

Cluster analysis for genotypes of bread wheat (*Triticum aestivum* L.)

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Abstract

A field experiment was carried out at the Agricultural Research and Experiment Station in the Sayada area of the College of Agriculture – at the University of Kirkuk for the winter agricultural season 2021/2022 by designing random complete block designs with a split-plan system of 30 experimental units per block to know the effect of spraying with three concentrations of silica fertilizer (0, 2, and 4) ml.l⁻¹. The ten genotypes of bread wheat are (Wafiya, Al-Fayyad, Abu Ghraib 3, Baghdad 1, Jihan 99, Adna, Sham 6, Bora, Al-Rasheed, and Monnllles). 24.332 and the highest distance between the two genotypes Abu Ghraib and Baghdad with a distance of 130.975 when focusing (2). The lowest distance between the Italian and Baghdad genotypes is 28.288, and the highest distance factor between the two genotypes is below and Baghdad with a distance of 139.055 at a concentration (4).

Keywords: bread wheat, silica fertilizer, cluster analysis, genotypes

1. Introduction

The wheat crop, *Triticum aestivum* L, is one of the oldest and most important crops known to people as it constitutes the basic material in their diet and a source of energy needed by their body because it contains a high proportion of carbohydrates rich in calories) [1]

Silicon is the second most abundant element in the earth's crust, and many studies have shown that the use of silicon increased plant growth significantly, and the positive effects of silicon are more evident when plants are exposed to multiple stresses, including biotic and abiotic stresses. It is also known that silicon increases plant tolerance for plants from drought by maintaining the water balance in the plant and increasing the photosynthetic activity of the leaves, the use of silicon increases the drought tolerance of wheat plants [2].

Cluster analysis is to collect and test desirable genotypes with a good basis for classifying high-yielding genotypes with high-yielding constituent traits according to the environmental conditions in which they are planted. It is a multivariate analysis that has the function of minimizing differences within groups and maximizing differences between groups, testing genotypes in large numbers causes a high level of difficulty, cluster analysis can be used to classify genotypes and determine the best combination [3].

The study aims to find out how the genotypes of bread wheat are distributed using cluster analysis at three levels of silica fertilizer.

2. Material and Method

The field experiment was carried out at the Agricultural Research and Experiment Station in the

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Sayada area, which belongs to the College of Agriculture, University of Kirkuk, during the winter season (2021-2022), according to the split-plot system within the randomized complete block design (R.C.B.D) and with three replications [4]. Agricultural operations were conducted. On an experimental land of plowing and leveling, then the land is divided into three replications. The first factor was sprayed with silica fertilizer with three concentrations (0, 2, and 4) ml.l⁻¹, symbolized by S₂, S₁, and S₀, respectively. It was placed in the main plots and sprayed twice at the beginning of the elongation phase. After 15 days the second factor includes 10 genotypes of bread wheat, which were placed in the secondary plots. The cultivation took place on 15/11/2021 in the form of lines, where one replicate included 30 experimental units, and each experimental unit contained 4 lines, the length of the line was 3 m, and the distance between one line and another was 0.25 m, using a seeding rate of 350. M-2 grain for each line, and the field fertilization process was carried out with 320 kg.h⁻¹ Dab fertilizer (N18%, P2O246%), then (200) kg urea (N46%) was added as a second batch in the branching stage, and the broadleaf weeds were controlled with D. 2.4 At a concentration of 125 ml in 100 liters-1 of water, the thin-leaved weeds were controlled with Topic pesticide 5/3/2022, at a concentration of (500) ml in 100 liters-1 of water, and the weeds were controlled manually as needed. Cluster analysis of genotypes was carried out at each level of silica fertilizer, as well as using the (SPSS) program.

3. Results and Discussion

Cluster analysis is one of the statistical methods through which variables are classified in certain ways and arranged into groups where they are

homogeneous and reduce the differences within one group and the heterogeneous and large differences with other groups.

Cluster analysis of genotypes at (0) ml.l-1 concentration of silica fertilizer

It is noted in Figure (1) the tree diagram that shows the genetic relationships between the genotypes and based on the distance factor depending on the concentration of silica fertilizer at a concentration of (0) ml.l-1, as you find that the genotypes were formed from two main groups, the first main group was divided into two secondary groups, Al-Rasheed and Jihan, as for the second main group, it was divided into two secondary groups, the first secondary group was divided into two groups under the secondary school, Port Italia and Baghdad, the second secondary group was divided into two groups under the first secondary school, where it was divided into two groups under secondary school. Fayyad, as a group under the second secondary school, was divided into two groups under the third secondary school, Wafia, under the first third secondary school, Wafia, while under the third secondary school, a second group was divided into Monnllles and Abu Ghraib, with good potential in the training program. [5]

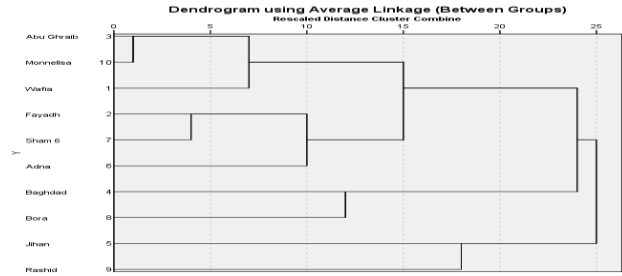


Figure (1) the tree diagram of the genotypes at (0) ml.l-1 concentration of silica fertilizer

Matrix of consanguinity between genotypes at the concentration of silica fertilizer (0) ml.l-1 It is noted in table (2) the kinship matrix that explains the divergence between the genotypes, and to obtain the matrix, the clustering method was used, depending on the distance factor between the genotypes, and then distributed in groups using the hierarchical method through the clustering method, as it was the least factor between the Monnllles and Abu Ghraib genotypes It is 15.379, which indicates the strong relationship and convergence between the genotypes, and it was the highest distance factor between the two genotypes, Fayyad and Baghdad, with a distance of 160.952.

Table (2) Matrix of the relationship between genotypes at the concentration of silica fertilizer (0) ml.l-1

Genotypes	Euclidean Distance									
	Wafia	Fayadh	Abu Ghraib	Baghdad	Jihan	Adna	Sham 6	Bora	Rashid	Monnellsa
Wafia	.000	94.14	47.63	80.11	137.05	78.36	89.52	71.57	104.11	39.22
Fayadh		.000	78.30	160.95	138.97	62.14	29.33	125.10	151.23	79.98
Abu Ghraib			.000	97.66	101.71	52.30	68.63	80.07	85.39	15.37
Baghdad				.000	156.89	131.39	158.46	60.87	82.34	93.17
Jihan					.000	84.09	121.96	159.81	86.04	103.33
Adna						.000	48.36	113.88	102.36	49.26
Sham 6							.000	128.65	142.93	69.04
Bora								.000	102.54	78.75
Rashid									.000	85.94
Monnellsa										.000

This is a dissimilarity matrix

Hierarchical linkage (accumulation) at the concentration of silica fertilizer (0) ml.l-1 It is noted in table (3) the steps for collecting the vocabulary and how to form clusters at each stage of the cluster analysis, which numbered 9 stages, as the first stage was between the third and tenth genotypes, and the

distance difference during the clustering process reached 15.379, which is the least distance, while the second stage of the cluster analysis is between the second and seventh genotypes, and the distance difference between the two genotypes was 29.337, and so on for the rest of the complexation stages.

Agglomeration Schedule

Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
1	3	10	15.379	0	0	3
2	2	7	29.337	0	0	4
3	1	3	43.431	0	1	6
4	2	6	55.254	2	0	6
5	4	8	60.871	0	0	8
6	1	2	73.285	3	4	8
7	5	9	86.040	0	0	9
8	1	4	109.984	6	5	9
9	1	5	116.295	8	7	0

Cluster analysis of genotypes at the concentration of silica fertilizer (2) ml.l-1

Figure (4) notes the genetic relationships between the genotypes based on the distance factor depending on the concentration of silica fertilizer at a concentration of 2 ml.l-1, as we find that the genotype was formed from two main groups, the first

main group was divided into two secondary groups, the first group included Jihan and a secondary group Secondly, it was divided into two groups under the Baghdad and Wafia secondary and the second major group was divided into two secondary groups, the first secondary group was divided into two groups under the secondary under the first secondary Bora under a second high school, it was divided into under

the first high and the second in Fayyad, and under the second high school, it was divided into under the third high school, Rashid and Sham 6. The second high school was divided into two groups under the first high school, Abu Ghraib.

Matrix of consanguinity between genotypes at the concentration of silica fertilizer (2) ml.l-1 It is noted in table (5) the kinship matrix that explains the

divergence between the genotypes and to obtain the matrix, it was distributed in groups using the hierarchical method through the aggregation method, as the lowest factor between the genotypes Monnllles and below was 24.332, which indicates the strong relationship and convergence between the genotypes and was higher The distance factor between the two genotypes, Abu Ghraib and Baghdad, is 130.975.

Table (5) Matrix of the relationship between genotypes at the concentration of silica fertilizer (0) ml.l-1 Euclidean Distance

Genotypes	Wafia	Fayadh	Abu Ghraib	Baghdad	Jihan	Adna	Sham 6	Bora	Rashid	Monnellsa
Wafia	.000	51.2	121.48	24.73	68.09	95.13	46.45	84.25	59.07	82.27
Fayadh		.000	93.73	69.17	85.09	74.50	30.89	42.62	29.70	67.22
Abu Ghraib			.000	130.97	90.05	38.85	85.04	94.88	72.14	54.17
Baghdad				.000	64.45	100.98	57.30	96.79	74.76	86.25
Jihan					.000	63.68	59.92	107.19	67.61	54.51
Adna						.000	56.70	78.37	55.19	24.33
Sham 6							.000	56.39	26.49	48.79
Bora								.000	58.26	70.31
Rashid									.000	52.17
Monnellsa										.000

This is a dissimilarity matrix

Hierarchical linkage (acclamation) at the concentration of silica fertilizer (2) ml.l-1 It is noted in table (6) the steps for collecting the vocabulary and how to form clusters at each stage of the cluster analysis, which numbered 9 stages, as the first stage was between the sixth and tenth genotype, and the

distance difference during the clustering process reached 24.332, which is the least distance, while the second stage of the cluster analysis between the first and fourth genotypes, and the distance between the two genotypes reached 24.739, and so on for the rest of the clustering stages.

Table (6) hierarchical linkage (acclamation) at the concentration of silica fertilizer (0) ml.l-1 Agglomeration Schedule

Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
1	6	10	24.332	0	0	5
2	1	4	24.739	0	0	7
3	7	9	26.492	0	0	4
4	2	7	30.298	0	3	6
5	3	6	46.519	0	1	8
6	2	8	52.428	4	0	8
7	1	5	66.277	2	0	9
8	2	3	70.757	6	5	9
9	1	2	80.202	7	8	0

Cluster analysis of genotypes at the concentration of silica fertilizer (4) ml.l-1 It is noted in Figure (7) the genetic relationships between the genotypes and based on the distance factor depending on the concentration of silica fertilizer at a concentration of 4 ml.L-1, as we find that the genotypes were formed and were divided into two main groups, the first is Fayyad and the second main group was divided into two secondary groups, the first secondary group It was divided into two groups under the secondary Adna and Jihan, the second secondary group was divided into two groups under the first high school and a group under the first high the first was divided into under the first high which was divided under the third high which included Rashid Abu Ghraib, the second was divided under the second secondary which included Monnllles and Baghdad, good potential in the education program. [7]

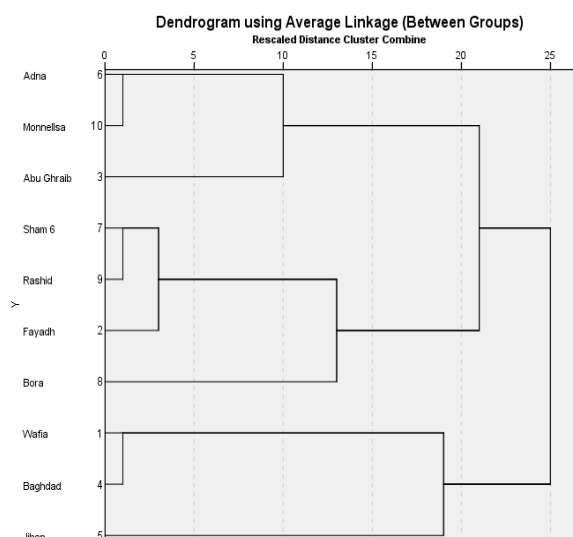


Figure (4): the tree diagram of the genotypes at the concentration of silica fertilizer (2) ml 1

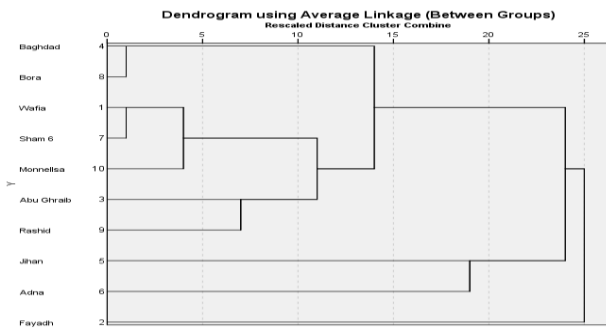


Figure (7) the tree diagram of the genotypes at the concentration of silica fertilizer (4) ml.l⁻¹

Matrix of consanguinity between genotypes at the concentration of silica fertilizer (4) ml.l⁻¹ It is noted in table (8) the kinship matrix that explains the

divergence between the genotypes. To obtain the matrix the clustering method was used depending on the distance factor between the genotypes and then distributed into groups using the hierarchical method through the clustering method as it was the least factor among the genotypes, Bora and Baghdad are 28.288, which indicates the strong relationship and convergence between the genotypes, and the highest factor was the distance between the two genotypes Adna and Baghdad, with a distance of 139.055, this is supported by the tree diagram of the genotypes, which indicates the genetic differences between them and other genotypes and may be due to the different genes in the genotypes.

Table (8) Matrix of the relationship between genotypes at the concentration of silica fertilizer (4) ml.l⁻¹

Genotypes	Euclidean Distance									
	Wafia	Fayadh	Abu Ghraib	Baghdad	Jihan	Adna	Sham 6	Bora	Rashid	Monnellsa
Wafia	.000	112.39	67.81	37.45	82.49	118.94	29.07	45.38	60.20	39.80
Fayadh		.000	54.62	114.26	133.38	86.65	95.15	106.57	85.14	114.77
Abu Ghraib			.000	77.29	93.45	74.87	48.94	76.16	46.68	67.68
Baghdad				.000	114.69	139.05	52.90	28.28	81.66	74.22
Jihan					.000	82.76	81.91	117.37	54.41	47.76
Adna						.000	105.90	134.27	64.30	96.48
Sham 6							.000	60.56	53.89	37.94
Bora								.000	80.88	81.05
Rashid									.000	45.75
Monnellsa										.000

This is a dissimilarity matrix

Hierarchical linking (acclamation) at the concentration of silica fertilizer (4) ml.l⁻¹ It is noted in table (9) the steps for collecting the vocabulary and how to form clusters at each stage of the cluster analysis, which numbered 9 stages, as the first stage was between the fourth and eighth genotypes, and

the distance difference during the clustering process reached 28.288, which is the least distance, while the second stage of the cluster analysis between the first and seventh genotypes, and the distance difference between the two genotypes reached 29.073, and so on for the rest of the clustering stages

Table (9) hierarchical linkage (grouping) at the concentration of silica fertilizer (4) ml.l⁻¹

Agglomeration Schedule						
Stage	Cluster Combined		Coefficients	Stage Cluster First Appears		Next Stage
	Cluster 1	Cluster 2		Cluster 1	Cluster 2	
1	4	8	28.288	0	0	6
2	1	7	29.073	0	0	3
3	1	10	38.874	2	0	5
4	3	9	46.686	0	0	5
5	1	3	57.382	3	4	6
6	1	4	66.760	5	1	8
7	5	6	82.768	0	0	8
8	1	5	94.711	6	7	9
9	1	2	100.331	8	0	0

4. Conclusion

The result 24.332 and the highest distance between the two genotypes Abu Ghraib and Baghdad with a distance of 130.975 when focusing (2) The lowest distance between the Italian and Baghdad genotypes is 28.288, and the highest distance factor between the two genotypes is below and Baghdad with a distance of 139.055 at a concentration (4).

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