Quest Journals
Journal of Architecture and Civil Engineering
Volume 6 ~ Issue 2 (2021) pp: 20-27
www.questjournals.org

Research Paper

Genetic Diversity Assessment of Bread Wheat Genotypes Using Cluster Analysis

M. A. H. Al-Falahi* Kh. M. Dawod** M.Othman Mohammed ***
** Faculty of Agricultural and Forestry Engineering Sciences, University of Duhok*
*** College of Agriculture and Forestry, University of Mosul*
**** College of Science, Biology Dip. University of Zakho*

ADSTRACT
The study included nineteen bread wheat genotypes, their seeds 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. 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, then it was analyzed statistically to identify the nature of the differences between the genotypes. The cluster analysis was conducted with the aim of collecting similar genotypes into homogeneous groups and estimating the degree of genetic difference between them through the use of hierarchical clustering technology, which includes creating a degree of similarity matrix and estimating the distances between groups of genotypes formed. The results showed that the mean square of genotypes was significant at a 1% probability level for all studied traits. The stages of the cluster analysis showed that the genotypes were distributed into 12 groups, and the first, second, fourth, seventh and tenth groups included one genotype for each of them, they are respectively, IPA 99, Buhooth4, Apst-6, Maoroot and Azmar, indicating that these genotypes differ 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: Jihan 99 with Hasad, Apst-36 with Apst-26, Alwan with Tamoz2, Sham 6 with IPA95 and Howlier with Alla, because they had the highest degree of similarity (0.960, 0.897, 0.868, 0.852 and 0.849 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, Italy and Apst-12, indicates the high genetic variation between them and the other genotypes, which may be due to the variation in the genetic origin, or to they have preferred genes that are not found in other genotypes, which encourages their introduction into crosses with those that have shown distinct genetic variation to take advantage of the heterosis phenomenon and the segregations that result from it.
KEYWORDS*: genetic variation; cluster analysis; similarity; wheat (Triticum aestivum L.)*

Received 28 Jan, 2021; Revised: 10 Feb, 2021; Accepted 12 Feb, 2021
Published with open access at www.questjournals.org

I. INTRODUCTION

Breeding of bread wheat through crossing, followed by the desired choice of individuals in segregation generations, depends on the presence of genetic diversity among the parents, and therefore the first step in wheat crossbreeding program is the choice of the parents, and the analysis of the genetic diversity of genetic resources is a prerequisite for their efficient exploitation in the plant breeding program. The accurate determination of the genotype is very important during all steps of the breeding program, start from the choice of parents for crossbreeding to obtain new varieties for use in the production of the crop. Talking about genetic diversity helps the wheat breeder to find desirable traits to improve wheat varieties and achieve high production potential (Mwale *et al*., 2016). Estimation of genetic diversity on the basis of genetic distance is useful for wheat breeding as a tool of the parental selection for promoting new genetic recombination to increase the grain yield (Khodadadi *et al*., 2011, and Poudel *et al*., 2017). Crossbreeding and subsequent selection is one of the important methods of wheat breeding, and choosing the parents is the first step in the plant breeding program through crossbreeding. In order to benefit from transgressive segregation, genetic distance between parents is essential (Joshi *et al*. 2004). With the greater genetic distance between the parents, the higher heterosis could be observed in the resulting offspring (Anand and Murrty, 1968). Narouee (2006) determined the genetic diversity of local wheat lines in western Iran using cluster analysis, and six groups were identified for different regions.

Fang *et al*. (1996) found through a cluster analysis that 120 durum wheat genotypes were distributed into five groups based on the date of maturity, plant height, spike length, number of seeds per spike, 1000 grains weight, and seed yield per spike. The estimation of genetic distance is one of the appropriate tools for selecting parents in the crossbreeding programs in wheat, and the appropriate selection of parents is necessary for use in crossbreeding nurseries to enhance genetic recombination to increase the grain yield (Islam, 2004). There are some suitable methods such as cluster analysis, principal component analysis and factorial analysis, which are used to determine genetic diversity (Eivazi et al., 2007). Usually, before calculating the genetic distance, the variables are standardized so that they are all of equal importance in determining the distance. The results of the clusters analysis and principal components may have relative differences with each other. Therefore, before using a cluster analysis, the principal components can be avoided, and on the other hand, when the first two principal components represent a high ratio of variation, grouping according to these two components can be useful for finding the groups (Fotokian *et al*. 2002). Various algorithms have been used to study genetic diversity in cluster analysis, as UPGMA and Ward's methods being known as the most popular methods. Among the algorithms, UPGMA, Ward, SLINK, and CLINK, were applied in the past in cluster analysis, genetic diversity exploration and grouping of plant material, and UPGMA is the most correct method according to the family relationship based on its genetic material (Mohammadi and Prasanna, 2003).

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 them. 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, nineteen genotypes of bread wheat were selected (some of them were introduced and some were cultivated in different parts of Iraq), and then planted and analyzed for their genetic diversity based on the studied traits which explained in this research using cluster analysis and based on the analysis of the principal components, to identify the excellent and promising genotypes that could be used as parents in crossbreeding programs for the bread wheat crop.

II. MATERIALS AND METHODS

Nineteen 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. The total rainfall during the season was 779.54 mm, distributed over the months as follows: 43.34, 19.3, 137.8, 110.7, 101.7, 282.0, 68.5 and 16.2 mm for the

Table (1): The bread wheat genotypes used in the study with their pedigree and origin

sq	Genotype	Pedigree	Origin
1	Italy	Introduced	Int. Center for Agric. Res. in Dry Areas (ICARDA)
2	Jihan 99	Certified in Kurdistan region	Agricultural Research Directorate - Dohuk
3	Howlier	Certified in Kurdistan region	Agricultural Research Directorate - Dohuk
4	Azmar	Certified in Kurdistan region	Agricultural Research Directorate - Dohuk
5	Hasad	introduced	Int. Center for Agric. Res. in Dry Areas (ICARDA)
6	Sham 6	Certified in Baghdad	General Commission for Agric. Res., Baghdad
7	Alwan	Introduced	Int. Center for Agric. Res. in Dry Areas (ICARDA)
8	Maoroot	Introduced	Int. Center for Agric. Res. in Dry Areas (ICARDA)
9	Alla	Introduced	Int. Center for Agric. Res. in Dry Areas (ICARDA)

10	Apst-35	Introduced	Int. Center for Agric. Res. in Dry Areas (ICARDA)
11	Apst-33	Introduced	Int. Center for Agric. Res. in Dry Areas (ICARDA)
12	Apst-6	Introduced	Int. Center for Agric. Res. in Dry Areas (ICARDA)
13	IPA95	Certified in Baghdad	General Commission for Agric. Res., Baghdad
14	Buhoth4	Not Certified in Dohuk	Agricultural Research Directorate - Dohuk
15	Apst-36	Introduced	Int. Center for Agric. Res. in Dry Areas (ICARDA)
16	Apst-12	Introduced	Int. Center for Agric. Res. in Dry Areas (ICARDA)
17	Apst-26	Introduced	Int. Center for Agric. Res. in Dry Areas (ICARDA)
18	Tamoz2	Certified in Baghdad	General Commission for Agric. Res., Baghdad
19	IPA99	Certified in Baghdad	General Commission for Agric. Res., Baghdad

months of October, November and December (2019), December, January, February, March, April and May (2020) respectively. 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 19 genotypes using a randomized complete block design with three replications, where each block contained 19 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 with the 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 seeds per spike (NS/S), seed weight per spike (g) (SW/S), 1000 seed weight (g) (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 principal 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), and

III. RESULTS AND DISCUSSION

Table (2) shows the analysis of variance results of the bread wheat traits under study, and it is noticed that the mean square of the genotypes was highly significant for all studied traits, and this is an indication of the presence of high genetic variations between the genotypes which could be utilized in breeding programs for improvement of bread wheat genotypes to enhance the crop

Table (2): Analysis of variance results for studied traits of bread wheat.

Source	df	Traits							
		PH	LA	SL	NS/S	SW/S	1000GW	GY/U	GY/h
Reps.	2	2.123	2.182	0.049	1.105	0.0002	0.066	14.875	0.002
Genotypes	18	771.76**	66.819**	11.541**	244.67**	0.808**	184.25**	52930.5**	6.481**
Error	36	0.919	1.015	0.012	1.642	0.0011	0.034	19.092	0.0036
Determination Coefficient		99.763	97.061	99.788	98.676	99.741	99.964	99.928	99.889

(**) Significance at 1% probability level.

productivity, and these results confirmed by the high values of the determination coefficients, which ranged between 97.061% for the leaf area and 99.964% for the 1000 grains weight, which means that more than 97% of the changes in all traits are caused by differences 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 genotypes performance means for studied traits are shown in Table (3). For the plant height trait, it is noted that the genotypes, Apst-33, Apst-36 and Apst-26 surpassed by giving lower height plants (61,000, 60,333 and 61,667 cm, respectively), with a significant difference than all other genotypes, while the highest significant mean of plant height was 115,667 cm for the Maoroot genotype, and the Howlier genotype

was surpassed by giving highest leaf area of 35,450 cm^2, with an insignificant difference from the genotype IPA 99, and a significant difference from all other genotypes. For the number of

Table (3): Means of bread wheat genotypes for studied traits.

genotypes	Traits							
	PH	LA	SL	NS/S	SW/S	1000SW	GY/U	GY/h
Italy	72.000 ij	21.453 g	7.067 k	56.333 a	2.333 b	41.193 f	247.03 j	2.741 j
Jihan 99	73.333 i	27.727de	10.600 e	29.000fg	0.970 j	41.180 f	198.85 k	2.212 k
Howlier	81.000 ef	35.450 a	8.367 i	25.667 h	1.310 e	39.600 g	145.66 n	1.611 m
Azmar	80.000 f	20.830 g	12.567 c	31.667 e	0.913 k	38.520 h	183.73 l	2.033 l
Hasad	75.333 h	28.93 cd	10.500 e	27.000gh	1.087ghi	42.033 e	189.75 l	2.104 l
Sham 6	82.667 e	32.42 b	10.067 f	41.667 b	0.883 k	20.793 p	106.59 r	1.278 p
Alwan	85.000 d	26.59 e	10.567 e	27.333gh	1.137 fg	42.380 d	421.01 b	4.670 b
Maoroot	115.667a	26.047 e	12.100 d	26.000 h	0.827 l	33.640 k	117.95 q	1.307op
Alla	103.000c	30.207 c	9.167 h	29.000fg	1.073 hi	36.807 j	153.02 m	1.693 m
Apst-35	71.000 j	27.157 e	8.100 j	26.000 h	0.630 m	25.400 n	278.06 h	3.085 h
Apst-33	61.000 k	29.047cd	10.100 f	39.000 c	0.923 jk	24.940 o	307.25 g	3.411 g
Apst-6	78.333 g	32.823 b	10.200 f	35.000 d	1.083ghi	31.863l	380.72 d	4.226 d
IPA95	76.667 h	26.973 e	9.000 h	38.667 c	1.077 hi	28.893 m	134.56 o	1.489 n
Buhoth4	102.667c	23.633 f	12.100 d	32.000 e	1.497 d	46.170 b	363.16 e	4.030 e
Apst-36	60.333 k	20.830 g	9.000 h	30.000ef	1.123fgh	37.257 i	317.73 f	3.526 f
Apst-12	81.667 ef	21.620 g	7.000 k	38.000c	1.643 c	43.130 c	125.46 p	1.385 o
Apst-26	61.667 k	22.300fg	9.400 g	37.000cd	1.170 f	31.783 l	265.53 i	2.941 i
Tamoz2	73.333 i	21.623 g	13.100 b	26.333 h	1.053 i	41.933 e	405.61 c	4.500 c
IPA99	111.000b	33.987ab	14.100 a	54.333 a	2.757 a	50.743 a	640.14 a	6.774 a
Mean	81.351	26.824	10.163	34.211	1.236	36.751	260.622	2.896

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

seeds per spike, the two genotypes, Italy and IPA 99 are identical in giving the highest number of 56,333 and 54,333 seeds, respectively, with a significant difference from all the other genotypes. As for the traits of spike length, grain weight per spike, 1000 grains weight, grain yield per unit area and grain yield per hectare, the genotype IPA 99 was significantly surpassed all other genotypes by highest means, which were 14.1 cm, 2.757 gm, 50.743 gm, 640.14 gm and 6.774 tons respectively. It is noticed that this genotype achieved an increase in the grain yield per hectare by 45.054% over the followed genotype in its importance (Alwan), and 133.909% over the general mean of all genotypes. The lowest means for spike length and grain weight per spike were 8,367 cm and 0.630 gm for the two genotypes, Howlier and Apst-35, respectively, and for traits, 1000 grains weight, grain yield per unit area, and grain yield per hectare were 20.793 gm, 106.59 gm and 1.278 tons, respectively in genotype Sham 6. It is concluded that the variety, IPA 99, which certified and registered in Iraq, was distinguished for all studied traits, followed in importance by the genotypes, Alwan, Tamoz 2 and Apst-6, and these results allow the possibility of making use of these genotypes in the crop breeding programs by crossbreeding to transmit desirable traits.

Through the clustering analysis, the variations between the genotypes were represented by the scheme shown in Figure (1), and it was shown that the genotypes were distributed into 12 groups (Table, 4) and also included 18 stages (Table, 5). It is noted from Table (4) that the genotypes IPA 99, Buhooth 4, Apst-6, Maoroot and Azmar (groups 1, 2, 4, 7 and 10) differed from all the other genotypes, as each of them represented an independent group by itself, and this indicates that it has a great genetic variation from the other genotypes, and what confirms this is its high Euclidean distances with the other genotypes as shown in Table (7). The remaining seven groups each contained two genotypes, as follows: the third group (Tamoz 2 and Alwan), the fifth group (Apst-26, Apst-36), the sixth group (Apst-33 and Apst-35), the eighth group (IPA 95 and Sham 6), the nineth group (Alla and Howlier), the eleventh group (Hasad and Jihan 99), the twelfth and final group (Apst-12 and Italy). These results indicate the possibility of forming a wide genetic base that helps in providing the opportunity to obtain the genetic crossover in the segregating generations through hybridization between genotypes that belong to genetically distant groups. As for Table (5),

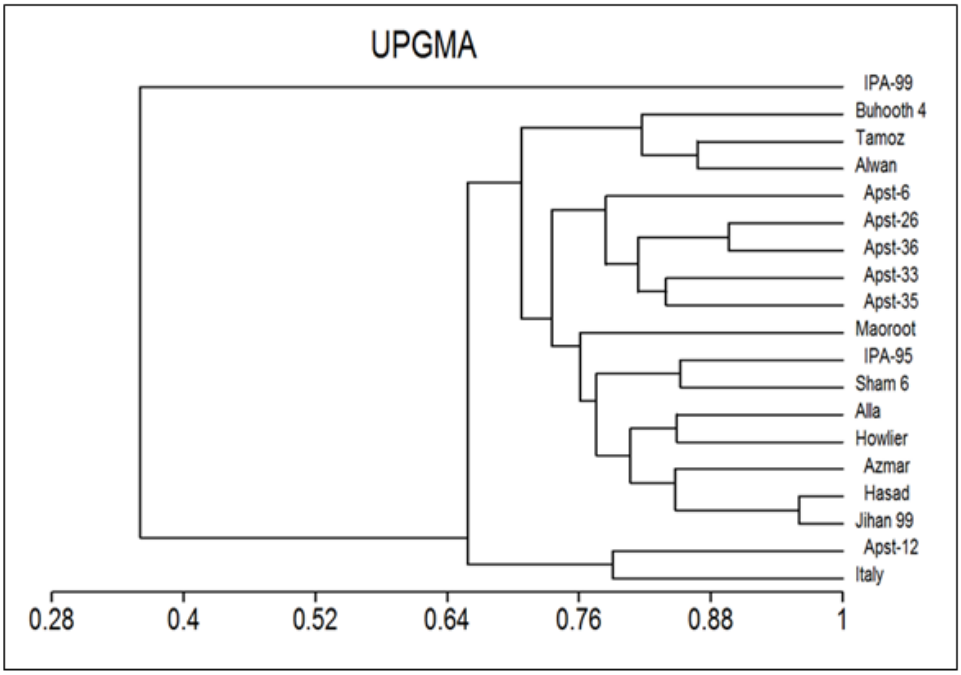

Figure 1. Distribution of bread wheat genotypes into groups according to cluster analysis

Table (4): 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	IPA 99	7	1	Maoroot
2	1	Buhooth 4	8	2	IPA 95, Sham 6
3	2	Tamoz 2, Alwan	9	2	Alla, Howlier
4	1	Apst-6	10	1	Azmar
5	2	Apst-26, Apst-36	11	2	Hasad, Jihan 99
6	2	Apst-33, Apst-35	12	2	Apst-12, Italy

Table (5): Distances between groups according to the stages of cluster analysis

Node	Group 1	Group 2	Similarity	Objects in group
1	Jihan 99	Hasad	0.96	2
2	Apst-36	Apst-26	0.897	2
3	Alwan	Tamoz	0.868	2
4	Sham 6	IPA-95	0.852	2
5	Howlier	Alla	0.849	2
6	Node 1	Azmar	0.847	3
7	Apst-35	Apst-33	0.839	2
8	Node 3	Buhooth 4	0.817	3
9	Node 7	Node 2	0.814	4
10	Node 6	Node 5	0.806	5
11	Italy	Apst-12	0.791	2
12	Node 9	Apst-6	0.784	5
13	Node 10	Node 4	0.775	7
14	Node 13	Maoroot	0.76	8
15	Node 14	Node 12	0.735	13
16	Node 15	Node 8	0.708	16
17	Node 11	Node 16	0.659	18
18	Node 17	IPA-99	0.361	19

and depending on Figure (1), it shows the stages of the formation of the cluster shape, where the first stage began with the merging of Jihan 99 with Hasad into one group because they had the highest degree of similarity of 0.960. It is noted in the sixth stage, in which the two genotypes in the first stage (Jihan 99 and Hasad) were combined with the Azmar genotype, with a degree of similarity of 0.847. It is evident that the degrees of similarity gradually decrease with the progression of the stages to reach in the last stage to 0.361 in which the genotype IPA 99 was combined with the genotypes of stage 17 (which includes the genotypes of the two stages 11 and 16), as the stage 11 in which the genotype Italy was combined with Apst-12 with a degree of similarity of 0.791, while the stage 16, the genotypes of stage 15 (Node 14 and Node 12) and 8 (Node 3 with the genotype Buhooth 4) were combined.

It is concluded from the foregoing that the lower euclidean distances (the higher degree of similarity) indicates the strong relationship or the closeness of genetic similarity between the genotypes, as is the case between the pairs of genotypes, Jihan 99 with Hasad, Apst-36 with Apst-26, Alwan with Tamoz 2, Sham 6 with IPA-95 and Howlier with Alla (Table 5), which had the lowest euclidean distances (the highest degree of similarity), which necessitates with this case avoiding crossing between them, and the lowest degree of similarity was 0.233 between the genotypes IPA 99 and Apst-35 (Table 6), an indication of their genetic variations with the other remainder genotypes, which may be due to their variations in the genetic origin or to their possession of certain genes not present in the other genotypes, which reflected on their positive performance for many of the studied traits, and accordingly, crossing between any of them with any

Table (6): Similarity matrix

	Italy	Jihan99	Howlier	Azmar	Hasad	Sham6	Alwan	maoroot	Alla	Apst35	Apst33	Apst6	IPA95	Buhooth4	Apst36	Apst12	Apst26	Tamoz2	IPA99
Italy	1																		
Jihan99	0.666	1																	
Howlier	0.594	0.810	1																
Azmar	0.653	0.858	0.727	1															
Hasad	0.643	0.960	0.843	0.837	1														
Sham6	0.531	0.743	0.754	0.698	0.746	1													
Alwan	0.585	0.831	0.710	0.738	0.835	0.617	1												
Maoroot	0.465	0.771	0.707	0.785	0.766	0.711	0.687	1											
Alla	0.567	0.839	0.849	0.765	0.854	0.769	0.736	0.827	1										
Apst35	0.626	0.808	0.735	0.705	0.788	0.712	0.742	0.693	0.734	1									
Apst33	0.605	0.787	0.650	0.694	0.771	0.793	0.727	0.626	0.702	0.839	1								
Apst6	0.567	0.777	0.738	0.702	0.784	0.764	0.827	0.634	0.744	0.756	0.835	1							
IPA95	0.655	0.828	0.790	0.774	0.823	0.852	0.701	0.755	0.828	0.805	0.814	0.774	1						
Buhooth4	0.596	0.726	0.611	0.759	0.716	0.536	0.823	0.711	0.710	0.623	0.646	0.728	0.620	1					
Apst36	0.704	0.795	0.692	0.801	0.772	0.598	0.783	0.627	0.729	0.791	0.804	0.759	0.746	0.736	1				
Apst12	0.79	0.744	0.761	0.774	0.747	0.691	0.663	0.655	0.73	0.650	0.622	0.620	0.808	0.681	0.726	1			

	1								0										
Apst 26	0.733	0.789	0.679	0.784	0.767	0.695	0.727	0.652	0.719	0.805	0.856	0.787	0.829	0.700	0.897	0.757	1		
Tamoz2	0.609	0.782	0.623	0.813	0.774	0.525	0.868	0.656	0.630	0.700	0.676	0.750	0.633	0.811	0.809	0.646	0.740	1	
IPA 99	0.426	0.346	0.338	0.325	0.356	0.315	0.481	0.340	0.373	0.233	0.345	0.477	0.281	0.550	0.285	0.296	0.290	0.438	1
	Italy	Jihan99	Howlier	Azmar	Hasad	Sham6	Alwan	maoroot	Alla	Apst35	Apst33	Apst6	IPA95	Buhooth4	Apst36	Apst12	Apst26	Tamoz2	IPA99

of the other genotypes may results in a desirable heterosis, as it is noticed that the degrees of similarity of them, which are shown in Table (6), were low with other genotypes. It was ranged for the genotype, IPA 99 between 0.233 with the Apst-35 genotype and 0.550 with Buhooth 4 genotype, while for the genotype Apst-35, the degree of similarity was ranged between 0.233 with the IPA 99 and 0.839 with the Apst-33. 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

The analysis of variance results for traits data of the genotypes groups that were formed by the cluster analysis are shown in Table (7), in which it is noticed that the mean square of the genotypes groups was highly significant for all the studied traits, indicating the presence of high genetic variations between the groups. The means of the twelve genotypes groups are shown in Table (8). It is noted that the first group that included the genotype IPA 99 only surpassed by highest means for the traits of leaf area (33.987 cm^2), spike length (14.100 cm), number and weight of grains per spike (54.333 grains and 2.757 gm respectively), grain yield per unit area (610.14 gm / 0.9 m^2) and grain yield per hectare (6,774 tons per hectare). For plant height trait, the plants of the third group, which include the Alwan and Tamoz 2 genotypes, were distinguished by lowest height, by a mean of 54.17 cm, with a significant difference from the first, second, seventh and ninth groups only, while the Maoroot genotype (the only representative of the seventh group) gave taller plants (115.67 cm), with a significant difference from those given by the first groups (IPA 99) and the second (Buhooth 4). These results indicate the possibility of adopting these groups in the hybridization programs to transfer the 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 reach distinct varieties with their production and quality specifications.

Table (7): Analysis of variance results for groups formed according to cluster analysis.

Source	df	Traits							
		PH	LA	SL	NS/S	SW/S	1000SW	GY/U	GY/h
Reps.	2	142.340	8.512	3.600	19.924	0.029	50.790	3328.08	0.418
Genotypes	11	1111.83**	94.793**	13.281**	277.39**	1.052**	201.022**	59393.2**	7.293**
Error	22	188.227	17.974	3.816	23.643	0.032	49.303	3875.041	0.477

(**) Significance at 1% probability level.

Table (8): Means of groups formed according to cluster analysis for studied traits.

Groups	Traits							
	PH	LA	SL	NS/S	SW/S	1000SW	GY/U	GY/h
1	111.00 a	33.987 a	14.100 a	54.333 a	2.757 a	50.743 a	610.14 a	6.774 a
2	102.67ab	23.633bcd	12.10 ab	32.000cd	1.497 c	46.170 ab	363.16 b	4.030 b
3	54.17 d	16.190 d	7.783 c	18.667 e	0.700 g	27.507 d	238.46 cd	2.646 cd
4	78.33bcd	32.823 a	10.20 bc	35.000cd	1.083def	31.863 cd	380.72 b	4.226 b
5	61.00 d	21.565 cd	9.200 bc	33.500cd	1.147 de	34.520bcd	291.63 bc	3.233 bc
6	66.00 cd	28.102abc	9.100 bc	32.500cd	0.777 fg	25.170 d	292.66 bc	3.248 bc
7	115.67 a	26.047abc	12.10 ab	26.000de	0.827efg	33.650bcd	117.95 e	1.307 e
8	79.67bcd	29.697 ab	9.533 bc	40.167bc	0.980 d-g	24.843 d	120.57 de	1.384 de
9	92.00abc	32.828 a	8.767 bc	27.333 d	1.192 d	38.203a-d	149.34 de	1.652 de
10	80.00bcd	20.830 cd	12.567ab	31.667cd	0.913 d-g	38.520a-d	183.73cde	2.033cde
11	74.33 cd	28.328abc	10.55abc	28.000 d	1.028 d-g	41.607abc	194.30cde	2.158cde
12	76.83bcd	21.537 cd	7.033 c	47.167ab	1.988 b	42.162abc	186.24cde	2.063cde

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

References

[1]. Al-Zubaidy, K. M. D. and M. A. H. Al-Falahy (2016). Principles and Proceedures of Statistics and Experimental Designs. Duhok University Press, Iraq.
[2]. Anand, I. J. and B. R. Murrty (1968). Genetic divergence and hybrid performance in linseed. Ind. J. Genet. plant Breed 28: 178-185.
[3]. Arain, S., K.D. Jamali, M. H. Naqvi, A.M. Soomro, M. A. Arain and S. A. Ali (2006). Genetic diversity for agronomic characters and their association with grain yield components in durum wheat. In: Proceedings of the International Wheat Seminar; 2006 Feb 20–22; Faisalabad, Pakistan. Faisalabad: Wheat Research Institute; 2006. p. 56–60.
[4]. Babay, E., R. Chaabane., R. M. Abdmouleh and M. Bennaceur (2015). Diversity of Tunisian bread wheat genotypes revealed by morpho-agronomical and microsattelite markers. Biosci. J., 31(3): 701-708.
[5]. Eivazi, A. R., M. R. Naghavi, M. Hajheidari, S. M. Pirseyedi, M. R. Ghaffari, S. A. Mohammadi, I.
[6]. Majidi, G. H. Salekdeh and M. Mardi (2007) Assessing wheat (*Triticum aestivum* L.) genetic diversity using quality traits, amplified fragment length polymorphisms, simple sequence repeats and proteome analysis. Ann Appl Biol 152:81-91.
[7]. Fang, X. W., E.H. Xiong and W. Zhu (1996). Cluster analysis of elite wheat germplasm. Jiangsu Agric Sci 4: 14-16.
[8]. Fotokian, M., A. Shahnejat bushehri and A. Taleie (2002) Cluster analysis based on PCA in rice genotypes. Paper presented at the 6rd international conference of Statistics, University of Tarbiat modares, Iran, 26-28 August 2002.
[9]. Fouad, H. A. (2020). Principal component and cluster analysis to estimate genetic diversity in breadwheat (*Triticum aestivum* L.) genotypes. J. of Pl. Prod., Mansoura Univ., 11(4): 325–331.
[10]. Islam, M. R. (2004). Genetic diversity in irrigated rice. Pak J Biol Sci 2: 226-229.
[11]. Jan, S., F. Mohammad and F. U. Khan (2015). Genetic potential and heritability estimates of yield traits F_3 segregating populations of bread wheat. International J. Environment,4(2): 106–115.
[12]. Joshi, B. K., A. Mudwari, M. R. Bhatta and G. O. Ferrara (2004). Genetic diversity in Nepalese wheat cultivars based on agromorphological traits and coefficients of parentage. Nep Agric., Res J 5: 7-17.
[13]. Kandel, M., A. Bastola., P. Sapkota., O. Chaudhary., P. Dhakal., P. Chalise and J. Shrestha (2018).
[14]. Analysis of genetic diversity among the different wheat (*Triticum aestivum* L.) genotypes.
[15]. Turkeish J. of Agric. and Nat. Sci. 5(2): 180–185.
[16]. Khodadadi, M., M. H. Fotokian and M. Miransari (2011). Genetic diversity of wheat (*Triticum aestivum* L.) genotypes based on cluster and principal component analyses for breeding strategies. Australian J. of Crop Sci. 5(1):17-24.
[17]. Mohammadi, S. A. and M. M. Prasanna BM (2003) Analysis of genetics diversity in crop plants: salient statical tools and considerations. Crop Sci 43: 1235-1248.
[18]. Motlatsi, E. and K. L. Mothibeli (2020). Characterization of wheat (*Triticum aestivum* L.) cultivars grown in Lesotho by morphological markers. Eur. J. of Agric. and Forestry Res. 8(1):28-35.
[19]. Mwale, V. M., X. Tang and E. Chilembwe (2016). Assessment of genetic diversity among sixty bread wheat (*Triticum aestivum*) cultivars using microsatellite markers. African J. of Biotechnology. 15(21): 960-973.
[20]. Narouee, R. M. (2006) Evaluation of genetic diversity and factor analysis for morphologic traits of wheat landraces of Sistan-Baloochestan. J Pajouhesh-va-Sazandegi in Persian, abstract in English 73: 50-58.
[21]. Pooja, D. S. S. and R. S. Beniwal (2018). Genetic diversity based on cluster and principal component analyses for yield and its contributing characters in RILs of bread wheat (*Triticum aestivum* L.), Int. J. Pure App. Biosci. 6(2): 242-247.
[22]. Poudel, A., D. B. Thapa and M. Sapkota (2017). Assessment of genetic diversity of bread wheat (*Triticum aestivum* L.) genotypes through cluster and principal component analysis. Int. J. Exp. Res. Rev., 11: 1-9.
[23]. Rani, K., V. Singh., V.S. Mor and G. Singh (2018). Genetic diversity analysis for seed vigour, yield and its component traits in bread wheat (*Triticum aestivum* L.). Chem. Sci. Rev. Lett. 7(28): 855-859.
[24]. Santosh, J. P., A. S. Jaiswal and N. C. Gahatyari (2019). Genetic diversity analysis in bread wheat (*Triticum aestivum* L.em.Thell.) for yield and physiological traits. Int. J. Curr. Microbiol. App. Sci. 8(2): 3059-3068.
[25]. Sneath, P. H. A. and R. R. Sokai (1973). Numerical Taxonomy: The Principal and Practice of Numerical Classification, W. H. Freeman and Co., San Francisco.

تقييم التنوع الوراثي لتراكيب وراثية من حنطة الخبز باستخدام التحليل العنقودي

محمد علي حسين الفلاحي* خالد محمد داؤد** محمد عثمان محمد***

* كلية علوم الهندسة الزراعية والغابات ، جامعة دهوك

** كلية الزراعة والغابات ، جامعة الموصل

*** كليه العلوم قسم البايولوجي جامعه زاخو

الخلاصة

اشتملت الدراسة على تسعة عشر تركيباً وراثياً من حنطة الخبز، زرعت بذورها خلال الموسم الزراعي 2020/2019 باستخدام تصميم القطاعات العشوائية الكاملة بثلاثة مكررات في محطة أبحاث كلية علوم الهندسة الزراعية، جامعة دهوك. تم تسجيل البيانات عن صفات ارتفاع النبات والمساحة الورقية وطول السنبلة وعدد ووزن الحبوب في السنبلة ووزن 1000 حبة وحاصل الحبوب لوحدة مساحة وحاصل الحبوب للهكتار، ثم حللت البيانات احصائياً للتعرف على طبيعة الاختلافات بين التراكيب الوراثية. واجري التحليل العنقودي بهدف تجميع التراكيب الوراثية المتشابهة في مجاميع متجانسة وتقدير درجة الاختلاف الوراثي بينها من خلال استخدام تقانة التجميع الهرمي التي تتضمن تكوين مصفوفة درجة التشابه وتقدير المسافات بين مجاميع التراكيب الوراثية المتكونة. أظهرت النتائج ان متوسط مربعات التراكيب الوراثية كان معنوياً عند مستوى احتمال 1% للصفات جميعها. واظهرت مراحل التحليل العنقودي ان التراكيب الوراثية توزعت في 12 مجموعة، ضمت المجموعات الاولى والثانية والرابعة والسابعة والعاشرة تركيباً وراثياً واحداً لكل منها هي على التوالي 99 IPA و4 Buhooth و6-Apst وMaoroot و Azmarدلالة على اختلاف هذه التراكيب الوراثية عن التراكيب الاخرى بسبب اختلافها في اصوها الوراثية، والذي انعكس بالتالي على أدائها، اما المجموعات الاخرى ضم كل منها تركيبين وراثيين. ويستنتج من نتائج التحليل العنقودي وجود تقارب قوي بين ازواج التراكيب الوراثية التالية: 99 Jihan مع Hasad و36-Apst مع 26-Apst وAlwan مع 2Tamoz و6 Sham مع IPA95 وHowlier مع Alla لامتلاكها اعلى درجات التشابه (0.960 و0.897 و0.868 و0.852 و0.849 على التوالي) واقل المسافات الاقليدية، وهذا يستوجب تجنب اجراء التهجينات بين هذه الازواج، بينما كانت أقل درجة تشابه بين التركيبين الوراثيين Italy و12-Apst، دلالة على الاختلاف الوراثي العالي بينهما وبقية التراكيب الاخرى، والذي قد يعود الى الاختلاف في الاصل الوراثي أو الى امتلاكهما جينات رئيسة مفضلة تخلو منها التراكيب الاخرى، مما يشجع ادخالهما في تهجينات مع التراكيب التي اظهرت تغايراً وراثياً متميزاً للاستفادة من ظاهرة قوة الهجين والانعزالات التي تنتج عنها.