

AMMI ANALYSIS FOR GRAIN YIELD IN BREAD WHEAT RECOMBINANT INBRED LINES

Sajid MUHAMMAD, Sultan AKBAR JADOON*, Fida MOHAMMAD, Iftikhar HUSSAIN
KHALIL, Sheraz AHMAD, Fahim ULLAH KHAN

Department of Plant Breeding and Genetics, Faculty of Crop Production Sciences,
The University of Agriculture, Peshawar-Pakistan

Muhammad S., S. Akbar Jadoon, F. Mohammad, I. Hussain Khalil, S. Ahmad, F. Ullah Khan (2023). *AMMI analysis for grain yield in bread wheat recombinant inbred lines*. - Genetika, Vol 55, No.1, 125-140.

Identification of high yielding relatively stable genotypes is an integral objective of plant breeding programs. Testing of genotypes across environments is required to determine yield stability of genotypes. The specific objective of the current study was to analyze genotype by environment interaction (GEI) for grain yield of 44 bread wheat recombinant inbred lines (RILs) and six check cultivars using additive main effect and multiplicative interaction (AMMI) model. Experiments were planted using alpha lattice design with two replicates in Peshawar (E-1 and E-3), Hangu (E-2 and E-4) and Kohat (E-5) Khyber Pakhtunkhwa province, Pakistan. Analysis of variance revealed significant differences among RILs for all traits while interactions due to genotype by environment were significant for all traits except days to emergence and 1000-grain weight. Significant GEI justified environment-specific as well as AMMI analysis to identify RILs with specific and wider adaptation. The AMMI analysis revealed that the first interaction principal component analysis (IPCA 1) captured 64% of GEI sum of squares while the second interaction principal component analysis (IPCA 2) explained 25.8% of the interaction sum of square. The AMMI biplot identified G30 as high yielding genotype followed by G19 and G49, whereas low yielding RILs were G13, G8 and G7. Similarly G30, being close to IPCA1 axis, was the most stable RIL with wider adaptability followed by G31 and G25. Based on AMMI stability value (ASV), RILs G18 (2.15), G5 (2.78), G27 (3.72), G44 (4.31), G25 (4.43), G42 (4.57), G43 (5.78), G11 (5.82), G1 (7.66) and G29 (7.81) were recognized in the given order of relative stability. Stability analysis identified G49 (Wafaq × Ghaznavi-98-3) as high yielding stable genotype among RILs which can be commercialized after fulfilling procedural requirements.

Key words: AMMI, Bi-plot, principal components, RILs, yield stability

Corresponding author: Sultan Akbar Jadoon, Department of Plant Breeding and Genetics, Faculty of Crop Production Sciences, The University of Agriculture, Peshawar-Pakistan, sultan@aup.edu.pk

INTRODUCTION

Prime objective of any plant breeding program is to develop broad-based relatively high yielding stable genotypes. Therefore, evaluation of genotypes across year and location is imperative to identify relative stable high yielding genotypes (AHMED *et al.*, 2019). Stability in performance of genotypes becomes important in environments where conditions vary considerably. Hence, the development of high yielding genotypes accompanied with relatively stable performance is of paramount importance for environments with the desired conditions. Various univariate and multivariate methods have been established to analyze and interpret genotypic performance across environments with varying levels of accuracy and complexity (MAFOUASSON *et al.*, 2018). ZOBEL *et al.* (1988) described the limitations of classical stability models as analysis of variance fails to capture significant portion of GEI while principal component analysis captures only highly significant GEI sum of squares and advocated the use of AMMI analysis. AMMI is a powerful tool in diagnosing GEI patterns by using the PCA (principal component axis) scores and AMMI stability value (ASV). The AMMI model combines the ANOVA for the genotypes and environment main effects with the principal components of the GEI. Results obtained can be graphed in a biplot to indicate both main and interaction effects for genotypes and environments (GEORGE and LUNDY, 2019). Further, AMMI model is a useful technique to capture the non-linear interaction, when joint regression technique fails to perceive important effects of GEI (RAJU, 2002). The AMMI model (GAUCH and ZOBEL, 1996) is more efficient in determining the most stable and high yielding genotypes in multi environment trials as compared to other procedures. Biplot analysis is the most powerful interpretive tool for AMMI models. Biplot is a graphical technique where aspects of both genotypes and environments are plotted on the same axes so that interrelationships can be visualized. In AMMI biplot, the main effects (genotypes mean and environments mean) are plotted on X- axis and IPCA 1 score is plotted on Y-axis to identify stable genotypes. The effectiveness of AMMI procedure has been clearly demonstrated (AHMED *et al.*, 2019; SINGH *et al.*, 2019). AMMI is suitable in the initial statistical analysis because it gives analytical tool for diagnosing other stability models. Secondly, AMMI clarifies the GEI and its analyses summarize the pattern and relationships of genotypes and environments. The third utility is to improve accuracy of the yield estimates. Multi-location yield trials facilitate quantification of environment and GEI effects (GOKSOY *et al.* 2019, JAFARI NAZARABADI *et al.*, 2022). However, there is always need for appropriate analysis of multi-location yield trials to establish genotypic differences as a result of diverse environments (TARAKONVAS and RUZGAS, 2006, ANURADHA *et al.*, 2022).

The objectives of this study were to; i) interpret GEI obtained by AMMI analysis of yield, ii) assess grain yield performance of genotypes based on the biplot, and iii) determine genotypes with high yield, depending on the differential genotypic response to environments.

MATERIALS AND METHODS

This study was conducted to interpret GEI for grain yield of 44 wheat RILs and six check cultivars across five environments using AMMI models. Breeding history of plant material, experimental design and statistical model used are explained as under; *Breeding history of plant material*: Forty-four F_{5:7} RILs-derived bread wheat populations (Table 1) were

originally developed in the Department of Plant Breeding and Genetics (AHMAD *et al.*, 2007). The segregating populations were advanced in bulk till F₄ generation. In F₅ generation, single heads were selected from the bulk populations based on agronomic fitness and disease resistance. The F_{5:6} heads were raised as head-to-row for seed multiplication and disease screening against stripe rust. Forty-four F_{5:7} RILs were selected for further evaluation in multi-location trials over years.

Table 1. List of bread wheat RILs and check cultivars evaluated across five environments

Code	Parentage	Code	Parentage
G1	Atta-Habib (Check)	G26	Tatara × Inqilab -1
G2	Margalla × Ghaznavi-98-9	G27	Tatara × Wafaq-2
G3	Takbeer × Khattakwal -1	G28	Wafaq × Ghaznavi-98-1
G4	Tatara × Inqilab -5	G29	Wafaq × Ghaznavi-98-5
G5	Tatara × Ghaznavi-98-6	G30	Sehar (Check)
G6	Margalla × Inqilab -1	G31	Tatara × Ghaznavi-98-1
G7	Tatara × Ghaznavi-98-4	G32	Tatara × Inqilab-7
G8	Wafaq × Ghaznavi-98-6	G33	Ghaznavi-98 × Khattakwal-4
G9	Tatara × Takbeer -7	G34	Margalla × Inqilab -2
G10	Sern (Check)	G35	Takbeer × Inqilab -8
G11	Tatara × Ghaznavi-98-3	G36	Tatara × Ghaznavi-98-3
G12	Wafaq × Takbeer -6	G37	Tatara × Ghaznavi-98-2
G13	Margalla × Inqilab -9	G38	Tatara × Wafaq-4
G14	Takbeer × Khattakwal -2	G39	Takbeer × Inqilab -1
G15	Ghaznavi-98 × Tatara-1	G40	Barsat (Check)
G16	Tatara × Ghaznavi-98-7	G41	Tatara × Takbeer-5
G17	Wafaq × Tatara-1	G42	Wafaq × Inqilab -2
G18	Tatara × Inqilab -7	G43	Tatara × Margalla-1
G19	Tatara × Takbeer -1	G44	Takbeer × Inqilab-8
G20	Janbaz (check)	G45	Takbeer × Inqilab-8
G21	Ghaznavi-98 × Khattakwal -1	G46	Pirsabak 2005 (Check)
G22	Tatara × Ghaznavi-98-6	G47	Tatara × Inqilab-3
G23	Wafaq × Ghaznavi-98-8	G48	Tatara × Ghaznavi-98-4
G24	Wafaq × Ghaznavi-98-4	G49	Wafaq × Ghaznavi-98-3
G25	Wafaq × Ghaznavi-98-7	G50	Takbeer × Margalla-4

Experimental design and procedure: Fifty genotypes including 44 F_{5:7} RILs and six check cultivars (Table 1) were evaluated in five environments. Experimental material was planted at the University of Agriculture Peshawar (E-1) and Hangu (E-2) during 2011/12 while at the University of Agriculture Peshawar (E-3), Hangu (E-4) and Kohat (E-5) during 2012/13 crop season. Hereafter, environments will be referred as E-1, E-2, E-3, E-4 and E-5. Experimental material was planted in 5×10 alpha lattice design with two replicates at each environment. Each plot had 4 rows of 5 meter length and a row-to-row space of 30 cm. Standard dose of nitrogen (120 kg ha⁻¹) and phosphorous (60 kg ha⁻¹) was applied. Uniform cultural practices required for wheat crop were followed throughout the growing season. Information regarding total precipitation, average temperature and humidity is presented in Figure A.

Statistical analysis

AMMI Analysis: The AMMI analysis of variance and AMMI biplots were carried out using computer software GenStat v. 12 (VSN INTERNATIONAL, 2009). Each location under respective

year was considered as individual environment. Means were adjusted for blocks and replications in each environment before subjecting to AMMI analysis.

The AMMI model is given as:

$$Y_{ij} = \mu + \alpha_i + \beta_j + \sum_{n=0}^N \lambda_n Y_{in} \delta_{jn} + \theta_{ij} + \varepsilon_{ij}$$

Where,

Y_{ij} = the mean yield of genotype i in environment j

μ = the grand mean

α_i = the deviation of the genotype mean from the grand mean

β_j = the deviation of the environment mean from the grand mean,

λ_n = the singular value for the IPCA n

N = the number of PCA axis retained in the model

Y_{in} = the PCA score of a genotype for PCA axis n

δ_{jn} = the environmental PCA score for PCA axis n

θ_{ij} = the AMMI residual and ε_{ij} = the residuals.

The degrees of freedom (df) for the IPCA axis were calculated as suggested by ZOBEL et al. (1988).

AMMI biplot: The AMMI biplot graphically displays GEI with AMMI interaction parameters. Two type of plotting is possible with estimated AMMI interaction parameters. First PCA scores of genotypes and environments are plotted against their respective means. In biplot, the IPCA1 is used as ordinate (Y-axis) and the mean effect for genotypes or environment and or both represent abscissa (X-axis). Likewise, the IPCA1 is the abscissa and IPCA2 represents the ordinate to further explore the stability. This biplot formulates the interactions and referred as AMMI1 model while IPCA1 score is plotted against IPCA2 score which is termed as AMMI2 model.

AMMI stability value: The ranking of genotypes based on their stability was computed following PURCHASE et al. (2000).

$$ASV = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1 \text{ Score})^2 + (IPCA2 \text{ Score})^2}$$

Where SS_{IPCA1}/SS_{IPCA2} is the weight given to the IPCA1 value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares

RESULTS AND DISCUSSION

AMMI analysis of variance: AMMI analysis of variance of 44 bread wheat RILs and six check cultivars over five environments for grain yield is given in Table 2. Significant differences were detected among environments, genotypes and GEI. This means that the genotypes showed different behavior in the environments. This enables the breeder to justify the selection of genotypes based on the magnitude of interaction with the environment (ERDEMCI, 2018, ADIL *et al.*, 2022). Genotypes explained 34.7% of the total phenotypic variation. Environments gathered the least sum of squares (8%) which indicated that environments were steady for grain yield of genotypes hence selection of genotypes based on environment is not effective in this case. Interaction due to genotype by environment explained 57.3% of the total phenotypic variation in the grain yield performance of genotypes, indicating that change in ranking of genotypic performance was mainly the result of GEI. This suggests that different sets of genotypes appeared high yielding in different environments. Differential environmental conditions may have triggered some yield enhancing genes in different genotypes which may have resulted in significant GEI and eventually higher proportion in total phenotypic variation (Fig. A). While studying genotypic performance across environments, MOHAMMAD *et al.* (2011); BACHA *et al.* (2015); NOORUL *et al.* (2015); ROOSTAEI *et al.* (2022) also reported that the performance of wheat genotypes was environment-specific. Likewise, GAUCH and ZOBEL (1996) reported that sizable proportion of environment and GEI in total variation implies the presence of different mega-environments with different sets of high yielding genotypes. In light of this explanation, the current experiment may also have different mega-environments which could be used for screening bread wheat lines.

Table 2. Analysis of variance based on AMMI model for yield of 50 wheat genotypes across five environments during 2011-13

Source	Df	SS	MS	Total variation explained (%)	GE explained (%)	Cumulative (%)
Total	249	155023847				
Genotypes	49	53867397	1099335**	34.7		
Environments	4	12401839	3100460**	8.0		
Interactions	196	88754611	452830**	57.3		
IPCA1	52	56831385	1092911		64.0	64.0
IPCA2	50	22931377	458628		25.8	89.9
Residuals	94	8991849	95658			

GEI was further partitioned into two principal components. The first two principal components were significant and cumulatively explained 89.8% of the variation due to GE interaction (Table 2). This indicated that first two principal components were sufficient to explain the complex patterns of GE interaction. Therefore, most information regarding GE interaction can be drawn by plotting these two principal components. HOMMA (2015), TEMBO (2021) also reported highly significant PCA 1 and PCA 2 components and concluded that AMMI model with first two IPCA was the best predictive model in explaining GEI. The current findings validated the results obtained by earlier researchers that first two principal components of AMMI model were more important in explaining GEI (BRANDLE and MCVETTV (1988); TARAKANOVAS and RUSGAZ (2006), MOHAMMED *et al* (2010); GUPTA *et al.*, 2022; OMRANI *et al.*, 2022; SIME *et al.*, 2022).

AMMI biplot: Yield performance of 50 genotypes across five environments based on AMMI model is presented in Figures 1, 2, 3 and 4. The IPCA of genotypes in AMMI analysis could predict stability of genotypes over environments (GAUCH and ZOBEL., 1997, YAN *et al.*, 2007; KYRATZIS *et al.*, 2022; ÖZTÜRK, 2022)). Higher IPCA score (both positive and negative) for a genotype is an indication of the instability of genotype over environments. Mean grain yield of genotypes was plotted against first principal component (Fig.1).

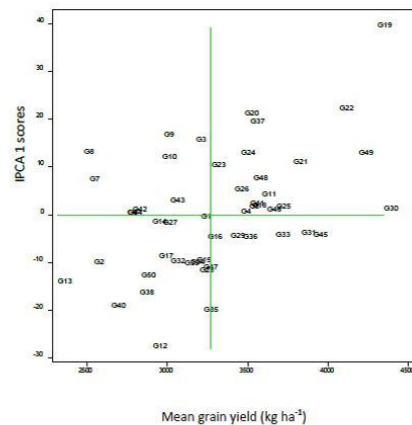


Figure 1 AMMI1 biplot of 50 genotypes based on IPCA1 scores against mean yield.

It is clear that G30 was high yielding genotype, followed by G19 and G49. The lowest yielding genotype was G13 followed by G8 and G7. The most stable genotype being close to the IPC1 axis was G30 followed by G31 and G25 and thus can be used as widely adapted genotypes. The most unstable genotypes were G19 and G22 as these were lying far away from IPC1 axis. However, due to their high yield they could be considered for specific environment. The closer the IPCA value of genotype to zero, more stable will be the genotypes across their testing environments (PURCHASE *et al.*, 2000). The PCA scores of genotypes in the AMMI analysis

shows the magnitude of stability of genotypes over environments. Greater PCA score is an indication of specific adaptation of a genotype to a specific environment (KAYA *et al.*, 2002, FERNEY *et al.*, 2022), The PCA scores of stability of genotypes over environment is an indication of specific adaptation of a genotype to a specific environment.

against environment E-4 and E-5 (i.e., Peshawar) might have been the most favorable for wheat. Conversely, genotype G19 did not respond to environment E-1 (JAFARI NAZARABADI *et al.*, 2022; MUHAMMAD *et al.*, 2022).

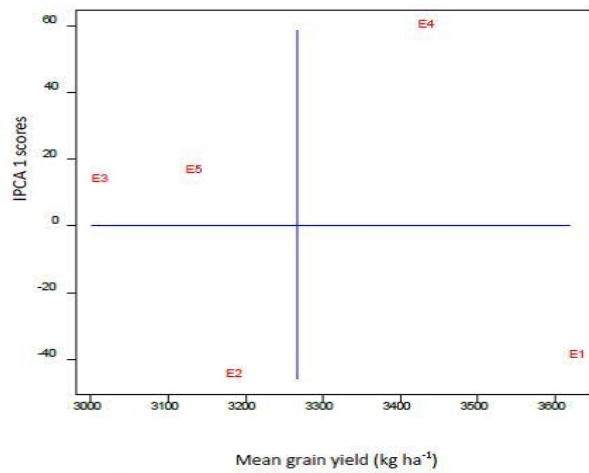


Figure 2 AMMI biplot of five environments based on IPCA1 scores of environments against mean yield.

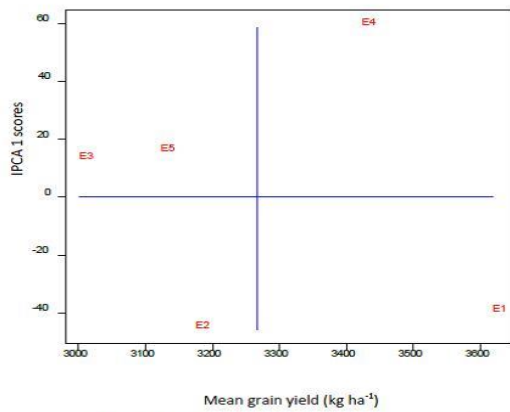


Figure 2 AMMI biplot of five environments based on IPCA1 scores of environments against mean yield.

Genotypes that were in close proximity of environments or with each other indicated specific adaptation to that environment or had similar performance (AYALNEH *et al.*, 2014; ABYAR *et al.*, 2022). The interaction of genotypes with specific environment based on mean grain yield is illustrated in Fig. 3. Genotypes G19 and G22 were highly responsive to environment E4 while G35 was responsive to environments E1 and E2. Genotypes and environments located on the positive x-axis (right quadrants) had positive association while

those located on the negative x-axis (left quadrants) had negative association. Positive association indicates superior performance in that environment while negative association indicates poor performance.

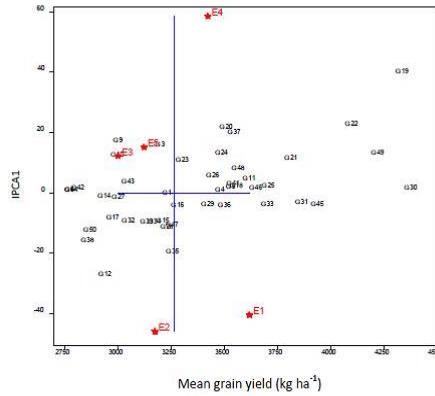


Figure 3 AMMI biplot of 50 genotypes based on their IPCA 1 scores against mean yield.

AMMI biplot constructed on the basis of AMMI1 model explained 64% of total variation (Table 2). Similarly, AMMI2 biplot was constructed by plotting principal component 1 against principal component 2 as shown in Figure 4.

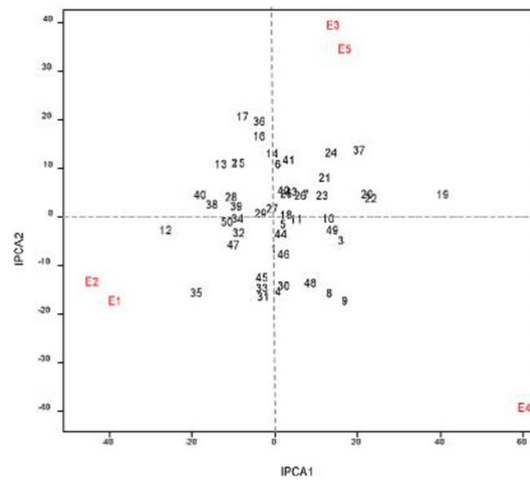


Figure 4 AMMI 2 biplot of 50 genotypes based on their IPCA 1 scores against IPCA 2 scores.

The first two principal components cumulatively explained 89.8% of variation due to GE interaction, and thus making AMMI2 model a better fit than AMMI1 (Table 2). MOHAMMAD *et al.* (2011); FARSHADFAR *et al.* (2012); ANURADHA *et al.* (2022) had also reported importance of the first two PCs in explaining the genotype by environment interaction. Since PC2 also plays significant role in explaining the GEI therefore, PC1 was plotted on x-axis and PC2 was plotted on y-axis for grain yield. The greater the IPCA scores, the more specifically adapted a genotype to a certain environment. The more IPCA score approached to zero the more stable could be a genotype to all environments (ADUGNA and LABUSCHAGNE, 2002; YAN *et al.*, 2007; NAJAFI *et al.*, 2021). Genotypes that are grouped in the same quadrant of the biplot are closely associated, while genotypes in the opposite direction of the quadrant have no association. Based on AMMI2 model, G18, G27, G11 and G5 were stable and widely adapted genotypes as indicated by their vicinity to the origin although yield ranking of these genotypes was 13th, 36th, 11th and 16th, respectively. Similarly genotypes G9, G17, G19, and G35 could be considered as less stable genotypes as lying far away from the origin of the biplot. However, genotype G19 can be considered as specifically adapted genotype due to its higher mean yield. YAN and TINKER (2006); YAN *et al.* (2007); SOLOMON *et al.* (2012); ABRAHA *et al.* (2019) reported that AMMI biplot could clearly facilitate identification of environments and cultivars for specific recommendations. The environment differences in terms of temperature, rainfall, altitude and soil fertility etc. affected the performance of genotypes, justifying the need to identify high yielding stable genotypes in wide range of environments or to breed cultivars specifically adapted to specific environments (DURSUN, 2020; ADIL *et al.*, 2022; VERMA and SINGH, 2022). ADUGNA and LABUSCHAGNE (2002); TARAKANOVAS and RUZGAS (2006); ROOSTAEI *et al.* (2022) documented the efficiency of AMMI analysis in partitioning genotype by interaction for grain yield stability in winter wheat.

AMMI stability value: AMMI model provides no provision to rank genotypes based on their stability. Therefore, PURCHASE *et al.* (2000) proposed AMMI stability value (ASV) based on the principal components of AMMI analysis. The ASV is the method of calculating the distance from the origin in an AMMI2 model using Pythagoras theorem (PURCHASE *et al.*, 2000). Hence, genotype with smaller ASV is the most stable across environments, while the one with larger ASV, the more specifically adapted a genotype is to certain environment. The ASV and ranking of genotypes based on ASV and mean grain yield are given in Table 4..

Table 4. Mean performance of top four wheat genotypes at each environment

Environment	Mean	Score	1	2	3	4
E4	3423	58.6	G19	G22	G49	G30
E5	3122	15.2	G19	G22	G49	G37
E3	3001	12.3	G19	G22	G37	G49
E1	3618	-40.4	G30	G35	G45	G31
E2	3174	-45.8	G30	G35	G45	G31

Table 5. Genotypes ranking based on AMMI stability value (ASV) and mean yield ($Kg\ ha^{-1}$) of 50 wheat genotypes across five environments

Line	ASV	ASV Rank	IPCA [1]	IPCA [2]	Mean Yield	Yield Rank
G18	2.15	1	-1.05	-7.48	3525	13
G5	2.78	2	-10.43	10.43	3508	16
G27	3.72	3	15.09	-5.87	2971	36
G44	4.31	4	0.07	-16.36	2751	44
G25	4.43	5	1.06	-2.22	3676	8
G42	4.57	6	-0.06	10.16	2781	43
G43	5.78	7	6.92	3.83	3017	34
G11	5.82	8	12.55	-16.52	3586	11
G1	7.66	9	16.18	-18.07	3208	27
G29	7.81	10	11.45	-1.34	3391	22
G26	8.10	11	3.61	-1.25	3415	21
G46	8.75	12	-27.98	-3.67	3617	10
G6	10.16	13	-14.43	10.16	2748	45
G41	11.38	14	-2.08	12.09	3511	15
G7	11.55	15	-10.16	10.35	2514	48
G14	12.53	16	-5.20	15.84	2904	40
G30	14.93	17	-9.28	19.76	4346	1
G45	15.22	18	1.32	-0.56	3906	5
G23	15.80	19	39.01	3.69	3272	23
G4	16.36	20	20.69	3.74	3457	19
G34	16.63	21	10.45	7.14	3140	31
G32	16.78	22	21.72	2.84	3019	33
G39	16.91	23	9.79	3.45	3104	32
G33	17.12	24	12.25	12.50	3672	9
G16	17.83	25	1.18	4.02	3249	24
G21	17.93	26	4.67	3.42	3783	7
G10	18.07	27	-2.32	0.73	2966	37
G48	18.43	28	-12.19	3.32	3534	12
G31	18.58	29	-4.96	-0.24	3833	6
G15	19.05	30	0.68	-14.89	3181	29
G47	19.20	31	-4.30	-17.31	3224	26
G2	19.46	32	-10.31	-4.26	2542	47
G28	19.47	33	-4.73	-15.42	3199	28
G49	19.71	34	-10.53	-1.35	4190	3
G36	20.45	35	-20.55	-16.43	3470	18
G50	20.89	36	-5.20	18.74	2837	41
G24	22.98	37	18.98	13.05	3457	20
G3	24.47	38	-16.90	1.79	3176	30
G17	24.57	39	-10.70	1.42	2945	38
G13	24.88	40	-19.65	3.79	2315	50
G8	25.75	41	1.84	11.00	2479	49
G38	26.66	42	0.55	4.49	2826	42
G40	31.17	43	2.51	4.21	2649	46
G9	31.23	44	-0.18	-4.30	2977	35
G37	32.60	45	-4.74	-13.26	3515	14
G20	32.79	46	0.59	-8.71	3478	17
G22	34.31	47	-11.49	-6.44	4067	4
G35	36.28	48	7.15	-14.60	3226	25
G12	44.20	49	12.30	-3.67	2908	39
G19	61.53	50	-13.23	-1.75	4306	2

Based on ASV, G18 (2.15), G5 (2.78), G27 (3.72), G44 (4.31), G25 (4.43), G42 (4.57), G43 (5.78), G11 (5.82), G1 (7.66) and G29 (7.81) had low ASV and thus were widely stable genotypes (Table 4.14). Similarly, due to large ASV, G19 (61.53), G12 (44.20), G35 (36.28) and G22 (34.31) were the most unstable genotypes, wherein, G19 and G22 were superior in yield ranking, and thus had specific adaptation (Table 5). Current results validate the previous

finding of FARSHADFAR *et al.* (2012); AHMED *et al.* (2019); KHAN *et al.* (2020) who used ASV as a technique for evaluating grain yield stability of wheat cultivars. Earlier researchers have also used ASV to determine stability in genotypes for grain yield (DESALEGN *et al.*, 2004; FERNEY *et al.*, 2006; AHMED *et al.*, 2019; JĘDZURA *et al.*, 2022).

CONCLUSIONS

Significant GEI for most of the traits indicated that genotypic performance was not stable across five environments. AMMI analysis of variance indicated highly significant differences among genotypes, environments and GEI. Biplot based on the first principal components and mean grain yield of the genotypes and environments identified genotypes G49, G30, G22 and G45 as high yielding genotypes, whereas G49 was the perfect genotype due to its proximity to the “ideal genotype”. Genotypes G37, G20, G35 and G12 were the least stable in addition to their below average performances. Among environments, E-4 appeared to be the most productive and discriminating environment, whereas, E-1 and E-2 were the least representative environments.

ACKNOWLEDGMENTS

The principal author is highly obliged to the Higher Education Commission (HEC) of Pakistan for providing financial support and department of Plant Breeding and Genetics for providing all relevant material for conducting this research.

Received, March 26th, 2022

Accepted November 28th, 2022

REFERENCES

- ABRAHA, M.T., H. SHIMELIS, T. SOLOMON, A. HAILU (2019): Genotype-by-environment interaction and selection of elite wheat genotypes under variable rainfall conditions in northern Ethiopia. *J. Crop Improv.* 33(6): 797–813.
- ABYAR, S., S. NAVABPOUR, R. KARIMIZADEH, A. GHOLIZADEH, G. KIANI (2022): Grain yield stability evaluation of bread wheat genotypes using AMMI multivariate methods. *Isfahan Univ. Technol. Crop Prod. Process.* 12(1): 119–132.
- ADIL, N., S.H. WANI, S. RAFIQEE, S. MEHRAJUDDIN, N.R. SOFI, A.B. SHIKARI, A. HUSSAIN, F. MOHIDDIN, I.A. JEHANGIR, G.H. KHAN (2022): Deciphering genotype \times environment interaction by AMMI and GGE biplot analysis among elite wheat (*Triticum aestivum* L.) genotypes of Himalayan region. *Ekin J. Crop Breed. Genet.* 8(1): 41–52.
- ADUGNA, W., and M. T. LABUSCHAGNE (2002): G \times E interaction and phenotypic stability analysis of linseed in Ethiopia. *Plant Breed.*, 121: 66-71.
- AHMAD, F., F. MOHAMMAD, M. BASHIR, SAIFULLAH, H. KHAN (2007): Inheritance of important traits in bread wheat over different planting dates using diallel analysis. *Sarhad. J. Agric.*, 23(4): 955-964.
- AHMED, S., F. MOHAMMAD, N. U. KHAN, Q. AHMED, S. GUL, S. A. KHAN, M. H. ROMENA, M. FIKERE, I. ALI, A. DIN (2019): Assessment of flue-cured tobacco recombinant inbred lines under multi-environment yield trials. *Intl. J. Agric. Biol.*, 22(3): 578–586.
- AL-ASHKAR, I., M. SALLAM, N. AL-SUHAIBANI, A. IBRAHIM, A. ALSADON, A. AL-DOSS (2022): Multiple stresses of wheat in the detection of traits and genotypes of high-performance and stability for a complex interplay of environment and genotypes. *Agronomy* 12(10): 2252.
- ALEMU, G., N. GELETA, A. DABI, A. DELESSA, R. DUGA (2021): Stability models for selecting adaptable and stable bread wheat (*Triticum aestivum* L.) varieties for grain yield in Ethiopia. *J. Agric. Sci. Eng* 7: 14–22.

- ANURADHA, N., T. PATRO, A. SINGAMSETTI, Y. SANDHYA RANI, U. TRIVENI, A. NIRMALA KUMARI, N. GOVANAKOPPA, T. LAKSHMI PATHY, V.A. TONAPI (2022): Comparative study of AMMI-and BLUP-based simultaneous selection for grain yield and stability of finger millet [*Eleusine coracana* (L.) Gaertn.] genotypes. *Front. Plant Sci.* 12: 3117.
- AYALNEH, T., T. LETTA, M. ABINASA (2013): Assessment of stability, adaptability and yield performance of bread wheat cultivars in South Eastern Ethiopia. *Plant Breed. Seed Sci.*, 67(1): 3-11.
- BACHA. T., S. ALMEREW, Z. TADESSE (2015): Genotype \times environment interaction and yield stability of bread wheat genotype in Ethiopia using the AMMI analysis. *J. Bio. Agric. Healthcare.*, 5(11): 129-139.
- BRANDLE, J. E., and P. B. E. MCVETTV (1988): Genotype \times environment interaction and stability analysis of seed yield of oilseed rape grown in Manitoba. *Canad. J. Plant Sci.*, 68: 381-388.
- DESALEGN, D., S. GELALCHA, B. YAIE, B. GIRMA, B. MAMO, D. MASRESHA (2004): Grain yield stability of bread wheat genotypes in favorable and stressed environments. Proceedings of the 12th Regional *Wheat Workshop for Eastern, Central and Southern Africa* Nakuru, Kenya.
- DURUSUN, K. (2020): Stability analyses for interpreting genotype by environment interaction of selected oriental tobacco landraces. *Turkish J. Field Crop.* 25(1): 83–91.
- ERDEMSI, I. (2018): Investigation of genotype \times environment interaction in chickpea genotypes using AMMI and GGE biplot analysis. *Turk J Field Crops.*, 23(1): 20-26.
- FARSHADFAR, E., N. MAHMODI, A. YAGHOTIPOOR (2011): AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat. *Aust. J. Crop Sci.*, 5(13): 1837-1844.
- FERNEY, G.H., M. ALEXEI, A. AIGUL (2006): Evaluation of grain yield stability, reliability and cultivar recommendations in spring wheat from Kazakhstan and Siberia. *J. Cent. Eur. Agric.*, 4: 649-660.
- GAUCH, H. G., AND R. W. ZOBEL (1996): AMMI analysis of yield trials. In: Kang MS, Gauch H.G (eds) *Genotype by environment Interaction*. CRC Press. Boca Raton, FL. 85-122.
- GAUCH, H. G. AND R. W. ZOBEL (1997): Identifying mega-environments and targeting genotypes. *Crop Sci.*, 37: 311-326.
- GEORGE, N. AND M. LUNDY (2019): Quantifying genotype \times environment effects in long-term common wheat yield trials from an agroecologically diverse production region. *Crop Sci.*, 59(5): 1960–1972.
- GOKSOY A. T., M. SINCIK, M. ERDOGMUS, M. ERGIN, S. AYTAC, G. GUMUSCU, O. GUNDUZ, R. KELES, G. BAYRAM, E. SENYIGIT (2019): The parametric and non-parametric stability analyses for interpreting genotype by environment interaction of some soybean genotypes. *Turk J Field Crops.*, 24(1): 28-38.
- GUPTA, V., M. KUMAR, V. SINGH, L. CHAUDHARY, S. YASHVEER, R. SHEORAN, M.S. DALAL, A. NAIN, K. LAMBA, N. GANGADHARAIHAH (2022): Genotype by environment interaction analysis for grain yield of wheat (*Triticum aestivum* (L.) em. Thell) genotypes. *Agriculture* 12(7): 1002.
- HOMMA, S. (2015): AMMI, Stability and GGE biplot analysis of durum wheat grain yield for genotypes tested under some optimum and high moisture areas of Ethiopia. *Acad. J. Entomol.*, 8(3): 132-139.
- JAFARI NAZARABADI, T., A.A. NASROLLAHNEJAD GHOMI, A. KORDENAEJ, K. ZENALINEZHAD (2022): Stability analysis of advanced bread wheat (*Triticum aestivum* L.) lines using AMMI method. *J. Plant Prod. Res.* 29(3): 127–141.
- JĘDZURA, S., J. BOCIANOWSKI, P. MATYSIK (2022): The AMMI model application to analyze the genotype–environmental interaction of spring wheat grain yield for the breeding program purposes. *Cereal Res. Commun.*: 1–9.
- KARIM, M.H., M.A. JAHAN (2013): Comparative study of yield and yield contributing traits of different genotypes in bread wheat. *J. Agric. Biol. Sci.* 8(2): 147–151.
- KAYA, Y., PALTA, S. TANER (2002): Additive main effects and multiplicative interaction of yield performances in bread wheat genotypes across environments. *Turk. J. Agric. For.*, 26: 275-279.
- KHAN, M.A.U., F. MOHAMMAD, F.U. KHAN, S. AHMAD, M.A. RAZA, T. KAMAL (2020): Comparison among different stability models for yield in bread wheat. *Sarhad J. Agric.* 36(1): 282–290.

- KYRATZIS, A.C., A. PALLIDES, A. KATSIOTIS (2022): Investigating stability parameters for agronomic and quality traits of durum wheat grown under Mediterranean conditions. *Agronomy* 12(8): 1774.
- MAFOUASSON, H. N. A., V. GRACEN, M. A. YEBOAH, G. NTSOMBOH-NTSEFONG, L. N. TANDZI, C. S. MUTENGWA (2018): Genotype-by-environment interaction and yield stability of maize single cross hybrids developed from tropical inbred lines. *Agronomy*, 8(5):62
- MOHAMMAD, F., O. S. ABDALLA, S. RAJARAM, A. YALJAROUKA, N. U. KHAN, A. Z. KHAN, S. K. KHALIL, I. H. KHALIL, I. AHMAD AND S. A. JADOON (2011): Additive main Effect and multiplicative analysis of synthetic-derived wheat under varying moisture regimes. *Pak. J. Bot.*, 43(2): 1205-1210.
- MOHAMMED, M. I. (2009): Genotype x Environment interaction in bread wheat in Northern Sudan using AMMI analysis. *American-Eurasian J. Agric. Environ. Sci.*, 6(4): 427-433.
- MULUGETA, B., K. TESFAYE, M. GELETA, E. JOHANSSON, T. HAILESILASSIE, C. HAMMENHAG, F. HAILU, R. ORTIZ (2022): Multivariate analyses of Ethiopian durum wheat revealed stable and high yielding genotypes. *PLoS One* 17(8): e0273008.
- NAJAFI, M.T., S.M. AGAEE, A. MOAYEDI, A. KAFFASHI, M. SAYAHFAR (2021): Yield stability analysis of durum wheat genotypes using AMMI method.
- NEGASH, G., A. BIRR (2022): Adaptability study of yield and yield related trait performance of improved bread wheat (*Triticum aestivum* L.) varieties in North Shewa Zone Oromia, Ethiopia. *South Asian Res J Agri Fish* 4(6): 77–84.
- NOORUL, S., A. MUSHTAQ, V. RAKASH, B. ASIFA, A.D. ZAHOOR (2015): Stability analysis in Wheat: An application of additive main effects and multiplicative interaction. *African J. Agric. Res.* 10(4): 295–300.
- OMRANI, A., S. OMRANI, M. KHODARAHMI, S.H. SHOJAEI, Á. ILLÉS, C. BOJTOR, S.M.N. MOUSAVI, J. NAGY (2022): Evaluation of grain yield stability in some selected wheat genotypes using AMMI and GGE biplot methods. *Agronomy* 12(5): 1130.
- ÖZTÜRK, I. (2022): Environment by genotype interaction and stability of bread wheat (*Triticum aestivum* L.) genotypes under rainfed conditions in Trakia region. *Ekin J. Crop Breed. Genet.* 8(2): 118–127.
- PURCHASE, J. L., H. HATTING, C. S. VAN DEVENTER (2000): Genotype × environment interaction of winter wheat in South Africa: II. Stability analysis of yield performance. *S. Afr. J. Plant Soil*, 17: 101-107.
- RAJU, B. K. M. (2002): A study on AMMI model and its biplots. *J. Indian Society Agric. Stat.*, 55(3): 297-322.
- ROOSTAEI, M., J. JAFARZADEH, E. ROOHI, H. NAZARY, R. RAJABI, R. MOHAMMADI, G.R. KHALILZADEH, F. SEIF, S.M.M. MIRFATAH, S.S. AMIRI (2022): Genotype × environment interaction and stability analyses of grain yield in rainfed winter bread wheat. *Exp. Agric.* 58: e37.
- SIME, B., G. NEPIR, G. ALEMU (2022): Analysis of genotype by environment interaction for agronomic traits of bread wheat (*Triticum aestivum* L.) genotypes in Oromia, Ethiopia. *Am. J. Biosci. Bioeng.* 10(3): 70–77.
- SINGH, C., A. GUPTA, V. GUPTA, P. KUMAR, R. SENDHIL (2019): Genotype x environment interaction analysis of multi-environment wheat trials in India using AMMI and GGE biplot models. *Crop Breed. Appl. Biotechnol.*, 19(3): 309–318.
- SOLOMON, K. F., H. A. SMIT, E. MALAN, W. J. DUTOIT (2008): Parametric model based assessment of genotype × environment interactions for grain yield in durum wheat under irrigation. *Intl. J. Plant Prod.*, 2(3): 23-36.
- TARAKANOVAS, P. AND V. RUZGAS (2006): Additive main effect and multiplicative analysis of grain yield of wheat varieties in Lithuania. *Agron. Res.*, 4(1): 91-98.
- 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.

- TIWARI, J.K. (2019): GGE biplot and AMMI model to evaluate spine gourd (*Momordica dioica* Roxb.) for genotype \times environment interaction and seasonal adaptation. *Electron. J. Plant Breed.* *10*(1): 264–271.
- VERMA, A., G.P. SINGH (2022): Comparative analysis of genotype \times environment interaction for wheat genotypes by AMMI and BLUP for Peninsular zone. *J. Crop Weed* *18*(2): 191–199.
- VSN INTERNATIONAL (2009): *GenStat for Windows®*. 12th ed. VSN International Ltd, Hemel Hempstead, UK.
- YAN, W., M.S. KANG, B. MA, S. WOODS, P.L. CORNELIUS (2007): GGE biplot vs. AMMI analysis of genotype-by-environment data. *Crop Sci.* *47*(2): 643–655.
- YAN, W., N.A. TINKER (2006): Biplot analysis of multi-environment trial data: Principles and applications. *Can. J. Plant Sci.* *86*(3): 623–645.
- YAN, Z., J. G. LAUER, R. BORGES, N. DE LEON (2010): Effects of genotype \times environment interaction on agronomic traits in soybean. *Crop Sci.*, *50*(2): 696–702.
- ZOBEL, R. W., M. J. WRIGHT, H. G. GAUCH (1988): Statistical analysis of a yield trial. *Agron. J.*, *80*: 388–393.

AMMI ANALIZA ZA PRINOS ZRNA KOD PŠENICE SA REKOMBINATNIM INBRED LINIJAMA

Sajid MUHAMMAD, Sultan AKBAR JADOON*, Fida MOHAMMAD, Iftikhar HUSSAIN
KHALIL, Sheraz AHMAD, Fahim ULLAH KHAN

Department za oplemenjivanje bilja i genetiku, Fakultet za nauku o proizvodnji bilja,
Univerzitet za poljoprivredu, Peshawar-Pakistan

Izvod

Identifikacija relativno stabilnih genotipova visokog prinosa je integralni cilj programa oplemenjivanja biljaka. Testiranje genotipova u različitim sredinama je potrebno da bi se utvrdila stabilnost prinosa genotipova. Specifični cilj ove studije bio je da se analizira genotip po interakciji sa sredinom (GEI) za prinos zrna 44 rekombinantne inbred linije hlebne pšenice (RIL) i šest kontrolnih sorti korišćenjem modela aditivnog glavnog efekta i multiplikativne interakcije (AMMI). Eksperimenti su postavljeni korišćenjem alfa rešetkastog dizajna sa dve replike u Pešavaru (E-1 i E-3), Hangu (E-2 i E-4) i Kohat (E-5) u provinciji Hajber Pahtunkva, Pakistan. Analiza varijanse je otkrila značajne razlike među RIL-ovima za sve osobine, dok su interakcije zbog genotipa prema sredini bile značajne za sve osobine osim dana do nicanja i mase 1000 zrna. Značajan GEI opravdao je specifičnu okolinu kao i AMMI analizu kako bi se identifikovali RIL sa specifičnim i širim prilagođavanjem. AMMI analiza je otkrila da je prva analiza glavne komponente interakcije (IPCA 1) obuhvatila 64% GEI zbira kvadrata, dok je druga analiza glavne komponente interakcije (IPCA 2) objasnila 25,8% zbira kvadrata interakcije. AMMI biplot je identifikovao G30 kao genotip visokog prinosa, a zatim G19 i G49, dok su RIL sa niskim prinosom bili G13, G8 i G7. Slično tome, G30, koji je bio blizu IPCA1 ose, bio je najstabilniji RIL sa širom prilagodljivošću praćen G31 i G25. Na osnovu AMMI vrednosti stabilnosti (ASV), RILs G18 (2,15), G5 (2,78), G27 (3,72), G44 (4,31), G25 (4,43), G42 (4,57), G43 (5,78), G11 (5,82), G1 (7,66) i G29 (7,81) su prepoznate po datom redosledu relativne stabilnosti. Analiza stabilnosti identifikovala je G49 (Vafak × Ghaznavi-98-3) kao stabilan genotip visokog prinosa među RIL-ovima koji se može komercijalizovati nakon ispunjavanja proceduralnih zahteva.

Primljeno 26.III.2022.

Odobreno 28. XI. 2022.