UDC 575. 630
https://doi.org/10.2298/GENSR2502191Q
Original scientific article

YIELD STABILITY STUDY THROUGH GENOTYPE × ENVIRONMENT INTERACTION USING AMMI AND GGE BIPLOT ANALYSIS IN *Brassica juncea* (L.)

Huma QAMAR[1], Muhammad AHMAD[2]*, Rujaab NADEEM[2], Huda Sarwar MAQBOOL[2], Arzish JAVAID[2,5], Sundus SHAHZAD[1], Mariam HASSAN[1], Muhammad JAHANZAIB[3], Haris KHURSHID[3], Amir HAMEED[4], Younas JAVED[1], Ghulam SARWAR[6]

[1] Oilseeds Research Institute, Ayub Agricultural Research Institute Faisalabad, Pakistan
[2] Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan
[3] Oilseeds Research Program, Crop Sciences Institute (CSI), National Agricultural Research Centre (NARC), Islamabad, Pakistan
[4] Statistical Section, Ayub Agricultural Research Institute, Faisalabad, Pakistan
[5] Plant Genomics and Molecular Breeding Laboratory, National Institute for Biotechnology and Genetic Engineering (NIBGE), Faisalabad, Pakistan
[6] Cotton Research Institute (CRI), Multan, Pakistan

Qamar H., M. Ahmad, R. Nadeem, H. S. Maqbool, A. Javaid, S. Shahzad, M. Hassan, M. Jahanzaib, H. Khurshid, A. Hameed, Y. Javed, G. Sarwar (2025). *Yield stability study through genotype × environment interaction using AMMI and GGE biplot analysis in Brassica juncea (L.)*- Genetika, Vol 57, No. 2, 191-208.

In the fluctuating agro-climatic conditions breeders are concerned with information regarding combined effect of Genotype × Environment interaction (G×E) and stability of the crop to boost up the breeding program. In the current work, an assessment was conducted on eleven different genotypes of *Brassica juncea* (L.) across five distinct locations to determine their grain yield. The experimental design employed a randomized complete block design with a factorial arrangement during the period of 2017-18. A

Corresponding author: Muhammad Ahmad, Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan, Phone: +92 303 718 7813, Email: ahmaduaf2013@gmail.com, ORCID: 0000-0002-7813-0433, H.Qamar ORCID: 0000-0002-2412-6519, R.Nadeem ORCID: 0009-0009-2296-6387, H.S.Maqbool ORCID: 0009-0000-1992-7699, A.Javaid ORCID: 0009-0007-0256-8811, S.Shahzad ORCID: 0009-0009-4333-9569, M.Hassan ORCID 0000-0003-4259-1569, M.Jahanzaib ORCID: 0009-0009-3945-1734, H.Khurshid ORCID: 0000-0002-2660-2240, A.Hameed ORCID: 0009-0008-8789-1083, Y.Javed ORCID: 0009-0006-1494-4493, G.Sarwar ORCID: 0000-0002-7180-9670

combined analysis of variance (ANOVA) was performed, revealing significant variations in the yield among the genotypes. Stability was analysed using multiple parameters (regression slope, stability variance, etc.) on multi-environment trial data. Furthermore, the AMMI analysis demonstrated that the genotype ZBJ-10021 exhibited a highly desirable, high-yielding characteristic that was least influenced by environmental factors. Moreover, ZBJ-12011 exhibited the highest yield (2454 kg ha^{-1}), followed closely by ZBJ-10021 (2367 kg ha^{-1}). The implementation of a multivariate approach known as the Genotype main effect plus (GGE) biplot allowed for the exploration of 86% of the total yield variability, effectively representing the best-performing genotypes and environments in a graphical manner. The findings revealed that both ZBJ-10021 and ZBJ-12011 genotypes exhibited high grain yield with a relatively stable performance across various environments. Consequently, these genotypes hold potential for utilization in breeding programs aimed at developing stable genotypes with high yield. Additionally, to gain higher yield, cultivation of environment-specific genotypes is recommended.

Keywords: Agro-climatic conditions, AMMI analysis, GGE biplot, Genetic variation, Grain yield, Stability analysis

INTRODUCTION

Indian mustard (*Brassica juncea* L.), commonly known as rai or brown mustard, is a member of the Brassicaceae family. It is classified as a naturally occurring amphidiploid species, characterized by a genome composition of AABB and a chromosome count of 2n=36. The parental species of Indian mustard are *B. rapa* (AA, 2n=20) and *B. nigra* (BB, 2n=16) (YADAVA *et al*., 2010; RAO *et al*., 2025). It is a *Rabi* crop classified as a long-day plant and grows well in temperate regions. The *B. juncea* L. plant requires 25-33°C for optimum germination and seed development (YOUNG *et al.,* 2004; SHARMA *et al*., 2023). The seeds of *B. juncea* L. contain 37-42% oil which includes commercially important fatty acids *i.e.,* erucic acid and linoleic acid, making it an important raw material for the food and oil industry (RAI *et al*., 2022).

Globally, the crop is ranked as the third most important edible oilseed crop after soybean and palm (TANIN *et al.,* 2018). In Pakistan rapeseed-mustard (*B. juncea* L.) is the second most important crop after cotton grown for its edible oil (KHAN *et al*., 2024). Due to peculiar eating preferences, edible oil is one of the country's largest consumed food items while the demand for it is bound to increase with the rapid growth of population and improved living standards (AMJAD *et al.,* 2014). This gap of supply is primarily filled by heavy imports of oil which have surged with an annual increase of 12.5% since the 1970s. The oil content of the mustard seed is 37-42% which makes it an important commodity for utilization in Pakistan's oilseed sector. In the year 2020-21, the share of rapeseed and mustard in Pakistan's edible oil production was recorded at 0.486 million tonnes (GOVT. OF PAKISTAN, 2024-2025).

Despite favourable farmer perceptions (tolerance to lodging, drought, shattering, and pests), mustard yields fluctuate markedly across Pakistan's production zones (AKHATAR *et al*., 2025). A major contribution to area and production of mustard is from Southern regions of Punjab followed by marginal production in Sindh and Khyber Pakhtunkhwa provinces. But with the fluctuating environment in these areas, the genotypes fail to perform and contribute well across a wide range of climates which ultimately results in lower yield.

Because grain yield is highly polygenic and environment-sensitive, mustard shows substantial across-site and across-year yield variation driven by G×E. The diverse genetic makeup of plants with differential responses in terms of yield and other agronomic traits is the result of genotype to environment interaction (JAHANZAIB *et al*., 2019). Economically important traits of *B. juncea* (L.) *i.e.,* number of seeds per siliqua, number of siliqua per plant, number of siliqua per main raceme, hundred seed weight and oil content are largely influenced by environmental variation in such a way that deteriorates the ability of the plant to perform up to its maximum potential and the plant loses its adaptation and stability (IQBAL *et al*., 2017; DEY *et al*., 2024). This signifies that the plant's genetic expression of these traits is diversely affected by the differential variation that occurred in environmental conditions, by the environmental stresses such as heat, salinity, and drought conditions, etc. as well as by the biotic stresses (IQBAL *et al*., 2017).

In a prevailing scenario of climate change, environmental yield stability is an important parameter for breeding new cultivars with improved adaptation. Cultivar's stability is the consistency in the performance of genotypes over a wide range of environments (ANSARI *et al*., 2024). For a plant breeder, keeping in view the negative effects of G × E interaction on stability as mentioned by Eberhart and Russell in 1966, an efficient performing genotype would be the one that ensures its maximum performance to be retained even under the diversified environment. Over five decades of research have established stability as a core breeding objective and clarified complementary ways to quantify it (SAINI *et al*., 2013). Thus, stability analysis is incorporated in studies while evaluating the best performing genotype under specified or a wide range of environments and for the selection of promising and stable genotypes. The yield stability of *B. juncea* L. relies upon the tolerance and resistance to environmental factors. Although stability is the main concern it is not the only way for choice as the most stable genotype would not always be the best yielding genotype. For this reason, both yield and stability need to be incorporated in the ideotype criteria. Several methods have been developed to reveal patterns of G × E interaction *i.e.,* FRANCIS and KANNENBERG (1978) CV%, eco-valence, absolute rank method of NASSAR and HUEHN (1987). Moreover, additive main effects and multiplicative model (AMMI) (GAUCH, 1992) and GGE biplot (YAN, 2001) are preferable choices while studying the response of genotypes *viz a` viz* multiple variables such as climatic or pedological data over a wide range of environments (SANCHEZ-GARCIA *et al.,* 2012). These methods not only explain a larger portion of the genotype × environment interaction but also simplify the results by representing the products of the environmental and genotypic sensitivity scores in a biplot (BASSI and SANCHEZ-GARCIA, 2017). Principle Component Analysis (PCA) is the most widely used estimation tool of genetic variation present in the germplasm which, furthermore, graphically illustrates the questions presented in the genotype × environment table. The validity and reliability of stability parameters in the Additive Main Effects and Multiplicative Interaction (AMMI) model can be enhanced by incorporating a greater number of Principal Component Analysis (PCA) axes. This approach has been effectively utilized in the development of a novel stability measure for the AMMI model (ZALI *et al*., 2012). It is worth noting that biplots have certain limitations when it comes to drawing stability conclusions. To overcome these limitations, an endeavour has been made to establish a more comprehensive stability method that considers all available "N" PCA axes within the fitted AMMI model. The proposed stability measures exhibit precision in accordance with the increasing amount of information yielded by the model.

Recent AMMI and GGE studies on B. juncea across South Asia reveal strong genotype × environment (G×E) interactions, with only a few genotypes showing stable, high yields. A 2024 Jharkhand analysis identified mustard lines with near-unit regression and broad adaptability suitable for wide release (KUMAR *et al*., 2024). Another study confirmed environment dominance and highlights the utility of environment grouping via vector relationships for yield interpretation (SHOJAEI *et al*., 2023). Therefore, the present study was conducted to identify high-yielding and persistent genotypes of *B. juncea* (L.) under five different regions of Punjab-Pakistan through stability analysis and to perform GGE biplot analysis to evaluate the genetic variability present among the local *B. juncea* L. genotypes. In addition, to select the best performing genotypes across environments.

MATERIALS AND METHODS

The experiment was conducted at five separate locations across Punjab during the Zaid-Kharif season 2017-2018. The material used for this experiment consisted of eleven entries of *B. juncea* L. named *viz*. ZBJ-14013, ZBJ-13012, ZBJ-12011, ZBJ-11002, ZBJ-10021, ZBJ-14017, ZBJ-14005, ZBJ-13006, ZBJ-15020, ZBJ-15018, and one check AARI Canola. The seed yield data of eleven *B. juncea* (L.) genotypes were evaluated at five ecologically distinct locations; oilseed section Ayub Agriculture Research Institute Faisalabad (E1); Regional Agriculture Research Institute (RARI), Bahawalpur (E2); Oilseeds Research sub-station, Piplan, District Mianwali (E3), Oilseed Research Station, Khanpur (E4), and Agronomic Research Station Karor (Layyah) (E5). The experiment was laid out in a randomized complete block design (RCBD) under factorial with three replications having plot size 5×1.8m. Each replication consisted of four rows, each of 5m in length. Plant-to-plant and row-to-row distances were maintained by 15×45cm, respectively. Experiments were sown with recommended seed rate followed by adequate irrigations. The sowing of Zaid-Kharif *B. juncea* (L.) genotypes was done on September 15, 2017. As the research is based on the evaluation of genotypes, three irrigations were applied as is the normal procedure. Fertilizer applied by the ratio of 80:60:60 of N:P:K, respectively. The plots were harvested in March 2018. In the Faisalabad region, data were recorded for eight characters, *i.e.,* days to 50% flowering, days of maturity, plant height (cm), no. of branches, siliqua length (cm), seeds per siliqua, 1000 seed weight (g), and yield (recorded in grams per plot and converted into kg per ha). For other locations, only yield data were considered for analysis.

Statistical Analysis

The data of the combined eleven mustard genotypes were analysed over five dissimilar locations for grain yield. The responses of genotypes to changes in the environment were quantified with linear regression models according to EBERHART and RUSSEL (1966) and PERKIN and JINKS (1968) where each genotype yield was regressed on the environmental index. Other parameters for stability *i.e*., FRANCIS and KANNENBERG'S, (1978) Coefficient of variance (CV_i), Shukla's (1972) stability variance (σ^2_i), Wricke's (1962) ecovalence (W_i), LIN and BINNS (1988) cultivar performance measure (P_i) and NASSAR and HUHN's (1987) mean absolute rank difference (S1, S2) were computed using GEA-R (Genotype × Environment Analysis with R) for

Windows Version 4.0. AMMI (additive main effects and multiplicative interaction) analysis of variance was also used to determine genotype (G), environment (E), and Genotype-Environment interactions effects (G × E), Mean yield values of eleven genotypes in each environment and across environments were analysed to check the potential of the genotypes. AMMI and GGE biplot models were used to identify stable, best performing, environment-specific genotypes and genotypes were ranked based on higher grain yield and stability. Interaction Principal Component Axis (IPCA) scores were used to calculate AMMI-based measures. R-Statistical software package GEA-R3.5.1 was used to conduct the analyses.

RESULTS

The results of an AMMI (Additive Main effects and Multiplicative Interaction) analysis of variance for grain yield in *B. juncea* (L.) as shown in Table 1. across different genotypes and environments. The purpose of the analysis is to study the yield stability of different mustard genotypes by examining the interaction between genotypes and environments. The genotypes have a statistically significant effect on grain yield (P value = 0.001**), explaining 3.16% of the total variation while environments also have a highly significant effect on grain yield (P value = 0.000***), explaining 88.06% of the total variation. The interaction between genotypes and environments (G × E) is highly significant (P value = 0.000**), explaining 8.78% of the total variation. This indicates that the performance of different genotypes varies across different environments, suggesting the presence of genotype × environment interaction.

IPCA1, IPCA2, IPCA3, and IPCA4 represent the Interaction Principal Component Analysis components, which capture additional sources of variation not explained by the main effects of genotypes and environments. IPCA1 has a statistically significant effect, but IPCA2, IPCA3, and IPCA4 do not show significant effects.

Table1. AAMI analysis of variance for grain yield of eleven mustard genotypes across five environments

Source	D.F	SS	MS	P value	Explained SS %
Genotypes	10	1421750	142175	0.001**	3.16
Environment	4	39577000	9894250	0.000***	88.06
G × E Interaction	40	3948266	98707	0.000***	8.78
IPCA1	13	3063593	235661	0.000***	
IPCA2	11	522840	475301	0.086	
IPCA3	9	275134	30570	0.123	
IPCA4	7	86703	12386	1.000	
Total	54	44947016			

*, ** and *** indicate significances at P< 0.05, P<0.01 and P< 0.001, respectively

Yield stability analysis

The yield data for all eleven genotypes in five locations were presented in a graph against CV_i values to measure the stability and performance of genotypes concurrently (Fig. 1; Table 2). The average CV_i for all genotypes was 44.09. Cultivar ZBJ-10021 showed minimum variability (CV_i =37) followed by ZBJ-12011 (CV_i = 39.29) while cultivar ZBJ-14005 exhibited maximum variability of grain yield across environments (CV_i =50.43). As the trend line indicates, the genotypes with above-average yield *i.e.,* ZBJ-10021 and ZBJ-12011 were comparatively stable under different environments. The linear regression procedure was used to check the yield of each genotype based on the mean yield of the locations. According to this procedure, a genotype with a higher mean yield, regression coefficient b=1.0, and deviation S^2d_i =0 is considered stable. Genotypes ZBJ-12011 and ZBJ-15020 were stable with minimum S^2d_i and regression coefficient *b* value near to unity (Table 1). A comparison plot of these values was generated to interpolate these genotypes on an XY plane (Fig. 2). Genotype ZBJ-10021 is both stable and adaptable and all other genotypes were classified as adaptable except for ZBJ-13006 which remained highly responsive to the environment. The graph also depicted that genotype ZBJ-12011 and ZBJ-15020 were found to be closer to the ideal values of stable genotypes. However, ZBJ-13012, AARI canola, and ZBJ-11002 were found to be highly unstable with divergent yields at separate locations. Values of other stability indices are given in Table 2.

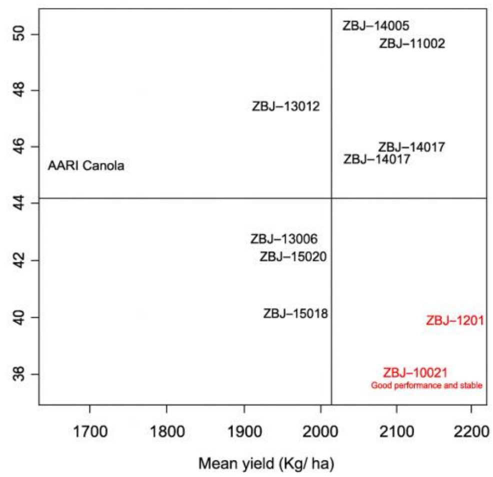

Figure 1. Mean yield of eleven genotypes vs. Francis' Coefficient of variation

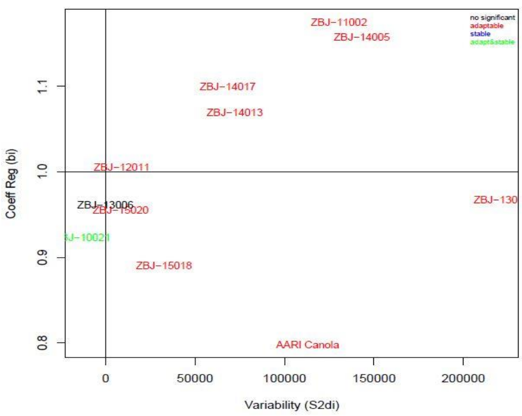

Figure 2. EBERHART and RUSSEL (1966) stability plot for the coefficient of yield

Table 2. Comparison of stability indices for eight Brassica juncea L. genotypes grain yield

GEN	Mean	SD	CV_i (%)	b_i	S^2d_i	R^2	σ^2_i	βi	S^2d_i	W_i	P_i	*Si* 1	*Si* 2
ZBJ-10021	2130.33	788.22	37.00	0.92	-13088.0	1.00	-3092.20	-0.08	574.21	18940.06	48216.94	0.65	3.06
ZBJ-11002	2117.67	1055.43	49.84	1.18	130441.5	0.90	150484.5	0.18	144103.7	521554.7	46902.50	1.90	11.81
ZBJ-12011	2209.00	867.99	39.29	1.01	9016.04	0.98	11934.59	0.01	22678.22	68118.64	16986.94	0.61	1.06
ZBJ-13006	1947.33	826.07	42.42	0.96	-200.29	0.99	4842.00	-0.04	13461.90	44906.52	109191.1	0.82	4.75
ZBJ-13012	1950.67	925.99	47.47	0.97	221409.5	0.79	207577.2	-0.03	235071.7	708403.5	217991.7	1.85	17.31
ZBJ-14005	2073.67	1045.78	50.43	1.16	143268.6	0.89	157035.6	0.16	156930.8	542994.6	57186.94	1.40	9.00
ZBJ-14013	2077.67	947.58	45.61	1.07	72164.37	0.93	74112.27	0.07	85826.55	271609.3	99543.61	2.70	13.06
ZBJ-14017	2117	970.75	45.85	1.1	68256.99	0.93	75046.53	0.1	81919.17	274666.8	33752.5	1.55	7.06
ZBJ-15018	1968.33	782.27	39.74	0.89	32611.62	0.94	44288.54	-0.11	46273.8	174004.3	107059.2	1.00	15.75
ZBJ-15020	1971	824.9	41.85	0.95	8394.52	0.98	13174	-0.05	22056.71	72174.9	99439.17	1.00	7.5
AARI Canola	1643	747.29	45.48	0.8	112951.3	0.83	143661.5	-0.2	126613.5	499225	370190.3	0.55	2.12

CV_i (%) = Francis' Coefficient of variance, b_i =regression coefficient, S^2d_i=deviation from the regression, R^2 =coefficient of determination, σ^2_i =Shukla's stability variance, β_i=Perkins and Jinks' linear regression coefficient, S^2d_i= deviation from the regression, $W_{I=}$ Wrickes's ecovalence, P_i=Lin and Binns's cultivar performance measure, *S1*, *S2* Nassar and Huhn (1987) mean absolute rank difference

Comparison of grain yield stability indices

A summary of different stability parameters with mean grain yield for all genotypes is given in Table 2. According to the stability variance (ri^2) value, the genotypes ZBJ-13006 and ZBJ-12011 were stable *i.e.,* ZBJ-11002, ZBJ-13012, and ZBJ-14005 were prone to environmental stimuli. PERKINS and JINKS'S (1968) regression coefficient β_i accounts for all or most of the GE interaction. A genotype with average sensitivity to the environment has a (1+ β_i) value of 1 and a β_i value of zero. This genotype is considered non-responsive to GE interaction. A genotype responsive to GE has a (1+ β_i) value greater than 1 hence has a β_i value greater than zero. However, a stable genotype that is indifferent to environmental variation has a value (1+ β_i) less than 1 and hence has a significantly negative β_i value. Therefore, ZBJ-13012 (β_i= -0.03), ZBJ-13006 (βi= -0.04) and ZBJ-15020(β_i= -0.05) were stable genotypes with a 1+ β_i<1. WRICKE'S (1962) ecovalence (W_i) or the stability of the genotype is its interaction with environments, summed and squared for all environments.

Thereby a genotype with less ecovalence has fewer fluctuations under different environments and is considered stable. V1 (ZBJ-10021) has minimum ecovalence (W_i =18940.06) followed by V4, ZBJ-13006 (W_i =44906.52) and V3, ZBJ-12011 (W_i =68118.64). On the contrary, genotype V10, ZBJ-15020 (W_i =72174.9), and other genotypes had higher ecovalence hence their yield was relatively more prone to environmental variation. The superiority measure (P_i) is calculated by squared differences between a genotype and the maximum mean of a genotype's yield at a given location, summed, and divided by two times the number of locations. Genotypes with lower values of P_i are considered stable. Genotype ZBJ-12011 (P_i=16986.94) and ZBJ-11002 (P_i=46902.5) had the lowest P_i values and hence considered relatively stable.

AMMI Analysis

AAMI biplot analysis helps in the assessment of stability and adaptability of genotypes where genotypes scatter according to their principal component scores (DE VITA *et al*., 2010). Moreover, it offers selection criteria for further genetic improvements in desirable genotypes. In the AMMI biplot X-axis represents genotype and environment main effects for grain yield (kg ha^{-1}) and Y-axis show the PC1 scores (Fig. 3). In biplot the middle of the vertical line denotes the grand mean of the grain yield, on the contrary, the middle of the horizontal line shows a PC1 value of zero (TOLESSA, 2015). The genotypes placed at right hand side of the biplot are high yielding *i.e.*, V1 (2367 kg/ha), V2 (2353 kg/ha), V3 (2454 kg/ha), V6 (2304 kg/ha), V7 (2309 kg/ha) and V8 (2352 kg/ha). Similarly, "FSD" (Faisalabad) and "KR" (Karor) are the highest grain yielding environments since these also positioned on the right-hand side. On the other hand, the rest of the genotypes and environments located on the left-hand side of the biplot considered low yielding. Genotypes or environments that appear almost on a horizontal line to the zero PC1 line have similar interaction effects while those which occur on the perpendicular line to the grand mean line have similar mean effects (BADU-APRAKU *et al*., 2003). Therefore, ZBJ-10021(V1) and ZBJ-15018 (V9) genotypes had the same interaction patterns while genotypes ZBJ-10021 (V1), ZBJ-11002 (V2), ZBJ-14017(V8); ZBJ-14005 (V6), ZBJ-14013 (V7); ZBJ-13006 (V4), ZBJ-13012 (V5), ZBJ-15018 (V9), and ZBJ-15020 (V10) revealed similar meaning effects. None of the environments exhibited the same interaction patterns or means, hence indicating significant variation in environments. Furthermore, the AMMI biplot depicted ZBJ-10021 (V1), ZBJ-13006 (V4), ZBJ-15018 (V9), ZBJ-15020 (V10), ZBJ-11002 (V2), ZBJ-14005 (V6), and ZBJ-14017 (V8) genotypes and "Pi" (Piplan) and "Ka" (Karor) environments as least interactive. While ZBJ-13012 (V5) and AARI Canola (V11) genotypes presented the highest G × E interaction in "BPR" (Bahawalpur) and "KP" (Khanpur) regions and genotype ZBJ-14013 (V7) in Fa (Faisalabad) environment. Although stability is accompanied by high yield performance, V1 was high grain yielding and the most stable genotype. However, because of the highest grain yield and relative stability, V3 was the most desirable genotype.

Genotypes (Figure 4) that exhibit least deviation from the average IPCA score are considered to have lower levels of genotype-by-environment interaction and are more stable across different environments. Positive interaction occurs by the same sign of both the genotype and environment on the IPCA axis while different sign indicates negative interaction. AMMI Biplot is divided into four distinct sections (Figure 4): upper left (section 1), lower left (section 4), upper right (section 2), and lower right (section 3). Upon analysis, it is observed that the upper and lower left sections represent environments characterized by low grain yield. Conversely, the upper and lower right sections correspond to environments that exhibit high grain yield.

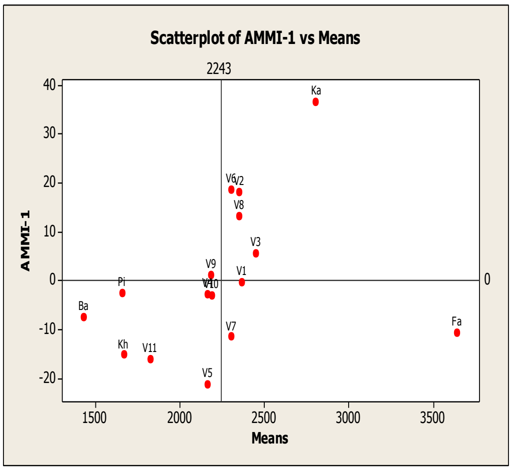

Figure 3. AMMI 1 Biplot for mean grain yield (kg ha^{-1}) of eleven *Brassica juncea* L. genotypes (V) and five environments using genotypic and environmental scores

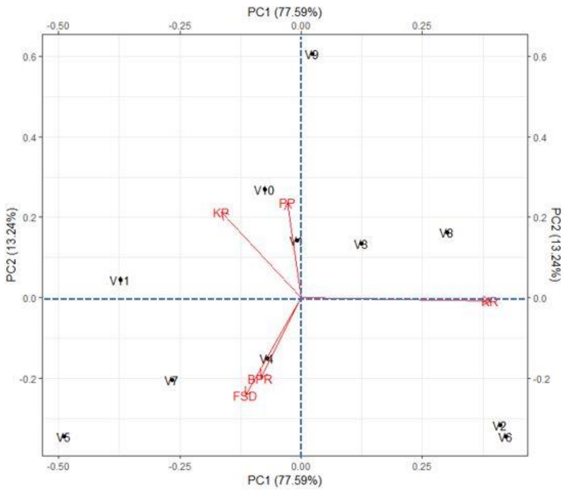

Figure 4. AMMI 2 Biplot for grain yield (kg ha^{-1}) showing the interaction of IPCA2 against IPCA1 scores of eleven mustard genotypes (V) in five environments

The genotypes positioned on the right-hand side of the grand mean value, with IPCA scores approaching zero, demonstrate high mean performance, a general adaptability to all environments, and low genotype-by-environment interaction. These genotypes exhibit consistent and stable performance across various environments, making them favourable candidates for cultivation due to their reliable and high overall performance. However, the genotype with a larger IPCA score and high average performance displayed specific adaptability to the environments. The presence of interaction in the AMMI Biplot is determined by the distance of genotypes and environments from the origin. When genotypes and environments are located within the same sector of the Biplot, it indicates a positive interaction, suggesting that those genotypes perform well in those specific environments. Conversely, when genotypes and environments are positioned in different sectors, it suggests a negative interaction, implying that the genotypes may not perform optimally in particular environments (OSIRU *et al*., 2009). A genotype is the best representative of a specific environment when it shows a high positive association in that environment. Genotypes V3 and V8 are exposed to specific adaptation for Piplan and Karor with positive interaction (GEI) and high seed yield (2209 and 2117 kg/ha) more than mean yield, respectively.

The genotype V1 exhibited stability and general adaptability in terms of seed yield, with a value of 2130.33 kg/ha, which is close to the mean yield. Additionally, it demonstrated low interaction as indicated by its IPCA score, which was close to zero. This finding aligns with the observations made by PURCHASE (1997), who stated that genotypes located closer to the pivot point are generally regarded as more stable. The genotypes V7 and V11, possessing positive interaction, were identified for specific adaptation for Faisalabad and Khanpur environment. In biplot, the distribution of genotype V1 seemed relatively close to the origin and revealed its minimum interaction with environments while the other ten genotypes were more influenced by environment as these spread away from the origin. The genotypes V2 and V6 had a positive correlation with the environment of the Karor region, exhibiting specific adaptability in this environment. Genotypes V4, V5 and V7 showed a positive association with the environment of Faisalabad and Bahawalpur.

GGE BIPLOT

Analysis of Genotype × Environment Interaction

A GGE biplot is an efficient way of analysing adaptive and stable genotypes based on yield performance across environments. Hence, in the present study, a GGE biplot was constructed to portray the interaction between both components. Cumulatively, the first two principal components described 86.95% of the variation. The variation was explained in terms of “which won where/what,” “relationship among environments” and “ranking of genotypes” for only these components.

Which Won Where/What

Which won where/what pick out the most desirable, adaptable, and high yielding genotypes for each environment or group of environments (Fig. 5). By connecting the markers for six of the genotypes a polygon is formed, while five genotypes are inside the shape of the polygon. For the marking of a specific environment/location or their group, red rays are drawn perpendicular to the sides of the polygon. In the current case, six rays divide this biplot into six different sections in which five of our locations fall into three of these sections. The genotypes present at the apex for each quadrant are the ones possessing the highest yield for that location and fall within that quadrant. The plot indicated genotype V2 (ZBJ-11002) performed well at

Karor (KR) and V3 (ZBJ-12011) as high yielding at Bahawalpur (BPR) district. Genotypes V11 (AARI Canola), V10 (ZBJ-15020), V9 (ZBJ-15018), V7 (ZBJ-14013), V5 (ZBJ-13012), and V4 (ZBJ-13006) did not perform well in all environments.

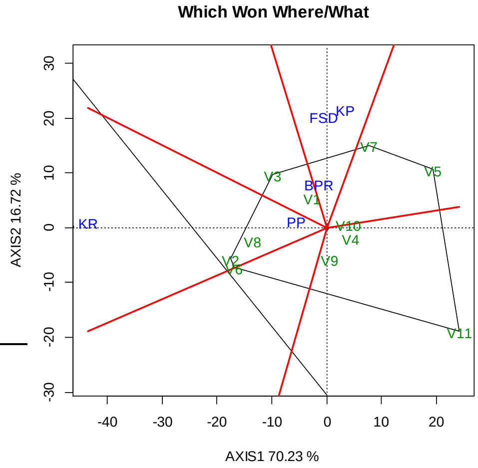

Figure 5. Performance of eleven genotypes in five separate locations for grain yield
FSD: Faisalabad, KP: Khan Pur, KR: Karor, PP: Piplan, BPR: Bahawalpur

Relationships among Environments

A summary of the relationship among various locations of the study is given in Figure 6.

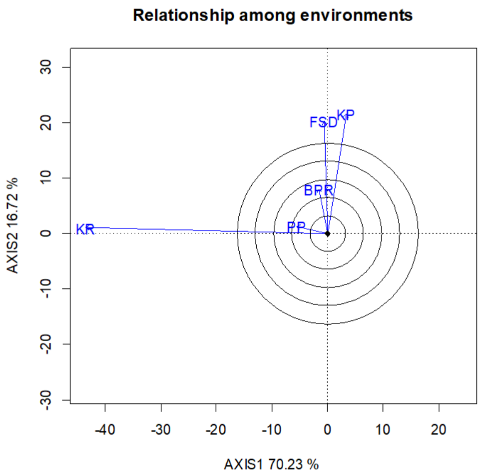

Figure 6. Inter-relationship among five different environments/locations
FSD: Faisalabad, KP: Khan Pur, KR: Karor, PP: Piplan, BPR: Bahawalpur

The environment vectors were represented by lines connecting origin and markers of the plot and locations, respectively. The inter-relationship plot drawing the cosine angle of the environmental vector was proportioned following the correlation coefficient between them. In this plot, environmental vectors of Karor (KR) and Piplan (PP); Faisalabad (FSD) and Bahawalpur (BPR) had the smallest angle, therefore can be placed in a solitary group. While the environmental vectors of Khanpur (KP) and Piplan (PP); Khanpur (KP) and Karor (KR) had the largest angle. The arrangement of different environment patterns correlates with the type of the site and geographic distance.

Ranking of Genotypes based on GGE Biplot

An ideal genotype is characterized by having the highest mean performance and displaying stability by consistently performing well across various environments. While it is acknowledged that such an elite genotype may only exist in theory, it can serve as a reference point for evaluating and comparing other genotypes (EMAMI *et al.*, 2015). By defining ideal genotypes, genotypic status is accomplished. Mean yield or stability or both decrease due to the distances from the ideal genotype. In the evaluation process of genotypes, distances are considered as rank indicators. Biplot indicated genotype V3 (ZBJ-13006) as the most favourable genotype followed by V1 (ZBJ-10021) (Figure 7). By the inspection of distances from the centre of the circle, genotypes V10 (ZBJ-15020), V7 (ZBJ-14013), V8 (ZBJ-14017), V4 (ZBJ-13006), V9 (ZBJ-15018), V2 (ZBJ-11002), V6 (ZBJ-14005), V5 (ZBJ-13012), and V11 (AARI Canola) ranked further in decreasing order.

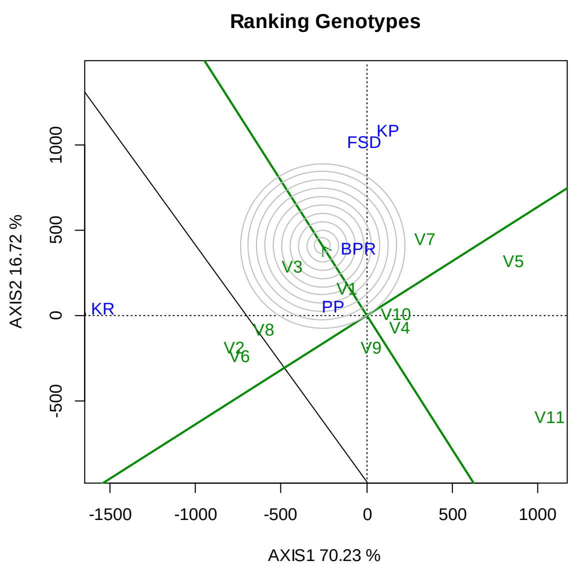

Figure 7. Ranking of genotypes for Brassica data using GGE biplot.
FSD: Faisalabad; KP: Khan Pur; KR: Karor; PP: Piplan; BPR: Bahawalpur

DISCUSSIONS

Stability analysis is one of the key methods to potentially characterize elite genotypes under diverse environmental conditions by their relative performance and to identify stable and high-yielding genotypes. Many researchers have studied the genotype × environment relationship and its effect on the yield stability of important crop species (YADAVA *et al*., 2010; BIBI *et al*., 2016; PRIYAMEDHA *et al*., 2017; TANIN *et al*., 2018, JAHANZAIB *et al.,* 2019; BOJOVIĆ *et al*., 2019). In the present work, eleven mustard genotypes were analysed for stability analysis at five separate locations. All the genotypes were supposed to give a variable response at different environments due to the unique genetic makeup and physiological response mechanism (HAFEEZ et al.,2024). Genotype V3 (ZBJ-12011) has minimum regression coefficient b_i and S^2d_i=0 followed by V10 (ZBJ-15020) index values. SHOJAEI (2023) reported that genotypes showing b_i values of unity gave an average performance to different environmental conditions. EBERHART and RUSSELL (1966) and FINLAY and WILKINSON (1963) described genotypes as having a regression coefficient of unity (b_i= 1), and deviation as zero (S^2d_i = 0), giving an excellent mean performance. These genotypes also acclimatized better across different environments.

AMMI Analysis indicated that V1 (ZBJ-10021) and V9 (ZBJ-15018) had the same interaction patterns because of occurrence on a horizontal line to the zero PC1 line. Environment “PP” (Piplan) and “KR” (Karor); and genotypes V1 (ZBJ-10021), V2 (ZBJ-11002), V8 (ZBJ-14017); V6 (ZBJ-14005), V7 (ZBJ-14013); V4 (ZBJ-13006), V5 (ZBJ-13012), V9 (ZBJ-15018), and V10 (ZBJ-15020) had similar mean effects. V5 (ZBJ-13012) and V11 (AARI Canola) showed the highest G × E interaction in the “BRP” (Bahawalpur) and “KP” (Khanpur) environment and V7 (ZBJ-14013) in the “FSD” (Faisalabad) region. “FSD” (Faisalabad) and “KR” (Karor) were high-yielding environments. Furthermore, the analysis exhibited a positive association of V2 (ZBJ-11002) and V6 (ZBJ-14005) genotypes with the environment of the Karor region. Similarly, genotypes V4 (ZBJ-13006), V5 (ZBJ-13012) and V7 (ZBJ-14013) indicated a positive correlation with the environment of Faisalabad and Bahawalpur. Hence, the AMMI analysis is a valuable tool for identifying the most suitable genotypes for specific environments. It has been extensively utilized in stability studies across various crops, including chickpea (ZALI *et al*., 2011), barley (ROMAGOSA *et al*., 2013), rapeseed (BIBI *et al*., 2018) and Ethiopian mustard (*B. carinata* L.) (TADESSE *et al*., 2018). It is important to note that the AMMI model is particularly well-suited for genotypes that exhibit specific adaptations to their respective environments. By considering genotype-by-environment interactions, the AMMI analysis can effectively identify genotypes that demonstrate superior performance and stability in particular environmental conditions. The results reported by JAHANZAIB *et al*. (2019) conformed to our findings who found most of the variation for yield in eight groundnut genotypes across six separate locations. YADAVA *et al*. (2010) also found a similar pattern of G × E interaction while studying thirty mustard genotypes under four environments. An earlier study by BIBI *et al.* (2018) also observed the effect of the environment on mustard yield stability and reported significant variability response.

GGE biplot is a powerful tool to select high-performing, adaptable and stable genotypes over multiple locations. It depicts genotype, the main effect along with genotype-environment interaction that is represented by additive main effect and the multiplicative interaction. The biplot depicts genotype-environment interaction. The most stable and adaptive cotton cultivars were identified using GGE biplot over six different environments (ALI *et al*., 2017). For the identification and screening of elite genotypes, YAN and HUNT (2001) described patterns of polygon based on "which-won-where" for GGE interaction at single or multiple environments. ALI *et al*. (2017) also used this model for the screening of best-performing genotypes of pine and cotton, respectively. In this investigation mean grain yield data were used to construct a GGE biplot of eleven genotypes for five distinct locations. The "which-won-where" plot represented a higher mean performance of V2 (ZBJ-11002) at Karor (KR). Similarly, V3 (ZBJ-12011) yielded higher seeds in Bahawalpur (BPR). Karor (KR) and Piplan (PP); Faisalabad (FSD) and Bahawalpur (BPR), corroborated with their climatic and geographical proximity in environmental comparison plots. The ranking and stability section revealed V3 (ZBJ-12011) as a high mean yielding genotype followed by V1 (ZBJ-10021) owing to closeness to circle.

Identifying ZBJ-12011 and ZBJ-10021 as both high-yielding and stable provides actionable material for mustard breeding programs in Pakistan. These lines can serve as (i) parents in crossing blocks to introgress broad adaptation, and (ii) direct cultivar-release candidates for irrigated and semi-arid zones. Conversely, specifically adapted genotypes ($\beta < 1$) could be exploited for stress-prone, low-input regions, complementing wide-adapted cultivars.

The combined AMMI–GGE framework also refines test-site selection, suggesting that environments such as Faisalabad and Bahawalpur are efficient "core sites" representing broader agro-ecological diversity. These insights facilitate strategic allocation of resources for future national performance trials.

CONCLUSIONS

The multi-environment evaluation of eleven B. juncea genotypes revealed significant genotype × environment interaction for seed yield. Among them, ZBJ-10021 and ZBJ-12011 consistently combined high productivity with dynamic stability, maintaining near-average responsiveness and minimal deviation across diverse locations. In contrast, AARI Canola exhibited environment-specific adaptation, performing well only under favourable conditions. The predominance of environmental variance underscores the need for region-focused testing and climate-resilient breeding strategies. The integrated use of AMMI and GGE biplot models efficiently identified both stable genotypes and representative testing sites such as Faisalabad and Bahawalpur. These results suggest that ZBJ-10021 and ZBJ-12011 are promising candidates for wide release and valuable parental lines for developing stable, high-yielding mustard cultivars. The study reinforces that multi-environment stability analysis is essential for achieving consistent mustard yields and strengthening Pakistan's edible-oil self-sufficiency

Received, September 25th, 2024
Accepted, September 30th, 2025

REFERENCES

AKHATAR, J., P. UPADHYAY, H. KUMAR (2025): Crop cultivation and hybrid seed production strategies in rapeseed-mustard. In: Hybrid seed production for boosting crop yields: Applications, challenges and opportunities**,** Springer Nature, Singapore, pp: 177–224.

ALI, I., N.U. KHAN, F. MOHAMMAD, M.A.IQBAL, A. ABBAS, D. FARHATULLAH, Z. BIBI, S. ALI, I.A. KHALIL, S. AHMAD, M.RAHMAN (2017): Genotype by environment and GGE-biplot analyses for seed cotton yield in upland cotton. Pak. J. Bot., *49*(6): 2273-83.

AMJAD, M. (2014): Oilseed crops of Pakistan, National Coordinator (Oilseed Crops), PARC, Pakistan, pp: 5-9.

ANSARI, A.A., J. AKHATAR, S. SHARMA, S.S. BANGA, C.ATRI (2024): Integrating multiple statistical indices to measure the stability of photosynthetic pigment content and composition in *Brassica juncea* (L.) Czern germplasm under varying environmental conditions. Photosynth. Res., *162*(1): 63–74.

BADU-APRAKU B., F. ABAMU, A. MENKIR, K.OBENG-ANTWI (2003): Genotype by environment interactions in the regional early maize variety trials in West and Central Africa. Maydica, *48*(2): 93-104.

BASSI, F.M., M. SANCHEZ-GARCIA (2017): Adaptation and stability analysis of ICARDA durum wheat elites across 18 countries. Crop Sci., *57*(5): 2419-2430.

BIBI, T., H.S. MUSTAFA, T.MAHMOOD, A. HAMEED, Q.ALI (2018): Multivariate analysis for adaptability and yield stability of rapeseed (*Brassica napus* L.) strains in different agro-climatic zones. Genetika, *50*(2): 369-378.

BIBI, T., RAUF, S., MUSTAFA, HSB., MAHMOOD, T., SALAH-UD-DIN (2016): Selection of stable mustard (*Brassica juncea* L.) genotypes through genotype × environment interaction and stability analysis suitable for Punjab, Pakistan. J. Agric. Basic Sci., *1*(1): 14-17.

BOJOVIĆ, R., V. POPOVIĆ J. IKANOVIĆ LJ. ŽIVANOVIĆ N. RAKAŠČAN, S. POPOVIĆ, V. UGRENOVIĆ, D.SIMIĆ (2019): Morphological characterization of sweet sorghum genotypes across environments. The J. of Animal and Plant Sci., *29*(3): 721-729.

DE VITA, P., A.M. MASTRANGELO, L. MATTEU, E. MAZZUCOTELLI, N. VIRZI, M. PALUMBO, M.L. STORTO, F. RIZZA, L.CATTIVELLI (2010): Genetic improvement effects on yield stability in durum wheat genotypes grown in Italy. Field Crop Res., *119*(1): 68-77.

DEY, S.R., M. SHARMA, P. KUMAR, P. DWIVEDI (2024): Genetic improvement of mustard. In: Genetic engineering of crop plants for food and health security, Springer Nature, Singapore, *2*: 227–259.

EMAMI, E., E. FARSHADFAR, H. SAFARI (2015): GGE Biplot analysis of genotype × environment interaction in Agropyron intermedium. J. Biodivers. Environ. Sci., *6*(4): 260-267.

FRANCIS, T.R., L.W. KANNENBERG (1978): Yield stability studies in short-season maize. I. A descriptive method for grouping genotypes. Can. J. Plant Sci., *58*(4): 1029-1034.

GAUCH, H.G. JR (1992): Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Elsevier, Amsterdam, Netherlands, pp: 278.

GOVT. OF PAKISTAN (2024-2025): Pakistan Economic Survey. Ministry of Economics, Pakistan, 2: 17-41.

HAFEEZ, A., H.G.M.D. AHMED, Y. ZENG, M.I. AKRAM, R. IQBAL, M.S. ALWAHIBI, M.S. ELSHIKH (2025): Genetic variability and trait correlations in Brassica genotypes for yield optimization. Appl. Ecol. Environ. Res., *23*(2): 3231–3244.

HAO, D.C., X.J. GU, P.G. XIAO (2015): High throughput sequencing in medicinal plant transcriptome studies. Medicinal plants. In: Medicinal Plants: Chemistry, Biology and Omics. Cambridge, Woodhead Publishing, Elsevier, pp: 49-96.

IQBAL, Z., N. NAWAZ, U.A. MUSHARAF, HSB. MUSTAFA, T. MAHMOOD, M. AFTAB (2017): An overview: Effect of different abiotic stresses on quantitative traits of Brassica, Sunflower, and Soybean due to climate change. Nat. Sci., *5*(5): 74-81.

JAHANZAIB, M., N. NAWAZ, H. KHURSHID, S.A. JAN, M. ARSHAD, I.HASSAN (2019): Estimating genotype× environment interaction for groundnut seed yield across different ecological zones. Int. J. Agric. Biol., *22*: 139-45.

KHAN, A., A.A, AWAN, M. YASIN, A. RAMZAN, M.W.A. CHEEMA, A.JAN (2024): Edible oilseeds: Historical perspectives, recent advances, and future directions. Intechopen.

KUMAR, V.A., N. KUMAR, K. JAGADEESH, A. KUMAR, C. MAHTO, H. LAL, H.DUBEY (2024): Stability assessment for improved mustard production in ecologically diverse regions of Jharkhand: Insights from AMMI and GGE. Res. Square https://doi.org/10.21203/rs.3.rs-4145405/v1

LIN, C.S., M.R. BINNS (1988): A superiority measure of cultivar performance for cultivar×location data. Can. J. Plant Sci., *68*(1): 193-198.

NASSAR, R., M.HUEHN (1987): Studies on estimation of phenotypic stability: Tests of significance for nonparametric measures of phenotypic stability. Biometrics, *1*: 45-53.

OSIRU, M.O., O.M. OLANA, E. ADIPALA, R.E. KAPINGA, B.E. LEMAGA (2009): Yield stability analysis of *Ipomoea batatus* L. cultivars in diverse environments. Aust. J. Crop Sci., *3*(4): 213-20.

PRIYAMEDHA, A.K., Z.A. HAIDER (2017): Stability for seed yield and component traits in Indian mustard (*Brassica juncea* L.) under Jharkhand condition. J. Oilseed Brassica, *1*(1): 37-42.

PURCHASE, J.L. (1997): Parametric analysis to describe genotype x environment interaction and yield stability in winter wheat. Univ. Free State, Bloemfontein, South Africa.

RAI, P.K., P. YADAV, A. KUMAR, A. SHARMA, V. KUMAR P. RAI (2022): *Brassica juncea*: A crop for food and health. In: The *Brassica juncea* genome, Springer Int. Publ., Cham, pp: 1–13.

RAO, M., A. KASHYAP, P. GARG, S.S. SHARMA, N.C. GUPTA, R. CHAMOLA, R. BHATTACHARYA (2025): An indigenous germplasm of *Brassica rapa* var. yellow NRCPB rapa 8 enhanced resynthesis of *Brassica juncea* without in vitro intervention. Genet. Resour. Crop Evol., 72(2): 1769–1782.

SAINI, P., C. SANDHYA (2015): A review on genotype environment interaction and its stability measures. Int. J. Sci. Res., *4*(1): 1210-1223.

SANCHEZ-GARCIA, M., F.,ÁLVARO, J.A. MARTÍN-SÁNCHEZ, J.C. SILLERO, J. ESCRIBANO, C.ROYO (2012): Breeding effects on the genotype × environment interaction for yield of bread wheat grown in Spain during the 20th century. Field Crop Res., *126*: 79-86.

SINGH, V.V., P.K. RAI, S.A. SIDDIQUI, V. VERMA, R. YADAV (2011): Genetic variability and relative drought tolerance in interspecific progenies of *Brassica juncea*. Agric. Biol. J. N. Am., *2*(1): 34-41.

SHARMA, P., N. LAKRA, Y. AHLAWAT, A. ZAID, A.M. ABD-ELGAWAD, H.O. ELANSARY, A.GUPTA (2023): Putrescine mitigates high temperature effects by modulating morpho-physiological and biochemical attributes in *Brassica juncea* seedlings. Agron., 13(7): 1879.

SHOJAEE, S.H., K. MOSTAFAVI, S.H. GHASEMI, M.R. BIHAMTA, A. ILLES, C. BOJTOR, S.M.N. MOUSAVI (2023): Sustainability on different canola (*Brassica napus* L.) cultivars by GGE biplot graphical technique in multi-environment. Sustain.**,** 15(11): 8945.TADESSE, T., SEFERA, G., TEKLIGN, A. (2018): Genotypes environment interaction analysis for Ethiopian mustard (*Brassica carinata* L.) genotypes using AMMI model. J. Plant Breed. Crop Sci., *10*(4): 86-92.

TOLESSA, T. (2015): Application of AMMI and Tai's stability statistics for yield stability analysis in faba bean (*Vicia faba* L.) cultivars grown in Central Highlands of Ethiopia. J. Plant Sci., *3*(4): 197-206.

YADAVA, D.K., S.C. GIRI, S. VASUDEV, A. KUMAR YADAV, B. DASS, R.S. RAJE, M. VIGNESH, R. SINGH, T. MOHAPATRA, K.V. PRABHU (2010): Stability analysis in Indian mustard (*Brassica juncea*) varieties. Indian J. Agric. Sci., *80*(9): 761.

YAN, W., L.A. HUNT (2001): Interpretation of genotype×environment interaction for winter wheat yield in Ontario. Crop Sci., *41*(1): 19-25.

YAN, W., H.X. WU (2008): Application of GGE biplot analysis to evaluate genotype (G), environment (E), and G×E interaction on *Pinus radiata*: A case study. For. Sci., *38*(1): 132-142.

YOUNG, L.W., R.W. WILEN, P.C. BONHAM-SMITH (2004): High temperature stress of *Brassica napus* during flowering reduces micro-and megagametophyte fertility, induces fruit abortion, and disrupts seed production. J. Exp. Bot., *55*(396): 485-95.

ZALI, H., E. FARSHADFAR, S.H. SABAGHPOUR (2011): Non-parametric analysis of phenotypic stability in chickpea (*Cicer arietinum* L.) genotypes in Iran. Crop Breed. J., *1*(1): 89-101.

ZALI, H., E. FARSHADFAR, S.H. SABAGHPOUR, R.KARIMIZADEH (2012): Evaluation of genotype × environment interaction in chickpea using measures of stability from AMMI model. Ann. Biol. Res., *3*(7): 3126-3136.

STABILNOST PRINOSA KROZ INTERAKCIJU GENOTIPXSPOLJAŠNJA SREDINA PRIMENOM AMMI I GGE BIPLOT ANALIZE KOD *Brassica juncea* (L.)

Huma QAMAR[1], Muhammad AHMAD[2]*, Rujaab NADEEM[2], Huda Sarwar MAQBOOL[2], Arzish JAVAID[2,5], Sundus SHAHZAD[1], Mariam HASSAN[1], Muhammad JAHANZAIB[3], Haris KHURSHID[3], Amir HAMEED[4], Younas JAVED[1], Ghulam SARWAR[6]

[1] Ayub Poljoprivredni istraživački isntitut, Faisalabad, Pakistan
[2] Odeljenje za oplemenjivanje i genetiku, Univezitet Poljoprivredni Faisalabad, Pakistan
[3] Istraživački program uljarica, Institut za biljne nauke (CSI), Nacionalni poljoprivredni istraživački centar (NARC), Islamabad, Pakistan
[4] Odelejnje za statistiku, Ayub Poljoprivredni istraživački institut, Faisalabad, Pakistan
[5] Laboratorija za biljni genom i molekularno oplemenjivanje, Nacionalni institut za biotehnologiju i genetski inženjering (NIBGE), Faisalabad, Pakistan
[6] Institut za istraživanje pamuka (CRI), Multan, Pakistan

Izvod

U promenljivim agro-klimatskim uslovima, uzgajivači su zainteresovani za informacije o kombinovanom efektu G × E i stabilnosti useva kako bi poboljšali selekcionarske programe. U ovom istraživanju sprovedena je procena jedanaest različitih genotipova *Brassica juncea* L. na pet različitih lokacija kako bi se odredio prinos zrna. Eksperimentalni dizajn koristio je slučajni blok dizajn s faktorijalnom raspodelom tokom perioda 2017-18. Izvršena je kombinovana analiza varijanse (ANOVA), koja je otkrila značajne varijacije u prinosu među genotipovima. Dalje, AMMI analiza je pokazala da je genotip ZBJ-10021 pokazao visoko željeni karakteristiku visokog prinosa koja je najmanje uticala na faktore okoline. Takođe, ZBJ-12011 je pokazao najviši prinos (2454 kg ha-1), a blisko za njim je bio ZBJ-10021 (2367 kg ha-1). Primena multivarijantnog pristupa poznatog kao Genotip glavni efekat plus interakcija Genotip × Okolina (GGE) biplot omogućila je istraživanje 86% ukupne varijabilnosti prinosa, efikasno prikazujući najbolje genotipove i okoline na grafikonu. Rezultati su pokazali da su genotipovi ZBJ-10021 i ZBJ-12011 ispoljili visok prinos zrna sa relativno stabilnom performansom u različitim okruženjima. Stoga, ovi genotipovi imaju potencijal za korišćenje u selekcionarskim programima usmerenim ka razvoju stabilnih genotipova sa visokim prinosom. Dodatno, preporučuje se uzgajanje genotipova specifičnih za okolinu kako bi se postigao veći prinos.

Primljeno 25.IX.2024.
Odobreno 30. IX. 2025.

How to cite this article: Qamar H., M. Ahmad, H. S. Maqbool, A. Javaid, S. Shahzad, M.Hassan, M. Jahanzaib, H. Khurshid, A.Hameed, R. Nadeem (2025). *Yield stability study through genotype × environment interaction using AMMI and GGE biplot analysis in Brassica juncea (L.))*- Genetika, Vol 57, No.2, 191-208.