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### Article

# **Estimation of genetic parameters for new entries of bread wheat** (*Triticum aestivum* L.)

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## ABSTRACT

The study was conducted in one of the fields of the Al-Yamja area, south of Mosul, which is (5) km from the city Centre for the season (2020-2021). Five genotypes of soft wheat were used, which were obtained from the Organization (C.I.M.M.Y.T.), adding an approved local cultivar (Abu Ghraib). The cultivation was carried out on lines with a length of (2) m and the distance between one line and another (30) cm using a randomized complete block design (R.C.B.D.) with three replications and in the manner explained by <sup>1</sup>. The study included the following traits: number of days to flowering at (50%), plant height (cm), spike length (cm), number of grains/spike, number of spikes/plant, vital yield (g/plant) and grain yield (g /plant). The weight of 100 grains and the harvest index %, where the analysis of variance table shows that all the genotypes showed significance at the probability level of 1% except for the trait number of spikes/plant, which was significant at the probability level of 5% and trait of the harvest index %. The statistical significance was not reached, and the studied phenotypic, genetic and environmental variance values showed that they were more significant than zero for all studied traits except for the genetic variance for the characteristic of harvest index %. Where it did not differ significantly from zero, it was noted that the values of heritability in the broad sense were high and for all the studied traits except for the trait number of spikes/plant was medium. The recipe of harvest index % was low. The values of the expected genetic improvement were as an average percentage for the traits of plant height, spike length and the number of grains/spike. The vital vield, grain vield and weight of 100 grains were low for the characteristics of the number of days to flowering at (50%), the number of spikes/plant and harvest index %. We note that the values of the genetic variation coefficient were the highest for a trait of spike length, number of grains/spike and biological yield, and the values of the phenotypic variation coefficient were the highest for the traits of spike length, number of grains/spike and biological yield.

Keywords: genetic parameters, bread wheat, Triticum aestivum L.

#### INTRODUCTION

Bread wheat (Triticum aestivum L.) is one of the most important food crops in the world; people all over the world depend on foods made from wheat, which are of important nutritional value because they contain proteins and carbohydrates as well as quantities of fats, vitamins, some mineral salts and amino acids. The basic human need is food. The estimated wheat production in Iraq is (4234) thousand tons for the season 2021, and the cultivated area of the wheat crop in Iraq is estimated (9464) thousand acres for the season 2021<sup>2</sup>. Studies in this field have been found. <sup>3</sup> found that the values of genetic and phenotypic variation coefficients were close to the traits of plant height, grain yield, number/spike, the weight of 1000 grains, and spike length <sup>4</sup> on high values of heritability in the broad sense of the second generation of bread wheat for the traits of plant height, flag leaf area, number of grains per spike, the weight of one thousand grains, biological yield, grain yield, harvest index and average spike length.<sup>5</sup> indicated that the values of the coefficient of variation were high for the grain yield, g/m2, and medium for the traits of the number of spikes/m2, the biological yield, g/m2, and the number of grains/spike, and low for the traits of plant height, the weight of 1000 grains and harvesting index, while the values of the genetic variation coefficient were high for the two traits of the number of grains/spike, grain yield, g/m2, the average for plant height, number of spikes/m2, biological yield, g/m2, the weight of 1000 grains, and harvest index. The values of the phenotypic variation coefficient were greater than those of the genetic variation coefficient for all traits. <sup>6</sup> found that the expected genetic improvement was high for spike length and 1000-grain weight. <sup>7</sup> reported that the expected genetic improvement values were less than 10% for the characteristics of the number of days until the expulsion of the spikes, the height of the plant, the number of grains per spike, the weight of one thousand grains and the yield of the individual plant <sup>5</sup> explained that the values of genetic variance were significant for the characteristics of plant height, grain/spike, weight of 1000 grains, harvest index and protein percentage.<sup>8</sup> found that the values of genetic and phenotypic variance were higher than those of environmental variance for all traits except for spike length, biological yield, g/plant, and harvest index%. This is due to genetic changes and their effects on traits and their effects on traits and little effect on the environment, where the selection is effective. At the same time, the environmental variance was higher than the genetic variance in the traits of spike length, biological yield, g/plant, and harvest index%.

#### MATERIALS AND METHODS

The study was conducted in one of the fields of Al-Yarmoja area, south of Mosul city, which is (5) km from the city center for the season (2020-2021), where five genotypes of soft wheat were used, which were obtained from Smit Organization (C.I.M.M.Y.T.) adding an approved local cultivar (Abu Ghraib) whose details are shown in Table (1)Cultivation was conducted on 11/26/2020 on lines with a length of (2) m and the distance between one line and another (30) cm using the randomized complete block design (R.C.B.D.) with three replications and in the manner explained by <sup>1</sup>.

genotype number	name	Source	lineage
1	GEROMTEL-3/12/ARTICO/AJAIA-3 //HUAL- ITA/10/	(C.I.M.M.T)	CDSS10Y00334S-099Y-055M- 7Y-0M-06Y-0B
2	SILVER-14/MOEWE//BISU-1/PATKA-3/3/PO- RRON-4/	(C.I.M.M.T)	CDSS11B00066S-086Y-031M- 15Y-0M
3	GUAYACAN INIA/GUANAY/8/GE- DIZ/FGO//GTA/3/	(C.I.M.M.T)	CDSS10Y00524T-099Y-044M- 5Y-2M-06Y-0B
4	CALERO/6/BCRIS/BICUM//LLARETA INIA/3/	(C.I.M.M.T)	CDSS12Y00036S-049Y-038M- 16Y-0M
5	CBC 509 CHILE/6/ECO/CMH76A.722//BIT/3/	(C.I.M.M.T)	CDSS12Y00724T-066Y-055M- 9Y-0M
6	Abu Ghraib	Inspection and certification of seeds - Nineveh branch	local cultivar

Table 1. shows the genotypes us	sed and their sources
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Triple superphosphate fertilizer was added at a rate of 160 kg/ha during the preparation of the land and urea fertilizer at an average of 240 kg/ha at an average of two batches, the first during the preparation of the land and the second when the plant reached the flowering stage <sup>9</sup>. The following traits were studied: number of days to flowering at (50%), plant height, spike length, number of grains/spike, number of spikes/plant, biofilm, grain yield, the weight of 1000 grains, and harvest index % for ten plants taken randomly from each experimental unit after excluding the terminal plants. Phenotypic, genetic, and environmental variances were estimated according to the method explained by <sup>10</sup>, heritability was estimated by the method explained by Singh and Chaudhary (1977), and the evidence shown by <sup>11</sup> was adopted. Heritability values in the broad sense are less than 40% and low, and from 40-60, The percentage is medium and from 60% or more high. The expected genetic improvement was estimated at 5% in the manner explained by <sup>16</sup> according to the data suggested by <sup>12</sup> for the expected genetic improvement limits, which are less than (10%) and low, between (10-30)%, medium and more than (30%). Also, the percentage of expected genetic improvement was calculated from the following equation:

$$EGA=i \sqrt{\frac{2}{\sigma}\rho} H2$$
(1)

$$EGA\% = (EGA/X) \times 100$$
(2)

H2 Inheritance in the broad sense

The standard deviation of phenotypic variance

E.G.A% represents the expected genetic improvement as a percentage of the overall mean of the trait.

E.G.A. represents the expected genetic improvement

X represents the mean of the adjective

i = 2.06

The process of calculating the values of genetic, environmental and phenotypic variation coefficients was conducted according to the method explained by <sup>13</sup> as in the following equation

#### RESULTS

Table (2) analysis of variance for the season (2020-2021) shows that the genotypes were significant at a probability level of 1%, and for all studied traits, the number of spikes/plant, which was significant at the probability level of 5%, and for the trait of harvest index %, which did not reach the statistical significance limit. These results agree with <sup>8, 14</sup>.

			mean squares M.S.								
sources of varia- tion(s.o.v)	de- grees of free- dom D.F.	Har- vest in- dex %	100- grain weight (gm)	Grain yield (gm/plant )	Biologi- cal Yield (gm/plant	Num- ber of spikes /plant	Number of grains /spike	Spike length (cm)	Plant height (cm)	Num- ber of days to 50%	
Replica- tion	2	5.712	0.005	0.418	1.998	0.767	16.948	0.204	0.365	0.167	
Genotypes	5	24.363	** 0.212	** 5.841	** 43.264	* 0.591	** 109.779	** 2.961	** 70.472	** 17.467	
Error	10	16.926	0.036	0.868	3.771	0.152	8.337	0.412	4.860	0.433	

# Table 2. Analysis of variance using a randomized complete block design for the studied traits in bread wheat for the season (2020-2021)<sup>1</sup>\*\* Scaled at 1% probability level, <sup>2</sup>\*Significant at a 5% probability level

Table (3) indicates the average values of the genotypes of the studied traits, where the characteristic of the number of days to flowering at (50%) showed that genotype (2) was earlier, with an average of (124.333) days, with a significant difference from all other genotypes, The trait of plant height (cm) showed that genotype (5) was the highest genotype, with an average of (85.267) cm, while genotype (1) was the lowest, with an average of (72.933) cm. The genetics used for this vary in plant height from one variety to another. The trait of spike length (cm) indicated that genotype (5) had the highest mean of (10,800) cm, while genotype (4) gave the lowest average of (8.066). These differences are due to the genetic factor between the genotypes, which led to some structures being distinguished from others in these cultivars. As for the trait of the number of grains/spike, genotype (5) gave the highest average (57,681), while genotype (6) gave the lowest average (41.199) for the recipe of the number of spikes/plant. It indicated that genotype (4) gave the highest average (9.433), while genotype (5) gave the lowest average (8.167). This trait is one of the components of the plant yield that is affected by genetic factors and many of the surrounding environmental conditions and agricultural processes in the plant. As for the characteristic of the biological yield, gm/plant, genotype (3) gave a higher average (34,809) g, while genotype (6) gave a lower average of (24.065) g, and these differences are due to genetic interaction with environmental conditions. At the same time, genotype (6) gave a lower average of (11.655) the increase in grain yield, which is an important achievement for the plant breeder. This is due to the phenotypic and physiological traits of the plant and the weight of 100 grains. It was found that genotype (1) gave a higher average of (3,850) g, while genotype (6) gave a lower average of (3,100) g. Thus, one genotype can be entered into breeding programs with other varieties to transfer the genes of high yield, weight of 100 grains. It is one of the main components of the yield. As for the trait of harvest index % in plants, genotype (2) gave the highest average of

Geno- types	Har- vest index %	100- grain weight (gm)	Grain yield (gm/plant )	Biological yield (gm/plant)	Num- ber of spikes /plant	Num- ber of grains /spike	Spike length (cm)	Plant height(cm)	Num- ber of days to50%
1	a	a	a	a b	b	bg	b	d	a
	47.494	3.850	15.689	33.301	8.433	50.560	8.400	72.933	130.333
2	a	b	a	g	b	a b	b	g d	d
	49.298	3.316	14.968	30.333	8.333	55.341	8.400	73.267	124.333
3	a	b	a	a	b	a b	b	g d	a b
	41.758	3.223	14.526	34.809	8.600	54.420	9.100	77.333	129.667
4	a	b	a	g	a	g	b	b	b
	49.240	3.267	14.368	29.171	9.433	47.819	8.066	80.500	129.000
5	a	b	a	a b g	b	a	a	a	b
	46.460	3.210	14.869	32.112	8.167	57.681	10.800	85.267	129.000
6	a	b	b	d	b	d	b	g d	g
	48.549	3.100	11.655	24.065	8.667	41.119	8.600	74.400	125.667
The gen- eral aver- age of traits	47.133	3.328	14.346	30.632	8.606	51.157	8.894	77.283	128.000

(49.298), while genotype (3) gave the lowest average of (41.758) and did not differ significantly from the traits of the genotypes.

Table 3. Averages of genotypes and cultivars for nine traits of the season (2021-2020)

Table (4) indicates the phenotypic, genetic and environmental variances. The values of phenotypic and environmental variance were significant from zero for all studied traits, and the values of genetic variance were significant from zero for all traits except for the traits of harvest index %, which did not differ significantly from zero. The performance of the genotypes in these traits is due to a degree. These results are consistent with <sup>8, 5, and 3</sup> in most studied traits.

Table (5) shows heritability in the broad sense and the expected genetic improvement as a percentage of the mean trait and the coefficients of genetic and phenotypic variation. The values of heritability in the broad sense were high, and for all the studied traits except for the trait of the number of spikes/plant was medium. For the trait of harvest, the index % was low, while the values of the expected genetic improvement were as a mean percentage for all traits except for the traits of the number of days to flowering at (50%) and the number of spikes/plant and index harvest% These results agree with <sup>8</sup> and <sup>5</sup>.

ge-					traits	}			
netic	Har-	1000-	Grain	Biologi-	Number of	Number of	Spik	Plant	Num-
con-	vest	Grain	yield	cal yield	spikes/plan	grains/spik	e	height(cm)	ber of
stant	index	weigh	(mg/pla	(gm/plan	ts	es	lengt		days
S	%	t	nt	t)			h		to50
		(gm)					(cm)		%
$\sigma^2 P$	19.40	0.095	2.526	16.936	0.298	42.151	1.26	26.730	6.111
S.E.	5						1		
	±	±	±	±	±	±	±	±	±
	3.543	0.017	0.461	3.092	0.054	7.696	0.23	4.880	1.116
							0		
σ²G	2.479	0.059	1.658	13.164	0.146	33.814	0.85	21.871	5.678
S.E.							0		
	±	±	±	±	±	±	±	±	±
	3.220	0.025	0.692	5.109	0.071	12.957	0.35	8.316	2.059
							1		
$\sigma^2 E$	16.92	0.036	0.868	3.771	0.152	8.337	0.41	4.860	0.433
S.E.	6						2		
	±	±	±	±	±	±	±	±	±
	4.370	0.009	0.224	0.974	0.039	2.153	0.10	1.255	0.112
							6		

Table 4. Phenotypic, genetic and environmental variances for the season (2020-2021)

Traits	inher- itance of broad sense	Expected genetic im- provement	Expected genetic im- provement as a per- centage of the mean of the trait	genetic variation coefficient	coefficient of phenotypic variation
Number of days to50%	0.929	4.731	3.696	1.862	1.931
Plant height(cm)	0.818	8.714	11.276	6.051	6.690
Spike length (cm)	0.673	1.558	17.519	10.636	12.627
Number of grains/spikes	0.802	10.729	20.973	11.367	12.691
Number of spikes/plants	0.491	0.552	6.418	4.447	6.347
Biological yield (gm/plant)	0.777	6.590	21.512	11.845	13.435
Grain yield(mg/plant)	0.656	2.149	14.977	8.974	11.078
1000-Grain weight (g)	0.620	0.393	11.805	7.278	9.244
𝔅 Harvest index	0.128	1.159	2.460	3.341	9.346

Table 5. heritability in the broad sense and the expected genetic improvement as a percentage of the mean of the trait

#### DISCUSSION

We note that the highest coefficient of genetic and phenotypic variation was (11.845 and 13.435), respectively, for the characteristic of the bio-crop, g/plant and that the values of the coefficient of phenotypic variation were higher than the values of the coefficient of genetic variation for all the studied traits, and this indicates the great role of the environmental influence in changing the traits. These results are consistent with <sup>8, 15.</sup>

#### CONCLUSIONS

The study concludes the evaluation and estimation of the genetic, phenotypic and environmental variations of the traits of new inputs of soft wheat sourced from S.M.T., in addition to studying the heritability and genetic improvement expected in percentage to benefit from these methods in determining the appropriate breeding method.

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