018	0.33	2.33	1.00	0.11
20C201	1718	0.95	10.80	3.64	18973	74895	28193	3.33	28.00	3.33	0.67
20C202	1725	0.89	4.17	1.37	-1569	3680	33372	1.00	4.33	1.33	0.19
20C203	1191	0.72	37.50	-7.64	273582	957539	438371	4.67	65.30	4.67	0.31
20C204	1436	0.69	11.70	-2.83	48962	178855	183033	4.00	48.00	4.00	0.29
20C205	1785	0.81	13.50	4.36	42075	154982	12418	3.00	39.00	4.00	1.00
20C206	1806	0.95	11.40	4.06	26329	100395	12583	4.00	41.30	4.00	1.33
20C207	1788	1.00	5.95	2.14	1087	12889	21638	1.83	8.58	1.83	0.61
20C208	1912	0.67	15.00	4.74	68687	247235	876	2.33	49.00	4.67	4.67
20C209	1706	0.88	7.85	2.54	6527	31749	32058	1.00	6.33	1.67	0.28
20C210	1480	0.93	3.22	-0.93	8081	37135	132655	3.00	22.30	3.00	0.25
Barani-17	1672	0.96	8.29	2.74	6841	32835	41308	2.50	14.60	2.50	0.31

Mean = Rank according to mean grain yield (kg ha-1), CV% = Coefficient of variability, R_i^2 = Coefficients of determination, b_i = Regression coefficient, σ_i^2 = Shukla's stability varianc, Wi = Wricke's ecovalence, Pi = Superiority index, S_i^2 = Genotype absolute rank difference mean over 'n' environments and S_i^2 = Ranks variance over 'n' environments, N_i^1,: N_i^2Thennarasu's (1995) non-parametric stability indices.

Genotype 20C200 was ranked as the first or second by the majority of stability models. Models S_i^1, S_i^2, N_i^1 and N_i^2, ranked it on number one whereas R_i^2, σ_i^2, and W_i placed it on second position. The details of rankings are given in the Table 4.

Table 4. Rank order of fifteen advanced wheat cultivars cultivated in three different Barani zones in Punjab Province using different stability models

Gen	Mean	R_i^2	CV(%)	b_i	σ_i^2	Wi	P_i	S_i^1	S_i^2	N_i^1	N_i^2
20C197	13	14	3	4	5	5	13	3	7	6	4
20C198	11	12	5	6	9	9	11	7	9	7	6
20C199	10	6	1	1	1	1	10	3	3	2	2
20C200	9	2	4	3	2	2	9	1	1	1	1
20C201	6	4	9	11	10	10	5	8	10	8	12
20C202	5	7	3	2	3	3	7	2	2	2	3
20C203	15	10	14	15	15	15	15	10	15	10	9
20C204	14	11	11	10	13	13	14	9	13	9	8
20C205	4	9	12	13	12	12	2	7	11	9	13
20C206	2	4	10	12	11	11	3	9	12	9	14
20C207	3	1	6	7	4	4	4	4	5	4	11
20C208	1	13	13	14	14	14	1	5	14	10	15
20C209	7	8	7	8	6	6	6	2	4	3	7
20C210	12	5	2	5	8	8	12	7	8	7	5
Barani-17 (Check)	8	3	8	9	7	7	8	6	6	5	10

CONCLUSIONS

The AMMI model demonstrated that interaction genotype and environment (GEI) is highly significant for grain yield. Various parametric and nonparametric stability statistics used in the current study assessed the stability of wheat genotypes in terms of yield, stability, or a combination of both. According to R^2 method, the genotypes 20C207, 20C200, Barani-17 (Check), 20C201 and 20C206 which showed above-average yield were identified as more stable compared to the other genotypes. Based on the present results, out of 10 stability models studied, genotype 20C200 were declared as stable by 9 models and 20C1991 and 20C202 by 8 models.

According to Shukla stability variance of genotypes 20C199, 20C200, 20C202 and 20C207 was pointed as desirable genotypes. According to Wricke method the genotypes 20C199, 20C200, 20C202 and 20C207 had low Wricke's ecovalence values and hence were stable. The findings indicated that using stability measures such as P_i, CV%, b_i , S_i^1, S_i^2, S_i^2, N_i^1 and N_i^2 tends to favor genotypes with below-average yield rather than those with high yields. Consequently, the AMMI and GGE biplot methods emerged as effective tools for classifying diverse environments and identifying genotypes that are stable and adaptable across varying conditions.

Based on these analyses, genotypes 20C208, 20C206, 20C207, 20C209, and 20C205 are recommended as valuable genetic resources for wheat production, due to their optimal balance of yield and stability in fluctuating environments. As a result, the Attock area was found to be the most perfect environment trial, followed by Chakwal.

ACKNOWLEDGEMENTS

The authors extend their appreciation to the Researchers Supporting Project number (RSP2025R98), King Saud University, Riyadh, Saudi Arabia, for financial support.

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