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Evaluation of the Performance and Productivity of Triticale (X. *Triticosecale Wittmack*) Genotypes under Foliar Super Nano-Fertilizer Application

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ABSTRACT

Background: Triticale (X. *Triticosecale Wittmack*) is an important cereal crop characterized by its potential for high grain yield and adaptation to diverse environmental conditions. Understanding the genetic variability, heritability, genetic advance, stability and divergence among triticale genotypes is essential for identifying superior genotypes for breeding programs. The present study aimed to evaluate the genetic parameters and performance stability of four triticale genotypes under different concentrations of super nano fertilizer.

Methods: The field experiment was conducted during the cold winter months of 2024-2025 at the Field Crops Department, Agriculture College of, Karmat Ali site, Basrah University, Iraq, using silty loam soil. Four triticale genotypes (Mohannad, Amal-7, Liron-5 and Farah) were evaluated under three concentrations of super nano fertilizer (0, 4 and 6 g L^{-1}), applied by foliar spraying at the tillering and beginning of flowering stages. The experiment was conducted using a randomized complete block design with three replications. Genetic, phenotypic and environmental variances, broad-sense heritability, genetic and phenotypic coefficients of variation, genetic advance, stability and genetic divergence were estimated.

Result: The estimated genetic, environmental, phenotypic, 0.369182, 0.011310 and 0.380492, respectively. Broad-sense heritability for grain yield was high (97.02%), while the phenotypic and genotypic coefficients of variation were 18.11172% and 17.84051%, respectively. The highest genetic advance values were recorded for flag leaf area (55.98) and Spikes number m^{-2} (50.03). Stability analysis identified Amal-7 (G2) as the most desirable genotype, combining high grain yield with superior genetic stability. Genetic divergence analysis revealed the smallest genetic distance between Liron-5 and Farah (282.437), indicating greater genetic similarity, whereas the largest genetic distance was observed between Amal-7 and Farah (35079.583), indicating substantial genetic divergence. The results demonstrated considerable genetic variability among the evaluated triticale genotypes, with high heritability for grain yield and substantial potential for genetic improvement. Among the tested genotypes, Amal-7 (G2) exhibited superior yield performance and genetic stability and may therefore be considered a promising genotype for cultivation and future triticale breeding programs.

Key words: Genetic parameters, Genotypes, Super nano-fertilizer, Triticale.

INTRODUCTION

Among the crops of high importance belonging to the Poaceae family is (X. *Triticosecale Wittmack*). Triticale grains are generally richer in vitamins and minerals than wheat and rye, with strong nutritional value and a high protein content, particularly the amino acid lysine. Although bread made from triticale is lower in quality, it has greater nutritional value than wheat bread. The grains are associated with improved bone growth and digestion, better blood sugar control and stimulated blood circulation. They also contain phenols and dietary fiber. Cereals contain (3.7%) lysine and (11.5-22.5%) other proteins (Sadeeq *et al.*, 2019; Kamanova *et al.*, 2023). Its genetic makeup makes triticale suitable for cultivation under diverse environmental conditions, while varieties differ in their growth and yield characteristics (Al-Zubaidi, 2022). Ultimately, productivity depends on suitable environmental conditions, crop maintenance, growth factors and soil. One of the most important practices is the application of nano-fertilizers, including super-nano fertilizer. These fertilizers supply plants with essential elements, which can increase production and improve quality. Selecting new varieties and evaluating their responses to different concentrations of nano-super fertilizer are also important, particularly because these varieties can contribute to higher yields in

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crops such as Triticale Crop. Their responses vary according to each variety's genetic capacity to convert manufactured nutrients from the source to the destination. Foliar feeding is another important factor for achieving the highest yield at present, increasing production and reducing pollution associated with fertilizer use (Hassan *et al.*, 2019; Al-Abody, 2015). Materials that raise yield without damaging the environment are needed and nano-phosphate fertilizer is among the most significant options. This experiment was conducted because few studies have estimated specific genetic characteristics, examined stability and genetic divergence and assessed the responses of four Triticale Crop varieties to three different amounts of nano-super fertilizer.

MATERIALS AND METHODS

An experiment was carried out in silty loam soil during winter 2024-2025 at the "Karma Ali" site - the Department of Field Crops, College of Agriculture, Basra Governorate. Selected genetic parameters have been studied for the following Triticale cultivars (genotypes): "Mohannad", "Amal-7", "Leron-5" and "Farah". Also, the effect of three concentrations of "nano-super fertilizer" (0, 4 and 6 g/L) was studied (Table 1). Factorial experiment in RCBD design was conducted, where three replications were used and treatments were randomly allocated to blocks. The field was divided into experimental units (plots) with the size of 1.5 m × 2 m, containing 10 rows with the length of 1.5 m and 20 cm distance between the rows. Sowing was performed throughout all experimental units on November 1, 2024. The plots were irrigated right after sowing and irrigation was continued when necessary. Nano-fertilizer was used for foliar sprays twice in the early morning hours: once at the beginning of flowering and once in the vegetative growth stage. "Zahi" solution was used as the spreading agent to decrease the surface tension of water, while in the control treatments-distilled water was sprayed. The amount of the nitrogen fertilizer was urea (with 46% of nitrogen) at the level of 120 kg N/ha; the fertilization was conducted in two stages: the first one 15 days after planting and the second - in the elongation stage of the plants (Abdelaal *et al.*, 2019). The phosphorus fertilizer (as P_2O_5) in the amount of 100 kg/ha was used before planting based on the results of soil analysis of its physical and chemical characteristics (Table 2) (Al-Morshedy, 2023). Manual weeding was done when necessary and the irrigation was provided according to the needs of the crop. Genetic parameters that were estimated in this experiment include genotypic variance (σ^2G), environmental variance (σ^2E) and phenotypic variance (σ^2P) (Walter, 1975). The formula of broad-sense heritability estimation (h^2b.s. %) proposed by Hanson *et al.* (1956) was used. Phenotypic coefficient of variation was estimated using the formula developed by Dudley and Moll (1969) and genotypic coefficient of variation - with the help of the formula by Burton (1952). Moreover, genetic stability was studied using the methods developed by Burton (1952), El-Sahookie (1985), Finlay and Wilkinson (1963) and Eberhart and Russell (1966). Also, the estimation of genetic divergence was conducted in four varieties of "tortilla" crops based on mean grain yield and its components, as described by Hamdalla (2011).

Calculation of genetic parameters:

Calculation genetic, environmental and phenotypic variances:

Variations of genetic and phenotypic were by Walter, (1975) as following:

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

$$\sigma^2E = Mse$$

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

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

Heritability was Estimated using the following method, (Hanson *et al.,* 1956):

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

Where,

$h^2_{b.s.}$ = Broad sense-heritability.

σ^2G = Trait genetic variance.

σ^2P = Trait phenotypic variance.

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

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

Hierarchical cluster analysis

Hamdalla (2011) explains that the Agglomerative approach was applied to Triticale Crop genetic patterns are divided

Table 1: Studied genotypes and fertilizer concentrations in the environments (test environments).

Genotypes	Symbol	Genetic ratios	Fertilizer concentrations (Environments)	Symbol
Mohannad	G1	Local check	0 g L^{-1}	E1
Amal-7	G2	Individual selection from second-generation hybrids	4 g L^{-1}	E2
Liron-5	G3	LIRON2/5/DIS B5/3/SPHD/PVN//YOGUI_6/4/KER_3/6/ BULL_10/CTSS02B00419S-10Y-5M-3Y-4M-2Y-OM	6 g L^{-1}	E3
Farah	G4	Local check		

into groups, making the data easier to use in cluster analysis (Sneath and Sokai, 1973; Williams, 1976). The process consists of several stages, beginning a straightforward technique (Sneath and Sokai, 1973). Based on the preceding formula, the resulting values indicate the degree of similarity between the sum rates across the matrix of proximities produced in the first stage using SPSS version - 22.

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

RESULTS AND DISCUSSION

The results in Table (3) indicate the influence of genotypes on the studied traits. The genotype Liron-5 performed best, yielding the greatest plant height 95.09 cm. The genotype Amal-7 excelled in several parameters, producing the largest flag leaf area 41.12 cm^2, the highest spikes number 424.90 m^{-2}, the greatest grains number in spike 45.493 and the highest grain yield 4.380 t ha^{-1}. Meanwhile, the genotype Mohannad recorded the highest weight 1000 grains 36.40 g. Conversely, the genotype Farah showed the lowest mean values for all the studied traits; this may be attributed to genetic differences among the Genotypes, a finding consistent with AL-Asadi and AL-Abody, (2025); Laouar and Hafsi, (2024).

The results presented in Table (4) indicate that the 6 g L^{-1} concentration was superior, yielding the highest mean values for all studied traits specifically 91.11 cm, 32.87 cm^2, 330.00 m^{-2}, 40.358, 33.31 g and 3.987 t ha^{-1}, respectively. Conversely, the 0 g L^{-1} concentration recorded the lowest mean values for all studied traits. This can be attributed to the role of nano-fertilizer in enhancing the studied characteristics and producing higher mean values, given the significant function it performs. This finding is consistent with AL-Abody *et al.* (2020).

The results in Table (5) indicate an interaction effect between the genotypes and the concentrations of nano-fertilizer. The genotype Amal-7, at a concentration of 6 g L^{-1}, outperformed the others, yielding the highest mean values for most of the studied traits; specifically, it recorded the highest averages for flag leaf area, spikes number, grains number in spike and grain yield 44.32 cm^2, 441.50 m^2, 48.260 and 4.790 t ha^{-1}, respectively. This can be attributed to the interactive effect between the genotypes and the nano-fertilizer concentrations, a finding that aligns with (AL-Abody *et al.,* 2020).

Table 2: Some chemical and physical properties of field soil before planting.

Traits		Values	Units
Soil reactivity level (pH)		7.11	-
Electrical conductivity (E.C)		7.13	dS m^{-1}
Organic matter		10.2	g kg^{-1}
Items prefab	Nitrogen	51.11	mg kg^{-1} Soil
	Phosphorus	5.25	
	Potassium	135	
Soil separates	Sand	363	g kg^{-1} Soil
	Silt	541	
	Clay	96	
Texture	Silty loam		

Analysis of variance

According to Table (6), the effects of the four genotypes were all highly significant. Differences in the traits under study may be attributed to the inherited characteristics of these genotypes and their sensitivity to environmental conditions. Similar results were reported by (Al-Abody, 2020; Sheera, 2023; Al-Samarraie, 2024), who found highly significant effects among genotypes. The concentrations of super nano fertilizer also had highly significant effects on all studied traits, with values of 607.921**, 107.3343**, 6561.50**, 154.2586**, 94.6992** and 5.13670**, respectively. Applying super nano fertilizer may activate enzymes responsible for essential plant functions, thereby improving growth characteristics. These results agree with

Table 3: Effect of genotypes, in the studied traits.

Genotypes	Plant height (cm)	Flag leaf area (cm^2)	Spikes number (m^{-2})	Grains number in spike	Weight of 1000 grains(g)	Grain yield (t ha^{-1})
Mohannad	82.41	34.30	339.87	41.371	36.40	3.343
Amal-7	83.21	41.12	424.90	45.493	28.93	4.380
Liron-5	95.09	25.45	246.97	34.933	35.25	3.187
Farah	73.26	19.52	238.57	27.643	22.66	2.713
L.S.D (0.05)	2.230	0.914	5.029	0.4467	0.739	0.1040

Table 4: Effect of super nano fertilization concentrations, in the studied traits.

Fertilization (g L^{-1})	Plant height (cm)	Flag leaf area (cm^2)	Spikes number (m^{-2})	Grains number in spike	Weight of 1000 grains (g)	Grain yield (t ha^{-1})
0	77.02	26.93	286.00	33.388	27.77	2.697
4	82.35	30.49	321.73	38.335	31.35	3.532
6	91.11	32.87	330.00	40.358	33.31	3.987
L.S.D (0.05)	1.931	0.791	4.355	0.3868	0.640	0.0900

(Devi *et al.*, 2022 Al-Samarraie, 2024). The interaction between the two study factors genotypes and super nano fertilizer concentrations was highly significant for every trait examined, with values of 140.975**, 4.3246**, 1047.07**, 0.7031**, 7.0197** and 0.09577**, respectively. This occurred because the phenotypic variance of the genetic compositions reflected the interplay of genetic and environmental variation. These findings are consistent with (Khaskheil *et al.*, 2017; Al-Azzawi, 2020; Al-Samarraie, 2024).

Table (7) showed that the genetic variation values for the plant traits listed were 59.68692, 68.10361, 5783.652, 45.61822, 40.25681 and 0.369182, respectively. These values reflect the magnitude of genetic variation and its importance in the selection process, which results from the variance of genetic factors. For environmental variation, the highest values for plant height and number of spikes m^2 were 5.202 and 26.46, respectively. The phenotypic variation values were 64.88892, 68.97731, 5810.112, 45.82692,

Table 5: Effect of interactions between genotypes and super nano fertilization concentrations, in the studied traits.

	0	4	6	0	4	6
	Plant height (cm)			**Flag leaf area (cm^2)**		
Mohannad	76.22	83.55	87.46	32.25	34.19	36.47
Amal-7	80.27	83.13	86.24	36.42	42.61	44.32
Liron-5	81.46	89.55	114.26	21.81	25.29	29.24
Farah	70.11	73.18	76.49	17.23	19.87	21.45
L.S.D (0.05)		3.862			1.583	
	Spikes number (m^{-2})			**Grains number in spike**		
Mohannad	286.30	353.80	379.50	37.403	42.250	44.460
Amal-7	394.40	438.80	441.50	41.440	46.780	48.260
Liron-5	231.50	252.80	256.60	31.520	35.850	37.430
Farah	231.80	241.50	242.40	23.190	28.460	31.280
L.S.D (0.05)		8.710			0.7736	
	Weight of 1000 grains(g)			**Grain yield (t ha^{-1})**		
Mohannad	32.35	36.56	40.29	2.560	3.540	3.930
Amal-7	25.73	29.47	31.58	3.770	4.580	4.790
Liron-5	31.43	35.75	38.58	2.410	3.430	3.720
Farah	21.57	22.62	23.79	2.050	2.580	3.510
L.S.D (0.05)		1.280			0.1801	

Table 6: Analysis of variance for genotypes, super nano fertilization concentrations and their interactions in the studied traits.

S.O.V.	D.F.	Plant height (cm)	Flag leaf area (cm^2)	Spikes number (m^{-2})	Grains number in spike	Weight of 1000 grains (g)	Grain yield (t ha^{-1})
Replicates	2	19.545	5.8102	1509.83	24.9700	8.7723	0.16568
Genotypes	3	721.445**	818.1170**	69430.28**	547.6273**	362.8823**	4.44149**
Super nano	2	607.921**	107.3343**	6561.50**	154.2586**	94.6992**	5.13670**
Genotypes × Super nano	6	140.975**	4.3246**	1047.07**	0.7031**	7.0197**	0.09577**
Error	22	5.202	0.8737	26.46	0.2087	0.5710	0.01131

ns, * and **: Non-significant, significant at 0.05 and 0.01 probability level, respectively.

Table 7: Estimates of genetic parameters for all studied traits of the triticale crop.

Traitsgenetic parameter	Plant height (cm)	Flag leaf area (cm^2)	Spikes number (m^{-2})	Grains number in spike	Weight of 1000 grains (g)	Grain yield (t ha^{-1})
σ^2G	59.68692	68.10361	5783.652	45.61822	40.25681	0.369182
σ^2E	5.202	0.8737	26.46	0.2087	0.5710	0.01131
σ^2P	64.88892	68.97731	5810.112	45.82692	40.82781	0.380492
$h^2_{b.s}$ (%)	91.98	98.73	99.54	99.54	98.60	97.02
PCV (%)	9.648011	27.59451	24.38566	18.1198	20.73893	18.11172
GCV (%)	9.253203	27.41919	24.33007	18.0785	20.5934	17.84051
GA (%)	18.29	55.98	50.03	37.13	35.80	36.00

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, GA(%): Genetic advance.

40.82781 and 0.380492, respectively. Broad-sense heritability was high for all traits, indicating that the study Features could be improved and that this improvement could be passed on to subsequent generations. The broad-sense heritability values also reflected greater genetic variation than environmental variation across all the studied traits, providing an opportunity to select for their improvement. In general, comparing the values shows that genetic variation was higher for all traits, a useful feature. Because their environmental impact was small, plant breeders should collect genetic material directly for breeding, development and selection of superior features. This agrees with AL-Abody, (2019); Mahmood *et al.* (2025). The flag leaf area, number of spikes m^{-2} and 1000-seed weight had the highest phenotypic and genetic coefficients of variation; plant height had the lowest. These findings are consistent with Al-Abody *et al.* (2020); Omar and Al-Layla, (2024); AL-Asadi and AL-Abody, (2025); Al-Mafarji *et al.* (2026a); Hindi *et al.* (2025) and Hindi *et al.* (2026). Based on these results, the traits can be selected because there were high significant differences. Flag leaf area and spike number m^{-2} were measured to estimate expected genetic improvement (GA%), expressed as a percentage. The highest values were recorded for these traits, reaching 55.98% and 50.03%, respectively. This suggests that flag leaf area and spike number m^{-2} are suitable for selection and may produce substantial genetic progress. Plant height, by contrast, showed the lowest genetic improvement, at 18.29. These results are consistent with the findings of Al-Samarraie (2024).

Stability analysis

The findings in Table 8 show differences in mean yield (YI) among the varieties studied. G2 produced the highest grain yield, at 4.380 t. ha^{-1}, because of differences in the genetic compositions of the genotypes, consistent with Al-Mafarji *et al.*, (2026b), Al-Asadi and Al-Abody (2025), Across the genetic-stability analysis and all methods examined, genotype G2 was identified as genetically stable while also producing the higher yield. According to (El-Sahookie, 1985), its H% was 87.703; under the method of (Finlay and Wilkinson, 1963), its bi value was 1.041. Using the method of (Eberhart and Russell, 1966), S^2di was (0.003), while the method of (Wricke, 1962) gave a Wi value of 0.011. Under the Geometric Adaptability Index method, the GAI value was 4.357. We conclude that genetic stability analysis identified genotype G2 as the ideal, genetically stable structure (Mesfin and Tulu, 2024; Al-Samarraie, 2024; Al-Zaidi, 2024). These findings also confirmed the usefulness of genetic stability analysis methods for detecting the ideal, genetically stable genetic structure.

GGE - Biplot stability

Nano-super fertilizers were foliar-applied to the genotypes at three different levels (0, 4 and 6 g L^{-1}) that correspond to environments E1, E2 and E3, respectively. Differences between the performance of genotypes and their responses under various conditions were observed within these environments. Fig (1) shows how the genotype responds to the environmental conditions by showing the connection between the genotypes and the environments where differences in the responses to the fertilizer levels are shown. The ideal genotype under the studied environments is shown in Fig (2). According to this figure, G2 genotype was found to be the closest to the ideal genotype due to its superior performance and desirable genetic composition. Fig (3) shows genotype preference for each environment that indicates differences in the responses of genotypes and the most suitable genotypes under the different concentrations of fertilizers. The polygon view shows the performance and adaptation of genotypes to the environments. As shown in Fig (4), the stability of the

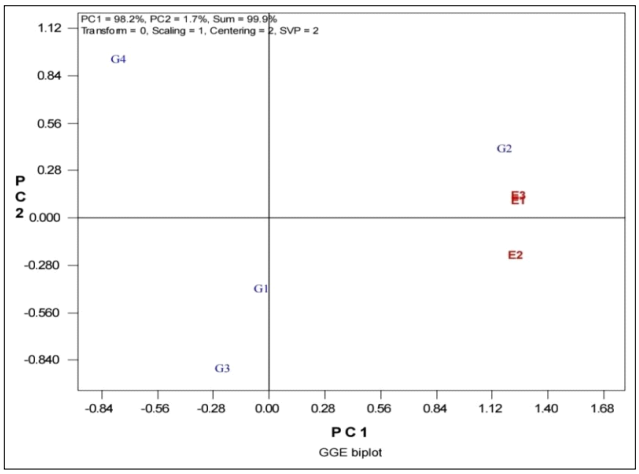


Fig 1: Relationship between genotypes and studied environments.

Table 8: Mean grain yield and estimates of stability parameters for grain yield of four genotypes in three environments.

Genotypes	YI mean yield	H% (EL-Sahookie, 1985)	Bi (Finlay and Wilkinson, 1963)	S^2di (Eberhart and Russell,1966)	Wi (Wricke,1962)	GAI (Geometric adaptability index)
G1	3.343	78.888	1.076	0.012	0.045	3.290
G2	4.380	87.703	1.041	0.003	0.011	4.357
G3	3.187	78.408	0.813	0.016	0.021	3.133
G4	2.713	72.761	1.070	0.109	0.116	2.648

Yi: Yield mean over all environments; bi: coefficient of regression; S^2di: Sum of squares deviation from regression; Wi; GAI.

genotypes under different environments was confirmed and G2 genotype showed the most desirable genotype stability. Among all environments E3 (6 g L^{-1}) was found to be the most favourable environment for the genotype performance. These results were in accordance with Daemo and Ashango (2024) and Sharif *et al.* (2026).

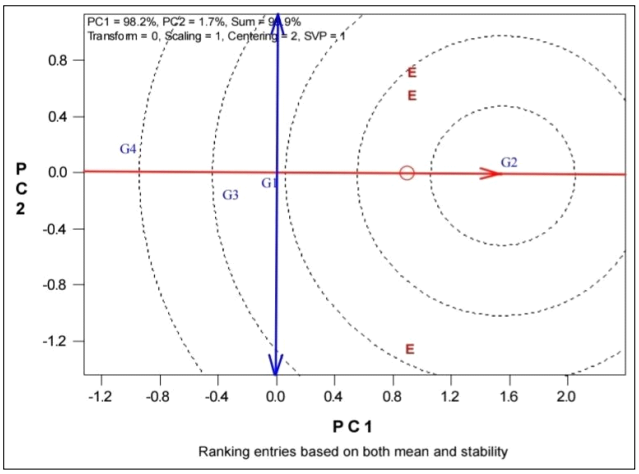


Fig 2: The ideal genotype across the studied environments.

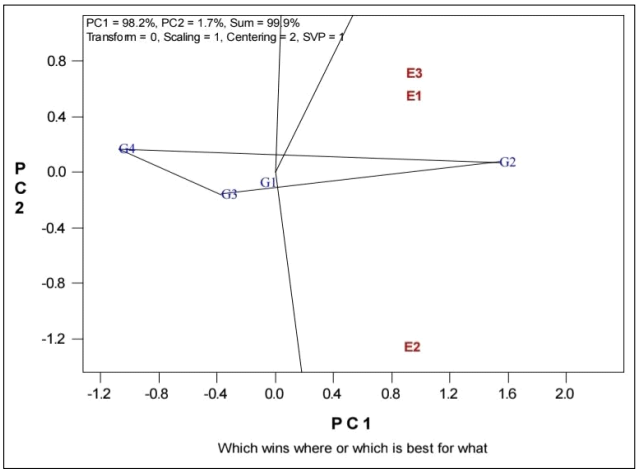


Fig 3: Genotype preferences for each environment.

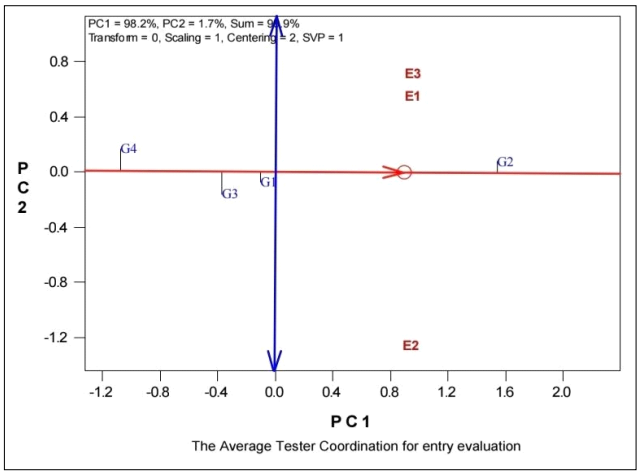


Fig 4: Stability of the studied genotypes across environments.

Clustering analysis

Varietal genetic divergence was analyzed to determine how the varieties could be grouped according to their genetic similarity or divergence, as shown in Table 9. The analysis classified the varieties based on their performance and genetic origin. The results presented in Table (9) and Fig (5) show that this method detected a genetic gap of 35,079,583 between the two genetic compositions, (G2) and (G4). This wide gap indicates that the two compositions contain genetically distant and different genes, reflecting a high level of genetic divergence. Crosses between them may therefore be made and used in future breeding work, particularly hybridization followed by selection to identify the optimal genetic profile with the preferred and desired genetic characteristics. This analysis also estimated the genetic distance between the two genetic compositions, G3 and G4, at 282.437. Their closeness may result from shared genetic material. At the same time, genetic compositions from different and genetically distant sources do not necessarily have to be identical. Because G3 and G4 are genetically similar, their performance may benefit from carrying some major preferred genes that could be used in subsequent breeding programs. One of the two closely related compositions could therefore replace the

Table 9: Genetic divergence.

Genotypes	Squared Euclidean Distance			
	1: Mohannad	2: Amal-7	3: Liron-5	4: Farah
1: Mohannad	0.000	7303.968	8673.205	10639.332
2: Amal-7	7303.968	0.000	31811.964	35079.583
3: Liron-5	8673.205	31811.964	0.000	282.437
4: Farah	10639.332	35079.583	282.437	0.000

Stage	Cluster combined		Coefficients
	Cluster 2	Cluster 1	
1	3	4	282.437
2	1	2	7303.968
3	1	3	21551.021

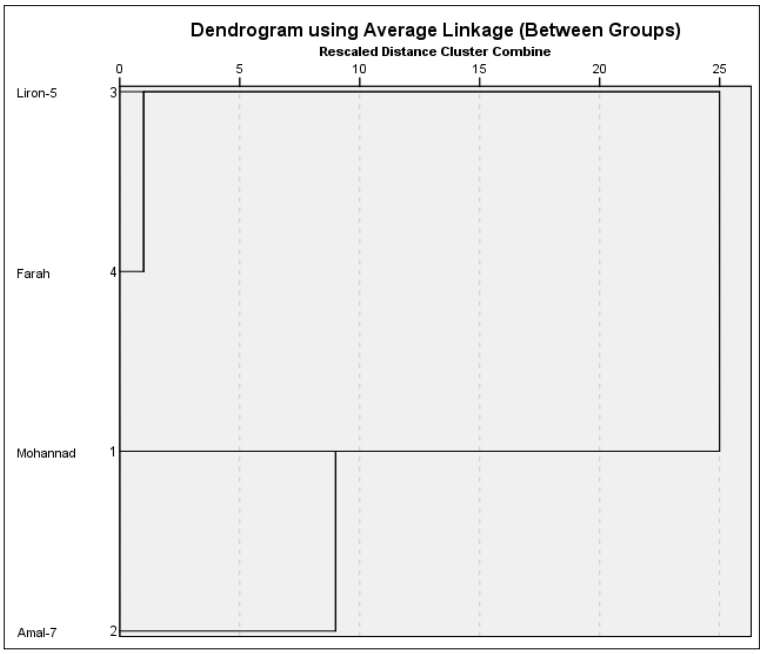


Fig 5: Genetic tree.

other if it were lost, eliminating the need to cross them. When molecular techniques are unavailable, this statistical method may serve as a successful alternative. This technique can make comparisons easier by showing the relationships among genetic compositions, helping select those that show genetic divergence while preserving their genetic origins. Khalil *et al.* (2020) and AL-Asadi and AL-Abody (2025), explained the benefits and importance of genetic divergence analysis for detecting genetically divergent structures for crossbreeding.

CONCLUSION

Analysis of variances results showed spikes number of (m^{-2}) recorded highest genetic, environmental variance, while area of flag leaf gave highest phenotypic variance and coefficients of variation. Spikes number (m^{-2}) and grains per spike recorded highest heritability degree in broad sense, while flag leaf area and Spikes number m^{-2} recorded highest percentage of genetic improvement. This indicates that these two traits are capable of achieving genetic progress and can be selected for. Genetic stability analysis showed that the genotype (G2) Amal-7 is the ideal variety with a high yield and genetic stability. The highest distance for the genes was found between Amal-7 and Farah genotypes and hybridization between them is possible to obtain a genotype with the desired traits.

Conflict of interest

The authors declare that they have no conflict of interest regarding the publication of this manuscript.

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