Plant Archives Vol. 20, Supplement 2, 2020 pp. 2396-2402 **e-ISSN:2581-6063 (online), ISSN:0972-5210**

STUDY OF GENETIC PARAMETERS AND CLUSTER ANALYSIS FOR NEW GENOTYPES OF BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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Abstract

The study was carried out in the fields of College of Agriculture and Forestry, University of Mosul to evaluate 15 genotypes source from the International Center for Agricultural Research in the Dry Areas (ICARDA) of bread wheat (*Triticum aestivum* L.), including two local varieties approved in Iraq (Pohoth-4 and Tal- Afar-3) using the of Random Complete Block Design (RCBD), with three replications and studied characteristics: (Number of flowering days at 50%, plant height, area of the flag leaf (cm), length spike (cm), number of spikes plant^{-1}, number of grains spike, grain yield plant^{-1}, biological yield plant^{-1}, harvest index (%), weight of 1000 grains and protein ratio (%)). The results showed that the values of genotype and phenotypic variances were significant at the level of 1% for all studied traits. The phenotypic correlation was significant and positive at 1% of the grain yield with the traits number of spikes plant^{-1}, biological yield plant^{-1} and protein ratio, while the values of the coefficients of genotype and phenotypic variation of the studied characteristics was varied, while heritability of broad sense was high for most traits except for spike length, harvest index and biological yield plant^{-1}. The expected genetic improvement values, as a percentage, were differentiated for the studied traits. The results cluster analysis showed that higher Genetic spacing was between the 15 and 11 genotypes as well Between 15 and 4.

Keywords: Bread wheat, phenotypic correlation, heritability of broad sense, expected genetic improvement.

Introduction

Wheat is considered one of the important food crops globally, covering about 17% of the total cultivated areas in the world Ojha *et al*. (2018) as the area planted with wheat in 2018 reached 214 million hect. and its productivity reached 34.254 tons / hect. (FAO, 2020) and reached The cultivated area by wheat in Iraq is 6331 thousand dunums for the winter season 2019, and its production capacity for the same year is about 4343 thousand tons CSO (2019).

Knowing the importance of genotypic, phenotypic and environmental variations, their correlations and heritability of broad sense and expected genetic improvement and phenotypic and genotypic difference coefficients is the most important step in planning genetic improvement programs, which enables plant breeders to expect the amount of genetic improvement resulting from selection. These genetic features in wheat yield have been estimated by several researchers, as Al-Maliki and others (2019) indicated that the values of genotypic and phenotypic correlations were significant and in the desired direction for the characteristics of plant height, spike length, number of grains spike^{-1}, weight 1000 grains, and grain yield plant^{-1} in nine varieties. From bread wheat, as he showed in his study that the values of the coefficient of genotypic and phenotypic variance were consistent with most of the traits studied in wheat bread. Ayyub (2019) stated that the heritability values of broad sense were high for the height of the plant, the number of spikes plant^{-1}, number of grains spike^{-1}, grain yield plant^{-1} and the weight 100 grains, Serhid (2018) show that the expected genetic improvement values were high for the trait of the yield and the biological yield, while it was low for the 1000-grain weight trait And the harvest Index and the number of grains spike^{-1}, as will as Jabour *et al.* (2019) showed the expected genetic improvement values were high for the traits of plant height, 1000 grains weight, spike length in durum wheat. The cluster analysis is considered a good tool for plant breeders to assess the genetic spacing, determine the locations of quantitative traits, and preserve the genetic origins, although it does not need to make hypotheses about the nature of data distribution (Yan and Ortiz, 1994), When using the cluster analysis to analysis the grain yield data, the results of the analysis showed that the cultivars were grouped into five groups and the highest genetic spacing was in the third group (Sabah and Ebaa 99), where as the lowest genetic spacing was in the fifth group (Maxi Pac) for the grain yield in the wheat bread (Al-Maliki, 2017).

The aim of this study is parameters genetics which include, genotypic, phenotypic and environmental variations, genotypic and phenotypic, correlations, broad sense heritability, expected genetic improvement studied and estimate the values of the genetic and phenotypic coefficients. As well as estimate the degree of genetic spacing between the genotypes for bread wheat.

Materials and Methods

The study was carried out in the fields of the College of Agriculture and Forestry, University of Mosul, where the planted of the seeds of the thirteen genotypes included the entry of the International Center for Agricultural Research in the Dry Areas (ICARDA) as well as the local cultivars (Pohoth-4 and Tal- Afar-3) cultivated locally and the following table shows:

Table 1 : Genotypic genetically and number used in study

No.	Genotypes	Pedigrees
1	Terbol	ICARDA
2	Atlas	ICARDA
3	Tesfa	ICARDA
4	ALMAZ-19/ETBW 4919/3/NING MAI 9558//CHIL/CHUM18	ICW08-50312-2AP-0AP-0AP-2TR
5	ASEEL-1//MILAN/PASTOR/3/SHAMISS-3	ICW08-50343-4AP-0AP-0AP-3TR
6	AZD-2//PFAU/MILAN	ICW07-0205-1AP-0AP-0AP-1AP
7	BAASHA-14//PFAU/MILAN	ICW07-0746-3AP-0AP-0AP-1AP
8	BAOBAB-1//MILAN/PASTOR	ICW07-0407-0AP-0AP-0AP-6AP
9	DAJAJ-5/4/CHEN/AEGILOPSSQUARROSA (TAUS)//BCN/3/KAUZ/5/WBLL1*2/KIRITATI	ICW08-50152-2AP-0AP-0AP-4TR
10	DEBEIRA//SHUHA-8/DUCULA/3/PASTOR/SERI//PFAU	ICW08-50013-8AP-0AP-0AP-2TR
11	GOUMRIA-3//PFAU/MILAN	ICW07-0581-4AP-0AP-0AP-4AP
12	HUBARA-5//PFAU/MILAN	ICW07-0583-6AP-0AP-0AP-5AP
13	JAWAHIR-2//MILAN/DUCULA	ICW07-0279-8AP-0AP-0AP-1AP
14	Tal- Afar-3	Local check
15	Pohoth-4	Local check

The experiment was carried out according to Randomized Complete Block Design (RCBD), Al-Rawy and Khalaf Allah (2000), by three replicates, where by the genotypes were randomly distributed in each repeater by two rows for each genotype. The length of the line ranged between 2 meters and the distance between the rows 30 cm and urea fertilizer was added at a rate of 20 kg (nitrogen For a dunum (Al-Kubaisi and others 2000), equivalent to 43.47 kg of urea, in two batches, the first - when planting, and the second - before flowering. The study was conducted on 10 plants randomly taken with the exclusion of peripheral plants from each streak in the season (2018-2019) and the characteristics were studied: number of days for flowering at 50%, plant height (cm), spike length (cm), area of flag leaf (cm^2) , number of spikes $Plant^{-1}$, number of grain $spike^{-1}$, Biological yield $plant^{-1}$ (gm), grain yield $plant^{-1}$ (gm), harvest Index (%), 1000 grain weight (g), and protein ratio (%).

Data were statistically analyzed using the SAS program, and genetic and environmental variations were estimated and the coefficient of genetic difference and coefficient of phenotypic and the broad sense heritability as explained by Singh and Chaudhary (1977). The ranges shown were approved by Ali (1999). The broad sense heritability values are less than 40% low, 40-60% medium, and 60% or more high.

$$\sigma^2_g = (M.St - M.se)/r \qquad \sigma^2_e = M.S.e \qquad \sigma^2_p = \sigma^2_g + \sigma^2_e$$

$$Genotypic\ Coefficient\ of\ Variation\ (G.C.V.) = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

$$Phenotypic\ Coefficient\ of\ Variation\ (P.C.V.) = \frac{\sqrt{\sigma^2_P}}{\bar{X}} \times 100$$

$$H^2 = \frac{\sigma^2_G}{\sigma^2_P}$$

The expected genetic improvement was estimated at the selection of 5% of plants, according to Johanson *et al.* (1955). The ranges proposed by Agarwal and Ahmad (1982) were adopted for expected genetic improvement as a percentage of average: less than 10% low, 10-30% medium and more than 30% high.

The expected genetic improvement was also calculated at the intensity selection of 5%, according to the following formula:

$$EGA = (h^2{}_N\%)(\sigma P)(i)$$

The percentage of genetic improvement expected from the following equation was calculated:

$$EGA\% = (EGA/X) \times 100$$

The phenotypic variance was estimated from the sum of the genotypic and environmental variations on the assumption of the absence of genetic-environmental interference (Falconer, 1964) and the standard error of genetic and environmental variation was calculated according to Kempthorne (1957) according to the following equations**:**

$$SE(\sigma^2 G) = \sqrt{\frac{1}{r^2}\left[\frac{2(msg)^2}{k+2} + \frac{2(mse)^2}{k+2}\right]}$$

$$SE(\sigma^2 E) = \sqrt{\frac{2(mse)^2}{k+2}}$$

k = degrees of freedom for each source (genotypes or experimental errors).

r = the number of repeats

The standard error of phenotypic variance was estimated according to Mather and Jinks (1981) according to the formula:

$$SE(\sigma^2 p) = \sqrt{\frac{2(\sigma^2 p)^2}{N}}$$

Where N = the sum of degrees of freedom for the genotypes and the experimental error

The phenotypic (rP) and genetic (rG) correlations were estimated by the manner explained by Walter, (1975), as the variations of the phenotypic and hereditary co-influences shown in the equations were estimated:

$$\sigma_{Pxy} = \sigma_{Gxy} + \sigma_{Exy} \qquad \sigma_{Vxy} = \sigma_{Gxy} = \frac{MSgxy - MSexy}{r}$$

Genetic variation common to the traits X and Y = σ_{GxGy}

The phenotypic contrast between the traits X and Y = σ_{PxPy}

Environmental variation common to the traits X and Y σ_{ExEy} = Mse $_{xy}$

Then the phenotypic (rP) and phenotypic correlation coefficients (rG) between the studied trait pairs were estimated, and their significance was tested Al-Rawy (1980).

$$rP = \frac{\sigma_{Pxy}}{\sqrt{\sigma^2_{Px}\,\sigma^2_{Py}}} \quad rG = \frac{\sigma_{Gxy}}{\sqrt{\sigma^2_{Gx}\,\sigma^2_{Gy}}}$$

Cluster analysis was performed by means of the rate of each of the genotypes of the studied traits with the aim of placing the genotypes in groups according to the Sneath and Sokai response pattern (1973), The analysis was in two phases, the first includes the analysis of the basic components method, and the second includes a cluster analysis that includes several steps that begin with the formation of a proximities matrix and then the formation of the Dendogram according to the UPGMA method Sneath and Sokai , (1973) Distances are estimated that express the degree of similarity between the rates of the sum of the totals of the indicated matrix.

Results and Discussion

It is noted from Table (2) that the average squares of genotypes differed significantly at the level of 1% for all studied traits, and the presence of such a discrepancy between the genotypes in the traits gives an appropriate opportunity for plant breeders to conduct the evaluation Perform these genotypes and for important traits that can be used in future breeding programs. This study is consistent with (Ali *et al.,* 2008).

Table 2 : Analysis of variance for genotypes of traits studied in bread wheat

S.O.V.	Replications	Genotypes	Error
D.F. / Characters	**2**	**14**	**28**
Number of days at 50%	0.955	** 15.260	0.549
Plant height (cm)	106.621	** 63.932	8.501
Area flag leaf (cm^2)	63.741	** 80.020	7.708
Spike length (cm)	2.024	** 0.588	0.162
Number of spike $plant^{-1}$	6.342	** 4.620	0.701
Number of grains $spike^{-1}$	232.685	** 137.186	8.540
Grain yield (g)	23.888	** 13.331	2.215
Biological yield%	64.549	** 58.698	16.476
Harvest index**%**	168.220	** 28.589	7.821
1000grain weight (g)	2.0**02**	** 25.170	0.956
Protein ratio%	5.806	** 1.830	0.195

** Level of significance at 1%

The results shown in Table (3) indicate the significance of the phenotypic, genotypic and environmental variations of all studied traits. Observing the averages of the studied traits, there were differences between the values of the averages and the range. These differences were high for the characteristics of plant height, the flag leaf area, the number of grains $spike^{-1}$, biological yield $plant^{-1}$, harvest index and protein ratio, while the differences were low for the rest of the traits. Also, the coefficients of genotypic and phenotypic variation for all traits, as the highest values for coefficients of genotypic and phenotypic variation were for the grain yield and the number of spikes / plant and the lowest value for the number of days for flowering was 50% and average for the rest of the traits. Heritability values in the broad sense were high for all studied traits except for the spike length and biological yield characteristics, which were of medium value. The expected genetic improvement values as a percentage were average for the grain yield, number of grains $spike^{-1}$, weight of 1000 grains, number of spikes $plant^{-1}$, flag leaf area, and biological yield. While it is low for the rest of the trait the results show that the expected genetic improvement values were between medium to high for the majority of traits, and this indicates the importance of selection in improving these traits (Al-Taweel, 2009).

Table 3 : Average and range the estimation parameters and variations of genetic traits studied

Characters Genetic Parameter	Number of days at 50%	Plant height (cm)	Area flag leaf (cm^2)	Spike length (cm	Number of spike /plant	Number of grains /spike	Grain yield (g)	Biological yield%	Harvest index%	1000 grain weight (g)	Protein ratio%
Genotypic variance	4.904 ± 1.534	18.477 ± 6.455	24.104 ± 8.062	0.142 ± 0.060	1.306 ± 0.467	42.882 ± 13.802	3.705 ± 1.349	14.074 ± 6.020	6.923 ± 2.929	8.071 ± 2.531	0.545 ± 0.184
Environmental variance	0.549 ± 0.359	8.501 ± 5.565	7.708 ± 5.046	0.162 ± 0.106	0.701 ± 0.459	8.540 ± 5.591	2.215 ± 1.450	16.476 ± 10.786	7.821 ± 5.120	0.956 ± 0.626	0.195 ± 0.128
Phenotypic variance	5.453 ± 1.129	26.978 ± 6.995	31.812 ± 7.685	0.304 ± 0.095	2.007 ± 0.537	51.422 ± 11.467	5.920 ± 1.620	30.550 ± 9.589	14.744 ± 4.596	9.027 ± 1.881	0.740 ± 0.183
Mean	134.085	81.476	40.445	9.189	7.080	55.060	11.399	30.349	37.455	37.917	13.367
Rang	136-127	93.5 - 72.13	48.11-31.96	10-8.4	9.10-5.20	67.33-42.60	14.04-6.78	34.70-21.22	42.50-31.50	43.87-33.36	15.40-12.20
Genotypic coefficient variation	1.652	5.276	12.139	4.101	16.143	11.893	16.886	12.361	7.025	7.493	5.523
Phenotypic coefficient variation	1.741	6.375	13.946	6.000	20.011	13.024	21.345	18.212	10.252	7.924	6.436
Broad sense heritability	0.899	0.685	0.758	0.467	0.651	0.834	0.626	0.461	0.470	0.894	0.736
expected genetic improvement	4.326	7.328	8.804	0.531	1.899	12.319	3.137	5.245	3.714	5.534	1.305
expected genetic improvement%	3.226	8.994	21.767	5.774	26.827	22.373	27.520	17.284	9.916	14.595	9.764

Table (4) indicates the values of the genetic correlation coefficients (upper part) for the traits studied in bread wheat, It turns out that the adjective number of flowering days at 50% showed a positive and unimportant genetic correlation with all studied traits. With the exception of the protein ratio, weight of 1000 grains, and the length of the spike, as it was not significant in the negative direction, While we find that the genetic correlation for the height of the plant was positive and not significant for weight of 1000 grains As for the correlation with the other characteristics, it was not significant in the negative direction. The flag leaf area showed a positive and non-significant genetic correlation for all studied traits, except the protein ratio that was not significant and negative. The characteristic of the spike length showed a negative and genetically correlation non-significant for all studied traits, except for the protein ratio and number of grains spike^{-1} characteristics, which gave a positive and non-significant genetically correlation, and from the results of the table, we find that the number of spike plant^{-1} characteristics were genetically correlation non-significant and according to the characteristics of grain yield, harvest index, biological yield, number of grains spike^{-1}, while the genetic correlation was negative and non-significant for the protein ratio and weight of 1000 grains. We also find that the number of grains spike^{-1} characteristic was genetically positive and non-significant for all traits except the weight of 1000 grains that were correlated with negative and non-moral correlation with it. As for the weight of 1000 grains, harvest index, and protein ratio, the correlation was non-significant and negative. In the of the harvest index, it was found that the genetic correlation was insignificant according to the characteristics of grain yield and protein ratio and non- significant in the negative direction of weight of 1000 grains. As for the quality of the weight of 1000 grain, it was of a negative and non-significant genetic correlation for the two grain yield and protein ratio traits. Likewise, the genetic correlation of the protein ratio did not reach a significant and negative level with the grain yield trait.

Table (4) also shows the values of the correlation coefficients (the bottom part) of the traits studied in bread wheat It is noticed that the phenotypic correlation of the number of days of flowering at 50% was positive and significant at the level of 5% with the characteristics of grain yield and harvest index, and correlated significantly and positively with the area of the science leaf at the level of 1%. The height of the plant showed a significant and positive phenotypic correlation at the level of 1% for the weight of 1000 grains and the number of grains spike^{-1}. The phenotypic correlation of the trait of flag leaf area was significantly positive at the level of 5% of the traits of the grain yield, the biological yield, the number of grains spike^{-1}. The phenotypic correlation of the number of spike plant^{-1} traits was significant and positive at the level of 1% with the characteristics of grain yield and biological yield and was significant and negative at the 5% probability level for the protein ratio trait. The number of grains spike^{-1} had a positive and significant correlation at the level of 1% with the harvest index and negative and significant at the same level for the trait of the weight of 1000 grains. While the biological yield trait was correlation with positive and significant phenotypic correlation at the level of 1% with the trait of grain yield, negative and significant at the same level for the protein ratio trait. The protein ratio gave a negative phenotypic correlation at the 1% chance level with the grain yield characteristic. From the foregoing, the positive genetic correlation between two traits means that the genetic improvement of one of the two traits will be associated with the genetic improvement of the other trait and vice versa Al-Taweel (2017).

Table (5) shows the values of the genetic dimension between the studied genotypes Where he notes from a matrix Genetic affinity (15) and genotype (11) The relationship between them is high, followed by genetics (15) and genetics

(4). Next comes the genetic makeup (15) and the genetic makeup (12). Thus, the gradations between the values are from the main groups to the secondary and then the sub groups, The values of this dimension of these genotypes were consistent with their average performance in the outcome trait starting with genotype 11. From the foregoing, it is clear that the values of the genetic dimension can be inferred by predicting the superior genotypes. Similar results were indicated for this study by (Arain *et al.*, 2018; Al-Maliki, 2017).

Table 4 : Genetic correlation coefficients (upper part) and phenotypic (lower part) of the studied traits of bread wheat.

Characters	Correlations	Grain yield (g)	Protein ratio%	1000 grain weight (g)	Harvest index %	Biological yield %	Number of grains/ pike	Number of spike /plant	Spike length (cm)	Area flag leaf (cm^2)	Plant height (cm)
Number of days at 50%	G	0.139	-0.013	-0.043	0.125	0.081	0.057	0.093	-0.021	0.152	0.025
	P	*0.357	-0.166	-0.101	*0.346	0.178	0.189	0.219	-0.037	**0.413	0.085
Plant height (cm)	G	-0.061	-0.150	0.204	-0.070	-0.026	-0.256	-0.012	-0.199	-0.050	
	P	-0.106	*-0.372	**0.586	-0.218	0.069	**-0.637	0.031	*-0.347	-0.094	
Area flag leaf (cm^2)	G	0.101	-0.028	0.064	0.009	0.102	0.124	0.065	0.003		
	P	*0.350	-0.084	0.172	0.030	*0.365	*0.366	0.273	0.074		
Spike length (cm)	G	-0.038	0.048	-0.074	-0.059	-0.065	0.015	-0.077			
	P	0.124	0.154	-0.226	-0.117	0.125	0.179	-0.012			
Number of spike /plant	G	0.252	-0.142	-0.040	0.023	0.246	0.017				
	P	**0.852	*-0.376	-0.157	-0.019	**0.881	0.083				
Number of grains/spike	G	0.073	0.104	-0.193	0.116	0.027					
	P	0.287	0.278	**-0.555	**0.383	0.162					
Biological yield **%**	G	0.245	-0.190	-0.005	-0.009						
	P	0.921**	-0.457**	-0.059	-0.134						
Harvest index**%**	G	0.069	0.130	-0.087							
	P	0.183	0.179	-0.206							
1000grain weight (g)	G	-0.053	-0.078								
	P	-0.184	-0.208								
Protein ratio**%**	G	-0.145									
	P	-0.405**									

**،*at level 1 %, 5% at respectively.

Table 5 : the values of the genetic dimension between the genotypes studied in bread wheat

Case	Proximity Matrix														
	Squared Euclidean Distance														
	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15
G1	1	31.414	409.232	393.002	168.283	29.509	131.269	140.582	102.106	353.803	273.508	191.042	223.354	280.739	712.626
G2		1	346.014	405.130	110.984	14.853	124.807	171.193	81.654	287.029	209.382	165.628	159.697	254.072	709.018
G3			1	247.702	135.982	417.924	239.100	224.471	211.871	129.693	346.117	248.648	110.778	303.932	468.245
G4				1	312.364	404.672	394.900	441.363	417.405	462.016	233.313	124.640	304.889	780.797	986.300
G5					1	128.722	161.013	109.723	43.501	195.277	129.976	205.683	10.175	220.453	622.949
G6						1	169.630	188.948	101.152	376.128	180.045	186.599	175.732	321.328	840.862
G7							1	109.044	105.656	144.050	392.854	258.936	177.348	177.308	329.970
G8								1	44.640	213.934	378.567	363.988	123.597	126.761	389.397
G9									1	156.883	262.871	275.997	68.865	132.251	526.000
G10										1	534.730	351.405	197.590	184.484	402.913
G11											1	182.508	148.782	645.554	1127.980
G12												1	229.246	513.227	915.215
G13													1	232.004	613.259
G14														1	377.364
G15															1

It is noted from Figure (1) that the genotypes, including the two varieties accredited in Iraq (Tal Afar-3 and Bahut-4), were distributed in two main groups: the first main group which included the genetic makeup 15 while the second main group included two subgroups: The first sub-group that included the two genotypes 11 and 4, while the second sub-

group was divided into three subgroups: the first group, which included the genotype 3, and the second group that included the genotype 14, while the third group included two groups: the first group, the two genotypes 1 and 2, and the second group .The second group included the two genotypes 9 and 8, and the second group included the two genotypes 13 and 5.

From the cluster analysis in Figure (1), it was found that the two cultivars accredited in Iraq came in two main groups, the first was Bahut-4 (15), where it came alone in the first main group and has a genetic difference with the rest of the inserted genotypes and the adopted variety Tal Afar -3 (14) It came in the second subgroup, It is clear from the above that the inter of genotypes belonging to different groups starts from the main to the secondary and the sub to include all genes in the parental genotypes Which will enter into crosses to ensure their genetic spacing and obtain high results in terms of hybrid strength and Special federal ability in hybrids, and these results are in line with (Abu Al-King *et al.,* 2019; Poudel *et al.*, 2017).

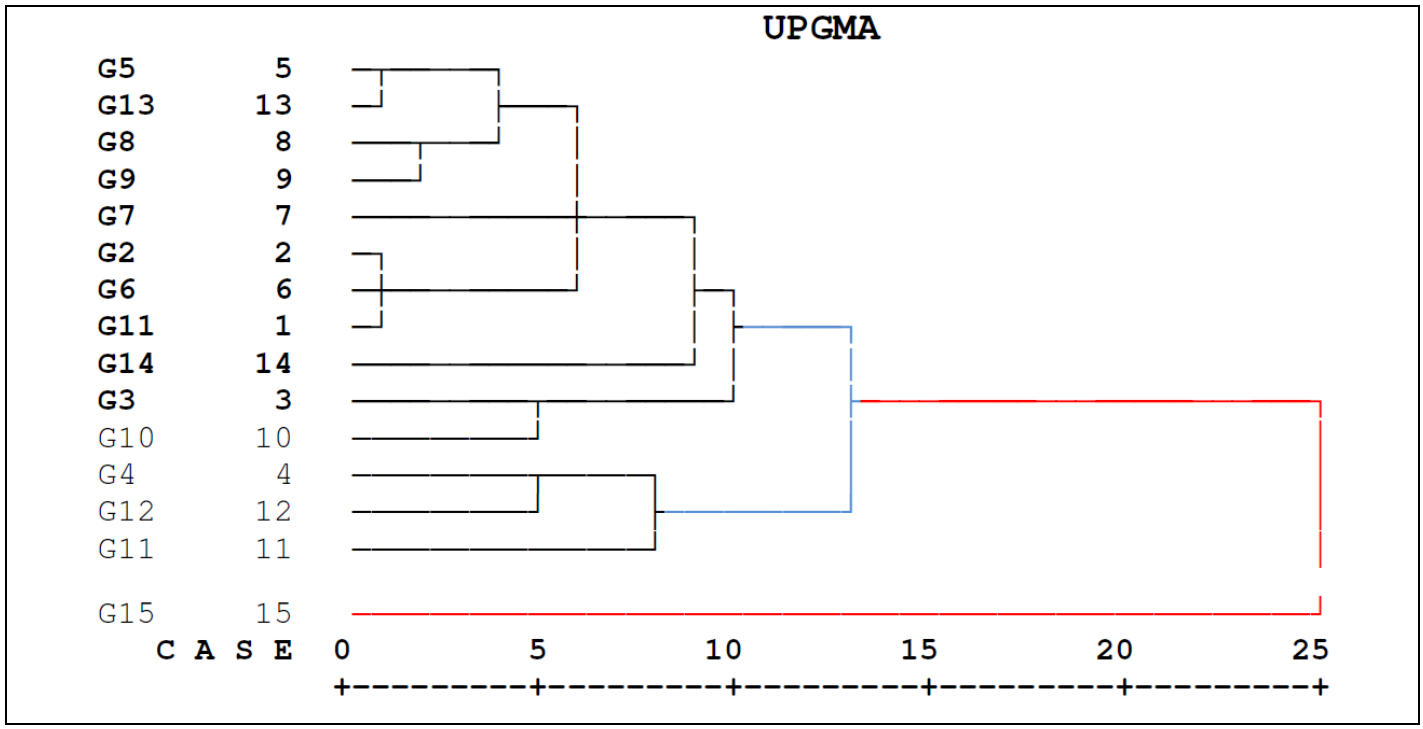

Fig. 1: Genetic relationships and groups of genotypes of wheat bread

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