The Genetic Diversity of Bread Wheat (*Triticum aestivum* L.) Genotypes Based on Cluster Analysis

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Abstract

The study included twenty bread wheat genotypes, which were sown during 2019/2020 agricultural season, using randomized complete block design with three replications at the Research Station of the Faculty of Agricultural Engineering Sciences, University of Duhok, Iraq. The data were recorded on plant height, leaf area, spike length, number and weight of grains per spike, 1000 grains weight, grain yield per unit area, and grain yield per hectare. The cluster analysis was conducted with the aim of collecting similar genotypes into homogeneous groups depending on the degree of genetic difference between them. The results showed that the mean square of genotypes was highly significant for all studied traits. The cluster analysis showed that the genotypes were distributed into 14 groups, and the first, third, fifth, seventh and ninth, eleventh, twelfth and thirteenth groups included one genotype for each of them, they were respectively, Wafia, Al-Rasheed, Latifia, Buhooth 10, IPA 95, Baghdad, Baghdad3 and Variety 158 indicating that these genotypes differed from the others due to their difference in their genetic origins, which is reflected in its performance, as for the other groups, each of them contained two genotypes. It was concluded from the results of the cluster analysis that there was a strong similarity between pairs of the following genotypes: Nora with Sham 6, IPA 99 with Tamoz 2, Babylon 113 with Fatih and Abo-Graib 3 with Pankal, because they had the highest degree of similarity (0.93, 0.91, 0.89 and 0.89 respectively) and the lesser Euclidean distances, and this requires avoiding crossing between these pairs, while the lowest degree of similarity was between the two genotypes, Buhooth 22 and Al-Baraka, which indicated a high genetic variation between them and the other genotypes, which may be due to the variation in the genetic origin, or they had preferred genes that the other genotypes did not have, so it is recommended to crosses those genotypes with those that have shown distinct genetic variation to take advantage of the heterosis and the segregations that result from.

Key words: Bread wheat, Genotypes, Cluster analysis, Similarity.

Introduction:

Wheat (*Triticum aestivum* L.) is the world's main source of human food, and it occupies the central position in the agriculture. It ranks second, after rice, as a source of calories for consumers in developing countries (Braun *et al*., 2010). Wheat is grown on more than 240 million hectares with a production of 757.92 million metric tons (Statista, 2018). The yield can be enhanced by increasing the cultivated area or yield per unit area. However, it is difficult to increase the area of wheat cultivation mainly due to the need for agricultural diversification and the cultivation of other crops in the field. Thus, good management practices in the fields help in enhancing wheat productivity (Pingali, 2012). One of these beneficial practices is the development of improved genotypes with high grain yield characteristics, which is the constant option for breeders to increase the yield per unit area along with better management practices. Knowing the information that contributes to increasing the grain yield is complicated because the yield is polygenic in nature and influenced by environmental changes (Farooq, 2010). It is important to identify the traits that contribute to grain yield to enhance breeding efficiency through meaningful selection criteria (Gashaw and Mohammed, 2007). Traits such as plant height, number of grains per spike, and 1000 grain weight contribute to wheat production (Gupta, 2006). where the estimating of correlation coefficient to find the degree of the relationship between the different traits associated with the yield is an important issue that shows a complex series of correlations (Majumder *et al*., 2008). Therefore, it is important to work on the interrelationship between the yield and other contributed traits for the effective selection of the improved genotypes, followed by an evaluation of the similarity between these genotypes using a cluster analysis based on field and productivity traits by exploiting the Euclidean distances, as many researchers used clustering analysis to study Morphological similarities between genotypes (Awan *et al*. 2014 and Yadav *et al*. 2015). Whereas, the dendrogram based on Euclidean distances separates the different genotypes of wheat, allowing for better selection of parents in breeding programs and thus achieving a good response to beneficial agricultural properties.

The Euclidean distance is used to estimate the genetic distance between the parents in order to maximize the transgressive segregation. Babay *et al*., (2015) noted that there is a great variation between genotypes, due to the wide range of Euclidean distance between genotypes. Poodle *et al*., (2017) revealed that the choice of genotypes from Group 2 would result in the selection of superior genotypes to be used in wheat breeding. Rani *et al*., (2018) performed a cluster analysis using the WARD method and square Euclidean distance coefficient, and collected 40 genotypes in 6 groups, the fifth group had the highest grain yield (1014.4 g), number of spikes/m^2 (143.46), and the second lowest plant height. Thus, the presence of genotypes in clusters has excellent opportunities for improvement through large crossbreeding. Pooja and Binewal, (2018) revealed that the results of a cluster analysis could be used in planning and implementing a future genetic improvement program for wheat. Kandel *et al.*, (2018) identified surpassed genotypes after clustering based on their genetic diversity in performance. Santosh *et al*., (2019) revealed that genotypes carrying desired traits from different clusters could be exploited in a future wheat breeding programs to improve grain yield. The results of the cluster analysis showed that the varieties were genetically different from one another, which could give farmers a wider range to choose from it (Motlatsi and Mothibeli, 2020). Fouad (2020) reported that cluster analysis divided 22 genotypes of bread wheat used in his study into five clusters. Each of them contained 8, 1, 3, 9 and 1 genotypes for cluster 1, 2,3,4 and 5 respectively. Average observed gain of cluster 1 showed positive increase for day to heading, no. of spikelet's/spike and spike density. Nielain is separated in the second cluster and showed positive observed gain for plant height. Also, genotype Emaral is separated in cluster 5 and showed high positive observed gain for the most traits. So hybridization between Nielain of cluster 2 and Emaral of cluster 5 could give new recombination and transgressive segregation with long spike density in the progenies derived from their crossing.

According to the foregoing, twenty genotypes of bread wheat were selected (18 of them certified in Baghdad and Kurdistan region), and then planted and analyzed for their genetic diversity based on the studied traits which explained in this research using cluster analysis, to identify the excellent and promising genotypes that could be used as parents in crossbreeding programs for the bread wheat crop.

Materials and Methods:

Twenty genotypes of bread wheat (*Triticum aestivum* L.) were adopted in the current study (Their names and sources are shown in Table 1). The seeds of these genotypes were planted on 25 November, 2019, at the fields of the Faculty of Agricultural Engineering Sciences, Dohuk University, under rainy conditions. Table (2) shows the amounts of rainfall (mm) and its distribution through the growing season. The field soil was prepared by plowing by mold board plow twice and in a perpendicular manner, then smoothing, leveling and planning operations were carried out, and the planting was in lines, the distance between one line and another 0.30 m. Compound fertilizer (NPK 20:20:20) was added at a rate of 120 kg per hectare during land preparation before planting, and urea fertilizer (N% 46) at a rate of 160 kg per hectare in two periods, the first in the tillering stage and the second before flowering. The experiment was carried out that included twenty genotypes using a randomized complete block design with three replications, where each block contained twenty experimental units in which the genotypes were randomly distributed. Each experimental unit contained three lines of 3 m length for each line. Weed control was carried out using Top herbicide for thin-leaf and Gran Star for broad-leaf at 2-3 leaf stage for both types of weeds, with the scientifically recommended dosages for each herbicide. Data were recorded on plant height (cm) (PH), leaf area (cm^2) (LA), spike length (cm) (SL), number of grains per spike (NG/S), grain weight per spike (gm) (GW/S), 1000 grains weight (gm) (1000GW), grain yield per unit area (g/0.9 m) (GY/U) and grain yield (kg per hectare) (GY/h).

Depending on the means of the genotypes for studied traits, a cluster analysis was performed through the use of the available program SPSS, to place the genotypes in groups according to the type of response (Sneath and Sokai, 1973). The cluster analysis was of two stages, the first includes analysis by the principle components method, and the second is the cluster analysis, which includes several steps starting with the formation of the degree of similarity matrix between the genotypes (Proximities Matrix) and then the formation of Dendogram according to the UPGMA method (Sneath and Sokai, 1973), where distances are estimated expressing the degree of similarities between means of the groups from the indicated matrix. The genotypes data and that of genotypes groups formed according to cluster analysis for all studied traits were analyzed statistically according to the method of the experimental design used, with the help of the available program SAS (Statistical Analysis System), then, the differences between the means of the genotypes were compared by Duncan's multiple range test method (Al-Zubaidy and Al-Falahy, 2016).

Table 1. The bread wheat genotypes used in the study with their pedigree and origin.

No.	Genotype	Pedigree	Origin
1	AboGraib3	Certified in Baghdad	General Commission for Agric. Res., Baghdad
2	Buhoth22	Certified in Kurdistan region	Agricultural Research Directorate - Dohuk
3	Nora	introduced	Int. Center for Agric. Res. in Dry Areas (ICARDA)
4	Wafia	Certified in Kurdistan region	Agricultural Research Directorate - Dohuk
5	Urouk	Certified in Kurdistan region	Agricultural Research Directorate - Dohuk
6	Buhoth10	Certified in Kurdistan region	Agricultural Research Directorate - Dohuk
7	IPA95	Certified in Baghdad	General Commission for Agric. Res., Baghdad
8	Latifia	Certified in Baghdad	General Commission for Agric. Res., Baghdad
9	Baghdad3	Certified in Baghdad	General Commission for Agric. Res., Baghdad
10	Variety 158	Not Certified, Dohuk	Agricultural Research Directorate - Dohuk
11	IPA99	Certified in Baghdad	General Commission for Agric. Res., Baghdad
12	Pankal	Certified in Kurdistan region	Agricultural Research Directorate - Dohuk
13	Al-Rasheed	Certified in Baghdad	General Commission for Agric. Res., Baghdad
14	Baghdad	Certified in Baghdad	General Commission for Agric. Res., Baghdad
15	Al-Baraka	Certified in Baghdad	General Commission for Agric. Res., Baghdad
16	Babylon113	Certified in Kurdistan region	Agricultural Research Directorate - Dohuk
17	Tamoz2	Certified in Baghdad	General Commission for Agric. Res., Baghdad
18	Fatih	Certified in Baghdad	General Commission for Agric. Res., Baghdad
19	Sham6	Certified in Baghdad	General Commission for Agric. Res., Baghdad
20	Al-Faris1	Certified in Kurdistan region	Agricultural Research Directorate - Dohuk

Table 2. Amounts of rainfall (mm) during the growing season at the two locations

Months	October 2019	November 2019	December 2019	January 2020	February 2020	March 2020	April 2020	May 2020	Total
Duhok	43.34	19.3	137.8	110.7	101.7	282.0	68.5	16.2	779.54

Results and Discussion:

Table (3) shows the analysis of variance results of the bread wheat traits under study, in which it is noticed that the mean squares of the genotypes was highly significant for all studied traits, and this is evidence of the existence of high genetic variations between the genotypes. This result is confirmed by the high values of the determination coefficient, which ranged between 96.293% for spike length and 99.872% for the grain yield per unit area, and this means that more than 96% of the changes in all traits are caused by variations between genotypes. These results are in agreement with the previous work of Arain *et al.*, (2006), concerning agronomically important traits in bread wheat genotypes. Jan *et al*. (2015) also reported highly significant differentiation among the genotypes for grain yield and its components. The performance means of the genotypes for the studied traits are shown in Table (4). It is noted for plant height trait that the genotype Al-Rasheed was surpassed by giving it lower height plants (60,667 cm) with a significant difference from all other genotypes, followed by the genotype Al-Baraka with an average of plant height (69,000 cm), while the highest mean of plant height was 102,333 cm for the two genotypes Buhoth10 and Fatih. The two genotypes Urouk and Al-Faris1 surpassed others by giving highest leaf area of 5.644 and 5.504 cm^2 respectively, with a significant difference from all the other genotypes, while the lowest leaf area was 2.841 and 2.857 cm^2 for the genotypes Pankal and AboGraib3, respectively. For spike length, the genotype Nora was distinguished by giving the highest mean for the trait of 20.0 cm, with a significant difference from all other genotypes, followed by the genotype Sham6 with an average spike length of 17,000 cm, while the minimum length of the spike was 8,333 cm in the genotype Al-Rasheed. The genotype Wafia achieved significant superiority over all other genotypes for the traits of number and weight of grains per spike and 1000 grains weight with means amounted to (60,000 grains, 2,503 gm and 44,513 gm) respectively, followed in importance by the genotype IPA99 for number of grains per spike (49,000 grains) and genotype Sham6 for number of grains per spike and 1000 grains weight (1.923 gm and 42.413 gm, respectively). The lowest means for the three traits reached respectively, 29,000 grains for the genotype Al-Rasheed and (1.080 gm and 28.997 gm) for the genotype Latifia. As for the two traits grain yield per unit area and per hectare, the Urouk genotype surpassed others by highest grain yield equal to 507.97 gm / 0.9 m and 5.644 tons per hectare respectively, followed in importance for the two traits by genotype Al-Faris1, while the lowest grain yield was 195.57 gm/0.9 m2 and ^{2} and 2.173 tons per hectare in the genotype Variety 158. It is noted that the genotype Urouk achieved an increase in grain yield per hectare of 2.544% over the genotype Al-Faris1, which is followed in importance, and 98.662% over the genotype Pankal, which gave the lowest grain yield per hectare and 38.912 % over the general mean of all genotypes. It is concluded that the Urouk genotype surpassed the other genotypes for the traits of leaf area and grain yield per unit area and per hectare, in addition to giving good results for the remainder traits, followed in importance by the two genotypes Wafia and Al-Faris1. As the three genotypes are registered and certified in Kurdistan region. These results provide the possibility of making use of these genotypes in cross-breeding programs to transfer the desired traits.

Table 3. Analysis of variance results for studied traits of bread wheat.

SOV	**df**	**Traits**							
		PH	**LA**	**SL**	**NG/S**	**GW/S**	**1000GW**	**GY/U**	**GY/h**
Reps.	**2**	11.017	0.069	0.050	2.467	0.0012	1.074	153.54	0.069
Genotypes	**19**	328.86**	3.077**	25.378**	101.39**	0.314**	51.445**	24380.4**	3.077**
Error	**38**	1.596	0.016	0.489	0.923	0.0006	0.283	15.608	0.016
Determination Coefficient		99.042	98.966	96.293	98.217	99.624	98.913	99.872	98.966

(**) Significance at 1% probability level.

Table 4. Means of bread wheat genotypes for studied traits.

Genotypes	Traits							
	PH	LA	SL	NG/S	GW/S	1000GW	GY/U	GY/h
AboGraib3	91.00 cd	2.857 i	8.667 jk	46.333 c	1.387 ji	37.657 f	255.71 l	2.857 i
Buhoth22	96.00 b	4.791 c	10.000 hi	45.000 c	1.680 e	35.977 g	431.14 d	4.791 c
Nora	90.333 d	3.208gh	20.000 a	45.667 c	1.907bc	41.967bc	318.70 i	3.208 gh
Wafia	86.667 e	4.846 c	14.667 c	60.000 a	2.503 a	44.513 a	436.12 d	4.846 c
Urouk	92.333cd	5.644 a	14.667 c	41.000 d	1.673 e	41.273 c	507.97 a	5.644 a
Buhoth10	102.333a	4.020 f	12.000 ef	41.000 d	1.620 f	38.497ef	361.84 h	4.020 f
IPA95	76.000 h	3.416 g	10.000 hi	45.000 c	1.450 h	31.983 j	307.44 j	3.416 g
Latifia	93.333 c	4.558 d	13.667cd	42.333 d	1.080 m	28.997 k	410.22 f	4.558 d
Baghdad3	91.667cd	3.420 g	12.000 ef	45.333 c	1.867 c	39.800 d	307.85 j	3.420 g
V. 158	84.000 f	2.173 j	11.333 fg	45.333 c	1.763 d	39.353de	195.57 m	2.173 j
IPA99	82.000fg	3.985 f	9.333ijk	49.000 b	1.547 g	32.213 j	358.62 h	3.985 f
Pankal	84.000 f	2.841 i	11.333fg	45.667 c	1.353 j	34.773 h	255.71 l	2.841 i
Al-Rasheed	60.667 j	5.173 b	8.333 k	29.000 f	1.160 l	41.827bc	465.56 c	5.173 b
Baghdad	74.000 h	3.004 hi	10.33ghi	36.000 e	1.207 k	34.687 hi	270.39 k	3.004 hi
Al-Baraka	69.000 i	5.164 b	12.000ef	42.333 d	1.523 g	35.447gh	464.77 c	5.164 b
Babylon113	91.00 cd	4.243 e	13.000de	40.667 d	1.427 hi	35.940 g	381.88 g	4.243 e
Tamoz2	82.000fg	4.704 cd	9.667ij	46.000 c	1.427 hi	32.670 j	423.36 e	4.704 cd
Fatih	102.333a	4.674 cd	11.00fgh	41.000 d	1.367 j	33.840 i	420.64 e	4.674 cd
Sham6	91.00 cd	3.036 hi	17.000 b	46.667 c	1.923 b	42.413 b	273.22 k	3.036 hi
Al-Faris1	81.000 g	5.504 a	10.000hi	45.000 c	1.670 e	38.517ef	495.30 b	5.504 a
Mean	**86.017**	**4.063**	**11.950**	**43.917**	**1.577**	**37.117**	**367.101**	**4.063**

The values followed by the same letter for each trait are not significantly different from each other.

Through the cluster analysis, the variations between the genotypes were represented by the scheme shown in Figure (1), and it is noticed that the genotypes were distributed into 14 groups (Table, 5) and also included 19 stages (Table, 6). It is shown from Table (5) that the genotypes Wafia, Al-Rasheed, Latifia, Buhooth 10, IPA 95, Baghdad, Baghdad 3, and Variety 158 (groups 1, 3, 5, 7, 9, 11, 12 and 13) varied from all other genotypes, as each of them represented an independent group by itself, this indicates that it has a great genetic variation from other genotypes, and what confirms this its high Euclidean distances with other genotypes, which are shown in Table (7). The remaining six groups, each contained two genotypes, as follows: the second group (Sham6 and Nora), the fourth group (Al-Faris1 and Urouk), the sixth group (Fatih and Babylon 113), the eighth group (Tamoz 2 and IPA 99) the tenth group (Al-Baraka and Buhooth 22) and the fourteenth final group (Pankal and Abo-Graib 3). These results indicate the possibility of forming a broad genetic base that helps in providing the opportunity to obtain genetic crossing over in segregating generations through crossing between genotypes belonging to genetically distant groups. Table (6), and based on Figure (1), shows the stages of the formation of the cluster shape, where the first stage began by merging the two genotypes Nora and Sham 6 into one group because they had the highest degree of similarity of 0.925. It is noted in the fifth stage in which the two genotypes of the second stage (IPA 99 and Tamoz 2) were combined with the genotype IPA 95, with a degree of similarity of 0.885. It is evident that the degrees of similarity gradually decrease with the progression of the stages to reach in the last stage to 0.619, in which the genotypes of stage 17 were merged (from merging the genotypes of stage 16 and the genotype Al-Rasheed with a degree of similarity of 0.642) with the genotypes of stage 18 (which includes the two genotypes of first stage, Nora and Urouk genotype. From previous studies, Babay *et al*., (2015) noted that there is a great variation between genotypes, due to the wide range of similarity between them. Poodle *et al*., (2017), Rani *et al*., (2018), Pooja and Binewal, (2018), Kandel *et al*., (2018) and Fouad (2020) reported that cluster analysis divided the genotypes of bread wheat from their studies into different groups, and revealed that the choice of genotypes from different groups would result in the selection of superior genotypes to be used in wheat breeding programs to improve grain yield.

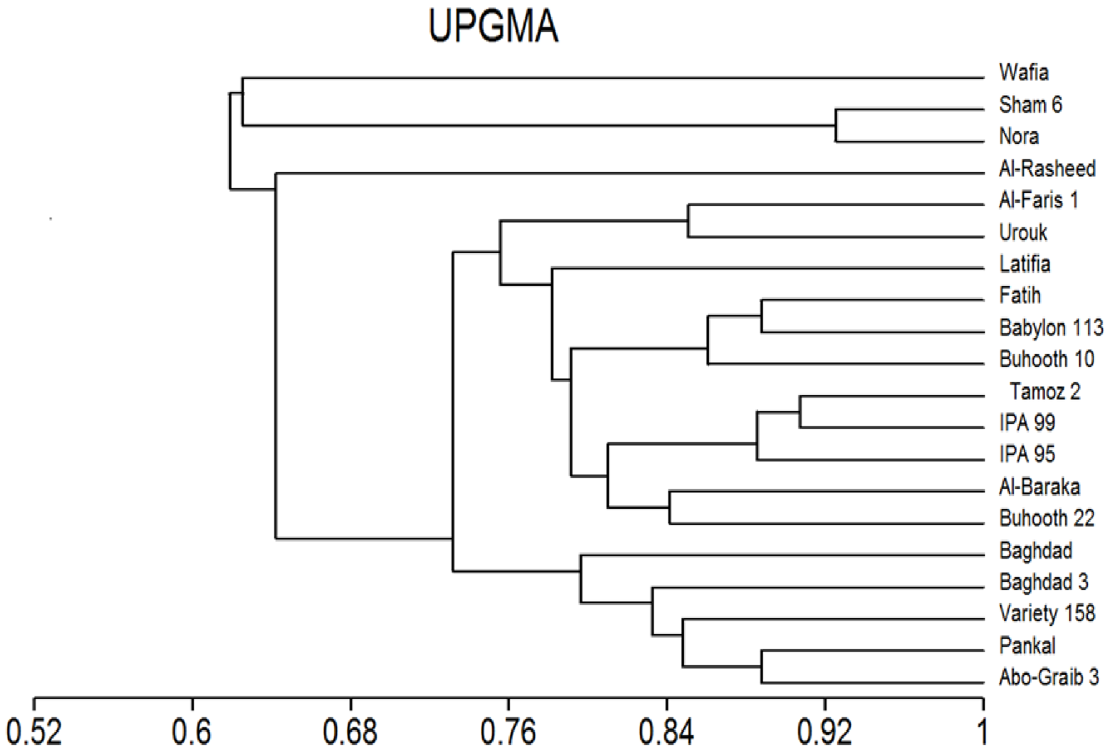

Figure 1. Distribution of bread wheat genotypes into groups according to cluster analysis

Table 5. Groups formed according to cluster analysis and genotypes they contain.

Groups	Genotype number	Names of the genotypes	Groups	Genotype number	Names of the genotypes
1	1	Wafia	**8**	2	Tamoz 2, IPA 99
2	2	Sham6, Nora	**9**	1	IPA 95
3	1	Al-Rasheed	**10**	2	Al-Baraka, Buhooth 22
4	2	Al-Faris1, Urouk	**11**	1	Baghdad
5	1	Latifia	**12**	1	Baghdad 3
6	2	Fatih, Babylon 113	**13**	1	Variety 158
7	1	Buhooth 10	**14**	2	Pankal, Abo-Graib 3

Table 6. Distances between groups according to the stages of cluster analysis

No.	Group 1	Group 2	Similarity	Objects in group
1	Nora	Sham 6	0.925	2
2	IPA 99	Tamoz 2	0.908	2
3	Babylon 113	Fatih	0.888	2
4	Abo-Graib 3	Pankal	0.888	2
5	IPA 95	Node 2	0.885	3
6	Buhooth 10	Node 3	0.861	3
7	Urouk	Al-Faris 1	0.851	2
8	Node 4	Variety 158	0.848	3
9	Buhooth 22	Al-Baraka	0.842	2
10	Node 8	Baghdad 3	0.833	4
11	Node 9	Node 5	0.81	5
12	Node 10	Baghdad	0.797	5
13	Node 11	Node 6	0.791	8
14	Node 13	Latifia	0.782	9
15	Node 14	Node 7	0.755	11
16	Node 12	Node 15	0.732	16
17	Node 16	Al-Rasheed	0.642	17
18	Node 1	Wafia	0.625	3
19	Node 17	Node 18	0.619	20

Sham 6 combined with the genotype Wafia). It was concluded from the above that the lower Euclidean distances (the higher degree of similarity) indicate the strong relationship or the closeness of genetic similarity between the genotypes, as is the case between the pairs of genotypes: Nora with Sham 6, IPA 99 with Tamoz. 2, Babylon 113 with Fatih and Abo-Graib 3 with Pankal (Table 6), which had the lowest Euclidean distances (the highest degree of similarity), which requires in this case to avoid crossing between them. The lowest degree of similarity for the least number of genotypes was 0.625 between the genotypes Nora and Sham 6 on the one hand and the genotype Wafia on the other hand, indicating their genetic variation with the remainder of the other genotypes, which may be due to the variation in the genetic origin or to having certain genes not present in the other genotypes. This was reflected in the positive performance of many studied traits, and accordingly, crossing between any of them with any of the other genotypes may result in a desirable heterosis, as it is noticed that the its degrees of similarity, which are shown in Table (7), were low with the other genotypes and ranged for the genotype Nora from 0.414 with the genotype Al-Rasheed to 0.925 with genotype Sham 6. The degree of similarity for the genotype Sham 6 ranged from 0.418 with the genotype Al-Rasheed and 0.925 with the genotype Nora. While for the Wafia genotype, the degree of similarity accounted 0.493 with Baghdad genotype.

Table 7. Similarity Matrix.

	Abo Graib3	Bhoth 22	Nora	Wafia	Urouk	Bhoth 10	IPA 95	Latifia	Bghdad 3	Variety 158	IPA 99	Pankal	Al Rasheed	Bghdad	Al Baraka	Babylon 113	Tamoz 2	Fatih	Sham 6	Al-Faris 1
Abo Graib 3	1																			
Bhoth 22	0.769	1																		
Nora	0.631	0.595	1																	
Wafia	0.526	0.689	0.614	1																
Urouk	0.609	0.790	0.649	0.749	1															
Bhoth 10	0.713	0.795	0.719	0.622	0.758	1														
IPA 95	0.808	0.770	0.625	0.552	0.620	0.723	1													
Latifia	0.693	0.810	0.533	0.594	0.717	0.713	0.734	1												
Bghdad 3	0.817	0.795	0.791	0.697	0.758	0.831	0.825	0.697	1											
Variety 158	0.831	0.722	0.661	0.574	0.623	0.703	0.768	0.610	0.847	1										
IPA 99	0.779	0.816	0.604	0.631	0.667	0.770	0.907	0.759	0.793	0.735	1									
Pankal	0.888	0.752	0.651	0.564	0.626	0.730	0.885	0.717	0.834	0.864	0.836	1								
Al Rasheed	0.598	0.691	0.414	0.539	0.677	0.570	0.622	0.630	0.574	0.540	0.629	0.573	1							
Bghdad	0.794	0.686	0.581	0.493	0.594	0.697	0.872	0.678	0.758	0.750	0.784	0.884	0.665	1						
Al Baraka	0.669	0.842	0.513	0.637	0.773	0.711	0.768	0.768	0.705	0.665	0.773	0.730	0.798	0.724	1					
Babylon 113	0.760	0.838	0.677	0.676	0.804	0.869	0.794	0.828	0.827	0.703	0.824	0.805	0.638	0.775	0.802	1				
Tamoz 2	0.759	0.887	0.550	0.657	0.716	0.721	0.864	0.823	0.739	0.703	0.908	0.809	0.714	0.751	0.849	0.829	1			
Fatih	0.700	0.863	0.574	0.628	0.764	0.853	0.762	0.822	0.743	0.629	0.791	0.760	0.641	0.736	0.783	0.888	0.858	1		
Sham 6	0.693	0.603	0.925	0.636	0.657	0.727	0.638	0.541	0.808	0.714	0.616	0.704	0.418	0.634	0.517	0.685	0.557	0.582	1	
Al-Faris1	0.666	0.837	0.597	0.686	0.851	0.764	0.736	0.665	0.746	0.679	0.777	0.696	0.716	0.670	0.824	0.778	0.727	0.780	0.601	1

Table (8), shows the analysis of variance results for the data of the traits of genotypes groups, which were formed by the cluster analysis, in which it is noticed that the mean squares of the genotypes groups was highly significant for all studied traits, indicating the presence of high genetic variations between these groups. The means of the fourteen groups of genotypes are shown in Table (9). It is noticed that the first group, which included the genotype Wafia only, surpassed by highest means for the traits of number of seeds per spike (60.000 grains), weight of grains per spike (2.503 g) and 1000 grains weight of (44.513 g). The second group, which included the genotypes Nora and Sham 6, was distinguished by the highest means of spike length, reached (18.500 cm), while the fourth group, which includes the two genotypes Al-Faris1 and Urouk, surpassed by a significant difference over all the other groups for the traits of leaf area (5.574 cm^2), grain yield per unit area (501.640 gm/0.9 m^2) and grain yield per hectare (5.574 tons). As for the plant height trait, the plants of the third group, which includes the genotype Al-Rasheed were distinguished by having the lowest height with an average of 60.667 cm, and a significant difference from all other groups, while the Buhooth 10 genotype (the only representative of the seventh group) gave taller plants (102.333 cm) by a significant difference with what was given by all the other groups. These results indicate the possibility of adopting these groups in crossbreeding programs to transmit distinct traits, as the possession of distinct genotypes with wide genetic variations is an important factor for the success of any breeding and improvement program, through which it is possible to collect the desired alleles and reached to distinct varieties with their production and quality specifications.

Table 8. Analysis of variance for studied traits of groups formed according to cluster analysis.

SOV	df	Traits							
		PH	LA	SL	NG/S	GW/S	1000GW	GY/U	GY/h
Reps.	2	7.625	0.039	0.095	1.327	0.0009	0.774	129.212	0.039
Genotypes	13	322.94**	3.061**	19.333**	136.56**	0.406**	58.181**	24333.74**	3.061**
Error	26	1.516	0.006	0.339	0.975	0.0006	0.114	8.971	0.006

(**) Significance at 1% probability level.

Table 9. Means of groups formed according to cluster analysis for studied traits

Groups	Traits							
	PH	LA	SL	NG/S	GW/S	1000GW	GY/U	GY/h
1	86.667 e	4.856 d	14.667 b	60.000 a	2.503 a	44.513 a	436.123 d	4.846 d
2	90.667 d	3.122 i	18.500 a	46.167bc	1.915 b	42.190 b	295.958 j	3.122 i
3	60.667 h	5.173 b	8.333 i	29.000h	1.160 j	41.827 b	465.557 b	5.173 b
4	86.667 e	5.574 a	12.333 d	43.000 e	1.672 e	39.895 c	501.640 a	5.574 a
5	93.333 c	4.558 e	13.667 c	42.333ef	1.080 k	28.997 h	410.220 e	4.558 e
6	96.500b	4.458 fe	12.000de	40.833 f	1.397 h	34.890 f	401.258 f	4.458 ef
7	102.333a	4.020 g	12.000de	41.000f	1.620 f	38.497 d	361.840 h	4.020 g
8	82.000 f	4.344 f	9.500 h	47.500b	1.487 g	32.442 g	390.988 g	4.344 f
9	76.000 g	3.416 h	10.000gh	45.000cd	1.450 g	31.983 g	307.440 i	3.416 h
10	82.500 f	4.978c	11.000efg	43.667de	1.602 f	35.712 e	447.957 c	4.978 c
11	74.000 g	3.004 i	10.333fgh	36.000 g	1.207 i	34.687 f	270.390 k	3.004 i
12	91.667cd	3.420 h	12.000de	45.333cd	1.867 c	39.800 c	307.853 i	3.420 h
13	84.000 f	2.173 k	11.333def	45.333cd	1.763 d	39.353 c	195.567 m	2.173 k
14	87.500 e	2.849 j	10.000gh	46.000bc	1.370 h	36.215 e	255.708 l	2.894 j

The values followed by the same letter for each trait are not significantly different from each other.

Conclusion:

It was concluded that there was a strong similarity between the pairs of the following wheat genotypes: Nora with Sham6, IPA99 with Tamoz2, Babylon113 With Fatih and Abo-Graib3 with Pankal, because they are distinguished by highest degree of similarity (0.925, 0.908, 0.888 and 0.888 respectively) and smaller Euclidean distances, and this requires avoiding hybridization between these pairs, while the lowest degree of similarity was found between the two genotypes Buhooth22 and Al-Baraka, which indicate their great genetic difference with other genotypes, which may be due to the difference in genetic origin or because they contain preferred genes not found in other genotypes, and this encourage their introduction into crosses with genotypes that have shown distinct genetic variation to take advantage from heterosis phenomenon and the segregations that result from it.

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