



Using AMMI Analysis to Select the Most Stable and Productive Varieties in Plant Breeding Programs. Review Article

Yaseen Obaid Noori Ahmed Sharif¹

Muhamed Auda Kalaf AL-Abody²

Tariq Raad Thaer Al-Mafarji³

Zakaria Al-Ajlouni⁴

¹Department of Field Crops, College of Agriculture, Kirkuk University, Kirkuk, IRAQ.

²Department of Field Crops, College of Agriculture, University of Basrah, IRAQ.

³Department of Medicinal and Industrial Plants, College of Medicinal and Industrial Plants, University Kirkuk, Kirkuk, IRAQ.

⁴Department of Plant Production, College of Agriculture, University of Science and Technology, Jordan.

*Corresponding Author: yaseenobaidnoori@uokirkuk.edu.iq

Received:09/08/2025

Revised: 25/11/2025

Accepted: 01/12/2025

Published: 17/12/2025

ABSTRACT

The genetic stability of genotypes under fluctuating environmental conditions is one of the most important elements in plant breeding programs. These factors enable breeders to make decisions regarding the adaptability of different genotypes to various environments. However, reactions of different genotypes to extreme environmental factors such as water stress, high temperatures, salinity, and other stresses complicate the choice of superior genotypes. So, analysis of genetic stability (in particular, the AMMI model) and estimation of GEI could be one of the most important criteria that plant breeders should take into consideration. In this regard, plant breeders use various statistical tools and methods for the detection of stable and high-yielding genotypes across environments. Of the many tools available, AMMI Biplot is one such important and effective methodology. This method is capable of showing those genotypes which combine genetic stability with productivity in various environments. Such genotypes are considered stable due to their superior genetic makeup and resilience to changeable environmental conditions. The AMMI-Biplot technique has been very efficient in the analysis of GEI and in the identification of superior genotypes. In the plant varieties, genetic stability is thought of as a multivariate character that is a consequence of the interaction of thousands of gene pairs with various environmental factors, therefore causing wide variations in the phenotypic expression of the characters. Genetically stable genotypes possess a high level of adaptability to diverse approved environments. The importance of this interaction in agriculture rests on the fact that testing of varieties in more than one environment is a pre-requisite for its approval, as well as for selecting a suitable environment and the development of genetically stable varieties resistant to environmental fluctuations. For this reason, the relevance of AMMI analysis rests on the possibility of classifying genotypes according to their stability in the environment, identification of optimal environments for each genotype, and realization of the analyses of the genotype-environment interaction through biplots. The final objective of AMMI analysis is thus to study the interaction of genotypes with environmental conditions for assessing productivity stability of varieties.

Keywords: AMMI Analysis, Varieties, Yield Stability, Biplot Analysis, Multi-Environment Trials, Plant Breeding Programs..

Copyright © 2025. This is an open-access article distributed under the Creative Commons Attribution License.

INTRODUCTION

The AMMI-Bi-plot analysis is a modern and highly efficient procedure for genetic stability analysis and variety selection based on high productivity and stability. The AMMI model (Additional Main Effects and Multiplier Interaction) tries to analyze interaction between genetic factors (genes) and various environments for the identification of those genotypes that interact positively with desirable environmental conditions. AMMI analysis helps to reveal the genotypes whose performance in the environment has been stable; this will enable plant breeders to identify the best varieties most adapted under differing conditions [1].

GEI interaction poses a constant challenge for plant breeders, as it weakens the correlation between phenotypic and genotypic values and complicates the selection of genotypes when assessed in multiple environments [2, 3, 4]. In the presence of GEI, breeders often use the analysis of genetic stability to discriminate between most productive and

stable genotypes. Several statistical methods have been developed and adopted regarding adaptability and stability under changing environmental conditions [5, 6]. Variability in genotype performance across environments is a key criterion for stability; a genotype is considered stable when its performance variability is low [7, 8].

Understanding the genotype \times environment interaction is important to predict the performance of genotypes across sites. Thus, considerable attention has been paid by researchers to assess this interaction through binary AMMI schemes to give appropriate recommendations about the suitable cultivars for each environment. A highly stable genotype shows a small sum-of-squared deviations and high coefficient of determination. Regarding this matter, the AMMI model currently has become one of the most applied models for differentiation between stable genotypes across multiple environments [9, 10].

The term "environment" embraces the entire range of physical, chemical, and biological factors that interact to influence plant growth; it often leads to a significant genotype-environment interaction [11]. Genetic variation is the basis of breeding programs, as described by [12, 13]. Genetic correlation is a measure of the extent to which particular genes controlling quantitative traits are associated together. This is frequently the reason why some varieties are economically important because of their combination of desirable traits [14, 15, 16]. It may arise from pleiotropy, gene clustering, or evolutionary relationships between traits [17, 18].

Analysis of genetic stability usually starts with ANOVA to estimate the main effects of genotypes and environments, followed by PCA to examine the interaction component of the GEI. According to [1], the AMMI model combines additive components due to main effects with multiplier components due to interaction effects. Where the genotype and environment have the same signal on the IPCA axes, the interaction is said to be positive; a difference in sign of the signal is taken to indicate a negative interaction. Large or positive IPCA values represent strong interaction, while values close to zero indicate a low interaction [19]. The AMMI model is a critical basis for the classification of genotypes by their stability, since IPCA1 values make important contributions to the genotype stability score. These scores need relative weighting based on the relative contributions of IPCA1 and IPCA2 to the mean squares of the interaction as reported in [20, 21]. The AMMI stability value is the Euclidean distance from the origin in a two-dimensional plot of the values of IPCA1 and IPCA2. It is calculated using the formula by [22]: $ASV = \frac{((SSPCA1/SSPCA2)(GPCA1))^2 + (GPCA2)}{1/2}$, $Y_{ijk} = \mu + G_i + E_j + \beta(E)k(j) + \sum M_m = 1\lambda m\gamma imamj + \xi_{ijk}$ ($m = 1 \rightarrow M$), where SSPCA1 and SSPCA2 are the sums of squares for PCA1 and PCA2, respectively, and GPCA1 and GPCA2 are the genotype scores for each principal component. The AMMI model, like other GEI models, expresses interaction effects as a sum of M multiplicative components that explain variation across M principal axes. When analyzing yield data, each combination of location and year is treated as a distinct environment, and the dataset is analyzed using an ANOVA-based framework.

Previous Studies On The Use Of The Ammi-Biplot Analysis Technique To Assess Genetic Stability:

Found [23] in their study on (19) yellow corn hybrids that the genotype G10 performed best in terms of performance, achieving the highest yield and greatest genetic stability across all environments, while genotype G1 was the least stable. Meanwhile, [24], in their study on (36) genetic combinations of bread wheat, showed that hybrid number 14 (Irena \times Veery) was the most stable under stress conditions, whereas combinations number 1 (S-78-11) and number 30 (Chamran \times Hirmand) were the least stable.

In the study by [25], which aimed to investigate the effect of ten environments on the yield of ten triple hybrids of yellow maize, AMMI-Biplot analysis demonstrated the significance of genotype-environment interaction, with the optimal hybrid being G10, which achieved the highest yield of 157.2 g per plant, followed by hybrid G8 with a yield of 143.8 g per plant. Similarly, [26] concluded in their study in Ethiopia on 10 genetic combinations of bread wheat that genotypes G9, G8, G10, and G4 were the most stable compared to other genotypes.

Another study [26] on (11) potato genotypes in Ethiopia found that the Ararsa genotype was the most stable, with an average yield of 30.18 tons/ha, while the Gera and Bulle genotypes were less stable. Gudanie and Gorebella combined high productivity and stability, with the Waka site recording the highest average grain yield of 33.52 tons/ha, while the Gendo site recorded the lowest at 24.18 tons/ha. Gudanie and Gorebella are considered the optimal choices for commercial production as they achieve a rare balance between high productivity and stability across different environments.

Regarding the study [28] on (20) barley genotypes in Iran, AMMI analysis showed that genotype G4 was the most stable across environments, while G5 and G6 exhibited general adaptability. The genotypes G7 and G13 showed specific adaptation to particular environments; G7 was specially adapted to the Neishabour environment, and G13 to the Esfehan environment. Genotype G1 produced high grain yield with stability.

In study [18] on (14) soybean genotypes grown at two locations in Iraq (Baghdad and Salahaddin), genotypes G11, G10, G7, G6, and G12 were found to be the most stable due to their general adaptability.

Found [29] in their study on (15) promising genetic compositions derived from a reciprocal hybridization program

involving six pure genetic lines of bread wheat that genotype G10 showed general adaptation and stability based on the ASV value (a measure of stability in the AMMI model useful for distinguishing yield stability among genotypes). [30], in their study on (8) bread wheat genotypes grown in (5) locations under heat stress, using two standard tests, reported significant differences ($p < 0.01$) in genotype and location effects. AMMI analysis and ASV values revealed that genotypes GEN4, GEN9, and GEN8 were genetically stable, whereas GEN5, GEN1, and GEN6 were most sensitive to stress.

Study [31] on (21) oat genotypes in Iran indicated that genotypes G21 (Brusher) and G6 (Mortlock) were the most adaptable due to their high stability and productivity under the conditions of Kermanshah province, with the highest grain yield recorded in environment E5 and the lowest in E11.

Study [32] on (150) coarse wheat genotypes across two locations using additive main effects and multiplicative interaction models found that the sum of squares was 59.8% for genotypes, 3.5% for environments, and 36.7% for genotype \times environment interaction (GEI).

In study [33] on (5) quinoa genotypes in Egypt, AMMI-Biplot analysis showed that the KVL-SRA3 genotype was broadly stable across all environments, confirming it as an ideal genotype and recommending the expansion of this nutritious crop's cultivation, especially in arid areas. These results open horizons for adopting quinoa as part of Egypt's food security strategy, while the Regalona genotype was the least stable.

Study [34] on (324) white corn genotypes showed that genotypes G148, G123, G110, G203, and G73 were the best in genetic stability and high yield compared to others.

In study [35] on (15) chickpea genotypes across eight environments in southeastern Turkey, AMMI analysis showed that genotypes G1 and G10 had genetic stability and high yield, being the best across all environments, while genotypes G2, G3, and G5 were adapted to specific environments.

In the study [36] on (32) barley genotypes, AMMI analysis showed that the most stable genotypes were R63N/22 and R63N/61. It is recommended to include the lines R63N/61, R63N/22, and R63N/1 in breeding programs due to their stability and their production of the highest average 1000-grain weight.

The study [37] on (30) peanut genotypes showed that AMMI analysis identified genotypes G18, G14, G7, G3, G1, and G5 as the best performers. Genotype G1 was the top performer with the highest average yield and high stability in the tested environment. According to the AEC line, genotypes G1 and G3 were highly stable, while genotypes G2 and G4 had low stability despite their high yield per hectare.

In study [38] on (18) chickpea genotypes in Iran, results showed that genotypes G5 and G9 were the most genetically stable, whereas genotypes G12, G7, and G8 were the least stable. Genotypes G6 and G18 achieved the highest seed yield.

In study [39] on (10) pea genotypes, it was found that the most genetically stable genotypes were 1, 4, and 8, while the optimal environments were MO7B, MA7B, and CE7B, which produced the highest protein content. Genotypes 6, 7, and 10 should be avoided due to their poor adaptation and stability in the studied environments.

Study [40] on (26) spring wheat genotypes confirmed through stability analysis that varieties STH 21-03, STH 21-09, and KOH 18279 recorded high yield and high genetic stability, making them ideal for breeding programs to achieve stable performance across diverse environments.

Study [41] on (23) sugar beet genotypes revealed that genotype G10 was the best performer, achieving the highest sugar beet yield (65.3 tons/ha), sugar content (15.68%), and sugar production (10.22 tons/ha), as well as the highest stability across different environments. Genotypes G2 and G14 were partially stable in beet yield and sugar content; G16 and G17 were stable in sugar content and production; while genotypes G8 and G11 had high yield but were less stable. Environment E3 showed the least interaction with varieties and achieved the best performance for most genotypes in beet yield and sugar content, while environment E1 excelled in sugar production. Genotype G11 was superior in environment E2 for beet yield; genotype G19 showed the highest sugar content in the same environment, and genotype G6 achieved the highest sugar production in environment E1.

In the study [42] on (11) peanut genotypes in Iran, genotypes ICG192 and ICG130 were adapted to environments TA1 and T Sequence, while genotype ICG178 was more adapted to environment MA2. Genotypes ICG140 and NC2 were the best in environment RA2. Genotypes ICG178, ICG115, and ICG201 were the most genetically stable, whereas NC2, ICG208, ICG130, and ICG192 were the least stable.

In study [43] on (20) bread wheat genotypes in Nepal under heat and drought conditions, AMMI analysis showed that genotype NL 1404 was the most stable across both environments, while NL 1346 was optimal for its high yield and genetic stability. Genotype NL 1350 was the least stable, and genotypes NL 1368 and BL 4407 had high yields but were genetically unstable. Genotype NL 1179 was the most stable according to stability analysis. Genotypes NL 1376, NL 1369, NL 1386, and NL 1387 were acclimated to heat stress environments, while NL 1384, Gautam, BL 4949, and NL 1412 adapted to heat and drought stress environments.

In study [44] on (11) oat genotypes, researchers reported that genotypes G6 and G5 were the best in terms of high

production and genetic stability across all studied environments.

Study [45] on (42) white corn genotypes showed that genotype G4 achieved the highest grain yield (4.648 tons/ha), followed by genotype G16 with a yield of 4.646 tons/ha. Genotypes G23, G18, G29, and G11 were sensitive to environmental changes due to strong genotype \times environment (G \times E) interaction. The optimal environments for testing and comparison were AS20 and PW20/JM20.

Study [46] on (12) bread wheat genotypes tested in three different environments in the Awi region of Ethiopia (E1, E2, E3) found that genotype G6 (Tay) had the highest productivity but was less stable, while genotype G7 (Hongolo) was the most stable with high productivity. Genotypes G5, G7, and G10 were the most stable according to AMMI analysis.

Study [47] on (20) barley genotypes grown in (5) locations in Iran concluded that AMMI analysis showed genotypes G3, G9, G10, and G14 were ideal due to their high productivity (above the general average of 4.56 tons/ha) and low IPCA values (high stability). Genotype G14 excelled in 6 out of 10 environments with high stability. These genotypes are suitable for wide adaptation in warm, dry, and humid regions of Iran.

Study [48] on (30) rice genotypes in Nepal found that AMMI analysis identified Samba Masuli Sub-1 and Sugandhit Dhan-1 as the most productive and genetically stable genotypes across tested environments. Promising genotypes like Kalo Basmati can be used in breeding programs to develop new varieties.

In study [49] on (16) sugar beet genotypes, researchers showed that environment was the most influential factor on sugar beet productivity, accounting for 74.25% of the variance. Genotype KWS4207 (G3) showed the highest stability in yield and sugar content, while KWS4027 (G14) excelled in sugar content (16.52%) with high stability. Genotype G3 was the most stable in yield and sugar content, and genotype G14 recorded the highest sugar content.

Finally, study [50] on (11) bread wheat genotypes in southern Ethiopia using AMMI analysis showed that genotype G8 was the most stable across all locations. Genotype G11 had the highest yield, while G2 was the least stable. Genotypes G11, G9, and G10 were suitable for Damot Gale and Kokate locations, with Damot Gale being the ideal environment for testing variety performance.

Conclusions:

From the above, it is evident that AMMI biplot analysis is promising and highly efficient for the selection of varieties with genetic stability influenced by the study factors. This technique allows the delimitation of varieties with a strong genetic structure and high genetic potential that can tolerate unpredictable environments. Therefore, we recommend the use of this technique in the identification of high-yielding and genetically stable varieties to ensure the selection of the best genotype. The new varieties will be used in subsequent breeding programs.

References

- [1]. Aljumaily, J. M. A. (2014). Analysis of genotype by environment interaction data using AMMI Biplot. The Iraqi Journal of Agricultural Sciences, 45 (2), 125–132.
- [2]. Comstock R. E. and R. H. Moll .1963. Genotype-Environment interaction. in Hanson W. D and H.E Robinson (ets.) Statistical genetics and plant breeding Nat. Acad Sci. Nat Res. council Publ Washington. P164-196.
- [3]. Jabbar, L. J., and Mohammed, M. I. (2022). Genetic variations, correlations, and path analysis of flax (*Linum usitatissimum* L.) genotypes at different concentrations of NPK nano complex fertilizer. Kirkuk University, College of Agriculture, Iraq, 13 (4), 364–381.
- [4]. Al-Abody, M. A. K., Al-Sabahi, W. A. J., and AL-Abdullah, S. A. M. (2020). Study of genetic and phenotype correlations and heritability for twelve varieties of wheat (*Triticum aestivum* L.) planting under different environmental of Basrah. Al-Muthanna Journal of Agricultural Sciences, 8(1):8-20.
- [5]. Lin, C. S.; M. R. Binns and L. P. Lefkovitch. (1986). Stability analysis where do we stand. Crop Sci. 26: 894-899 .
- [6]. Al-Samarrai, R., & Hindi, H. (2024). Stability Evaluation of Barley Genotypes grown in gypsum soil for Environmental variations. Journal of Medicinal and Industrial Plant Sciences, 2(2), 15-25. <https://doi.org/10.32894/MEDIP.24.2.2>
- [7]. Mosa, N. A., Ali, A. M., and Zibari, P. A. A. (2024). Assessment of genetic stability of *Magnolia grandiflora* L. by AFLP marker via tissue culture technology. Kirkuk University Journal for Agricultural Sciences, 15 (4):38-45.
- [8]. Al-Subhi, W. A., Ali, H. A., and Al-Asady, K. K. (2004). Yield stability in some varieties of sorghum under Basrah condition *Sorghum bicolor*, L. (Moench). Basrah J. Agric. Sci. 17(1):209 -216.
- [9]. Badu-Apraku, B., Fakorede, M. A. B., Menkir, A., Kamara, A. Y., and Dapaah, S. (2003). A multivariate analysis of the stability of extra-early maize inbred lines in *Striga*-infested environments. Maydica, 48 (4), 229-237.

- [10]. Sharif, Y. O. N. A., Madab, D. S., & Hindi, H. A. (2024). Estimation of Path Analysis and Genetic Parameters for Sorghum (*Sorghum bicolor* (L.) Moench) Varieties in Different Environments. IOP Conference Series: Earth and Environmental Science, 1371(5). <https://doi.org/10.1088/1755-1315/1371/5/052035>
- [11]. Al-Sahooki, M. M. (2000). Production and improvement of peanuts. Iraqi Journal of Agricultural Sciences, 31 (1), 9.
- [12]. Al-Mafarji, T. R. T., and Al-Jubouri, J. M. A. (2023). Heterosis, correlations and path analysis of grain yield components in bread wheat (*Triticum aestivum* L.). Kirkuk University Journal for Agricultural Sciences, 14 (3), 34–46
- [13]. Al-Abody, M. A. K., Al-Sabahi, W. A., and Al-Abdullah, S. A. M. (2019). Analysis of genetic stability using GGE-biplot technic to wheat cultivars (*Triticum aestivum* L.) under Basrah different environmental conditions. Plant Archives, 19 (2), 3597–3604.
- [14]. Omar, A., & Al-Layla, M. (2024). Estimation genetic parameter, genotypic and phenotypic correlation, path and cluster analysis of quantitative traits for Bread Wheat genotypes in Erbil under rain- fed condition. Journal of Medicinal and Industrial Plant Sciences, 2(3), 23-34. <https://doi.org/10.32894/MEDIP.24.3.4>
- [15]. Al-Abody, M. A. K. (2015). Response of Bread Wheat (*Triticum aestivum* L.) to Foliar Application of Iron and Manganese and their Interaction in Yield and Yield Components. Basrah Journal of Agricultural Sciences, 28 (2), 87-97.
- [16]. Al-Mafarji, T. R. T., Al-Jubouri, J. M. A., & Kanbar, A. (2024). Estimate Combining Ability and Gene Action of Yield, and Some Qualitative Traits of Bread Wheat Genotypes. (*Triticum aestivum* L.) of Half-Diallel Crosses. Tikrit Journal for Agricultural Sciences, 24(3), 182–196. <https://doi.org/10.25130/tjas.24.3.15>
- [17]. Al-Jubouri, R. M. A., Mohammed, M. I., & Al-Mafarji, T. R. T. (2024). Genetic Analysis of Heterosis and some Genetic Parameters of Half Diallel Crosses in Maize (*Zea mays* L.). IOP Conference Series: Earth and Environmental Science, 1371(5). <https://doi.org/10.1088/1755-1315/1371/5/052027>
- [18]. Al-Mafarji, T. R. T., & Al-Jubouri, J. M. A. (2023). Combining Ability and Gene Action of Half Diallel Crosses in Bread Wheat (*Triticum aestivum* L.). IOP Conference Series: Earth and Environmental Science, 1262(5). <https://doi.org/10.1088/1755-1315/1262/5/052027>
- [19]. Crossa, J. (1990). Statistical analysis of multi-locations trials. Advan. Agron. 44: 55-85.
- [20]. Mohammadi, R., M. Armion, A. Shabani and A. Daryaei. (2007). Identification of stability and adaptability in advanced durum wheat genotypes using AMMI analysis. Asian J. Plant Sci. 6: 1261-1268.
- [21]. Nassar, R., and M. Huehn. (1987). Studies on estimation of phenotypic stability: Tests of significance for non-parametric measures of phenotypic stability. Biometric 43: 45-53.
- [22]. Purchase, J. L., Hatting, H., & Van Deventer, C. S. (2000). Genotype× environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. South African Journal of Plant and Soil, 17(3), 101-107. <https://doi.org/10.1080/02571862.2000.10634878>
- [23]. Mitrović, B., Stanislavljević, D., Treski, S., Stojaković, M., Ivanović, M., Bekavac, G., and Rajković, M. (2012). Evaluation of experimental maize hybrids tested in multi-location trials using AMMI and GGE biplot analyses. *Turkish Journal of Field Crops, 17 (1), 35–40.
- [24]. Naroui Rad, M.R., Abdul Kadir, M., Rafii, M.Y., Jaafar, H.Z.E., Naghavi, M.R., and Ahmadi, F. (2013). Genotype × environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (*Triticum aestivum*) under normal and drought stress conditions. Australian Journal of Crop Science, 7(7), 956–961.
- [25]. Al-Rawi, O. H., Elsahookie, M. M., and Al-Jumaily, A. M. A. (2013). Stability estimates of some maize crosses by GR and AMMI equations. The Iraqi Journal of Agricultural Sciences, 44 (4), 427–433.
- [26]. Hagos, H. G., and Abay, F. (2013). AMMI and GGE biplot analysis of bread wheat genotypes in the northern part of Ethiopia. Journal of Plant Breeding and Genetics, 01, 12–18 .
- [27]. Daemo, B. B., & Ashango, Z. (2024). Application of AMMI and GGE biplot for genotype by environment interaction and yield stability analysis in potato genotypes grown in Dawuro zone, Ethiopia. Journal of Agriculture and Food Research, 18, 101287 .
- [28]. Mortazavian, S. M. M., Nikkhah, H. R., Hassani, F. A., Sharif-al-Hosseini, M., Taheri, M., and Mahlooji, M. (2014). GGE Biplot and AMMI Analysis of Yield Performance of Barley Genotypes across Different Environments in Iran. Journal of Agricultural Science and Technology (JAST), 16 (3), 609-622.
- [29]. Kadhem, F. A., and Baktash, F. Y. (2016). AMMI analysis of adaptability and yield stability of promising lines of bread wheat (*Triticum aestivum* L.). The Iraqi Journal of Agricultural Sciences, 47 (Special Issue), 35–43.
- [30]. Alam, A.; Farhad; A. Hakim; N. C. D. Barma; P. K. Malaker; M. A. Reza; A. Hossain and M. li. (2017).

- AMMI and GGE BIPLLOT Analysis for Yield Stability of Promising Bread Wheat Genotypes in Bangladesh. Pak. J. Bot., 49(3): 1049-1056
- [31]. Safavi, S. M., and Bahraminejad, S. (2017). The evaluation of genotype \times environment interactions for grain yield of oat genotypes using AMMI model. Journal of Crop Breeding, 9 (22), 125–132.
- [32]. Tekdal, S., and Kendal, E. (2018). Stability Parameters for Grain Yield of Emmer Wheat (*Triticum dicoccum* Schrank) Genotypes Turkish Journal of Field Crops, 23(2), 124-132 .
- [33]. Ali, M., Elsadek, A., and Salem, E.M. (2018). Stability Parameters and AMMI Analysis of Quinoa (*Chenopodium quinoa* Willd.). Egyptian Journal of Agronomy, 40(1), 59–74.
- [34]. Enyew, M., Feyissa, T., Geleta, M., Tesfaye, K., Hammenhag, C., and Carlsson, A. S. (2021). Genotype by environment interaction, correlation, AMMI, GGE biplot and cluster analysis for grain yield and other agronomic traits in sorghum (*Sorghum bicolor* L. Moench). PLOS ONE, 16 (10), e0258211.
- [35]. Erdemci, I. (2018). Investigation of genotype \times environment interaction in chickpea genotypes using AMMI and GGE biplot analysis. Turkish Journal of Field Crops, 23 (1), 20–26.
- [36]. Bocianowski, J., Warzecha, T., Nowosad, K., and Bathelt, R. (2019). Genotype by environment interaction using AMMI model and estimation of additive and epistasis gene effects for 1000-kernel weight in spring barley (*Hordeum vulgare* L.). Journal of Applied Genetics, 60 (1), 127–135.
- [37]. Khan, M. M. H., Rafii, M. Y., Ramlee, S. I., Jusoh, M., and Mamun, M. A. (2021). AMMI and GGE biplot analysis for yield performance and stability assessment of selected Bambara groundnut (*Vigna subterranea* L. Verdc.) genotypes under the multi-environmental trials (METs Scientific Reports, 11(1), 22791
- [38]. Farayed, Y., Abdi, H., Ahakpaz, F., Kanouni, H., and Mahmoodi, A. A. (2021). Genotype and environment interaction analysis for grain yield of chickpea genotypes using AMMI and GGE biplot models. Iranian Journal of Field Crop Science, 52(1), 155-166.
- [39]. Cardona–Ayala, C. E., Aramendiz-Tatis, H., and Espitia-Camacho, M. (2021). AMMI and SREG analysis for protein content in *Vigna unguiculata* (L.) Walp. Revista Ciência Agronômica, 52(4), e20207650.
- [40]. Jedzura, S., Bocianowski, J., and Matysik, P. (2022). The AMMI model application to analyze the genotype–environmental interaction of spring wheat grain yield for the breeding program purposes. Cereal Research Communications, 50(4), 1213–1224.
- [41]. Oroian, C., Ugrujan, F., Muresan, I.C., Oroian, I., Odagiu, A., Petrescu-Mag, I.V., and Burduhos, P. (2023). AMMI Analysis of Genotype \times Environment Interaction on Sugar Beet (*Beta vulgaris* L.) Yield, Sugar Content and Production in Romania. Agronomy, 13 (10), 2549 .
- [42]. Navrood, F. F., Zakaria, R. A., Rad, M. M., Zare, N., and Ahrabi, M. M. (2023). Stability analysis of groundnut (*Arachis hypogaea* L.) genotypes using AMMI and GGE biplot models and ideal genotype selection indicator. Indian Journal of Genetics and Plant Breeding, 83 (4), 518–525.
- [43]. Chaudhary, E., Sharma, S., Gautam, P., Ghimire, S., Sapkota, S., Bhattarai, K., Roka, P., Poudel, R., Timalisina, B., Neupane, K., G.C., G., Pariyar, M., Aryal, A., Poudel, M. R., and Bhandari, R. (2023). AMMI and GGE biplot analysis of wheat genotypes under heat stress and heat drought environment. Archives of Agriculture and Environmental Science, 8 (4), 484–489.
- [44]. Wodebo, K. Y., Tolemariam, T., Demeke, S., Garedew, W., Tesfaye, T., Zeleke, M., Gemiyu, D., Bedeke, W., Wamatu, J., and Sharma, M. (2023). AMMI and GGE Biplot Analyses for Mega-Environment Identification and Selection of Some High-Yielding Oat (*Avena sativa* L.) Genotypes for Multiple.
- [45]. Demelash, H. (2024). Genotype by environment interaction, AMMI, GGE biplot, and mega environment analysis of elite *Sorghum bicolor* (L.) Moench genotypes in humid lowland areas of Ethiopia. Heliyon, 10, e26528
- [46]. Mullualem, D., Tsega, A., Mengie, T., Fentie, D., Kassa, Z., Fassil, A., Wondaferew, D., Gelaw, T. A., and Astatkie, T. (2024). Genotype-by-environment interaction and stability analysis of grain yield of bread wheat (*Triticum aestivum* L.) genotypes using AMMI and GGE biplot analyses. Heliyon, 10, e32918.
- [47]. Rahmati, S., Azizi-Nezhad, R., Pour-Aboughadareh, A., Etminan, A., and Shooshtari, L. (2024). Analysis of genotype-by-environment interaction effect in barley genotypes using AMMI and GGE biplot methods. Heliyon, 10, e38131.
- [48]. Tiwari, D. N., Pandey, M. P., Manandhar, H. K., and Bhusal, T. N. (2024). Genotype by environment interaction using AMMI, GGE biplot and multivariate analysis of Nepalese aromatic rice landraces. Agronomy Journal of Nepal, 8 (1), 34–51
- [49]. Dang, X., Hu, X., Ma, Y., Li, Y., Kan, W., and Dong, X. (2024). AMMI and GGE biplot analysis for genotype \times environment interactions affecting the yield and quality characteristics of sugar beet. PeerJ, 12, e16882.
- [50]. Alemayehu, L., Kebede M and Wada E. (2025). AMMI analysis of elite bread wheat (*Triticum aestivum* L.) selections for genotype by environment interaction and stability of grain yield in Southern Ethiopia. PLOS

استخدام تحليل AMMI لاختيار الأصناف الأكثر استقراراً وإنتاجية في برامج تربية النبات . مقالة مراجعة

محمد عودة خلف العبودي²
زكريا العجلوني⁴

ياسين عبيد نوري أحمد شريف¹
طارق رعد ثامر المفرجي³

¹ قسم المحاصيل الحقلية، كلية الزراعة، جامعة كركوك، كركوك، العراق .

² قسم المحاصيل الحقلية، كلية الزراعة، جامعة البصرة، العراق .

³ قسم النباتات الطبية والصناعية، كلية النباتات الطبية والصناعية، جامعة كركوك، كركوك، العراق .

⁴ قسم الانتاج النباتي، كلية الزراعة، جامعة العلوم والتكنولوجيا الأردنية، الأردن

الخلاصة

استقرار التراكيب الوراثية تحت الظروف البيئية المختلفة يُعد أمراً مهماً لمربي النباتات لتحديد مدى قابليتها للتكيف مع الظروف البيئية. ومع ذلك، فإن استجابة التراكيب الوراثية تحت الظروف البيئية القاسية (مثل الجفاف، والحرارة، والملوحة، وغيرها من الضغوطات) تجعل من الصعب على مربي النباتات تحديد التراكيب المتفوقة. لذلك، فإن تحليل الاستقرار الوراثي (AMMI) وتقدير التفاعل بين التراكيب الوراثية والظروف البيئية يُعدان من المعايير المهمة التي يجب أخذها بعين الاعتبار. وبناءً عليه، قد يلجأ الباحثون في برامج تربية النباتات إلى البحث عن أداة أو تقنية يمكنها الكشف عن التراكيب الوراثية المستقرة وراثياً وذات الإنتاجية العالية. وتُعد تقنية AMMI-Biplot من أهم هذه الأدوات، إذ يمكن استخدامها لتحديد التراكيب الوراثية المستقرة ومرتفعة الإنتاجية عبر مختلف البيئات. ويُعزى سبب الاستقرار الوراثي لهذه التراكيب إلى امتلاكها جينات وراثية فائقة وقدرتها على التحمل في ظل ظروف بيئية متغيرة. وقد أثبتت هذه التقنية فعاليتها العالية في دراسة التفاعل الوراثي-البيئي وتحديد التراكيب عالية الأداء. ويُعتبر الاستقرار الوراثي في الأصناف النباتية صفة متعددة الأبعاد ناتجة عن تفاعل آلاف أزواج الجينات مع العديد من العوامل البيئية، مما يؤدي إلى ظهور أشكال مختلفة للصفة في الكائن الحي. وتتميز التراكيب الوراثية المستقرة بقدرتها المثلى على التكيف مع مجموعة واسعة من البيئات المعتمدة. وتكمن أهمية التفاعل الوراثي × البيئي (GEI) في الزراعة في اختيار الأصناف التي يجب اختبارها في بيئات متعددة قبل التوصية بها، وتحديد البيئات المناسبة، وتطوير أصناف مستقرة وراثياً قادرة على تحمل التقلبات البيئية. لذا، فإن أهمية تحليل AMMI تكمن في تصنيف التراكيب الوراثية حسب استقرارها البيئي، وتحديد البيئات المثلى لكل صنف، وتحليل التفاعل الوراثي-البيئي باستخدام المخططات الثنائية (Bi-plots) ويكمن الهدف من تحليل AMMI في دراسة التفاعل بين التركيب الوراثي والظروف البيئية لاختبار استقرار إنتاجية الصنف.

الكلمات المفتاحية: تحليل AMMI، الأصناف، استقرارية الحاصل، تحليل المخطط الثنائي، تجارب متعددة البيئات، برامج تربية النباتات.