Study some of genetic constants in new entries of Durum wheat under dry land conditions

Whadhah Thabit Abd al-dahi ⁽¹⁾	Mohammad Subhi Al-Taweel ⁽²⁾
⁽¹⁾ Department of Plant Production/	⁽²⁾ Department of Field Crops/
College of Agricultural Technology /	College of Agriculture and
Northern Technical University – Mosul	Forestr /University of Mosul
wadah8324@ntu.edu.iq	draltwel@uomosul.edu.iq

Abstract

1

A field experiment was carried out during the season 2019/2020 in Mosul/Tilkif. It included six introduced genotypes of durum wheat originating from International Center for Agriculture Research Dry areas (ICARDA) (Nano, Uramy, Miki3, Ouhassan and Atlhagy) and local variety Svivo for control. Six durum wheat genotypes were grown by using R.C.B.D. design with three replications. The results indicated that the means of the genotypes squares were significant at a 1% probability level for the traits of the flag leaf area, plant height, spike length, number of grains per spike, biological yield, grain yield, harvest index, and 1000 grains weight. Genetic and phenotypic variation were significant for all the studied traits, except for the traits of the number of days until the beginning of flowering, number of tillers .m⁻², and protein percentage, for phenotypic variation were not significant. Grain yield had positively significant phenotypic correlation at a 1% probability level with traits: flag leaf area, spike length, number of grains per spike, biological yield and harvest index and protein percentage. Whereas, grain yield showed a positive significant environmental correlation by 5% probability level with the biological yield and weight of 1000 grains traits. However, the values of heritability of broad sense were high for all the studied traits, except for the traits of the number of days until the beginning of flowering and protein percentage was medium, while, heritability of the number of tillers .m⁻² was low.

Keywords: durum wheat, genetic correlation, heritability of broad sense. The research is based on the doctoral thesis of the first researcher

حنطة الخشنة في المناطق الديمية	در اسة بعض الثوابت الور اثية لمدخلات جديدة من اا
محمد صبحي الطويل	وضاح ثابت عبد الضاحي
سم المحاصيل الحقار فركار في الذير إعة ما اخارات	قسم الانتاج الزرات /الكارة التقارية الزر إعرية/
مم المحاصيل الحقية المية المرواعة والعابات	لسم ، 2 تاج (مبايي (ملعيه - المعيه - المرومي)
جامعة الموصل	الجامعة التقنية الشمالية-الموصل
	draltwel@uomosul.edu.iqWadah8324@ntu.edu.iq

الخلاصة

نفذت تجربة حقلية خلال الموسم 2020/2019 في الموصل/ قضاء تلكيف، تضمنت ستة تراكيب وراثية مدخلة من الحنطة (Atlhagy Ouhassan 'Miki3 'Uramy 'Nano' (ايكاردا) Ouhassan 'Miki3 'Uramy 'Nano' وبثلاث مكررات. اشارت اضافة ألى الصنف المحلي سفيفو بهدف المقارنة. وطبق تصميم القطاعات العشوائية الكاملة R.C.B.D. وبثلاث مكررات. اشارت النتائج الى أن متوسطات مربعات التراكيب الوراثية كانت معنوية عند مستوى احتمال 1. لصفة مساحة ورقة العلم، وارتفاع النبات، وطبق تصميم القطاعات العشوائية الكاملة Ouhassan 'قرون المرات الشارت النبات، النتائج الى أن متوسطات مربعات التراكيب الوراثية كانت معنوية عند مستوى احتمال 1. لصفة مساحة ورقة العلم، وارتفاع النبات، وطول السنبلة، وعدد الحبوب بالسنبلة، والحاصل الحيوي، وحاصل الحبوب، ودليل الحصاد، ووزن 1000 حبة. كما ان التباين الوراثي كان معنوي لجميع الصفات المدروسة فيما عدا صفة عدد الايام لغاية بداية التزهير، وعدد الأسطاء. م²، ونسبة البروتين، كان التباين الوراثي كان معنوي لجميع الصفات المدروسة فيما عدا صفة عدد الايام لغاية بداية التزهير، وعدد الأسطاء. م²، ونسبة البروتين، كان التباين الوراثي كان معنوي لجميع الصفات المدروسة فيما عدا صفة عدد الايام لغاية بداية التزهير، وعدد الأسطاء. م²، ونسبة البروتين، كان التباين الوراثي كان معنوي لجميع الصفات المدروسة فيما عدا صفة عدد الايام لغاية بداية التزهير، وعدد الأسطاء. م²، ونسبة البروتين، كما وارتبل كان التباين المظهري معنوي لجميع الصفات المدروسة. ارتبط حاصل الحبوب ارتباطاً مظهرياً موجب المعنوية عند مستوى احتمال 1. مع مساحة ورقة العلم، وطول السنبلة، وعدد الحبوب بالسنبلة، والحاصل الحيوي ودليل الحصاد، وزن 1000 حبة. في اورتبل حاصل الحبوب ارتباطاً مظهرياً موجب المعنوية. عند مستوى احتمال 2. مع مساحة ورقة العلم، وطول السنبلة، وعدد الحبوب بالسنبلة، والحاصل الحبوب بالسنبلة، والحاصل الحيوي ودليل الحصاد، ونسبة البروتين. كما وارتبل حاصل الحبوب ارتبل ليبي في ورين 1000 حبة. في مالتوريث بالمعنى حاصل الحبوب ارتباط بيئي موجب المعنوية عند مستوى احتمال 5. مع الحاصل الحبوي، ووزن 1000 حبة. فيمالتوريث بالمعنى حاصل الحبوب ارتبا بينما كان واطئ لصفة عدد الأشطاء. م².

كلمات مفتاحية: الحنطة الخشنة، المعالم الوراثية، الارتباط الوراثي، التوريث بالمعنى الواسع.

Introduction

Durum wheat (Triticum durum Desf.) Constitutes 8% of the global cultivated area The Mediterranean region is the largest production area for Durum wheat in the world (1). The cultivated area in Iraq, according to the Agricultural Statistics Directorate, is estimated at 571.000 hectares, with a productivity of 415.000 tons The (2). cultivation of Durum wheat is concentrated in the rainy-guaranteed area of Iraq, especially in the areas surrounding the province of Nineveh, and this is due to the reliance of a large number of the residents of these areas on it for food in the work of grain, macaroni, bulgur and sabkati. This type of wheat contains two types of chromosomes, namely A and B, in which the binary number of chromosomes 2n = 28. The use of promising varieties is a very important factor to increase the yield of wheat because the final yield is the result of the interaction of environmental and genetic factors and agricultural processes, and it is possible to increase the grain yield by 10% to 80% when selecting promising varieties under favorable environmental conditions (3). Aljehashy (4) showed that the values of genetic, environmental and phenotypic variation were significant for the number of tillers .m⁻², plant height, weight of 1000 grains, grain yield, and biological yield, and the environmental and phenotypic variances were also significant for the number of seeds per spike and harvest index. Al-Mailiky et al (5) showed that

genetic, phenotypic and environmental variations are significant and highest with traits: plant height, number of seeds per spike, grain yield, and weight of 1000 grains. Aljehashy (4) showed that the grain yield trait has a genetic, positive and significant correlation with each of the trait of the number of grains in spike, the biological yield, the weight of 1000 grains, and the harvest index. Al-Najjar (6) found that the heritability values in a broad sense were high for the traits of seed number per spike, weight of 1000 grains, plant height, and grain yield. Whereas, Azimi et al. (7) found that the values of heritability of broad sense were high for the trait of the number of days until flowering, plant height, number of grains per spike, weight of 1000 grains, grain yield, biological yield, and harvest index. The aim of the study is to identify some of the genetic constants, including genetic variances, environmental phenotypes, genetic, phenotypic, environmental correlation, and heritability of broad sense in traits of grain yield and its components.

materials and methods

The experiment was carried out in the 2019-2020 agricultural season in a semi-rainy area (Mosul / Telkif district), It included five insertion genotypes sourced from ICARDA (Nano, Uramy, Miki3, Ouhassan and Atlhagy) in addition to a local variety (Svivo) for control whose lineages are shown in Table (1).

NO.	name	Proportions
Genotype		^
		Icasyr1/3/Bcr/Sbl5//T.urartu/6/319-ADDO/5/D68-1-93A-
1	Nano	1A//Ruff/Fg/3/Mtl5/4/Lahn/7/Icamor-TA04-71//Icamor-TA04-
		59/Arislahn10/3/Mgnl3/Ainzen1
		Mrb3*2/Turartu500651//IcamorTA0463/Bigost2/3/Grvand1/Bushen3
2	Uramy	/5/Ter1/3/Stj3//Bcr/Lks4/4/Icajihan18
3	Miki3	Stj3//Bcr/Lks4
		Ouasloukos1/5/Azn1/4/BEZAIZSHF//SD19539/Waha/3/Gdr2/6/Agh
4	Ouhassan	rass1/Bezaiz981//Icajihan1
		Mgnl3/Aghrass2/4/IcamorTA0462/3/Arislahn7//CI115/Bcrch1/5/Belt
5	Atlhagy	agy1/7/Icasyr1//Mrf2/T.dids20123/6/319ADDO/5/D68193A1A//Ruff
		/Fg/3/Mtl5/4/Lahn
6	Svivo	Local

The experiment was carried out according to R.C.B.D. By three replicates, the genotypes were randomly planted. Each experimental unit contained four lines, 1 meter long and 15 cm distance between the lines. The experiment was fertilized with urea fertilizer at a concentration of 45% at a rate of 20 kg / dunum (8), and in two batches, the first when planting and the second before the spikes were expelled. Comparisons between the averages were made using the Duncan method. The following traits were studied, number of days until the beginning of flowering, flag leaf area, plant height, spike length, number of tillers.m⁻ , number of grains per spike, biological yield, grain yield, Harvest index, 1000 grains weight, and protein percentage, and the genetic constants of these traits including phenotypic, genetic and environmental variations were estimated according to the method explained by Walter (9).

$$\sigma_{v}^{2} = \sigma_{G}^{2} = \frac{Msg-Mse}{r}$$

$$\sigma_{E}^{2} = Mse$$

$$\sigma_{P}^{2} = \sigma_{G}^{2} + \sigma_{E}^{2}$$

Then the phenotypic (rP), genotype (rG) and environmental correlation coefficients were estimated between the studied trait pairs, and their significance was tested in the manner explained by the AL-Rawi and Khalaf Allah (10).

$$rP = \frac{\sigma_{Pxy}}{\sqrt{\sigma^2 P_x \sigma^2 P_y}}$$
$$rG = \frac{\sigma_{Gxy}}{\sqrt{\sigma^2 G_x \sigma^2 G_y}}$$

$$rE = \frac{\sigma_{Exy}}{\sqrt{\sigma^2_{Ex}\sigma^2_{Ey}}}$$

and heritability of broad sense according to the following equation:

$$H = \frac{\sigma_G^2}{\sigma_P^2} \times 100$$

The ranges shown were adopted by Ali (19). The values of heritability of broad sense are less than 40% low, 40-60 medium and more than 60 high. SAS, Microsoft Office Excel and Minitab were used in implementing all statistical procedures.

Results and discussion

Table (2) shows the results of the analysis of variance of six genotypes of durum wheat, as it is noticed that the mean of squares of the genotypes were significant at a probability level of 1% for all traits, except for the traits of the number of days until flowering and the number of tillers .m⁻², and the percentage of protein, which did not reach the level of significance, as the significance of the studied traits is important to continue the genetic analysis in order to identify the appropriate methods for breeding the crop, and this corresponds to what (11), and (12) and (6).

Table (3) shows the genotypes averages for eleven traits, and from it becomes clear that there are differences in the genotypes and for most of the studied traits, as the highest significant values of the flag leaf area and spike length were at each of the genotypes Ouhassan and Atlhagy, as for plant height, the genotype Miki3 and Atlhagy and the local genotype Svivo are superior. As for the number of seeds per spike, it surpasses the genotype Nano and Ouhassan, and Atlhagy genotype is unique in recording the highest biological yield. While the highest grain yield was at the Ouhassan genotype, while the Uramy genotype recorded the highest values of the evidence for harvesting index and the 1000 grains weight, while the genotypes did not show significant differences between them for both the trait, the number of days until the beginning of flowering, and the number of tillers .m⁻², and protein percentage. Through these results, we can select the Ouhassan genotype, as it was the record of the highest

grain yield and significantly among the genotypes used in the study.

Tab	ole (2)	the results	of the anal	ysis of	f varia	ance of t	he mean	squares of t	the studied tra	aits.
		-	-			-				

Sources of variance	replication	Genotypes	Error
D.f	2	5	10
Traits		M.S.	
NO. of days until flowering	0.351	0.766 n.s	0.611
Flag leaf Area (cm ²)	2.062	31.174**	1.129
Plant height (cm)	0.030	33.886**	0.693
Spike length (cm)	0.001	0.569**	0.038
number of tillers .m ⁻²	2082.350	1092.460 n.s	1572.180
No. of grains / spike	5.689	53.101**	2.373
Bio. yield (gm.m ⁻²)	538.869	49943.366**	45.077
grain yield (gm.m ⁻²)	21.390	8572.866**	0.447
Harvest index%	0.250	36.715**	0.028
1000- grains weight	1.560	14.929**	2.299
protein %	0.173	0.188n.s	0.166

(**) and (*) were significant at 1% and 5% likelihood levels, respectively.

Table (3): averages of genotypes for the studied traits.

Genotypes	Nano	Uramy	Miki3	Ouhassan	Atlhagy	Svivo
						local
Traits						
No. of days until	121.18 a	121.14 a	121.51 a	120.48 a	121.48 a	122.00 a
flowering						
Flag leaf Area	38.16 c	35.58 d	40.22 b	42.55 a	44.01 a	37.29 cd
(cm^2)						
Plant height (cm)	83.05 c	81.63 c	89.03 a	87.01 b	89.63 a	88.60 a
Spike length (cm)	6.24 b	6.29 b	5.98 c	6.77 a	6.84 a	5.73 c
No. of tillers .m ⁻²	348.59 a	322.04 a	355.63 a	365.44 a	373.85 a	370.30 a
No. of grains /	46.76 a	37.94 c	40.57 c	47.71 a	43.83 b	38.39 c
spike						
Bio. yield $(gm.m^{-2})$	1110.03	1177.03	1233.67	1359.42b	1396.73	1083.22
	e	d	с		а	f
Grain yield (gm.m ⁻	341.43	379.53 c	276.45 f	419.57 a	401.73 b	323.34 e
²)	d					
Harvest index%	30.76 b	32.24 a	22.41 e	30.86 b	28.76 d	29.85 c
1000- grains	43.49 b	49.78 a	45.00 b	45.00 b	45.73 b	44.10 b
weight						
Protein %	14.50 a	14.21 a	14.07 a	14.70 a	14.53 a	14.64 a

Values followed by similar letters do not differ significantly from each other at 5% Duncan teast.

Table (4) shows the phenotypic, genetic and environmental variance. The phenotypic variance was significant for all the studied traits. As for the genetic variation, it was significant for most of the studied traits, except for the traits of the number of days until the beginning of flowering, and the number of tillers $.m^{-2}$, and the percentage of protein, and this is consistent with what they found (13),(11),(14). As for the environmental variation, it did not reach the point of significance and for all the studied traits.

Table (A) the	genetic	nhenotypic	and	environmental	variation	of the	studied traits
Table (4) the	genetic,	phenotypic	anu	environmental	variation	or the	studied traits.

Traits	Phenotypic	Environmental	Genetic	
	variance	variance	variance	
No. of days until	0.391	0.204	0.188	
flowering	土	±	±	
	0.142	0.273	0.317	
2	10.642	0.376	10.266	
Flag leaf Area (cm ²)	±	±	±	
	3.886	0.504	6.591	
	11.450	0.231	11.219	
Plant height (cm)	±	±	±	
	4.180	0.310	7.150	
	0.198	0.013	0.186	
Spike length (cm)	±	±	±	
	0.072	0.017	0.121	
2	713.527	524.061	189.466	
No. of tillers .m ⁻²	±	±	±	
	260.543	703.101	739.861	
	18.228	0.791	17.437	
No. of grains / spike	±	±	±	
	6.655	1.061	11.245	
D: 11(-2)	16657.806	15.026	16642.780	
B10. yield $(gm.m^2)$	±	<u>±</u>	±	
	6082.570	20.159	10529.005	
~ · · · · · · · · · · · · · · · · · · ·	2857.722	0.149	2857.573	
Grain yield (gm.m ²)	±	±	<u>+</u>	
	1043.492	0.199	1807.319	
	12.245	0.010	12.235	
Harvest index%	±	<u>±</u>	±	
	4.471	0.012	7.740	
1000	5.487	0.766	4.721	
1000- grains weight	<u>+</u>	±	±	
	2.003	1.028	3.311	
	0.089	0.039	0.050	
Protein %	±	±	±	
	0.032	0.052	0.065	

Table (5) show that there is no significant genetic correlation, whether positive or negative, for all the traits included in the study except for the traits of the area of the leaf flag, where it was genetically positively correlated with the moral with the biological yield at a probability level of 5% This result is consistent with what he found (4). The environmental correlation was negative in significance and at a probability level of 1% between the number of days until the beginning of flowering and each of the traits of protein percentage, number of tillers .m⁻², spike length, and flag leaf area, While the positive morale was at a probability level of 5% with the height of the plant and did not reach the level of significance with grain yield, 1000 grains weight, harvest index, biological yield, and the number of grains per spike. The traits of plant height were correlated with a positive environmental correlation at a probability level of 1% with the number of tillers .m⁻² and at a probability level of 5% with the number of grains per spike. This trait was correlated with a negative environmental correlation with the significant one at the level of probability of 1% with the percentage of protein, while it did not reach one of the significant with the rest of the traits. flag leaf area was correlated with a positive environmental and significant correlation at a probability level of 1% with the traits of protein percentage, 1000 grains weight, biological yield, number of tillers $.m^{-2}$ and spike length. This correlation was negatively with the harvest index, while it did not reach the limit of significance with the yield of seeds and the number of grains per spike. spike length was correlated with a significant positive environmental correlation at a probability level of 1% with the 1000 grains weight, and the number of tillers .m⁻², while it did not reach the significant level with the grain yield, protein percentage, harvest index, biological yield, and number of seeds per spike. The number of tillers .m⁻² correlated positively with the environment at the 5% probability level with 1000 grains weight, while it did not reach the significant level with the rest of the traits. The number of grains per spike was correlated with a significant negative environmental correlation

at a probability level of 5% with the grain yield, and the significant level did not reach the other traits. The biological yield was correlated with a positive and significant environmental correlation at the 5% probability level with the and a negative significant yield, grain correlation at the 1% probability level with the harvest index. The 1000 grains weight were associated with a significant positive environmental association at a 5% chance level with the grain yield. The protein percentage correlated negatively with significant environmental correlation at a 1% probability level with grain yield. as for the phenotypic correlation, the trait of the number of days until the beginning of flowering was correlated with a negative morphological correlation at a probability level of 1% with the grain yield, the number of grains per spike, and spike length, while the negative significance was at a 5% probability level with the biological yield and flag leaf area and positive significance with plant high. The plant height was also correlated with a negative morphological correlation at the probability level of 1% with 1000 grains weight, the harvest index, and the positive significance with the biological yield, the number of tillers $.m^{-2}$ and the flag leaf area, while it did not reach the level of significance with another trait. flag leaf area, was also correlated with a positive and significant correlation at the probability level of 1% with the grain yield, biological yield, number of seeds per spike, number of tillers .m⁻² and the spike length, while the negative significance was at the 5% probability level with harvest index. Spike length was correlated with a positive significant phenotypic correlation at 1% probability level with grain yield, biological yield and number of grains per spike, and it was at 5% probability level with harvest index. The number of tillers .m⁻² was correlated with a positive significant phenotypic correlation at 5% probability with protein percentage and negative significant with a 1000 grains weight, while it did not reach the significance with other traits. The number of grains per spike was correlated with a positive-significant phenotypic correlation at the 1% probability level with the grain yield, protein percentage

and biological yield, and negative significance with the 1000 grains weight. The biological vield was correlated with a positive-significant phenotypic correlation at the 1% probability level with the grain yield while it did not reach the significant level with the rest of the traits. Harvest index also correlated positively with the significant phenotypic correlation at the 1% probability level with the grain yield and did not reach the significant extent with the rest of the traits. Protein percentage was correlated with positive significant phenotypic a correlation with grain yield. These results are in agreement with (15) and (16). Through these results, we conclude that the yield traits were correlated with a positive and significant environmental correlation with the biological yield and the weight of 1000 grains, and the grain yield was correlated with a positive morphological correlation with flag leaf area, spike length, number of grains per spike, biological yield, harvest index, and protein percentage. including It is the positive and significant value of the connection between two traits that are considered an indicator of the possibility of selecting the two traits at the same time, meaning that selecting one of them means selecting for the other trait.

traits	Correlation	Grain yield	Protein	Weight of	Harvest	Bio. yield	No. of	No. of	Spike length	Flag leaf	Plant
		$(gm.m^{-2})$	%	1000 grains	index%	$(gm.m^{-2})$	grains/spike	tillers .m ⁻²	(cm)	Area	height
										(cm^2)	(cm)
No. of days until	G	-0.213	0.045	-0.049	-0.117	-0.161	-0.236	0.230	-0.185	-0.060	0.118
flowering	Ε	0.264	-0.442 **	-0.114	-0.027	0.208	0.197	-0.422 **	-0.566 **	-0.613 **	0.291 *
	Р	-0.473 **	-0.081	-0.158	-0.263	-0.352 *	-0.462 **	-0.103	-0.589 **	-0.290 *	0.315 *
Plant height (cm)	G	-0.059	0.080	-0.157	-0.207	0.148	-0.001	0.268	0.006	0.227	
	Ε	0.193	-0.475 **	-0.014	0.117	-0.079	0.420 *	0.409 **	-0.048	-0.266	
	Р	-0.175	-0.146	-0.435 **	-0.615 **	0.438 **	0.023	0.599 **	0.013	0.648 **	
Flag leaf Area	G	0.132	0.073	-0.122	-0.101	0.295 *	0.206	0.207	0.228		
(cm^2)	E	-0.022	0.656 **	0.490 **	-0.504 **	0.382 **	-0.051	0.421 **	0.516 **		
	Р	0.389 **	0.209	-0.268	-0.302 *	0.872 **	0.589 **	0.511 **	0.699 **		
Spike length (cm)	G	0.285	0.095	0.050	0.100	0.285	0.213	0.004			
	E	0.205	0.138	0.445 **	-0.240	0.259	0.164	0.466 **			
	Р	0.830 **	0.261	0.215	0.288 *	0.832 **	0.623 **	0.188			
No. of tillers .m ⁻²	G	0.019	0.201	-0.284	-0.092	0.128	0.094				
	E	0.011	0.000	0.300 *	-0.245	0.103	0.240				
	Р	0.036	0.303 *	-0.339 *	-0.188	0.251	0.254				
No. of grains /	G	0.151	0.156	-0.163	0.052	0.150					
spike	E	-0.306 *	0.241	-0.178	-0.266	0.197					
	Р	0.443 **	0.422 **	-0.473 **	0.149	0.442 **					
Bio. yield (gm.m	G	0.202	0.043	0.044	-0.048						
²)	E	0.354 *	0.260	0.075	-0.933 **						
	Р	0.605 **	0.110	0.124	-0.145						
Harvest index%	G	0.233	0.191	0.098							
	Е	-0.078	-0.496	0.036							
	Р	0.699 **	0.434	0.274							
1000- grains	G	0.108	-0.151								
Weight	Е	0.383 *	-0.065								
	Р	0.304	-0.360								
	G	0.187									
Protein %	Е	-0.621 **									
	Р	0.435 **									

Table (5) the genetic correlation coefficients (upper part), environmental (middle part) and phenotypic (lower part) for the studied traits.

(**) and (*) were significant at 1% and 5% likelihood levels, respectively.

Table (6) shows heritability of broad sense of the studied traits, as it is noticed that the values of heritability of broad sense were high for all the studied traits except for the two traits of number of days until the beginning of flowering, and protein percentage where heritability of broad sense was average, while the trait of the number of tillers $.m^{-2}$ was low. The high values of heritability are an indication of the possibility of inferring the genotype of the desired traits through the phenotype of the trait. These results are consistent with the findings of the trait (17), (18) and (4).

Table (6):	Heritability	values i	n the	broad	sense	of the	studied	traits.
1 4010 (0).	including	raraes i		orouu	001100	01 1110	braarea	u ai coi

NO.	traits	Heritability of broad sense
1	No. of days until flowering	47.959
2	Flag leaf Area (cm ²)	96.465
3	Plant height (cm)	97.982
4	Spike length (cm)	93.588
5	No. of tillers .m ⁻²	26.554
6	No. of grains / spike	95.660
7	Bio. yield $(gm.m^{-2})$	99.910
8	Grain yield (gm.m ⁻²)	99.995
9	Harvest index%	99.921
10	1000- grains Weight	86.034
11	Protein %	56.198

References:

- (1) Bonjean (A.P.; W.J. Angus; and M. van Ginkel (2016). The World Wheat Book: A History of Wheat Breeding. Vol3. Paris: Lavoisier.
- (2) Agricultural Statistics Directorate / Central Statistical Organization / Iraq. Wheat production for the year 2020.
- (3) Al-sarag 'E.I. 'and R.I.M. Ismaeil ' (2015). Evaluation of some bread wheat cultivars productivity as affected by sowing dates and water stress in semiarid region. Asian J. Crop Sci. '5(2): 167-178.
- (4) Al-jehashy 'Abdullah Khder Mohammad (2020). Cluster Analysis of Genotypes in bread Wheat Triticum eastivum L. and study of genetic architecture for grain yield traIts and it's components using dialed cross analysis. Master Thesis. Field Crops Department. College of Agriculture and Forestry. University of Al Mosul.
- (5) Al –Mailiky 'R. J. M. 'M. S. Mizel and M. I. Zaid (2019). Estimation of some

genetic parameters and correlation in varieties of bread Wheat under the conditions of Wasit Governorate. Muthanna journal of Agriculture Science. 7 (3): 316-324.

- (6) Al-Najjar 'Safwan Mohammad Younis (2020). Estimation of Genetic parameters 'path analysis and Genetic distance of introduced genotypes from bread wheat for different cultivation spaces. Master Thesis. Department of Field Crops. College of Agriculture and Forestry. University of Mosul.
- (7) Azimi 'A. M. 'S. Marker and I. Bhattacharjee (2017). Genotypic and phenotypic variability and correlation analysis for yield and its components in late sown wheat (*Triticum aestivum* L.). J. of Pharmacognosy and Phytochemistry. 6(4): 167-173.
- (8) Al-Kubaisi Ahmad Madloul Muhammad and Hamad Muhammad Salih (2000). Schedule irrigation and fertilization of the wheat and barley crops using the pivot irrigation method. Ministry of Agriculture - General

Authority for Agricultural Extension and Cooperation.

- (9) Walter A. B (1975). Manual of quantitative genetics (3rd edition) Washington State Univ press U.S.A.
- (10) AL-Raawi 'Khashi Mahmoud and Abdulaziz Khalaf Allah (2000). Design and analysis of agricultural experiments. Ministry of Higher Education and Scientific Research 'University of Mosul.
- (11) Degewione 'A.' T. Dejene and M. Sharif (2013). Genetic variability and traits association in bread Wheat (*Triticum aestivum* L.) genotypes. Inter. Res. J. of Agric. Sci. '1(2): 19-29.
- (12) Al-Daoudi, Sabah Ahmad Mahmoud and Daoud Suleiman Madab Al-Obaidi (2014). Estimation of some genotypes and pathway coefficient analysis of quantitative and qualitative traits in genotypes of triticale (*Triticum aestivum* L.)). Tikrit University Journal of Agricultural Sciences, Volume (14), Issue (1): 246-261.
- (13) Ali 'I. H. and E. F. Shakor (2012). Heritability 'variability 'genetic correlation and path analysis for quantitative traits in durum and bread wheat under dry farming conditions. Mesoptamia J. of Agri. 40(4): 27-39.
- (14) Ghallab 'K. H. 'A. A. N. Sharran 'and N. A. S. Shalby (2016). Genetic parameters for yield and yield components traits of some wheat genotypes grown in newly reclaimed soils. Int. J. Agr. Agri. R. 9(4): 1-8.
- (15) Al-Tawil 'Muhammad Sobhi (2017). Correlations and their medical practices. Al-Rafidain Agriculture Journal. Volume (45) Issue (3).
- (16) Mirosavljevic 'Milan. 'Vojislava Momcilovic. 'Novo Przulj. 'Ivana Maksimovic. 'Marian Putnik Delic. ' (2018). Dry matter accumulation of winter wheat and barly at different

sowing dates. Original scientific paper. Ratar Povart. 55(2): 87-94.

- (17) Nukasani 'V. 'N. R. Potdukhe 'S. Bharad 'S. Deshmukh and S. M. Shinde (2013). Genetic variability ' correlation and path analysis in Wheat. J. Wheat Res. 5(2): 48-51.
- (18) Sabit ·Z. ·B. Yadav and PK. Rai (2017). Genetic variability ·correlation and path analysis for yield and its components in f5 generation of bread wheat (*Triticum aestivum* L.). Journal of Pharmacognosy and Phytochemistry. 6(4): 680-687.
- (19) Ali, abeda al-Kamil Abdullah (1999). Hybrid Potency and Genetic Action in Yellow Maize (Zea mays L.), PhD thesis, College of Agriculture and Forestry, University of Mosul.