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Genetic Parameters and Stability of Soybean [*Glycine max* (L.) Merr.] Cultivars under Nano-phosphorus Foliar Fertilization Levels

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ABSTRACT

Background: Soybean is considered one of the most important economic crops; however, its productivity is influenced by genetic variability among cultivars and their response to phosphorus fertilization levels. The use of nano-phosphorus fertilizer contributes to enhancing growth efficiency and yield, which necessitates genetic evaluation of soybean cultivars under such fertilization conditions.

Methods: A field experiment was conducted in northern Kirkuk during the summer season of 2024 to estimate genetic parameters and analyze genetic relationships among six soybean cultivars (Iman, Taqa-2, Taqa-3, Lee-74, Shaima, Senaia-2) under six levels of nano-phosphorus foliar fertilizer (0, 1000, 2000, 3000, 4000 and 5000 ppm). The experiment was laid out in a randomized complete block design (RCBD) with a split-plot arrangement and three replications. Sowing was carried out on May 20, 2024.

Result: The data showed high estimates of genetic variance (σ^2G), environmental variances (σ^2E) and phenotypic variances (σ^2P), while broad-sense heritabilities reached a high of 91.65%. There were significant positive genetic correlations between seed yield and number of pods per plant (0.731**), number of seeds per pod (0.819**) and 1000 seed weight (0.956**). The variances and coefficients of variation for total seed yield per plant were 41073.86, 3740.47, 44814.33 and 8.70% and 8.33%, respectively. GGE Biplot analysis revealed that the genotype Lee-74 was the most stable and superior line for seed yield per plant. The results from hierarchical cluster analysis revealed that the pair of Iman and Shaima was the closest in genetic relationship (248.27) and the most distant between Taqa-2 and Lee-74 (68233.67).

Key words: Genetic correlation, Genetic parameters, Genetic stability, GGE-biplot, Nano-phosphorus fertilizer, Soybean cultivars.

INTRODUCTION

Soybean [*Glycine max* (L.) Merr.] is known to be among the most valuable strategic legume plants globally (Abed al-Kader *et al*., 2013) because of its high nutritional importance. It has a rich nutritional composition with a high protein concentration ranging from 30% to 50% and oil contents from 14% to 24% in addition to containing high qualities of essential amino acids and vegetable oils required in high amounts in the food industries. Additionally, as a component in crop rotation agriculture practices, the contribution of the soybean plants in increasing fertility in the soils through their capability to fix nitrogen from the atmosphere using nodules found in their roots helps in conserving the environment because they reduce the usage of nitrogenous fertilizer

In Iraq, on the other hand, the area under cultivation of soybean is very limited despite its significance across the globe. Based on data from the Food and Agriculture Organisation (FAO, 2023), the estimated area under cultivation within Iraq does not exceed 39 hectares, contributing insignificantly to the agricultural area of Iraq, with an average yield of production amounting to 875.5 kg/ha, which is well below the global average. That this particular commodity has very low levels of production within Iraq indicates many limitations such as soil nutrient content and the absence of agriculture technology.

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One of the limiting factors, which is a major concern for soybean productivity, is phosphorus deficiency. This is an essential element in plant growth, root, nodulation and energy transfer in legume crops (Alshamary *et al*., 2025). The efficiency of phosphorus nutrients using the normal fertilization processes is generally low because of phosphorus fixation in the soil, thereby pushing scientists to seek new methods in fertilizers, including nano-fertilizers

(Ghasil *et al*., 2025). Nano-phosphorus fertilizers are distinguished by their high efficiency in absorption, enhanced phosphorus translocation in plant tissues and minimized loss in the environment compared to normal fertilizers (Hassan *et al*., 2019). Evidence has shown that the use of nano-phosphorus fertilizers increased physiological processes, hence influencing growth and yield attributes (Liu and Lal, 2015).

Besides the optimized nutrient management, the evaluation of genetic variability and the estimation of genetic parameters within the improved genotypes is a basic part of crop improvement. Genetic analysis gives very useful information on the genetic control of traits, heritability and the stability of genotypes in unique environments and crop management (Falconer and Mackay, 1996; Madab *et al*., 2025). The stability of the genotypes is critical in testing the performance of the genotypes involving the new adopted crop management techniques, such as nano-phosphorus foliar fertilizer, aiming to identify stable and high-yielding genotypes (Khomphet, 2025).

Thus, the aim of this research study is to estimate some parameters of the genetics of the selected soybean cultivars at various phosphorus nanoparticle foliar fertilizer concentrations. The study results will help fill a gap in existing knowledge and serve to generate accurate scientific information on soybean improvement for the development of superior varieties for use in high-performance agriculture.

MATERIALS AND METHODS

In the summer growing season of 2024, a field experiment was conducted on a farmer's field situated within the Koldara area, Altun Kupri subdistrict, Dibis district in the North of Kirkuk province, Iraq. The experiment performed the task of estimating certain genetic parameters for genetic stability and analyzing the genetic divergence of six soybean [*Glycine max* (L.) Merr.] cultivars in Table 1, in response to the foliar application of six levels of nano-phosphorus fertilizer, 0, 1000, 2000, 3000, 4000 and 5000 ppm, respectively used symbol (E1, E2, E3, E4, E5, E6). The experiment was laid out in a split-plots design within a randomized complete block design (RCBD) with three replications.

Plots of 3 m length, with four rows in each experimental unit, were provided within the field. Seeds were to be sown along the rows, thus providing a spacing of 70 cm between rows and 20 cm between planting holes. Sowing was done for all experimental units on May 20, 2024. The experimental treatments were irrigated immediately after sowing, with subsequent irrigations applied as needed. Nitrogen fertilizer was supplied in the form of urea (46% N) at a rate of 200 kg N ha^{-1} (Ali, 2012), applied in two equal splits, the first after sowing and the second at the beginning of the flowering stage. Weed control was carried out manually by hoeing whenever necessary (Sharif *et al.,* 2024a; Jauhar and Al-Mafrajy, 2023).

The genetic parameters, including genetic variance (σ^2G), environmental variance (σ^2E) and phenotypic variance (σ^2P), were estimated according to the method described by Walter (1975). Broad-sense heritability ($h^2b.s\%$) was calculated following Hanson *et al*. (1956), while the coefficient of phenotypic variation was estimated according to Dudley and Moll (1969) and the coefficient of genotypic variation was calculated according to Burton (1952). The GGE biplot analysis was performed as described by Hamdalla *et al*. (2014), while hierarchical cluster analysis of the mean grain yield and its components for the six soybean cultivars was performed following Hamdalla (2011).

RESULTS AND DISCUSSION

Genetic correlation

The results presented in Table 2 indicate the values of genetic correlation coefficients between total seed yield and its yield components. There was a positive and highly significant correlation between total seed yield and the number of pods per plant, the number of seeds per pod and the 1000-seed weight, with coefficients of 0.731**, 0.819** and 0.956**, respectively. Additionally, a positive and highly significant correlation was observed between 100-seed weight and both the number of pods per plant

Table 1: Shows the studied cultivars and fertilizer levels in the environments (Test environments).

Symbol	Cultivar	Origin	Source of seeds
G1	Iman	Iraq	General Company for Industrial Crops, Ministry of Agriculture
G2	Taqa-2	Iraq	Iraqi Atomic Energy Organization
G3	Taqa-3	Iraq	Iraqi Atomic Energy Organization
G4	Lee-74	USA	General Company for Industrial Crops, Ministry of Agriculture
G5	Shaima	Iraq	General Company for Industrial Crops, Ministry of Agriculture
G6	Senaia-2	Iraq	General Company for Industrial Crops, Ministry of Agriculture

Table 2: Genetic correlation coefficients among the studied traits.

Studied traits	Number of pods per plant	Number of seeds per pod	100-seed weight (g)
Number of seeds per pod	0.796**		
100-seed weight (g)	0.712**	0.852**	
Seed yield (kg ha^{-1})	0.731**	0.819**	0.956**

and the number of seeds per pod, with coefficients of 0.712** and 0.852**, respectively. Moreover, there was a positive and highly significant correlation between the number of seeds per pod and the number of pods per plant, which amounted to 0.796**.

These findings are consistent with those reported by Mehra *et al.* (2020), Dutta *et al*. (2021), Verma *et al*. (2021), Alizawee *et al.* (2025) and Mahmood *et al.* (2025), Khomphet, (2025). The reason for this strong correlation between seed yield and its components can be attributed to the effects of genetic factors as well as the influence of nano-phosphorus fertilization.

Genetic and environmental variances, heritability and phenotypic and genotypic coefficients of variation

The data presented in Table 3 indicated that the genetic variance components are greater than the environmental variance components for all traits studied, which confirmed the importance of genetic components in the emergence of these traits. Such high genetic variation is due to the association between genetic factors and environmental factors (in this case, nano-phosphorus fertilization treatment). The estimates of genetic variation for yield and its components (seeds per pod, number of pods per plant, weight of 100 seeds and seed yield) were 0.01962, 1278.167, 1.577477 and 41073.86, respectively (Al-Jubouri *et al*., 2024; Hindi *et al*., 2025). This made clear that the genetic stability is high due to the genes responsible for controlling these characters, which in turn caused high broad sense heritability estimates for the studied traits.

The values of environmental variance were 0.00043748, 7.04524, 0.05323167 and 3740.471, respectively, whereas phenotypic variance values for traits were 0.020058, 1285.212, 1.630709 and 44814.33, respectively. Broad-sense heritability percentages for traits were 97.81%, 99.45%, 96.73% and 91.65%, respectively (Kuswantoro, 2019; Al-Mafarji *et al*., 2024). The high broad-sense heritability percentages for traits suggest that those traits are determined

Apart from this, the phenotypic coefficient of variation was greater than the genotypic coefficient of variation and their values were 6.985425, 44.23141, 11.59175 and 8.699609, respectively, against genotypic coefficients of variation of 6.908825, 44.11001, 11.40098 and 8.328639, respectively. The above findings have been supported by Dutta *et al*. (2021) and Verma *et al*. (2021). The phenotypic and genetic variance values were particularly high for grain yield, which positively influenced the high broad-sense heritability estimate of 91.65% for this trait, indicating that the environmental influence was relatively limited compared to the genetic effect. This agrees with the conclusions reported by Sharif *et al*. (2024b); Dutta *et al*. (2021); Verma *et al*. (2021) and Mehra *et al*. (2020).

Accordingly, the traits of the number of branches per plant and the number of pods per plant showed high genotypic coefficients of variation, suggesting greater opportunities for successful selection for these traits, reflecting the substantial genetic variation present among them.

GGE-biplot stability analysis

The stability of the studied cultivars was tested across environments represented by different levels of nano-phosphorus fertilizer (0, 1000, 2000, 3000, 4000 and 5000 ppm), labeled as E1, E2, E3, E4, E5 and E6, respectively, using the GGE-Biplot technique to study the genotype × environment interaction. Fig 1 shows the relationship among the studied environments, where environments E3 and E5 were identified as the most desirable, having the highest PC1 values and the lowest PC2 values. An environment is considered ideal when it has a high capacity to discriminate among cultivars (high PC1) and is representative of all tested environments (PC2 close to zero) Habtegebriel and Abebe, (2023). Environments E3 and E5 contributed to increased grain yield, unlike environments E4, E2 and E1. PC1 accounted for 79.8% of the total variation, emphasizing the effect of environments on cultivar performance, whereas PC2 accounted for 16.1% of the total variation. The cultivars above zero on the positive axis of PC1 were favorably affected towards high grain yield, whereas near zero on the positive axis of PC2 were less

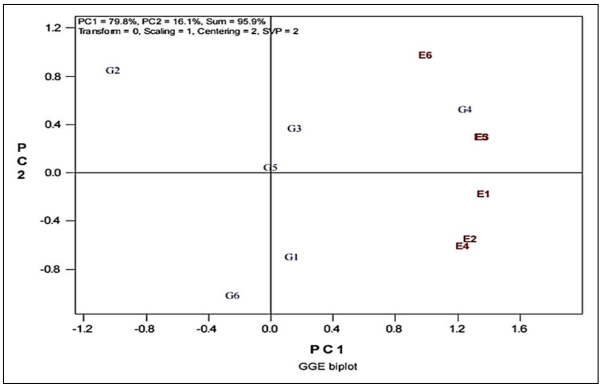


Fig 1: Relationship between genotypes and studied environments.

Table 3: Estimation of genetic, environmental and phenotypic variations and the degree of heritability in the broad sense and the coefficients of phenotypic and genetic variation of the studied traits of the soybean crop.

Traits	σ^2G	σ^2E	σ^2P	$h^2_{b.s}$	PCV (%)	GCV (%)
Number of seeds per pod	0.01962	0.00043748	0.020058	97.81	6.985425	6.908825
Number of pods per plant	1278.167	7.04524	1285.212	99.45	44.23141	44.11001
100-seed weight (g)	1.577477	0.05323167	1.630709	96.73	11.59175	11.40098
Seed yield (kg ha^{-1})	41073.86	3740.471	44814.33	91.65	8.699609	8.328639

productive. Cultivar G4 was observed to be the most productive cultivar.

The relationship between the preferred cultivars for different environments is depicted in Fig 2. Cultivar G4 preferred environments E3 and E5, as environments E3 and E5, as well as cultivar G4, were in the same quarter of the biplot diagram defined by similar scores of PC1 and PC2. The best-suited environment for cultivar G4 would be E4, showing genetic stability of the cultivar across different environments.

Fig 3 above illustrates the stability of a cultivar using the Average Environment Coordination (AEC) technique developed by Habtegebriel and Abebe, (2023). This graph is marked by two distinct lines. The first line marked by a red color passes through the origin, known as the average environment axis, where it reflects high trait expression in the direction of the arrowhead. Cultivar G4 contributed more towards yield, as well as mean performance. The other line, marked blue, is the stability axis, where arrows in both ends point perpendicular to the average environment axis. Cultivars close to the average environment axis contributed towards high stability, while those farther away contributed towards low stability. G4 contributed towards high stability, followed by G2, which contributed towards low stability.

Fig 4 above shows the relationships between the studied cultivars. The grain yield was highest in environments E3, E5 and other environments in cultivar G4, while the other environments have relatively low stability. The rays that originate from the origin indicate environmental vectors, which show the extent to which environments are correlated to each other. The cosine value between any pair of environmental vectors shows how environments are correlated, while the length of the vectors shows how environments can discriminate stable genotypes. The longer the vector, the better it can discriminate stable genotypes. The performance of the other environments was also observed, where those with longer projections performed above average, while those with shorter projections performed at or around average levels. The grain yield was highest in G4, while that of G2 was lowest.

Fig 5 identifies the ideal genotype across the studied environments. An ideal genotype combines high yield with high stability and suitability across diverse environments. The farther the positive PC1 values from the origin, the higher the yield and stability of the genotype, while longer

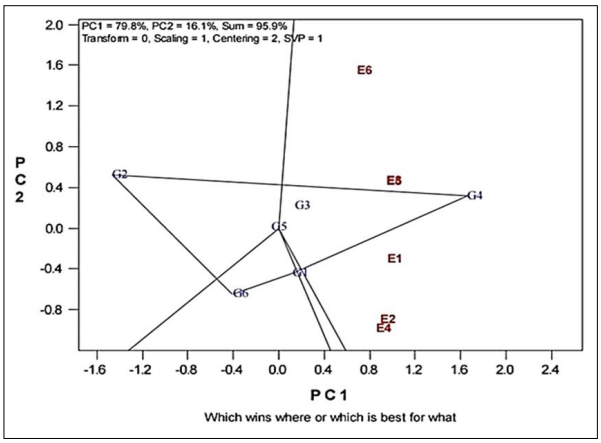


Fig 2: Genotype preferences for each environment.

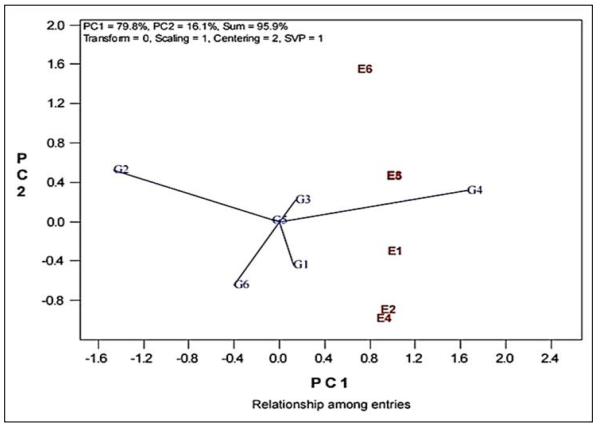


Fig 4: Relationships among the studied genotypes.

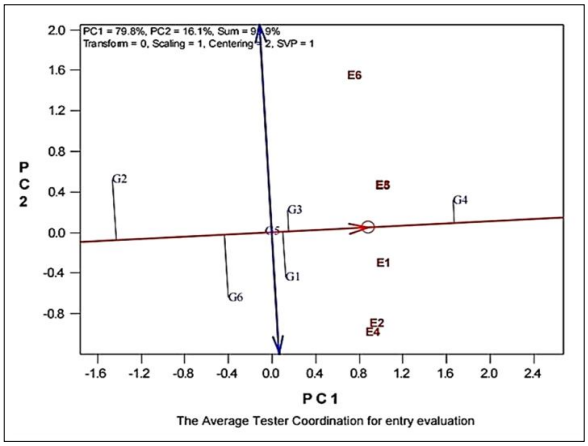


Fig 3: Stability of the studied genotypes across environments.

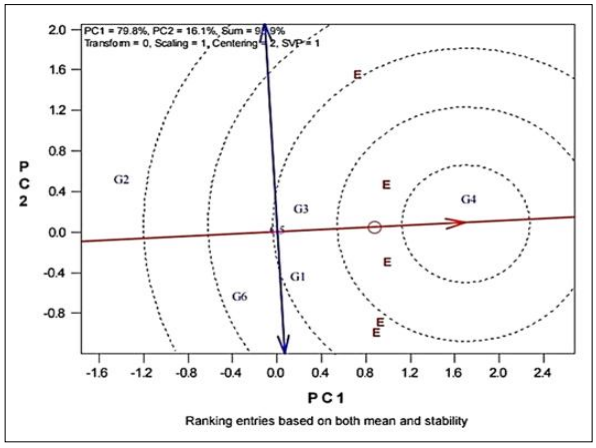


Fig 5: The ideal genotype across the studied environments.

PC2 vectors indicate lower yield and stability. The biplot analysis showed that cultivar G4 was the ideal genotype, combining high yield and stability, positioned in the first group represented by a concentric circle in the biplot. The second group included cultivar G3, which was closest to the ideal genotype.

Fig 6 shows the relationship among studied environments The most ideal environment will be characterized by high ability to distinguish among cultivars (high PC1) and will be well representative (close to PC2=0) (Habtegebriel and Abebe, 2023; Singamsetti *et al*., 2024). Environments E3 and E5 were deemed to be the most ideal environments, performing well on grain yield among all cultivars, followed by E1 that was similar in terms of grain yield, but E4 was the worst on grain yields among all cultivars. Cultivar G4 was most consistent across the four environments, outyielding all on grain yield. The most ideal environments were E3 and E5, while the least ideal were E2 and E4, which were farthest from the center of the concentric circles. The influence of environments on cultivars was well demonstrated using the PC1 and PC2 axes, establishing that G4 was the most ideal genotype.

The result from the GGE-Biplot showed efficiency in the search for the most stable genotypes over the environment and in the interpretation of the relationships among genotypes and the environment. These results agree with the findings from Ikeogu and Nwofia (2013); Carvalho *et al*. (2021); Al-Abody *et al*. (2019) and Obua *et al*. (2024), which showed that this method is effective in the search for stable genotypes and optimal environments.

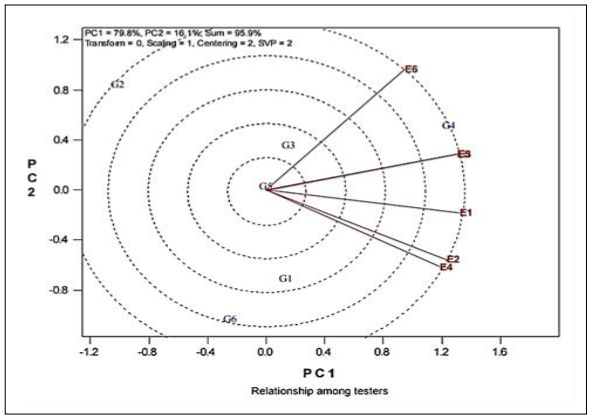


Fig 6: Relationships among the studied environments.

Hierarchical clustering analysis

Hierarchical cluster analysis was conducted based on the yield characters and their components for the varieties to establish their genetic similarity or divergence depending on their reaction to environmental factors (concentrations of nano-phosphorus fertilizer). This procedure is based on the measure of the distance showing the degree of divergence and the grouping based on performance and genetic make-up of the varieties. Genetic similarity between the varieties was established based on the degree of their genetic proximity as shown in Table 4 and Fig 7 showing the genetic similarity (difference) between the studied varieties.

The data showed that the genetic distance between the crops Iman and Shaima was 248.270, indicating that they have a close genetic relation, possibly because they possess similar genetic materials, meaning that crops from different origins may not always have large genetic distances. The fact that Iman and Shaima have a close genetic relation may be because they possess identical desirable genes, which would be valuable in breeding. This means that among the two crops that have a close genetic relation, one can replace the other in situations where one is lost, while breeding among them should not take place.

On the other hand, the highest genetic distance was noticed between Taqa-2 and Lee-74 cultivars (68233.667), representing the existence of a high degree of divergent genetic structures that could be effectively utilized through hybridization programs and subsequent selection to obtain superior cultivars adapted to the environmental conditions of this study. This statistical method could be considered an efficient and alternative method to biotechniques whenever the latter are unavailable or unattainable. The hierarchical

Table 4: Genetic divergence and kinship among six soybean cultivars according to cluster analysis.

Cultivars	Squared euclidean distance					
	1:Iman	2:Taqa -2	3:Taqa -3	4:Lee -74	5:Shaima	6: Senaia-2
1:Iman	0.000	15537.549	349.289	18916.089	248.270	1989.858
2:Taqa -2	15537.549	0.000	17120.897	68233.667	12854.295	6410.451
3:Taqa -3	349.289	17120.897	0.000	17074.153	335.958	2822.358
4:Lee -74	18916.089	68233.667	17074.153	0.000	21856.530	33045.167
5:Shaima	248.270	12854.295	335.958	21856.530	0.000	1213.676
6: Senaia-2	1989.858	6410.451	2822.358	33045.167	1213.676	0.000
Stage	Cluster combined			Coefficients		
	Cluster 1	Cluster 2				
1	1	5		248.270		
2	1	3		342.624		
3	1	6		2008.631		
4	1	2		12980.798		
5	1	4		31825.121		

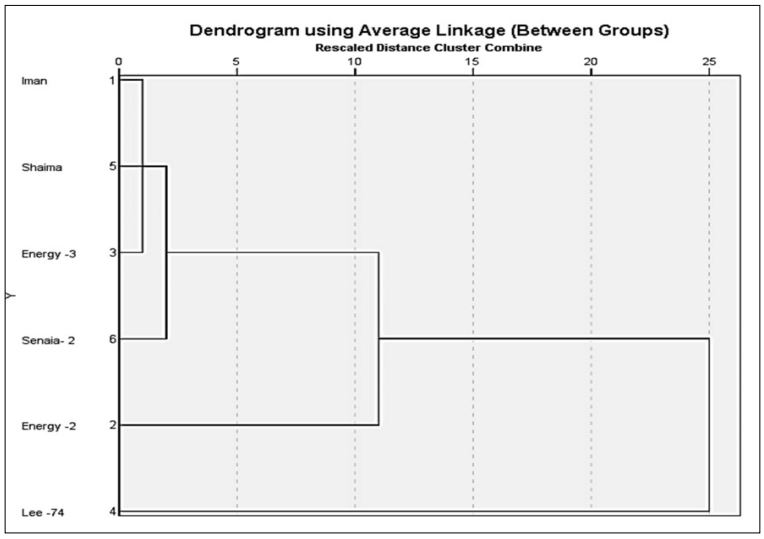


Fig 7: Dendrogram of the genetic relationships among four soybean cultivars based on similarity values using cluster analysis.

clustering method was effective in interpreting genetic relationships effectively to represent complex interactions of studied cultivars and enables comparison of them easily. Therefore, this supports genotypes with maximal genetic similarity or differences in addition to managing genetic resources effectively. The findings of this study are consistent with Khalil *et al*. (2020); Ragade *et al*. (2024); Chiemeke *et al*. (2024) and Al-Asadi and Al-Abody (2025), since all mentioned that this method was quite efficient to differentiate genetically divergent genotypes effectively.

CONCLUSION

The study demonstrated that the six evaluated soybean cultivars exhibited high genetic variability in yield and its components under the influence of nano-phosphorus foliar fertilization, with high broad-sense heritability estimates indicating the potential for direct selection improvement. The GGE-Biplot analysis identified cultivar Lee-74 (G4) as the most productive and stable across environments, particularly under E3 (2000 ppm) and E5 (4000 ppm) conditions. Hierarchical cluster analysis revealed close genetic proximity between Iman and Shaima and pronounced divergence between Taqa-2 and Lee-74, providing opportunities to exploit this genetic distance in hybridization programs. Therefore, it is recommended to adopt Lee-74 for cultivation under the agro-climatic conditions of northern Iraq, to utilize genetically distant parents in breeding programs for improving yield and stability and to expand research on nano-phosphorus applications in other legume crops to enhance sustainable productivity.

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.

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