AF-1047
[1-8]

RESEARCH ARTICLE Indian Journal of Agricultural Research

Estimation of Some Genetic Parameters of Different Genotypes of Maize Crop (*Zea mays* L.) under the Influence of Phosphate Fertilization

Muhamed A.K. AL-Abody[1], Fatimah A. Jamel[1], Taghreed M.K. Al-Farjawi[2]

ABSTRACT

Background: Maize crop is an important field crop, but its productivity is affected by the genetic factor (Genotypes) and the differences between them and their response to phosphate fertilization levels. Adding phosphate fertilizer contributes to improving growth efficiency and production, which necessitates conducting a genetic evaluation of Maize Genotypes under phosphate fertilization conditions.

Methods: Field experiment was carried out in the fall of 2023 in the Shatt Al-Arab district (Al-Hawta) in the east of Basrah Governorate in soil with a clay texture , in order to estimate certain genetic traits of maize crop genotypes (Rezer, Jemeson, Bohoth-106 and Baghdad-3) and their response to phosphate fertilizer (0, 120 and 240) kg P ha^{-1}, The treatments were applied in accordance with factorial type in three replications by randomized complete block design (RCBD). The different genotypes were randomly distributed within each block and agriculture was carried out on 20/8/2023.

Result: The analysis of genetic, environmental and phenotypic variances in grain yield were 0.132642, 0.00163 and 0.134272, respectively. The heritability degree was 98.78% and the phenotypic and genetic difference coefficients were 7.992387 and 7.943727 %, respectively. The results of the hierarchical cluster analysis also displayed the amount of genetic convergence between the genotypes Bohoth-106 and Baghdad-3 amounted to 216.449, which is the closest genetically between them and that the higher amount of genetic dimension was between the genotypes Rezer and Baghdad-3 amounted to 4282.256 and between the genotypes Rezer and Jemeson amounted to 1025.178,which can be used in hybridization to highlight the strength of the hybrid. While the genetic-distance between the genotype Jemeson and Bohoth-106 were 363.817, the genetic stability analysis showed that the genotype Baghdad-3 (G4) is the ideal genotype due to its high yield and genetic stability.

Key words: Cluster analysis, GGE-biplot analysis, Heritability, Maize (*Zea mays* L.) genotypes, Variations.

INTRODUCTION

The maize (*Zea mays* L.) is considered as main cereal crop as this crop comes next to the rice and wheat in terms of economic importance due to its versatility (Aziz and Sattar, 2024; Mauriya *et al.,* 2026) As maize is mostly cultivated as a grain diet crop, the bread and pastries are made by combining its flour with spelled wheat. The seed starch is used for making many type of sweets, Given the importance of this crop and due to its low productivity in Iraq, it invites us to seriously search for all possible means to increase the yield and among the most important means is the cultivation of genotypes that have high productivity to test the extent to which these genotypes respond to the conditions of the study area that achieve high productivity in quantity and quality (Mahmood *et al*., 2025), as well as many agricultural operations, foremost of which is the adding phosphate nourishment. Alongside the ongoing supply of novel genotypes, contemporary scientific techniques are being implemented for the benefit of the crop, beginning with planting in soil and concluding with harvesting and among those main agricultural operations is the implementation of adding varying phosphate fertilizer levels to reach the ideal amount that contributes towards increasing production per unit area (Ali *et al.,* 2025). It is known that the application of agricultural operations by correct scientific methods (such as the adoption of genotypes and different levels of phosphate fertilizer plays a significant part in raising agricultural production rates and adding different levels of phosphate fertilizer is one of the ways that facilitate agricultural operations effectively and help improve the characteristics of the yield (Sharif *et al.,* 2026). Suitable genotypes cultivation for the area

[1]Department of Field Crops, College of Agriculture, University of Basrah, Iraq.
[2]Date Palm Research Center, University of Basrah, Iraq.

Corresponding Author: Muhamed A.K. AL-Abody, Department of Field Crops, College of Agriculture, University of Basrah, Iraq. Email: mohammad.kalaf@uobasrah.edu.iq
ORCIDs: https://orcid.org/0000-0002-7380-5307, https://orcid.org/0000-0002-1750-4606, https://orcid.org/0000-0001-5440-3962

How to cite this article: AL-Abody, M.A.K., Jamel, F.A. and Al-Farjawi, T.M.K. (2026). Estimation of Some Genetic Parameters of Different Genotypes of Maize Crop (*Zea mays* L.) under the Influence of Phosphate Fertilization. *Indian Journal of Agricultural Research.* 1-8.

Submitted: 03-04-2026 **Accepted:** 25-06-2026 **Online:**

and the evaluation of the performance of these genotypes with the impact of varying phosphate fertilizer concentrations is an essential act that has to be followed in order to get the best harvest. Gaining insight into these genotypes' performance could assist researchers identify their genetic capabilities, which are reflected in increased productivity and thus will lead us to choose the appropriate genetic makeup. Phosphorus is an essential nutrient for plants because it plays a direct role in most physiological processes such as photosynthesis, respiration, cell division, seed formation and regulation of other cellular processes. It cannot occur inside plant cells (Al-Nuaimi, 1999), therefore, ensuring adequate levels of phosphorus in plant tissues will lead to increased root mass activity and increased branching and plant growth. Phosphorus plays an important role because it stimulates the action of enzymes and growth regulators. Building important compounds for plants such as carbohydrates and proteins (Al-Hamdany and Al-Hadethi, 2017). Due to the lack of studies on estimating some genetic parameters (Genetic, environmental, phenotypic and heritability variations in the broad-sense, hierarchical cluster analysis between the studied genotypes and genetic stability analysis) in the South Iraq region for maize crop, in addition to recognize the optimum genotypes and the most appropriate level of phosphate fertilizer to obtain maximum growth and harvest of grains, the idea of this research came.

MATERIALS AND METHODS

In the autumn of 2023, a field experiment was conducted in the Shatt Al-Arab district in the Al-Houta region, east of Basrah Governorate, Field Crops Department , College of Agriculture, in soil with a clay texture to estimate some genetic features of four genotypes of the maize crop (Rezer, Jemeson, Bohoth-106 and Baghdad-3) and their response to phosphate fertilizer (0, 120 and 240) kg P ha^{-1}. Before planting, composite soil samples were collected from the experimental field and analyzed to determine their physical and chemical properties. The results of the soil analysis are presented in Table (1). The treatments were constructed in accordance with factorial type in three replications by randomized complete block design (RCBD), divided land into experimental units and an area with 3 m x 4 m = 12 m^2. Every unit contains 5 lines with a 3 m distance with 75 cm distance between lines and between holes was 25 cm, planting was done on 20/8/2023 for all experimental units. The irrigation was given as needed, while nitrogen fertilizer was added as urea fertilizer (46% N) with 240 kg N ha^{-1} (Mohsen, 2007) and was added in two batches, one after planting and one in the stage of the beginning of male flowering (Cheyed and El- Sahookie, 2011) and potassium sulfate was applied as a potassium fertilizer (K_2O 54%) at once when planting, while phosphate fertilization was added according to the study treatments as triple superphosphate (46% P_2O_5) and by two batches, the first before planting and the other earlier flowering, The characteristics were height (cm), ear length (cm), grains number of ear (grains ear $^{-1}$), the weight of 500 grains (g) and the grain yield (t ha^{-1}).

Genetic parameters

Calculation genetic, environmental and phenotypic variances

Genetic and phenotypic variances are estimated (Walter, 1975) as following:

$$\sigma 2G = \frac{Msg - Mse}{r}$$

$$\sigma^2E = Mse$$

$$\sigma^2P = \sigma^2G + \sigma^2E$$

Whereas,
σ^2G= Genetic variance.
σ^2E= Environmental variance.
σ^2P= Phenotypic variance.
Msv= Mean squares genotypes.
Mse= Mean squares of experimental error.
r= number of replications.
a= Factor levels a.

Degree of heritability: Heritability in the broad sense ($h^2_{b.s}$)

Heritability was estimated as follows (Hanson *et al.,* 1956):

$$h^2_{(b.s)} = \frac{\sigma^2G}{\sigma^2P} \times 100$$

Whereas;
$h^2_{b.s.}$= Heritability in broad sense.
σ^2G= Trait genetic variance.
σ^2P= Trait phenotypic variance.

Table 1: Some chemical and physical properties of field soil before planting.

Traits		Values	Units
Degree of soil reaction (PH)		7.31	-
Electrical conductivity (E.C)		7.22	DC-Siemens M^{-1}
Organic matter		10.5	g kg^{-1}
Items prefab	Nitrogen	51.41	mg kg^{-1} Soil
	Phosphorus	5.15	
	Potassium	126	
Soil separates	Sand	250	g kg^{-1} soil
	Silt	300	
	Clay	450	
Texture	Clay texture		

Genotypes: of phenotypic and genetic coefficient of variation

$$PCV\ \% = \frac{\sqrt{\sigma^2 P}}{\bar{X}} \times 100$$

$$GCV\ \% = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

PCV (%)= Phenotypic coefficient of variation.
GCV (%)= Genetic coefficient of variation.
σ^2P= Phenotypic variance.
σ^2g= Genetic variance.
X =Arithmetic mean.

Hierarchical cluster analysis

Hamdalla (2011) states that the agglomerative approach was used to combine the oat genotypes into sets in order to simplify the data for the cluster analysis (Sneath and Sokai, 1973; Williams, 1976). The analysis is a multi-step procedure that initiates by the creation of degree of similarity matrix, which known as matrix proximities and ends with dendrogram creation. The euclidean distances were computed using the Un-weighted pair group method analysis (UPGMA) that is a straightforward technique (Sneath and Sokai, 1973). Based on the preceding formula, these values obtained indicate an amount of similarity between sums rates over matrix proximities that were created in the primary step with the SPSS version-22 (Punitha *et al*., 2010).

$$Distance\ (x, y) = [\Sigma i\ (xi - yi)^2\ ]^{1/2}$$

Cluster analysis was used to gather comparable genotypes in uniform categories. The tool of Hierarchical Clustering was applied to examine the genotype data and estimate the level of divergence of gene among genotypes. In order to classify the genotypes under study into sets for applications in upcoming breeding programs, the aforementioned approach was utilized to determine genetic spacing level between the genotypes' genes regard with yield components and seed production.

Genetic stability GGE-biplot analysis

analysis and graphing using GGE-Biplot software (Yan and Tanker, 2005). The genotypes were Rezer, Jemeson, Bohoth-106 and Baghdad-3 (G1, G2, G3 and G4) respectively and phosphate fertilizer levels were 0, 120, 240 kg P ha^{-1} (E1, E2 and E3), respectively.

RESULTS AND DISCUSSION

Genetic, environmental, phenotypic variations, degree of Heritability in the broad sense and phenotypic and genetic difference coefficients

The genetic differences of plant height (cm), ear length (cm), the grains number of ear (grains ear^{-1}), weight of 500 grains(g) and the grain yield (t ha^{-1}) amounted to 38.84433, 0.810733, 350.8133, 4.961333 and 0.132642, respectively Table (2). The environmental variations of the studied traits amounted to 1.288, 0.0301, 62.95, 0.041 and 0.00163, respectively. The phenotypic variation of the studied traits amounted to 40.13233, 0.84033, 413.7633, 5.002333 and 0.134272. Heritability degree amounted to 96.79, 96.42, 84.78, 99.18 and 98.78%, respectively. This shows that the genetic component is stable, this caused the overlap of genetic and environmental variation to result in a rise in the weight of phenotypic variation. The coefficient of phenotypic difference of the studied traits amounted to 4.659379, 4.802648, 5.01045, 2.264901 and 7.992387%, respectively and the coefficient of genetic difference was 4.584001, 4.71903, 4.613587, 2.2556 and 7.943727%, respectively. Ayoob (2019); Anees and Al-Majmai (2020); AL-Asadi and AL-Abody(2023); Sharif *et al*. (2024); AL-Asadi and AL-Abody (2025); Al-Mafarji *et al*. (2026a) found similar results.

Hierarchical clustering analysis

In order to identify the groupings of genotypes based on their convergence or genetic divergence based on how comparable their responses to environment factors were, the cluster analysis was carried out by means of the genotypes' examined features, because it relies on calculating spaces that convey the degree of this spacing and the genotype distribution within sets, based on their genetic sources and function and based on the values of genetic convergence between genotypes, the genetic relationship was found, which links them in groups (Table 3; Fig 1), which shows the amount of genetic convergence (distance genetics), which showed cluster

Table 2: Estimation of genetic, environmental and phenotypic variations and heritability degree at the broad sense and coefficients of phenotypic and genetic variation of the studied traits for maize crop.

Studied traits	σ^2G	σ^2E	σ^2P	$h^2_{b.s}$	PCV (%)	GCV (%)
Plant height (cm)	38.84433	1.288	40.13233	96.79	4.659379	4.584001
Ear length (cm)	0.810733	0.0301	0.84033	96.42	4.802648	4.71903
Grains number of ear (grains ear^{-1})	350.8133	62.95	413.7633	84.78	5.01045	4.613587
Weight of 500 grains (g)	4.961333	0.041	5.002333	99.18	2.264901	2.2556
Grain yield (t ha^{-1})	0.132642	0.00163	0.134272	98.78	7.992387	7.943727

σ^2G: Genetic variance, σ^2E: Environmental variance, σ^2P: Phenotypic variance, $h^2_{(b.s)}$: Heritability (Broad sense), PCV (%): Phenotypic Coefficient of variation, GCV(%): Genetic Coefficient of variation.

analysis between the genotypes Bohoth-106 and Baghdad-3 amounted to 216.449. They are the closest genetically between them and may be the reason for this convergence is their participation in the genetic material, as it is an indication that the genotypes that are from different sources are not necessarily genetically divergent. Also, the reason for the convergence of the two genotypes Bohoth-106 and Baghdad-3 is that they are the most similar to genes, which reflects positively on the performance of the two genetic structures, because they possess some of the main preferred genes and can be used in later breeding projects. Therefore, in the case that any of the two genotypes is lost, it is feasible to swap the other genotype that is genetically similar to it and prevent taxation between them and through this analysis it was found that the highest genetic dimension was between the genotypes Rezer and Baghdad-3 amounted to 4282.256 and between the genotypes Rezer and Jemeson amounted to 1025.178. As a result of the difference in its genetic origin and possession of the two genotypes to different genes were the reason for the widening of that distance between the two genotypes, while genetic distance between Jemeson and Bohoth-106 was 363.817. Because of their considerable genetic distance, the genotypes Rezer and Baghdad-3 can be used in breeding and development initiatives, particularly hybridization and then selection to catch better genetic makeup in the study area situations and this statistical technology can be a successful alternative to molecular technologies in the absence of the latter. By showing the relationships within the genotypes and making comparisons easier by illustrating the relationships between them, the cluster analysis process was effective in analyzing genetic kinship. It also made it easier to choose genotypes with elevated genetic kinship or genetic variation and maintain genetic assets and these results are consistent with Hamdalla (2011) finding. The effectiveness of this approach in identifying genetically similarity also recognized by Azzam and Al-Obaidi (2018); Jumaa and Madab (2018); AL-Gubouri and Jumaa (2018); Al-Sadoon *et al.* (2022); Omar and Al-Layla (2024); AL-Asadi and AL-Abody (2025); Hasan *et al.* (2026).

Table 3: The genetic divergence and kinship between four genotypes of maize crop according to cluster analysis.

Genotypes	Squared euclidean distance			
	1: Rezer	2: Jemeson	3: Bohoth-106	4: Baghdad-3
1: Rezer	0.000	1025.178	2580.394	4282.256
2: Jemeson	1025.178	0.000	363.817	1138.345
3: Bohoth-106	2580.394	363.817	0.000	216.449
4: Baghdad-3	4282.256	1138.345	216.449	0.000

Stage	Cluster combined		Coefficients
	Cluster 2	Cluster 1	
1	3	4	216.449
2	2	3	751.081
3	1	2	2629.276

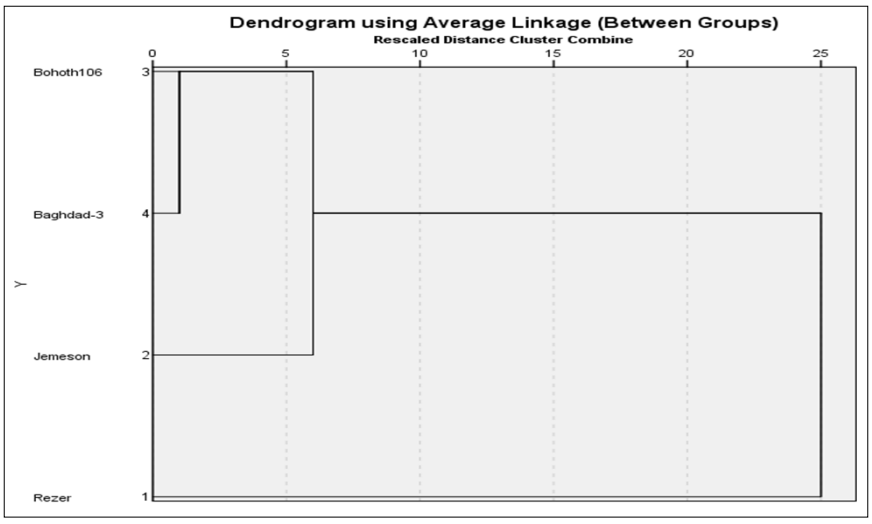


Fig 1: The genetic tree (Dendrogram) four genotypes of the maize crop using cluster analysis of similarity values.

Genetic stability: Analysis GGE-biplot

Phosphate fertilizer levels (0, 120, 240 kg P ha^{-1}) represented environments E1, E2, E3, sequentially. Fig (2) that the two environments E2 and E3 had an impact towards an increase in the rates of yield in contrast to the second environment E1, which reveals G4 is high-productivity of grain harvest at one group (first group) The second one was characterized in the genotype G3 and genotype G2 in another group while the least genotype is G1 in another group classified by Fig (2) in the form of concentric circles. Fig (3) shows the ideal genotypes makeup in the different environments under study based on the results achieved from this form, according to the stability of the genotypes in other environments, notes that the first group had a high-grain yield, which included G4 genotype is the ultimate genotype, represented by a concentric circle that represented genotype in the first group with the highest stability, while the second group included both the G3 genotype (close to ideal genotype), while remaining genotypes were present by other groups and outside that group (outside the three circles), which are the genotypes G2 and G1. Fig (4) also shows the preferred genotypes for each environment, as it is noted from the figure that the G4 genotype is the best in the E2 and E3 environments and the E2 and E3 environments share the stability of each of the genotypes confined to the polygonal angle, while the G1 genotype recorded less stability among the genotypes under study and this is consistent with Fig (2) as it turns out that the best the genetic structure was the G4 and that the best environments were the third environment E3, as shown in Fig (5) the stability of the studied genotypes and notes that the G4 genotype was the fixed and genetically stable genotype followed by the G3 genotype which is the genotype close to stability From the foregoing, it can be inferred that the GGE-Biplot technology testing of stability analysis was effective in analyzing the stability in displaying the associations between the genotypes and locations, enabling comparison by drawing such connections and making it easier to choose elevated stability genotypes and these effects align with Granato *et al*. (2016); Mousavi *et al*. (2019); AL-Abody *et al*. (2019); Mousavi *et al*. (2021); Al-Obaidi and Al-Jubouri (2023); Khan *et al*. (2023); Daemo and Ashango (2024) and Al-Mafarji *et al*. (2026b) they demonstrated how effective the method is in identifying genetically stable genotypes and most suitable conditions for them.

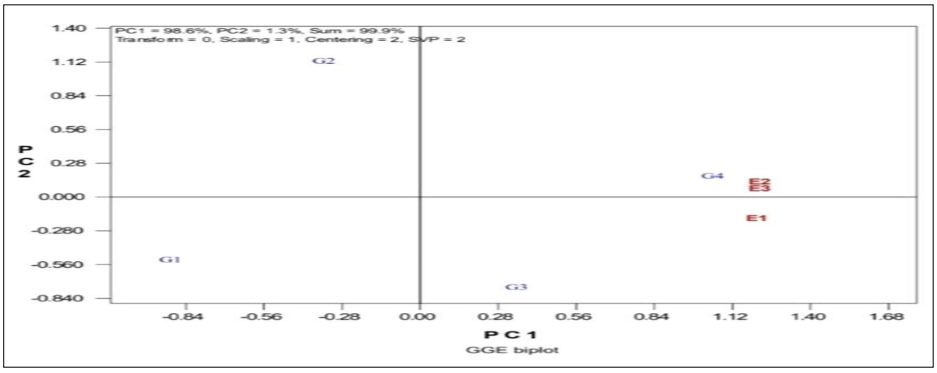


Fig 2: The relationship between genotypes and the environments.

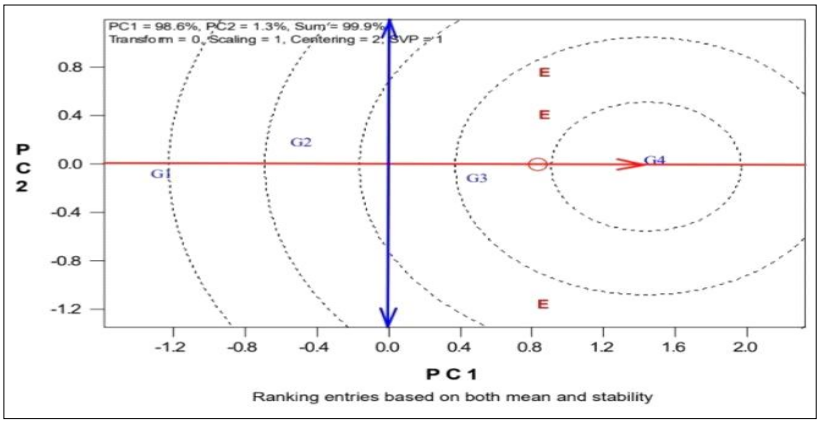


Fig 3: The ideal genotypes.

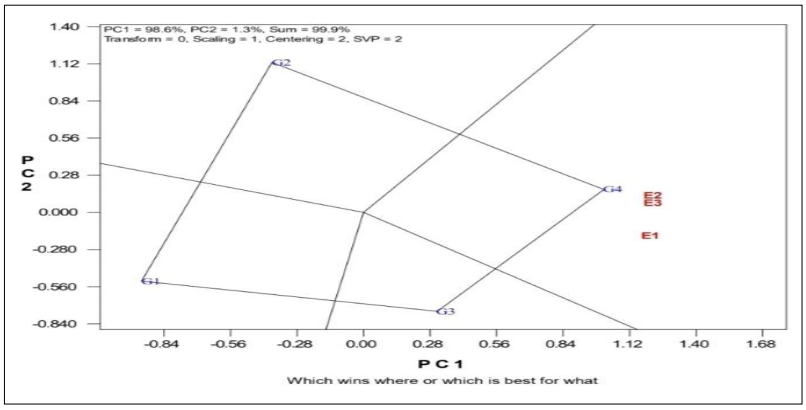


Fig 4: The preferred genotypes of each environment.

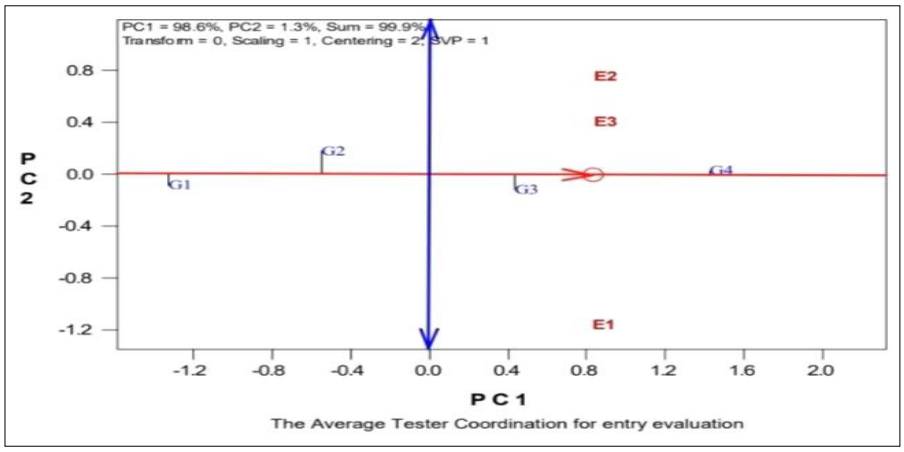


Fig 5: The stability of the studied genotypes.

CONCLUSION

The genetic, environmental and phenotypic variances in the characteristic of the grain yield, along with degree of heritability in the broad-sense and coefficient of phenotypic and genetic differences were high. Highest genetic-dimension was observed between the genotypes Rezer and Baghdad-3, which can be utilized in hybridization to enhance hybrid strength. By displaying the relationships between the genotypes, giving comparison by illustrating the relationships between them and streamlining picking process for genotypes of higher genetic kinship or genetic distancing and keeping genetic assets, also cluster analysis process showed effective genetic kinship exploring, genetic stability analysis showed that the ideal genotype was Baghdad-3 (G4), possessing both genetic stability and high yield and GGE-Biplot analysis of stability was able for knowing the ideal and genetically-stable genotypes.

Conflict of interest

I, the corresponding author, hereby declare on behalf of all co-authors that there is no conflict of interest regarding the publication of this manuscript. The authors declare that they have no known financial or personal relationships that could have appeared to influence the work reported in this paper. I confirm that all authors have read and approved this declaration, and I take full responsibility for its accuracy.

REFERENCES

Al-Abody, M.A.K., Al-Sebahi, W.A. and Al-Abdullah, S.A.M. (2019). Analysis of genetic stability using GGE-Biplot technique in wheat cultivars (*Triticum aestivum* L.) under different environmental conditions in basrah. *Plant Archives*. **19(2):** 3597-3604.

Al-Asadi, D.H.A. and Al-Abody, M.A.K. (2023). Analysis of path coefficient, correlations, variances and heritability of genotypes of maize (*Zea mays* L.). *Texas Journal of Agriculture and Biological Sciences*. **3(1):** 34-42.

Al-Asadi, E.Q.A. and Al-Abody, M.A.K. (2025). Genetic parameters of different oat genotypes using cluster analysis. *SABRAO Journal of Breeding and Genetics*. **57(1):** 86-93. https://doi.org/10.54910/sabrao2025.57.1.9.

Al-Gubouri, A.H.A. and Jumaa, A.E. (2018). The effect of genetic diversity of maize inbreds (*Zea mays* L.) by cluster analysis and assessment of half diallel hybrids. *Tikrit University Journal for Agricultural Sciences*. **18(1):** 1-13.

Al-Hamdany, F.M.A. and Al-Hadethi, R.Y.K. (2017). Effect of methods of addition of humic acid and levels of fertilizer recommendation on growth and yield of wheat. *Anbar Journal of Agricultural Sciences.* **15(2):** 372-381.

Ali, A.H., Sharif, Y.O.N.A., Raheem, A.H., Hussein, A.A.K. and Al-Mafarji, T.R.T. (2025). The effect of phosphorus levels on growth and yield components in sunflower (*Helianthus annuus* L.). *Agricultural Science Digest*. 1-6. doi: 10.18805/ag.DF-771.

Al-Mafarji, T.R.T., Aziz, J.M. and Zabin, K.M. (2026a). Study of nature of gene action, combining ability and heterosis in F2 half-diallel crosses for grain yield and its components in bread wheat. *Tikrit Journal for Agricultural Sciences*, **26(2):** 299-314. https://doi.org/10.25130/tjas.26.2.22.

Al-Mafarji, T.R.T., Abdullah, R.M., Zabin, K.M. and Hasan, S.A. (2026a). Genetic variability and stability of grain yield and related traits in barley genotypes across three seasons using Eberhart–Russell and GGE-Biplot analyses. *Egyptian Journal of Agronomy.* **48(2):** 751-765. https://doi.org/10.21608/agro.2026.450394.2007.

Al-Nuaimi, S. (1999). Fertilizers and Soil Fertility. Faculty of Agriculture, University of Mosul, Ministry of Higher Education and Scientific Research.

Al-Obaidi, O.N.J. and Al-Jubouri, J.M.A. (2023). Stability study of cotton genotypes cultivated in different environments. *IOP Conference Series: Earth and Environmental Science.* **1158(6):** 062030. https://doi.org/10.1088/1755-1315/1158/6/062030.

Al-Sadoon, A.W.M., Al-Qassi, E.K.K., Anees, A.H., Hussein, W.H. and El-Hosary, A.A.A. (2022). Determining the degree of kinship for the outward indicators of some Iraqi and Egyptian varieties and knowing their performance. *Journal of Plant Production.* **13(5):** 183-187.

Anees, A.H.A. and Al-Majmai, A.Y.M. (2020). Study of genetic and phenotypic variation in bread wheat (*Triticum aestivum* L.) for its productive indicators. *Journal of Plant Production*. **11(9):** 877-881.

Ayoob, M.H. (2019). Estimation of phenotypic variance components, heritability, average degree of dominance and genetic advance for early generations in bread wheat (*Triticum aestivum* L.). *Rafidain Journal of Science.* **28(1):** 11-23.

Aziz, J.M. and Sattar Ali, Z.A. (2024). Thermal accumulation for tasseling and silk stages and yield components for corn genotypes grown in planting dates during the autumn season. *IOP Conference Series: Earth and Environmental Science.* **1371(5):** 52091. https://doi.org/10.1088/1755-1315/1371/5/052091.

Azzam, M.R. and Al-Obaidi, M.O. (2018). Estimating some genetic parameters and genetic diversity by using cluster analysis for some traits in faba bean (*Vicia faba* L.). *Anbar Journal of Agricultural Sciences.* **16(2):** 3601-3612.

Cheyed, S.H. and El-Sahookie, M.M. (2011). Relationship between seed position on the cob, nitrogen level and harvesting date on maize seed quality. *Iraqi Journal of Agricultural Sciences.* **42(5):** 1-18.

Daemo, B.B. and 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. https://doi.org/10.1016/j.jafr.2024. 101287.

Granato, I.S.C., Fritsche-Neto, R., Resende, M.D.V. and Silva, F.F. (2016). Effects of using phenotypic means and genotypic values in GGE biplot analyses on genotype by environment studies in tropical maize (*Zea mays*). *Genetics and Molecular Research.* **15(4):** 1-11.

Hamdalla, M.S.H. (2011). Genetic diversity of sunflower based on cluster analysis. *Iraqi Journal of Agricultural Sciences.* **42(3):** 17-23.

Hanson, C.H., Robinson, H.F. and Comstock, R.E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza. *Agronomy Journal.* **48(6):** 268-272.

Hasan, S.A., Abdullah, R.M., Jaber, H.A. and Al-Mafarji, T.R. (2026). Genetic diversity of oat (*Avena sativa* L.) genotypes under different concentrations of potassium. *SABRAO Journal of Breeding and Genetics.* **58(1):** 285-293. https://doi.org/10.54910/sabrao2026.58.1.26.

Jumaa, R.F. and Madab, D.S. (2018). Estimation of genetic diversity using cluster, D^2 and principal component analyses of maize inbred lines (*Zea mays* L.). *Tikrit University Journal for Agricultural Sciences.* **18(4):** 39-50.

Khan, S.H., Aslam, M., Bibi, A. and Khan, H.Z. (2023). GGE biplot analysis for zinc quality and yield stability of exotic maize hybrids. *SABRAO Journal of Breeding and Genetics*. **55(1):** 268-278. https://doi.org/10.54910/sabrao2023.55.1.25.

Mahmood, E.T., Al-Mafarji, T.R.T., Al-Ethawi, M.B., Ahmed, K.K., Al-Ani, S.H.I. and Korolev, K.P. (2025). Correlation analysis of growth, yield and quality traits in maize (*Zea mays* L.) hybrids under different plant densities. *IOP Conference Series: Earth and Environmental Science.* **1538(1):** 12041. https://doi.org/10.1088/1755-1315/1538/1/012041.

Mauriya, A.K., Hashim, M., Verma, R.B., Kumar, P., Kumari, M., Sahu, R., *et al.* (2026). Evaluation of *rabi* maize-based intercropping system for augmenting productivity and profitability under irrigated conditions of Bihar. *Indian Journal of Agricultural Research,* **59(7):** 1131-1135. doi: 10.18805/IJARe.A-6213.

Mohsen, K.H. (2007). Response of Corn (*Zea mays* L.) to Different Levels of Nitrogen and Iron and Zinc Interaction Under South Iraq Conditions (Doctoral dissertation, University of Basrah, College of Agriculture).

Mousavi, S.M.N., Bojtor, C., Illés, Á. and Nagy, J. (2021). Genotype by trait interaction (GT) in maize hybrids on complete fertilizer. *Plants*. **10(11):** 2388. https://doi.org/10.3390/plants10112388.

Mousavi, S.M.N., Kith, K. and Nagy, J. (2019). Effect of interaction between traits of different maize genotypes under six fertilizer levels by GGE biplot analysis in hungary. *Progress in Agricultural Engineering Sciences*. **15(1):** 23-35. https://doi.org/10.1556/446.15.2019.1.2.

Omar, A. and Al-Layla, M. (2024). Estimation of genetic parameters, genotypic and phenotypic correlation, path and cluster analyses of quantitative traits in bread wheat genotypes under rain-fed conditions in Erbil. *Journal of Medicinal and Industrial Plant Sciences*. **2(3):** 23-34. https://doi.org/10.32894/MEDIP.24.3.

Punitha, B., Vindhiyavarman, P. and Manivannan, N. (2010). Genetic divergence study in sunflower (*Helianthus annuus* L.). *Electronic Journal of Plant Breeding.* **1(4):** 426-430.

Sharif, Y.O.N.A., Al-Abody, M.A.K., Muhammad, S.T. and Al-Mafarji, T.R.T. (2026). Genetic parameters and stability of soybean [*Glycine max* (L.) Merr.] cultivars under nano-phosphorus foliar fertilization levels. *Indian Journal of Agricultural Research.* **60(4):** 518-524. https://doi.org/10.18805/IJARe.AF-981.

Sharif, Y.O.N.A., Madab, D.S. and 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):** 52035. https://doi.org/10.1088/1755-1315/1371/5/052035.

Sneath, P.H.A. and Sokal, R.R. (1973). Numerical Taxonomy: The Principles and Practice of Numerical Classification. W. H. Freeman.

Walter, A.B. (1975). Manual of Quantitative Genetics (3rd ed.). Washington State University Press.

Williams, W.T. (1976). Pattern Analysis in Agricultural Sciences. Elsevier Scientific Publishing.

Yan, W. and Tinker, N.A. (2005). An integrated biplot analysis system for displaying, interpreting and exploring genotype × environment interaction. *Crop Science.* **45:** 1004-1016.