



## STABILITY ANALYSIS OF WHEAT THROUGH GENOTYPE BY ENVIRONMENT INTERACTION IN THREE REGIONS OF KHYBER PAKHTUNKHWA, PAKISTAN

I. KHAN<sup>1</sup>, S. GUL<sup>\*2</sup>, N.U. KHAN<sup>1</sup>, O.O. FAWIBE<sup>3</sup>, N. AKHTAR<sup>2</sup>, M. REHMAN<sup>4</sup>,  
 N. SABAH<sup>2</sup>, M.A. TAHIR<sup>2</sup>, A. IQBAL<sup>5</sup>, F. NAZ<sup>5</sup>, I. HAQ<sup>2</sup>, and A. RAUF<sup>6</sup>

<sup>1</sup>Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar, Pakistan

<sup>2</sup>University of Sargodha, Sargodha, Pakistan

<sup>3</sup>Federal University of Agriculture, Abeokuta, Nigeria

<sup>4</sup>Department of Agriculture, Hazara University, Mansehra, Pakistan

<sup>5</sup>Lasbela University of Agriculture, Water and Marine Sciences, Uthal - Lasbela, Pakistan

<sup>6</sup>Abdul Wali Khan University, Mardan, Pakistan

\*Corresponding author's email: samringulpbg@gmail.com

Email addresses of co-authors: imrankhans@hotmail.com, nukmarwat@aup.edu.pk, fawibeoo@funaab.edu.ng, naeem.uca@gmail.com, drmonsif@hu.edu.pk, soilscientist.uca@gmail.com, rai786@gmail.com, axhariqbal3@yahoo.com, farah.kaleri@gmail.com, drikramulhaq228@gmail.com, rauf77@awkum.edu.pk

### SUMMARY

Genotype-by-environment (GEI) interaction provides the basic information that helps breeders to select stable and superior genotypes for targeted environments. Climate change also alters the recommendations of the genotype for a specific condition. The field study carried out during the cropping seasons of 2015–2016 determined the performance of 16 wheat genotypes (13 lines and three cultivars) at three different locations: The University of Agriculture, Peshawar (UAP), Nuclear Institute of Food and Agriculture, Peshawar (NIFA), and Cereal Crops Research Institute (CCRI), Pirsabak-Nowshera, Khyber Pakhtunkhwa, Pakistan. Data on yield contributing parameters (days to heading, spike length, spikelets spike<sup>-1</sup>, grain weight spike<sup>-1</sup>, 1000-grain weight, and grain yield) were collected and analysed using analysis of variance (ANOVA) and stability analysis. Mean square values revealed highly significant results for all the traits under consideration for genotypes (G) and locations (L). Likewise, interactions (GEI) were highly significant for all the traits except grain weight spike<sup>-1</sup>. The performance of genotypes under different locations indicated no similarity. However, the overall performance of genotypes displayed better under environmental conditions of the Cereal Crops Research Institute (CCRI- Location No: 03). According to the Eberhart and Russell approach, the genotypes K-87, PR-113, Pak-13, PR-112, NR-449, and KT-338 were confirmed stable under tested locations for yield contributing traits as their regression coefficient (bi) value exhibited close to unity. Correlations of grain yield with yield contributing traits considered were significant and positive except for days to heading.

**Keywords:** Wheat (*Triticum aestivum* L.), stability, correlation, regression coefficient (bi), genotype by environment interaction, yield-related traits

**Key findings:** Significant results were obtained for the traits of wheat as influenced by genotypes (G), locations (L), and interactions (GEI). However, genotype by environment interactions had no significant effect on grain weight spike<sup>-1</sup>. Stability analysis identified stability of genotypes, i.e., K-87, PR-113, Pak-13, PR-112, NR-449, and KT-338 under tested locations, viz., The University of Agriculture, Peshawar (UAP), Nuclear Institute of Food and Agriculture, Peshawar (NIFA), and Cereal Crops Research Institute (CCRI), Pirsabak-Nowshera.

**Citation:** Khan T, Gul S, Khan NU, Fawibe OO, Akhtar N, Rehman M, Sabah N, Tahir MA, Iqbal A, Naz F, Haq I, Rauf A (2023). Stability analysis of wheat through genotype by environment interaction in three regions of Khyber Pakhtunkhwa, Pakistan. *SABRAO J. Breed. Genet.* 55(1): 50-60. <http://doi.org/10.54910/sabrao2023.55.1.5>.

Correlation of grain yield revealed significantly positive correlated with yield contributing traits under consideration, except for days to heading.

Communicating Editor: Dr. Kamile Ulukapi

Manuscript received: September 13, 2022; Accepted: November 14, 2022.

© Society for the Advancement of Breeding Research in Asia and Oceania (SABRAO) 2023

## INTRODUCTION

Wheat (*Triticum aestivum* L.) is known as the "King of Cereals" because of its high productivity and quality uses (Khan and Mohammad, 2018; Hadasch *et al.*, 2020; Dimitrov and Chipilski, 2022). It is a staple food in Pakistan and a cultivated major cereal worldwide. During the 2021–2022 cropping season, wheat cultivation in Pakistan covered an area of about 9.2 million hectares, with a production of around 27.5 million tons. It contributes 1.8% to the country's GDP and 9.2% value added in agriculture (PBS, 2021–22). In Pakistan, wheat yield is currently below its potential due to poor crop management, lack of water resources, biotic and abiotic stresses, and the effect of climate change (Coakley, 1978; Khan and Mohammad, 2018).

Climate change is an incipient matter, especially for agriculture in Pakistan, as the geographical location of Pakistan makes it vulnerable to environmental changes. The foremost cause of climate change is a boom in the emission of greenhouse gases, i.e., methane, carbon dioxide, and nitrous oxide. These gases trap sunlight and increase the temperature of the earth. The rise in temperature increases the transpiration rate, adversely affecting crop growth, especially wheat (Bayles *et al.*, 2000; Villareal *et al.*, 2002; Dimitrov and Chipilski, 2022).

It is imperative to develop stable wheat cultivars which can withstand harsh environmental conditions. Developing such genotypes can proceed by testing their performance under different environmental conditions. Then according to environment specificity, genotypes will be recommended for that location. This interaction of genotype with the environment is termed "Genotype by Environment Interaction (GEI)." A good genotype need not to perform accordingly in an environment it is not adapted, and such conditions generate ambiguity for breeders (Williams *et al.*, 2008; Tembo, 2021; Dimitrov and Chipilski, 2022). Therefore, GEI primarily plays a vital role in developing varieties, as it decreases genotypic stability under varied

environmental conditions (Zulkiffal *et al.*, 2022).

As GEI is a principal component in the recommendation of genotypes for stability in yield performance across environments, thus, multi-location trials are necessary to track the performance of genotypes (Ashraf *et al.*, 2001; Kalimullah *et al.*, 2012; Bonecke *et al.*, 2020). Stability among genotypes across locations/environments is a crucial step that has been defined and assessed by different biometrical methods like univariate and multivariate (Bayles *et al.*, 2000; Bonecke *et al.*, 2020; Naheed and Rehman, 2021). However, Finlay and Wilkinson (1963) introduced a suitable statistical approach according to the stability of a genotype assessed by mean and regression coefficient ( $b_i = 1.0$ ) values and later modified by Eberhart and Russell (1966). Deviation from regression coefficient ( $b_i = 1.0$ ) values changes the recommendation of genotype for an environment accordingly. If " $b_i = 1.0$ ," then the performance of a genotype is stable across environments for a trait, while if " $b_i > 1$ ," then genotypes are responsive and recommended for the specific environment; but, the " $b_i < 1$ " value for a trait regarded as suitable for unfavorable environmental conditions (Kalimullah *et al.*, 2012; Khan and Mohammad., 2018; Naheed and Rehman, 2021).

GEI is a key feature in the needed targeted genotypes that can withstand harsh environmental conditions. Therefore, this research studied variability among wheat genotypes, GEI, and correlation at three different locations in Khyber- Pakhtunkhwa (KPK)-Pakistan.

## MATERIALS AND METHODS

The research was carried out during the years 2015–2016 at three different locations in Khyber-Pakhtunkhwa, Pakistan, i.e. The University of Agriculture, Peshawar (UAP), Nuclear Institute of Food and Agriculture,

**Table 1.** Wheat genotypes used in the presented study.

Genotypes	Pedigree	Year of Release	Institute
DN-102	CHAM6/ATTILA//PASTOR	N.A.	ARI, D.I. Khan
Pakistan-13	Commercial Cultivar	2013	NARC, Islamabad
SRN-09111	PRL/2*PASTOR//PBW343*2/KUKUNA/3/ROLF07	N.A.	NIFA, Peshawar
NRL-1123	PSN/BOW//MILAN/3/2*BERKUT	N.A.	NIFA, Peshawar
NRL-1130	SOKOLL/EXCLAIBUR	N.A.	NIFA, Peshawar
Paseena-17	MTRWA92.161/PRINIA/5/SERI*3//RL06010/4*YR/3/PASTOR/4/	2017	CCRI, Nowshera
Khaista-17	KAUZ//ALTAR0B84/AOS/3/MILA/KAUZ/4/HUITIES/7/CAL/NH/H567 .71/3/SERI/4/CAL/NH//H567.71/5/5*KAUZ/6/PASTOR	2017	CCRI, Nowshera
PR-111	TOB/ERA//TOB/CN067/3/PLO/4/VEE#5/5/KAUZ/6/	N.A.	CCRI, Nowshera
Wadaan-17	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES/7/CAL/NH//H657. 71/3/SERI/4/CAL/NH//H567.71/5/5*KAUZ/6/PASTOR	2017	CCRI, Nowshera
PR-113	WHEAR//INQLAB91*2/TUKURU	N.A.	CCRI, Nowshera
NR-423	MTRWA92.161/PRINIA/5/SERI*3//RL6010/4*YR/3/PASTOR/4/BAV 92	N.A.	NARC, Islamabad
NR-429	CNO79//PF70354/MUS/3/PASTOR/4/BAV92/5/FRET2/KUKUNA//FR ET2/6/MILAN/KAUZ//PRINIA/3/BAV92	N.A.	NARC, Islamabad
NR-436	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/T.DICOCCONPI9 4624/AE.SQUARROSA(409)//BCN/6/WBLL4//BABAX.1B.1B*2/PRL/ 3 /PASTOR	N.A.	NARC, Islamabad
NR-449	SOKOLL//FRTL/2*PIFED	N.A.	NARC, Islamabad
Kohat-2017	SOKOLL/WBLLI	2017	BARS, Kohat
Khyber-87	KVZ/TRM//PTM/ANA-CM 43930	1987	CIMMYT, Mexico

Peshawar (NIFA), and Cereal Crops Research Institute (CCRI), Pirsabak-Nowshera. Sixteen (16) wheat genotypes (lines and varieties) collected from different research stations in Pakistan (Table 1) were grown in a randomized complete block design (RCBD) with three replications. Four rows had a 2 m length for each genotype, with a distance between each row at 30 cm. Data were taken on 10 randomly selected plants for days to heading, spike length, spikelet spike<sup>-1</sup>, grain weight spike<sup>-1</sup>, 1000-grain weight, and grain yield.

### Statistical analysis

Data were analysed using Analysis of Variance (ANOVA) proposed by Gomez and Gomez (1984) to assess variability and genotype by environment interaction (GEI) among genotypes. After getting significant results from the GEI, identifying the stability of genotypes ensued using Eberhart and Russell's (1966) statistical approach. Correlation among traits under observation determination was according to Kwon and Torrie (1964).

## RESULTS AND DISCUSSION

Previous studies showed an extensive range of variation in wheat germplasm for yield contributing traits (Ashraf *et al.*, 2001; Williams *et al.*, 2008; Naheed and Rahman, 2021) depicting the chance of selection and

improvement in germplasm following hybridization of superior genotypes. Hence, variation is a prime component of enhancement thus, the reason for its assessment through biometrical techniques and analysis of variance. Data subjected to ANOVA focused on yield contributing traits i.e., days to heading, spike length, spikelet spike<sup>-1</sup>, grain weight spike<sup>-1</sup>, 1000-grain weight, and grain yield. All under-consideration traits revealed highly significant variations for genotypes (G) and locations (L). However, genotype by environment interactions (GEI) average values were highly significant for all the traits except grain weight spike<sup>-1</sup> (Table 2). The observed variation among genotypes, locations, and GEI could be attributed to the variation in genetic makeup of genotypes and their interaction with the environment. Therefore, the interaction of the environment with the genotype is responsible for the recommendation of genotypes according to location since it reveals the impact of the environment on the genotype performance (Bayles *et al.*, 2000; Naheed and Rehman, 2021).

### Days to heading

Mean values for days to heading ranged between 107–114 days, but for G × E interactions, it ranged between 105–118 days. Genotype mean values revealed that minimum days to heading showed from PR-106

**Table 2.** Mean squares and coefficient of variation for various traits in wheat genotypes evaluated across three locations.

Traits	Locations (df = 2)	Genotypes (df = 15)	G × L (df = 30)	EMS	CV (%)
Days to heading	417.25**	25.56**	10.25**	3.18	1.60
Spike length	8.35**	189.45**	2.85**	1.20	8.71
Spikelets spike <sup>-1</sup>	24.80**	4.12 <sup>NS</sup>	3.38**	1.52	6.12
Grain weight spike <sup>-1</sup>	148.03**	55.53**	9.81 <sup>NS</sup>	9.54	13.92
1000-grain weight	43.21*	65.22**	15.09**	5.44	6.6
Grain yield	19897554.0**	15917542.4**	2711216.3**	706,227.5	18.50

\*,\*\* = Significant at  $p \leq 0.05$  and  $p \leq 0.01$ , NS = Non significant, df = Degree of freedom, CV = Coefficient of variation.

**Table 3.** Mean values and regression coefficient (bi) for days to heading in wheat genotypes evaluated across three locations.

Genotypes	Locations			Genotype means (days)	bi
	UAP	CCRI	NIFA		
DN-102	111	112	108	110	0.61
Pak-13	111	114	109	111	0.84
SRN-09111	113	115	109	112	1.05
NRL-1123	111	115	109	112	0.97
NRL-1130	112	115	108	112	1.11
PR-106	105	107	109	107	-0.23
PR-110	109	110	107	109	0.55
PR-111	110	115	108	111	1.14
PR-112	111	112	109	111	0.55
PR-113	111	118	108	112	1.67
NR-423	111	118	107	112	2.00
NR-429	113	116	110	113	1.08
NR-436	111	118	109	113	1.62
NR-449	111	117	108	112	1.49
KT-338	112	116	108	112	1.35
K-87	114	115	113	114	0.22
Location means (days)	111	115	109	-	-

LSD<sub>0.05</sub> Genotypes = 3.082, Locations = 1.117, GEI = 2.893

(107 days), whereas maximum days for heading from K-87 (114 days) (Table 3). Location means indicated that overall minimum days to heading emerged in NIFA (109 days) and maximum days in CCRI (115 days). Genotype × Environment Interaction (GEI) shows that minimum days to heading appeared at location AUP by genotype PR-106 (105 days), with maximum days (118 days) resulting from three lines, i.e., PR-113, NR-423, and NR-436 at location CCRI (Table 3). Days to heading is a pivotal trait in wheat as it decides grain filling duration. Delay in the heading resulted in shriveled seeds, while bold seeds were ascribed to early heading in wheat (Nasarullah *et al.*, 2017; Hadasch *et al.*, 2020).

Results for stability analysis values (bi) for days to heading ranged from -0.23 to 2.00, depicting an extensive range of stability among genotypes for days to heading (Table 3). Such an extensive range of differences were also reported by Tekdal and Kendal (2018) and Bonecke *et al.* (2020) for days to heading

depicting the response of different genotypes under different environmental conditions for the mentioned traits. Among 16 genotypes, seven genotypes, i.e., DN-102, Pak-13, NRL-1123, PR-106, PR-110, PR-112, and K-87, signified regression coefficient (bi) values as less than unity (<1.00). This low value specifies that genotypes showed resistance under unfavorable environmental conditions (Yaghotipoor *et al.*, 2017); hence, their recommendation for adverse environments. However, genotypes PR-111, PR-113, NR-423, NR-436, NR-449, and KT-338 showed bi value more than unity (>1.00). Observed results depict that genotypes SRN-09111 (1.05), NR-429 (1.08), and NRL-1130 (1.11) displayed bi values close to unity. Ali *et al.* (2012) discovered that if genotypes revealed regression coefficient (bi) values more than unity, those genotypes are best recommended for specific environments. However, if genotypes exhibited regression coefficient (bi) values close to unity or equal to unity for a

trait, then they are stable and better to be recommended for other environments. The reports of Polat *et al.* (2016) further supported the study results on the variation in regression coefficient ( $b_i$ ) values, with recommendations done according to  $b_i$  values for different environmental conditions (Ali *et al.*, 2012; Yaghotipoor *et al.*, 2017).

Correlation values for days to heading showed a significant negative relationship with grain yield (Table 9). This inverse relationship is needed when expected stress (terminal heat and drought stress) occurs in an environment. The results are in agreement with Ali *et al.* (2012), Polat *et al.* (2016), and Tekdal and Kendal (2018). They also reported a negative relationship between days to heading and grain yield among the advanced wheat population.

### Spike length

Spike length mean performance under study ranged from 10.01 to 15.02 cm, while for interaction ( $G \times E$ ) it varied from 9.30 to 15.77 cm (Table 4). Larger spikes surfaced in genotype PR-106 (15.02 cm), followed by Pak-13 (14.24 cm) and PR-110 (13.85 cm); however, small spikes resulted for K-87 (10.01 cm) and NR-423 (11.31 cm). Maximum spike length over locations came out for CCRI (12.99 cm), followed by NIFA (12.60 cm), with minimum spike lengths for UAP (12.16 cm). GEI revealed maximum spike length for two genotypes at different locations, i.e., PR-106 sown at UAP (15.77 cm) and Pak-13 at NIFA

(15.67 cm). Inversely, the minimum length was with K-87 sown at UAP (9.30 cm), with its performance at par with nine other genotypes sown at three locations ranging from 9.95 to 10.97 cm (Table 4). Spike length is an essential yield-contributing trait. The longer the spike, the more the obtainable spikelets, that in turn increase the grain yield (Shah *et al.*, 2009). Khan *et al.* (2014) supported the results as they also reported variations among wheat germplasm for spike length across different locations, while Khan and Mohammad (2018) observed that the performance of wheat genotypes under consideration was stable under different environments for spike length.

Regression coefficient ( $b_i$ ) values for spike length ranged from -1.28 to 3.00 (Table 4). Among all genotypes, three genotypes, i.e., NRL-1130 (0.53), KT-338(0.42), and K-87 (0.85), displayed regression values less than 1.00. It showed that these genotypes displayed resistance under adverse environmental conditions and could perform better under unfavorable conditions. Yaghotipoor *et al.* (2017) and Bonecke *et al.* (2020) supported these findings as they noticed that those genotypes which showed a  $b_i$  value lower than unity had resistance and perform well under poor environmental conditions. Genotypes DN-102 (1.37), NRL-1123 (2.56), PR-110 (1.31), PR-112 (3.00), NR-423 (2.33), NR-429 (2.60), NR-436 (2.36), and NR-449 (2.71) had  $b_i$  values more than unity (1).

**Table 4.** Mean values and regression coefficient ( $b_i$ ) for spike length in wheat genotypes evaluated across three locations.

Genotypes	Locations			Genotype means (cm)	$b_i$
	UAP	NIFA	CCRI		
DN-102	12.33	10.67	13.59	12.2	1.37
Pak-13	13.77	15.67	13.27	14.23	-0.47
SRN-09111	13.20	11.47	13.17	12.61	-0.14
NRL-1123	10.83	12.7	12.93	12.15	2.56
NRL-1130	11.47	12.83	11.85	12.05	0.53
PR-106	15.77	14.57	14.74	15.02	-1.28
PR-110	13.07	14.37	14.12	13.85	1.31
PR-111	13.57	13.7	12.52	13.26	-1.22
PR-112	10.90	11.77	13.43	12.03	3.00
PR-113	12.57	13.17	11.73	12.49	-0.94
NR-423	10.50	10.97	12.48	11.31	2.33
NR-429	11.57	12.07	13.77	12.47	2.60
NR-436	12.33	13.53	14.29	13.39	2.36
NR-449	10.57	12.60	12.78	11.98	2.71
KT-338	12.75	10.83	13.21	12.27	0.42
K-87	9.30	10.77	9.95	10.01	0.85
Location means (cm)	12.16	12.60	12.99	-	-

LSD<sub>0.05</sub> Genotypes = 4.26, Locations = 0.4, GEI = 1.77

These genotypes can perform better under specific environmental conditions. Polat *et al.* (2016) found that genotypes having values higher than unity can significantly perform differently under different environments. They also found higher values for spike length in wheat. One genotype, "K-87," had a value close to unity (0.85) for spike length, depicting stability in the performance of this genotype under different environmental conditions. Mohammadi *et al.* (2015) reported that those genotypes, which showed a bi value near one produced similar spike lengths under all the environments.

The correlation table revealed that spike length is in a positive and significant ( $P \leq 0.01$ ) link with grain yield (Table 9). A report of a significant positive correlation came from Fellahi *et al.* (2013). They noticed that those genotypes having long spikes are responsible for more grain on it, ultimately increasing yield (Nasarullah *et al.*, 2017).

### Spikelets per spike

From current research, mean genotype values for spikelets spike<sup>-1</sup> ranged from 18.63 to 21.57. The recorded minimum number of spikelets spike<sup>-1</sup> showed in NR-436 (18.63), whereas the maximum was in PR-112 (21.57). Mean values for GEI ranged from 17.42 (NR-436) to 22.87 (PR-112); however, overall highest values for spikelets spike<sup>-1</sup> appeared at location NIFA (20.94) and minimum at par values in CCRI (19.93) and AUP (19.54) (Table 5). Spikelets spike<sup>-1</sup> is an important yield-contributing trait in wheat as it directly

influences yield (Naheed and Rahman, 2021). Presented results aligned with Nasarullah *et al.* (2017) as they also found significant differences among genotypes for spikelets spike<sup>-1</sup> while checking the performance of genotypes under different environmental conditions.

Regression coefficient (bi) values for wheat genotypes ranged from -0.82 to 2.14 (Table 5). Results revealed bi values less than 1.00 for two genotypes, i.e., Pak-13 (0.86) and NR-436 (0.65). Therefore, these genotypes are suitable for unfavorable conditions when the focus is to increase the yield of wheat crops (Yaghotipoor *et al.*, 2017; Iltaf *et al.*, 2022). Further, bi values with more than 1.00 emerged for DN-102, SRN-09111, NRL-1123, NRL-1130, PR-106, PR-111, PR-113, NR-423, NR-449, KT-338, and K-87. These genotypes displayed responsiveness under specific environmental conditions. Notably, genotypes PR-113 (1.03), NR-423 (1.12), and Pak-13 (0.86) had values close to unity hence, considered desirable genotypes for both high- and low-yielding environments. Bassi and Garcia (2017) also found that different genotypes performed differently under multiple environments, and thus, recommendations of genotypes under various conditions proceeded according to bi values (Ali *et al.*, 2012).

Spikelets spike<sup>-1</sup> indicated significantly ( $P \leq 0.01$ ) positively associated with grain yield (Table 9). So, this trait is responsible for the increase in wheat grain yield. Fellahi *et al.* (2013) validated such findings. They also found a highly significant and positive correlation between spikelets spike<sup>-1</sup> and grain yield.

**Table 5.** Mean values and regression coefficient (bi) for spikelets per spike in wheat genotypes evaluated across three locations.

Genotypes	Locations			Genotype means (#)	bi
	UAP	NIFA	CCRI		
DN-102	18.52	21.53	20.47	20.17	1.95
Pak-13	20.05	21.10	19.8	20.32	0.86
SRN-09111	18.86	20.97	19.63	19.82	1.48
NRL-1123	19.58	21.67	19.43	20.23	1.64
NRL-1130	19.87	22.60	19.70	20.72	2.14
PR-106	18.29	20.90	20.63	19.94	1.56
PR-110	20.24	19.63	22.0	20.62	-0.82
PR-111	17.92	20.43	19.87	19.41	1.56
PR-112	21.25	20.60	22.87	21.57	-0.82
PR-113	20.00	21.20	19.47	20.22	1.03
NR-423	20.66	21.57	18.57	20.26	1.12
NR-429	21.81	20.43	19.83	20.69	-0.67
NR-436	17.42	18.83	19.63	18.63	0.65
NR-449	19.36	21.17	18.73	19.75	1.52
KT-338	18.48	20.20	19.33	19.34	1.16
K-87	20.37	22.13	18.93	20.48	1.65
Location means (#)	19.54	20.94	19.93	-	-

LSD<sub>0.05</sub> Locations = 1.770, GEI = 2.00

**Table 6.** Mean values and regression coefficient (bi) for grains weight per spike in wheat genotypes evaluated across three locations.

Genotypes	Locations			Genotype means (g)	bi
	UAP	NIFA	CCRI		
DN-102	1.92	2.09	1.69	1.90	1.09
Pak-13	2.03	2.75	1.77	2.19	2.89
SRN-09111	1.98	2.24	2.06	2.09	0.62
NRL-1123	2.09	2.43	2.03	2.18	1.20
NRL-1130	2.08	2.45	1.93	2.15	1.51
PR-106	2.37	2.48	2.32	2.39	0.45
PR-110	2.71	2.62	2.73	2.67	-0.34
PR-111	2.81	2.85	2.78	2.81	0.21
PR-112	2.21	2.29	2.10	2.20	0.52
PR-113	2.14	2.35	1.92	2.14	1.19
NR-423	2.26	2.26	2.04	2.19	0.54
NR-429	2.01	2.43	2.11	2.18	1.07
NR-436	1.84	2.24	1.79	1.96	1.38
NR-449	2.28	2.17	2.19	2.21	-0.14
KT-338	2.15	3.00	1.87	2.34	3.36
K-87	1.90	1.96	1.80	1.89	0.45
Location means (g)	2.17	2.41	2.07	-	-

LSD<sub>0.05</sub> Genotypes = 0.301, Locations = 0.093

### Grain weight per spike

Another yield-contributing parameter of wheat yield is grain weight per spike. If the grain is bold, then grain weight will be high, ultimately responsible for the increase in wheat yield. Mean values for grain weight spike<sup>-1</sup> ranged between 1.89 to 2.81 g. However, for GEI, it ranged from 1.69 to 3.00 g (Table 6). The maximum grain weight recording occurred in genotype PR-111 (2.81 g), followed by PR-110 (2.69 g), with minimum weight in genotype K-87 (1.89 g). Location mean values revealed that the environment of NIFA (2.41 g) is favorable for yield, followed by UAP (2.17 g) and CCRI (2.07 g). Values for interactions revealed non-significant, while KT-338 (3.00 g) sown at NIFA gave the highest grain weight spike<sup>-1</sup>, with minimum grain weight spike<sup>-1</sup> identified in genotype DN-102 (1.69 g) grown at CCRI (Table 6). Results agree with Bassi and Garcia (2017) and Hadasch *et al.* (2020) as they also observed variations among wheat genotypes for grain weight spike<sup>-1</sup>. Grain weight spike<sup>-1</sup> depends on environmental conditions if it is favorable, resulting in appropriate grain filling and the seed bold in size.

Correlation analysis revealed a significant ( $P \leq 0.01$ ) positive association between grain weight spike<sup>-1</sup> and grain yield (Table 9). Study findings relate to previous researchers' also acquiring a positive relationship between grain weight spike<sup>-1</sup> yield

in wheat genotypes grown across distinct environments (Yagdi and Sozen, 2009; Polat *et al.*, 2016; Bonecke *et al.*, 2020).

### 1000-grain weight

An influential quantitative trait of the wheat crop, 1000-grain weight directly alters the yield. The mean value for said character ranged between 33.54 to 43.48 g, while in the case of GEI, it ranged between 29.90 to 47.73 g (Table 7). Based on mean performance, genotype PR-111(43.48 g) exhibited the highest 1000-grain weight, followed by PR-112 (41.36 g), Pak-13 (40.36 g), SRN-09111 (39.87 g), NR-436 (39.83 g), and NR-449 (39.78 g). The lowest 1000-grain weight resulted in K-87 and DN-102. Location mean values show that genotypes performance for 1000-grain weight was maximum at location NIFA (39.33 g), followed by location UAP (37.94 g), whereas the minimum 1000-grain weight surfaced at CCRI (37.51 g). GEI exposed the maximum 1000-grain weight for PR-111 at UAP (47.73 g), and the minimum GEI mean value showed in DN-102 at UAP (29.90 g) (Table 7). Said results are consistent with Khan and Mohammad (2018). They also observed variations among wheat genotypes for 1000-grain weight when grown under different environmental conditions. Moreover, they said that variation is just because of the response of genotypes toward different environments (Iltaf *et al.*, 2022).

**Table 7.** Mean values and regression coefficient (bi) for 1000-grain weight in wheat genotypes evaluated across three locations.

Genotypes	Locations			Genotype means (g)	bi
	UAP	NIFA	CCRI		
DN-102	29.90	36.03	36.03	33.99	2.20
Pak-13	40.07	40.10	40.91	40.36	1.70
SRN-09111	39.90	42.27	37.46	39.87	2.27
NRL-1123	36.03	41.40	38.76	38.73	1.77
NRL-1130	36.97	34.57	33.02	34.85	2.67
PR-106	39.30	38.33	37.96	38.53	3.72
PR-110	34.70	38.60	37.63	36.98	2.19
PR-111	42.53	47.73	40.18	43.48	-1.96
PR-112	41.87	43.20	39.02	41.36	0.87
PR-113	38.73	41.10	37.18	39.00	2.29
NR-423	37.27	34.27	39.32	36.95	-1.95
NR-429	38.53	33.80	36.77	36.37	1.65
NR-436	37.97	42.33	39.19	39.83	-1.76
NR-449	41.10	40.77	37.47	39.78	0.64
KT-338	38.73	41.70	35.20	38.54	-0.28
K-87	33.50	33.03	34.08	33.54	-0.01
Location means (g)	37.94	39.33	37.51	-	-

LSD<sub>0.05</sub> Genotypes = 3.74, Locations = 1.48, GEI = 3.78

Regression coefficient (bi) values for 1000-grain weight ranged from -1.96 to 3.72 (Table 7). Genotypes NR-449 (0.64) revealed bi values less than 1.00, indicating the suitability of these genotypes under harsh environmental conditions. Similarly, the genotype PR-112 (0.87) value is close to 1.00, implying the stability of this genotype across environments. Genotypes DN-102, Pak-13, SRN-09111, NRL-1123, NRL-1130, PR-106, PR-110, PR-113, and NR-429 have values of more than 1.00 (Table 7). Jhinjer *et al.* (2017) and Yaghotipoor *et al.* (2017) proposed that genotypes having bi values lower than 1.00 can be endorsed for poor environments, while those genotypes showing bi values close to 1.00 are considered stable genotypes. However, genotypes having bi values of more than 1.00 are suitable under specific environmental conditions.

Correlation analysis shows that 1000-grain weight had a positive and highly significant relationship with yield (Table 9). Zafarnaderi *et al.* (2013) observed a highly significant positive correlation of 1000-grain weight with yield but negatively correlated with days to heading and days to maturity in bread wheat. The latest results concur with Bassi and Garcia (2017).

### Grain yield

Grain yield is a very complicated and imperative character to study. Therefore, improving this character is the main focus of every plant breeder. Regarding the current

experiment, the genotype mean value ranged from 3,218 to 8,128 kg ha<sup>-1</sup>; however, for interaction (GEI), it varies between 2,106–8,485 kg ha<sup>-1</sup> (Table 8). The mean performance revealed that the highest yield occurred in genotypes PR-112 (8,128 kg ha<sup>-1</sup>), PR-106 (6,519 kg ha<sup>-1</sup>), and PR-110 (6,381 kg ha<sup>-1</sup>). Conversely, the lowest yield appeared in 13 genotypes, varying from 3,218 to 4,605 kg ha<sup>-1</sup>. Location mean values revealed the maximum yield at NIFA (5,086 kg ha<sup>-1</sup>) and CCRI (4,712 kg ha<sup>-1</sup>), whereas the minimum at UAP (3,832 kg ha<sup>-1</sup>). Maximum and at par interaction values for yield resulted in four genotypes under different environments: PR-112 sown at UAP (8,485 kg ha<sup>-1</sup>); at NIFA (8,125 kg ha<sup>-1</sup>); at CCRI (7,775 kg ha<sup>-1</sup>), and PR-110 sown at UAP (7,665 kg ha<sup>-1</sup>). The minimum yield was in genotype NRL-1130 at UAP (2,106 kg ha<sup>-1</sup>), found at par with 14 other genotypes ranging from 2,278 to 3,454 kg ha<sup>-1</sup> grown at three previously mentioned locations (Table 8). Preceding research also found highly significant results for genotypes, environments, and their interaction with wheat yield. Observations for such type of variation came from Bassi and Garcia (2017), Polat *et al.* (2016), and Iltaf *et al.* (2022). They found that the environment always affects the performance of genotypes.

Stability analysis values (bi) stretched from -1.49 to 2.27 (Table 8). Two genotypes, PR-112 and NR-429, displayed a bi value of less than 1.00, revealing that they can perform well under unfavorable environmental conditions. Regression coefficient (bi) values of



**Table 8.** Mean values and regression coefficient (bi) for grain yield in wheat genotypes evaluated across three locations.

Genotypes	Locations			Genotype means (kg ha <sup>-1</sup> )	bi
	UAP	NIFA	CCRI		
DN-102	2285	4253	5279	3939	1.90
Pak-13	2956	6107	3964	4342	2.27
SRN-09111	3838	5638	4339	4605	1.28
NRL-1123	2506	5169	4089	3921	2.07
NRL-1130	2106	3372	5736	3738	1.57
PR-106	7293	6058	6207	6519	-1.03
PR-110	7665	6107	5369	6381	-1.49
PR-111	2978	5464	4083	4175	1.85
PR-112	8485	8125	7775	8128	0.37
PR-113	2278	4264	3322	3288	1.51
NR-423	3217	4991	3767	3992	1.27
NR-429	3411	4140	4864	4138	0.77
NR-436	3454	5900	4458	4604	1.81
NR-449	2633	3675	4757	3688	1.11
KT-338	3333	4883	3822	4013	1.11
K-87	2872	3228	3554	3218	-0.38
Location means (kg ha <sup>-1</sup> )	3832	5086	4712	-	-

LSD<sub>0.05</sub> Genotypes = 1,585, Locations = 518.5, GEI = 1,363

**Table 9.** Correlation of grain yield with various traits in wheat.

Traits	Correlation
Days to heading	-0.620*
Spike length	0.445**
Spikelets spike <sup>-1</sup>	0.379**
Grain weight spike <sup>-1</sup>	0.34**
1000-grain weight	0.327**

two genotypes, NR-449 and KT-338, showed close unity (1.11); hence, these two genotypes proved stable for all three locations. Highest bi values noticed in 11 genotypes included DN-102, Pak-13, SRN-09111, NRL-1123, NRL-1130, PR-111, PR-113, NR-423, NR-436, NR-449, and KT-338. Reports of such variation in stability among genotypes for 10 wheat cultivars studied at nine different locations came from Shah *et al.* (2009). Bonecke *et al.* (2020) and Naheed and Rahman (2021) also reported variations in the stability of wheat genotypes across environments. They proposed genotypes dappled with bi values lower than 1.00 are recommendable for poor environments, while those that showed bi values close to 1.00 are considered stable. However, genotypes having bi values of more than 1.00 are suitable under specific environmental conditions.

Grain yield mottled significant ( $P \leq 0.01$ ) and had a positive relationship with spike length, spikelets spike<sup>-1</sup>, grain weight spike<sup>-1</sup>, and 1000-grain weight. Yet, the significant and negative association turned up with days to heading (Table 9). The results agree with Aycecik and Yildirim (2006), who reported the

direct influence of spikelets spike<sup>-1</sup>, grain weight spike<sup>-1</sup>, and 1000-grain weight on grain yield. Dutamo *et al.* (2013) and Iltaf *et al.* (2022) also noticed that spikelets spike<sup>-1</sup>, grain weight spike<sup>-1</sup>, and 1000-grain weight directly affected grain yield.

## CONCLUSIONS

Significant results were obtained for all the traits under consideration for genotypes (G) and locations (L), while interactions (GEI) were highly remarkable for all the characters except grain weight spike<sup>-1</sup>. Grain yield showed a significant and positive correlation with spike length, spikelets spike<sup>-1</sup>, grain weight spike<sup>-1</sup>, 1000-grain weight, and grain yield, but was negatively correlated with days to heading. Stability analysis shows that genotypes - K-87, PR-113, Pak-13, PR-112, NR-449, and KT-338 were stable under tested locations for yield contributing traits, as their regression coefficient (bi) value resulted close to unity. Hence, these genotypes can serve as parental genotypes in the breeding program to develop stable genotypes.

## REFERENCES

- Ali A, Masood MA, Zahid MA (2012). Identifying the most promising genotypes in lentils for cultivation in a wide range of environments of Pakistan using various yield stability measures. *Pak. J. Bot.* 44(6): 1919-1922.
- Ashraf M, Qureshi AG, Ghafoor A, Khan NA (2001). Genotype-Environment interaction in wheat. *J. Biol. Sci.* 1(5): 356-367.
- Aycecik M, Yildirim T (2006). Path coefficient analysis of yield and yield components in bread wheat (*Triticum aestivum* L.) genotypes. *Pak J Bot.* 38(2):417-424.
- Bassi FM, Garcia MS (2017). Adaptation and stability analysis of ICARDA durum wheat elites across 18 countries. *Crop Sci.* 57: 2419-2430.
- Bayles RA, Flath K, Hovmoller MS, Pope CDV (2000). Break-down of the Yr17 resistance to yellow rust of wheat in northern Europe. *Agronomie.* 20: 805-811.
- Bonecke E, Breitsameter L, Bruggemann N (2020). The decoupling of impact factors reveals the response of German winter wheat yields to climatic changes. *Glob Change Biol.* 26:3601-3626.
- Coakley SM (1978). The effect of climatic variability on stripe rust of wheat in the Pacific Northwest. *Phytopathol.* 68: 207-212.
- Dimitrov E, Uhr Z, Chipilski R (2022). Study of yield and stability by common winter wheat varieties by changing climatic conditions in Sadovo region. *Bulg. J. Agric. Sci.* 28 (2), 271-278.
- Dutamo D, Alamerew S, Eticha F (2013). Path coefficient and correlation studies of yield and yield associated traits in bread wheat. *Germplasm* 33(11):1732-1739.
- Eberhart SA, Russell WA (1966). Stability parameters for comparing varieties. *Crop Sci.* 6: 36-40.
- Fellahi Z, Hannachi A, Bouzerzour H (2013). Correlation between traits and path analysis coefficient for grain yield and other quantitative traits in bread wheat under semiarid conditions. *J. Agric. Sustain.* 3(1): 16-26.
- Finlay KW, Wilkinson GN (1963). The analysis of adaptation in a plant breeding program. *Aust. J. Agric. Res.* 14: 742-754.
- Gomez KA, Gomez AA (1984). Statistical Procedures for Agricultural Research. *John Wiley and Sons Inc.* New York, USA.
- Hadasch S, Laidig F, Macholdt J, Bonecke E, Piepho HP (2020). Trends in mean performance and stability of winter wheat and winter rye yields in a long-term series of variety trials. *Field Crop Res.* 25(2): 1077-1092.
- Iltaf U, Raza H, Ali S, Fahad S, Ahmad A, Mukhtia SR, Samad N, Babar M (2022). Stability and yield performance of different wheat genotypes across multi locations of Khyber Pakhtunkhwa. *Pure and Applied Biol.* 11(3): 793-805.
- Jhinjer RK, Mavil GS, Malhotra A, Sood N, Singh B, Kaur B, Kumar V, Bhagat I, Sohu VS (2017). Stability analysis for grain yield and micronutrients in bread wheat genotypes. *Adv. Res.* 11(1): 1-8.
- Kalimullah SJ, Khan M, Irfaq, Rahman HU (2012). Genetic variability, correlation and diversity studies in bread wheat germplasm. *J. Anim. Plant Sci.* 22(2): 330-333.
- Khan MAU, Mohammad F (2018). Effect of genotype × environment interaction on grain yield determinants in bread wheat. *Sarhad J. Agric.* 34(1): 54-62.
- Khan S, Khan J, Khetran MA, Hanan A, Amanullah A, Kurd A, Naseer NS, Jaffar S (2014). Adaptation and stability of promising wheat genotypes for yield under rain-fed conditions of highland Balochistan. *J. Anim. Plant Sci.* 24(2): 521-525.
- Kwon S, Torrie J (1964). Heritability and interrelationship among traits of two soybean populations. *Crop Sci.* 4(2): 196-198.
- Mohammadi R, Farshadfar E, Amri A (2015). Interpreting genotype × environment interactions for grain yield of rain-fed durum wheat in Iran. *The Crop J.* 3(6): 526-535.
- Naheed H, Rahman HU (2021). Stability analysis of bread wheat lines using regression models. *Sarhad J. Agric.* 37(4): 1450-1457.
- Nasarullah, Uddin R, Uddin F, Jamal M (2017). Interpreting GE interaction of wheat genotypes for grain yield under different regimes of Khyber Pakhtunkhwa. *Pak. J. Agric. Res.* 30:107-121.
- PBS (2021-22). Year Book. Pakistan Bureau of Statistics (PBS), Ministry of Economic Affairs and Statistics, Govt. of Pakistan, Islamabad, Pakistan.
- Polat K, Cifci EA, Yagdi K (2016). Stability performance of bread wheat (*T. aestivum* L.) lines. *J. Agric. Sci. Tech:* 18: 553-560.
- Shah SIH, Sahito MA, Tunio S, Pirzada AJ (2009). Genotype-Environment interaction and stability analysis of yield and yield attributes of ten contemporary wheat varieties of Pakistan. *Sindh Univ. Res. J.* 41(4): 13-24.
- Tekdal S, Kendal E (2018). AMMI model to assess durum wheat genotypes in multi-environment trials. *J. Agric. Sci. Tech.* 20: 153-166.
- Tembo B (2021). Genotype by environment interaction analysis of wheat (*Triticum aestivum* L.) grain yield under rainfed conditions in Zambia. *SABRAO J. Breed. Genet.* 53(4): 609-619. <https://doi.org/10.54910/sabrao2021.53.4.5>.
- Villareal L, Christian L, Pope CV, Neema C (2002). Genetic variability in *Puccinia striiformis* f. sp. *tritici* populations sampled on a local scale during natural epidemics. *Appl Env Microbiol.* 68: 6138-6145.
- Williams RM, Brien OL, Eagles HA, Solah VA, Jayasena V (2008). The influences of genotype, environment, and genotype ×

- environment interaction on wheat quality. *Aust. J. Agric. Res.* 59(2): 95-99.
- Yagdi K, Sozen E (2009). Heritability, variance components and correlations of yield and quality traits in durum wheat (*T. durum* L.). *Pak. J. Bot.* 41(2): 753-759.
- Yaghotipoor A, Farshadfar E, Saeidi M (2017). Evaluation of phenotypic stability in bread wheat accessions using parametric and non-parametric methods. *J. Anim. Plant Sci.* 27(4): 1269-1275.
- Zafarnaderi N, Aharizad S, Mohammadi SA (2013). Relationship between grain yield and related agronomic traits in bread wheat recombinant inbred lines under water deficit condition. *Ann. Biol. Res.* 4(4):7-11.
- Zulkiffal M, Ahmed J, Riaz M, Ramzan Y, Ahsan A, Kanwal A, Ghafoor I, Nadeem M, Abdullah M (2022). Response of heat-stress tolerant and susceptible wheat lines in diverse planting environments by using parametric stability models. *SABRAO J. Breed. Genet.* 54(1): 127-140. <http://doi.org/10.54910/sabrao2022.54.1.12>.