



Heterosis, Correlations and Path Analysis of Grain Yield Components in Bread Wheat (*Triticum aestivum* L.)*

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Abstract

Seven genotypes of bread wheat (*Triticum aestivum* L.) were used (SK 95, Side14, Side 12, SK94, Giemiza 9, Giemiza 7, Al-Fayyad) and their 21 crosses from half diallel crosses, and they were planted at the Agricultural Research and Experiment Station of the Faculty of Agriculture, Agriculture - University of Kirkuk, using a randomized complete block design with three replicates in order to study the hybrid vigor, the genetic and phenotypic correlation, and the path analysis of the grain yield components. It is noted from the results that the hybrid 2*6 had the heterosis deviation from the average of the parents and the best of them are significant and in the desired direction in the number of active tillers plant⁻¹, the number of grains spikes⁻¹ and grain yield, and the genetic and phenotypic correlation was positive for the significant number of active tillers plant⁻¹, the number of spikelet's spike⁻¹ and the number of grain spike⁻¹, and significant positive for the weight of 1000 grains with the grains yield plant⁻¹, and the highest genetic and phenotypic correlation value of the number of grains spike⁻¹ was 0.8** and 0.785**, respectively with grain yield, and when the correlations were divided into direct and indirect effects, the number of grains spikes⁻¹ had the highest direct effect, which confirms the possibility of adopting it as a selective indicator to improve grain yield.

Key words: Heterosis, Correlations, Path Analysis, Bread Wheat.

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Introduction

Wheat is the most important strategic crop from an economic and nutritional point of view, and it is one of the first crops among cereal crops in the world in terms of importance, cultivated area, and global production volume. It is a major source of food for more than 35% of the world's population [1]. The introduction of several genotypes into diallel crossing is important for plant breeders, as it is one of the approved methods for obtaining recombination and exploiting the phenomenon of heterosis [2]. Determining the correlation between the different traits and dividing them into direct and indirect effects is one of the concepts adopted in determining the nature and direction of these relationships. The correlation coefficient is important in describing the common relationship between the variables in isolation from other factors, but it becomes unable to give full clarity of the interrelationships between more than two variables. Therefore, the path coefficient analysis is an effective measure in determining the promising components of the yield and at the same time reduces the number of indicators required in the program. Selection It is useful in dividing the correlation coefficient into direct effects and indirect effects of the components in order to estimate the relative importance and direction of effects in yield [3]. when [4] studying eight cultivars of soft wheat and their half-diallel crosses, found that the hybrids (K-50*K-76) and (K-50*K-77) showed positive hybrid vigor as a deviation from the mean and best of the parents at a weight of 1000 grain and number of active tillers plant⁻¹, number of spikelet's spike¹, and grain yield plant⁻¹. [5] showed that the majority of crosses showed a negatively significant superiority of the hybrid vigor of the first generation on the basis of its deviation from the average of the parents

and the best of them in the number of active tillers plant⁻¹, weight of 1000 grains, and grain yield plant⁻¹. [6] obtained two hybrids (DPW621-50*Raj4079) and (Raj4037*Raj4079) that showed significant and positive heterosis due to the deviation of the first generation from the average of the parents and the best of them in all the characteristics of the study. [7] noted that plant yield was genetically associated positively with the characteristic of the number of active tillers plant⁻¹, while plant yield was negatively associated with the number of spikelet's spike⁻¹, the number of grains spike⁻¹, and the weight of 1000 grains, while the plant yield was phenotypically correlated. and in the positive direction with the number of shoots plant⁻¹. [8] showed that the plant yield showed a positive genetic and phenotypic correlation with all the studied traits. [9] showed that the number of active tillers plant⁻¹ had a direct positive phenotypic effect on plant yield, while the number of grain spike⁻¹ and the weight of 1000 grains had a direct negative effect, and there were no direct and indirect effects for the other traits. [10] found direct positive phenotypic effects in the number of grains spikes⁻¹ on plant yield, and indirect genetic effects in the number of grains spike⁻¹ through the number of spikelet's spike⁻¹, and there were no direct and indirect effects for other traits. This study aims to evaluate the performance of the parents and their crosses and estimate heterosis as a deviation from the average of the parents and the best of them to follow up the superior ones in the following generations and the genetic and phenotypic correlations of the grain yield and its components and their division into direct and indirect effects to determine one or more traits by selecting them to improve the grain yield.

Materials and methods

Seven genotypes of bread wheat (*Triticum aestivum* L.) were used, six of

which were new from the Republic of Egypt which are ((1) SK95, (2) Giemiza9, (3) Side14, (4) Side12, (5) SK94, (6) Giemiza7, (7) Al-Fayyad)., in addition to the local variety approved for cultivation in Iraq (Al Fayyad variety). It was planted in the Agricultural Research and Experiment Station of the College of Agriculture - University of Kirkuk. The experimental land was prepared and plowed with a disc plow, then the land was smoothed and leveled, and DAP fertilizer (P2O5 46% +N18%) was added to it at once before planting at a rate of 200 kg.ha⁻¹, and urea fertilizer with a concentration of (46% N) in two batches, the first at the beginning of branching and the second in the elongation stage at a rate of 200 kg.ha⁻¹, and the varieties were planted in two planting dates, the first on 15 November 2021, and the second after 15 days of planting the first date on 1 December 2021. In order to ensure obtaining a sufficient number of first-generation hybrids, the cross-breeding process was conducted between the genotypes according to the half diallel crossing program, it was obtained (21) crosses, and the harvest was carried out on 1 June 2022. The parents and their crosses of twenty-one crosses were cultivated. Agricultural operations were carried out similarly to first season, and the experiment was conducted using a randomized complete block design (R.C.B.D) with three repetitions. Each repetition included (28) rows. The genotypes were randomly distributed on 15 October 2022, and the genotypes were harvested on 25 May 2023, by harvesting (10) plants from each experimental unit randomly after the terminal plants were excluded to calculate the grain yield and components.

The statistical analysis of the genotypes data was carried out by relying on the software SAS. The heterosis and Heterobeltiosis was also estimated on the

basis of the deviation of the first generation from the average and the best of the two parents as a percentage respectively, test (t) was used for the significance of the heterosis for genotypes at the level of probability (1%, 5%), and the correlation coefficient was calculated according to the following equation [11].

$$r(x_1x_2) = \frac{cov(x_1x_2)}{\sqrt{v(x_1)v(x_2)}}$$

The path coefficient was calculated, in which the direct and indirect effects of the components of the grain yield were calculated based on [11].

$$[P] = [R]^{-1}[r]$$

$r(x_1x_2)$ Correlation coefficient between the two traits (x_1) and (x_2).

$cov(x_1x_2)$ covariance between the two traits.

$v(x_1)$ The variance of the trait (x_1).

$v(x_2)$ The variance of the trait (x_2).

$[P]$ Direction of direct effects.

$[R]^{-1}$ the inverse of the matrix of correlation coefficients between all possible pairs of independent variables.

$[r]$ the direction of the correlation coefficients between the independent variables and the dependent variable.

Results and discussion

The analysis of variance table (1) shows that the parental genotypes differed significantly at the level of probability (1%) for all studied traits except for the number active tillers plant⁻¹, which differed significantly from the level of probability (5%), while the first-generation crosses (Table 2) differed significant in all the studied traits at the level of probability (1%) except for the characteristic of the number of spikelet's, spike⁻¹, which differed significantly at the level of probability (5%). This result agreed with [12], [13].

Table (1): Analysis of variance for parental cultivars and for all traits

S.O.V	D.F	Days 75% flowering	No. of active tillers plant ⁻¹	No. of spikelet's spike ⁻¹	No. of grains. spike ⁻¹	Weight 1000 grains	Single grains yield
Replicate	2	0.142	2.137	1.727	2.606	2.835	3.769
Genotype	6	17.746**	4.498*	5.754**	393.185**	54.328**	173.612**
Error	12	0.698	1.226	0.765	1.276	2.840	1.956

*, **: Significant at 5% and 1% levels, respectively

Table (2): Analysis of variance, for half diallel crosses and all traits

S.O.V	D. F	Days 75% flowering	No. of active tillers plant ⁻¹	No. of spikelet's spike ⁻¹	No. of grains. spike ⁻¹	Weight 1000 grains	Single grain yield
Replicate	2	0.015	13.803	1.701	0.514	4.000	4.862
Genotype	20	12.020**	17.489**	5.852*	553.258**	22.672**	479.614**
Error	40	0.549	2.027	2.530	5.589	4.121	3.284

*, **: Significant at 5% and 1% levels, respectively

Table (3) shows the averages of parental genotypes and for all studied traits. In the number of days for 75% flowering, parents (2), (5) and (7) showed significant precocity in the desired direction, it was (125.33, 125.33, 125.67) days, respectively. In the number of active tillers plant⁻¹ outperformed the parent (2), giving it the highest average of (17.58) tiller, while the parents (6), (5), (2), and (7) showed a significant superiority in the number of spikelet's spike⁻¹, which reached (21.9), 20.9, 20.7, 20.7) spikelet,

respectively, and in the number of grains, spike⁻¹, the parent (2) outperformed all the parents by giving him the highest average of (99.7) grains. While in the weight of 1000 grains, the parents (7), (4), and (3) excelled on the rest of the parents by giving them the highest average of (47.40, 46.76, 46.07) gm, and in the grain yield the parent (2) outperformed all the parents and gave the highest average of (67.862) gm. This result agreed with [14], [15], [16], [17].

Table (3): Averages of parents for all traits

Genotype	Days 75% flowering	No. of active tillers plant ⁻¹	No. of spikelet's spike ⁻¹	No. of grains. spike ⁻¹	Weight 1000 grains	Single grains yield
1	127.00 b	16.79 a	18.1 c	69.4 e	40.87 b	45.177 e
2	125.33 c	17.58 a	20.7 ab	99.7 a	36.77 c	67.862 a
3	130.67 a	14.07 b	20.0 b	90.6 b	46.07 a	62.916 b
4	127.00 b	15.65 ab	18.3 c	81.8 d	46.76 a	63.484 b
5	125.33 c	16.32 a	20.9 ab	88.4 c	39.52 bc	58.146 c
6	131.00 a	17.57 a	21.9 a	81.8 d	39.41 bc	58.096 c
7	125.67 c	15.98 ab	20.7 ab	67.7 e	47.40 a	52.355 d

Similar letters do not differ in terms of statistical significance

Table (4) shows the average values of traits for the half diallel crossing, and in the number of days for 75% flowering, the crosses (6x1), (2x1), (4x3), (4x5) and (4x7) were significantly earlier in the desired direction with a period of (123, 123.33, (124, 124,124) days, respectively. As for the number of active tillers plant⁻¹, the cross (3x4) was significantly superior to all hybrids and gave the highest average of (23.20) tiller , and in the number of spikelet's spike⁻¹ showed hybrids (2x6), (1x4), (2x4), (2x5) and (3x4) had a

significant superiority and gave the highest average of (23.80, 22.07, 21.23, 21.13, 20.93) spikelet, respectively, and for the number of grains spike⁻¹, crosses (2x4) and (2x6) and (4x6) were significant and gave the highest average of (115.73, 115.07, 111.67) grains, respectively, while in the weight of 1000 grains, the crosses showed (4x6), (5x6), (3x6), (3x4) , (2x4) and (2 x 6) had a significant superiority and gave the highest average of (48.36, 46.55, 46.52, 45.77, 45.71, 44.64) gm, respectively. This result agreed with [14], [15], [16], [17].

Table (4): Average of the hybrids, for half diallel crosses and all traits

Hybrids	Days 75% flowering	No. of active tillers plant ⁻¹	No. of spikelet's spike ⁻¹	No. of grains. spike ⁻¹	Weight 1000 grains	Single grains yield
1*2	123.33 f	16.77 d-g	20.07 bc	86.27 gh	36.50 g	52.77 ijk
1*3	128.67 a	18.38 b-e	18.87 c	87.67 fg	44.00 b-f	67.68 e
1*4	128.00 ab	14.07 gh	22.07 ab	107.87 b	40.93 ef	72.13 d
1*5	125.00 de	15.18 fgh	19.53 bc	78.73 ijk	42.46 c-f	53.78 hij
1*6	123.00 f	18.40 b-e	20.60 bc	90.40 ef	42.36 c-f	72.28 d
1*7	127.00 bc	16.77 d-g	19.53 bc	93.80 de	44.64 a-e	74.43 d
2*3	125.33 de	15.20 fgh	19.07 bc	77.93 jk	42.73 b-f	51.13 jk
2*4	128.67 a	13.93 h	21.13 abc	115.73 a	45.71 a-d	84.56 b
2*5	125.00 de	19.59 bc	21.23 abc	90.53 ef	41.82 def	72.24 d
2*6	125.00de	20.40 b	23.80 a	115.07 a	40.19 f	91.60 a
2*7	128.00 ab	20.40 b	19.80 bc	98.60 c	44.01 b-e	84.15 b
3*4	124.00 ef	23.20 a	20.93 abc	82.73 hi	45.77 abc	85.45 b
3*5	127.67 ab	17.18 c-f	18.40 c	79.67 ij	41.36 ef	56.75 gh
3*6	129.00 a	17.18 c-f	18.33 c	80.20 ij	46.52 ab	66.67 e
3*7	128.00 ab	18.79 bcd	18.47 c	74.80 kl	41.43 ef	58.12 g
4*5	124.00 ef	16.06 d-h	18.47 c	92.67 de	42.36 c-f	64.84 ef
4*6	129.00 a	13.67 h	19.20 bc	111.67 ab	48.36 a	77.54 c
4*7	124.00 ef	15.92 e-h	19.53 bc	82.07 ij	41.37 ef	54.95 hi
5*6	125.67 d	15.19 fgh	20.35 bc	71.80 l	46.55 ab	54.77 hi
5*7	125.00 de	17.19 c-f	20.20 bc	72.47 l	40.79 ef	50.37 k
6*7	128.67 cd	16.32 d-h	18.33 c	95.80 cd	40.09 f	63.49 f

Similar letters do not differ in terms of statistical significance

Table (5) shows that the crosses showed positive and negative heterosis as a deviation from the average of the parents, and that eleven hybrids showed negative heterosis desirable for the number of days for 75% flowering at the probability level

(1%) and ranged from (-4.65) for the hybrid (1× 6) to (-1.40) for the hybrid (3×6) and for the hybrid (1×5) at the level of probability (5%). The crosses that gave negative values for the heterosis an indicator of the over dominance of the lower paternal genes of the

number of days for 75% flowering, while in the number of active tillers plant⁻¹, six crosses showed positive, significant heterosis at the level of probability (1%), ranging from (56.16) for the (3×4) hybrid to (15.59) for the (2×5) hybrid, and for the hybrid (3× 5) at the probability level (5%), and in the number of spikelet's spike⁻¹ two hybrids (1×4) and (2×6) at the level of probability (1%) showed significant heterosis of (21.02, 11.74), respectively, and the hybrid (3×4) reached (9.22) at the level of probability (5%), while in the number of grains spike⁻¹, ten crosses showed positive, significant heterosis at the level of probability (1%), ranging from (42.68) in the hybrid (1×4) to (8.98) in the (4×5) hybrid, while in the weight of 1000 grains,

five crosses showed a positive and significant heterosis , ranging from (17.96) for the (5×6) hybrid to (8.84) for the (6×3) hybrid at the level of probability (1%), but for the characteristics of plant grain yield, thirteen crosses showed positive, significant, desirable heterosis, ranging from (52.64) for the (1×7) hybrid to (6.62) (4×5) at a probability level of (1%). The crosses that gave a significant heterosis resulted from the superiority of heterozygote over both the homozygous genes in parents, so the heterozygote genotype with dominance effect of gene becomes better than the homozygote genotype, or the heterosis may be due to the accumulation of different alleles of genes. This result agreed with [6], [18], [19], [20].

Table (5) Per cent heterosis in F1 over mid parent (MP) for traits of wheat.

Hybrids	Days 75% flowering	No. of active tillers plant ⁻¹	No. of spikelet's spike ⁻¹	No. of grains. spike ⁻¹	Weight 1000 grains	Single grains yield
1*2	-2.25**	-2.40	3.26	2.03	-5.97*	-6.62**
1*3	-0.13	19.12**	-1.05	9.58**	1.22	25.23**
1*4	0.79*	-13.27*	21.02**	42.68**	-6.58*	32.76**
1*5	-0.92*	-8.28	0.17	-0.21	5.64	4.09*
1*6	-4.65**	7.08	3.00	19.58**	5.53	39.98**
1*7	0.53	2.37	0.51	36.80**	1.14	52.64**
2*3	-2.08**	-3.93	-6.38	-18.09**	3.17	-21.81**
2*4	1.98*	-16.13**	8.19	27.53**	9.44**	28.76**
2*5	-0.27	15.59**	2.08	-3.74**	9.64**	14.67**
2*6	-2.47**	16.06**	11.74**	26.80**	5.49	45.44**
2*7	1.99**	21.55**	-4.50	17.78**	4.58	39.99**
3*4	-3.75**	56.16**	9.22*	-4.02**	-1.38	35.20**
3*5	-0.26	13.05*	-9.95*	-10.99**	-3.33	-6.25**
3*6	-1.40**	8.58	-12.42**	-6.96**	8.84**	10.19**
3*7	-0.13	25.04**	-9.33*	-5.52**	-11.36**	0.84
4*5	-1.72**	0.45	-5.78	8.89**	-1.81	6.62**
4*6	0.10	-17.73**	-4.48	36.51**	12.25**	27.56**
4*7	-1.72**	-0.39	-0.34	-3.56**	-4.09	-9.64**
5*6	-1.95**	-10.3855*	-4.76	-15.63**	17.957**	-5.76**
5*7	-0.40	6.428645	-2.88	-7.17**	-6.1341*	-8.83**
6*7	-1.82**	-2.71183	-13.92**	28.13**	-7.64076*	14.97**
SE(H)	0.532	0.966	1.026	4.536	3.709	2.912

*, **: Significant at 5% and 1% levels, respectively

Table (6) shows that the crosses showed negative and positive Heterobeltiosis due to the deviation of the first generation from the best parents, and that six crosses showed a significant negative hybrid vigor desirable for the characteristic of the number of days for 75% flowering at a probability level (1%) that ranged from (-4.79) in the hybrid (2×6) to (-1.06) in the hybrid (4×5), the crosses that gave negative values for the vigor of the hybrid for the characteristic of the number of days to 75% flowering indicate the superior dominance of genes in the lower parent, and in the number of active tillers plant⁻¹ showed five crosses, the positively significant hybrid vigor ranged from (48.26) in the (3×7) hybrid to (16.02) in the (2×6) and (2×7) hybrids at the level of probability (1%) and for the hybrid (2×5) at

the level of Probability (5%), while in the number of spikelet's spike⁻¹, the hybrid (1×3) showed positive, significant hybrid vigor at the level of probability (1%), outperforming all other hybrids. While the number of grains spike⁻¹ eight crosses were significantly superior and showed positive hybrids vigor ranging from (36.51) for the (4×6) hybrid to (4.83) for the (4×5) cross at a probability level of (1%), ten hybrids had a significant positive hybrid vigor at the level of probability (1%), reaching a maximum of (42.17) for the hybrid (1×7) and the lowest (5.96) for the hybrid (3×6) at the level of probability (1%). The crosses in which significant values were given indicate Heterobeltiosis, which is due to the heterozygote genotype. This result agreed with [5], [6], [21].

Table (6) Per cent Heterobeltiosis in F1 over better parent (BP) for traits of wheat.

Hybrids	Days 75% flowering	No. of active tillers plant ⁻¹	No. of spikelet's spike ⁻¹	No. of grains. spike ⁻¹	Weight 1000 grains	Single grains yield
1*2	-2.93**	-4.59	-3.22	-13.47**	-10.69**	-22.23**
1*3	1.31**	9.47	-5.67	-3.24*	-4.48	7.57**
1*4	0.79	-16.20**	20.36**	31.87**	-12.46**	13.62**
1*5	-0.27	-9.55	-6.39	-10.94**	3.89	-7.52**
1*6	-3.15**	4.69	-5.79	10.51**	3.65	24.42**
1*7	1.06*	-0.08	-5.79	35.16**	-5.82*	42.17**
2*3	0.01	-13.52*	-8.04	-21.83**	-7.23*	-24.65**
2*4	2.66**	-20.73**	1.93	16.08**	-2.24	24.61**
2*5	-0.27	11.45*	1.68	-9.19**	5.83	6.46**
2*6	-4.79**	16.04**	8.84	15.41**	1.96	34.98**
2*7	1.86**	16.04**	-4.50	-1.10	-7.14*	24.00**
3*4	-2.36**	48.26**	4.67	-8.68**	-2.11	34.60**
3*5	1.86**	5.25	-11.82*	-12.07**	-10.21**	-9.81**
3*6	-1.28**	-2.26	-16.16**	-11.48**	0.98	5.96**
3*7	1.86**	17.54**	-10.93*	-17.44**	-12.60**	-7.63**
4*5	-1.06*	-1.61	-11.50*	4.83**	-9.41**	2.15
4*6	1.57**	-22.23**	-12.20*	36.51**	3.44	22.15**
4*7	-1.33**	-0.38	-5.79	0.33	-12.71**	-13.44**
5*6	0.27	-13.58*	-6.94	-18.78**	17.80**	-5.80**
5*7	-0.27	5.33	-3.19	-18.02**	-13.94**	-13.37**
6*7	0.27	-7.11	-16.16**	17.11**	-15.42**	9.29**
SE(H)	0.614	1.116	1.184	1.739	1.573	1.393

*, **: Significant at 5% and 1% levels, respectively

Table (7) shows the genetic and phenotypic correlations, and it shows that the genetic correlation between the number of days to 75% flowering and the number of active tillers plant⁻¹, was significantly negative, and between the number of days to 75% flowering and the weight of 1000 seeds was significantly positive at the probability level (1%)., While the number of active tillers, plant⁻¹, and grain yield plant⁻¹ were significantly and positively associated (0.411**), and the number of spikelet's, spike⁻¹, was positively and significantly associated with the number of grains spike⁻¹, and grain yield plant⁻¹ (0.537** and 0.549**), and negatively with the weight of 1000 grains. At the level of probability (5%), the genetic correlation was positive and significant between the number of grains spike⁻¹ and the grain yield plant⁻¹ (0.800**), and the correlation between the weight of 1000 grains and the grain yield plant⁻¹ was positive and significant (0.268*). In the phenotypic correlation, the correlation between the number of days for 75% flowering and the weight of 1000 grains was positive and significant at the probability level (1%), and the number of active tillers plant⁻¹, was positively and significantly

associated with the grain yield plant⁻¹ (0.363**), and the number of spikelet's spike⁻¹ it was significantly positively associated with the number of grains spike⁻¹ and grain yield plant⁻¹ (0.343** and 0.363**).The number of grain spike⁻¹ was also significantly positively correlation with the grain yield plant⁻¹ (0.785**) and negatively with the weight of 1000 grains at a probability level (5%) , while the weight of 1000 grains was associated with the grain plant⁻¹ significantly positive (0.219 *). The interrelationships between the traits can determine the method of selection that is adopted with the aim of genetic improvement of the trait of economic importance, although they are sometimes shaded values, which requires path analysis, and from a genetic point of view, the positive correlation results from the coupling phase between the genes and the negative correlation from the repulsion phase. Temporary association may occur due to the imbalance due to the multiple effects of genes (pleiotropy), so the linkage between genes on the same chromosome is contiguous and the state of linkage can be changed by selection and hybridization. This result agreed with [8], [22], [23].

Table (7) Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for traits of wheat.

Traits	Days 75% flowering	No. of active tillers plant ⁻¹	No. of spikelet's spike ⁻¹	No. of grains spike ⁻¹	Weight 1000 grains	Single grains yield
Days 75% flowering	1.00	-0.319**	-0.112	0.157	0.346**	0.106
No. of active tillers plant ⁻¹	-0.207	1.00	-0.272*	-0.081	-0.211	0.411**
No. of spikelet's spike ⁻¹	-0.116	0.180	1.00	0.537**	-0.215*	0.549**
No. of grains spike ⁻¹	0.152	-0.065	0.343**	1.00	-0.043	0.800**
Weight 1000 grains	0.324**	-0.175	-0.218*	-0.218*	1.00	0.268*
Single grains yield	0.103	0.363**	0.363**	0.785**	0.219*	1.00

*,**: Significant at 5% and 1% levels, respectively

Table (8) shows the values of the direct and indirect effects and its fragmentation of the genetic correlation of the yield with the other traits. It shows that there are direct, high and positive effects for the traits of the number of active tillers plant⁻¹, the number of grain spike⁻¹, and the weight of 1000 grains with the grain yield plant⁻¹ amounted to (0.562, 0.842, 0.428) respectively, and the number of spike grains had the highest

genetic correlation coefficient and the highest direct effect on the grain yield plant⁻¹, so it is useful to select for it in order to improve the grain yield. It was also noted that there are indirect effects some of them positive and others negative, some of which are weak and neglected with grain yield through other characteristics. This result agreed with [10], [24], [25].

Table (8) Direct (diagonal) and indirect genotypic effect for some traits on grain yield in bread wheat.

traits	Days 75% flowering	No. of active tillers plant ⁻¹	No. of spikelet's spike ⁻¹	No. of grains spike ⁻¹	Weight 1000 grains
Days 75% flowering	0.009	-0.179	-0.004	0.132	0.148
No. of active tillers plant ⁻¹	-0.003	0.562	0.010	-0.068	-0.090
No. of spikelet's spike ⁻¹	-0.001	0.152	0.037	0.452	-0.092
No. of grains spike ⁻¹	0.001	-0.045	0.020	0.842	-0.018
Weight 1000 grains	0.003	-0.118	-0.008	-0.036	0.428

Table (9) shows the values of direct and indirect effects and the fragmentation of the phenotypic correlation of the plant yield with other traits and notes in it, that the direct effects were high, positive and significant for the qualities of the number of active tillers plant⁻¹, the number of grain spike⁻¹ and the weight of 1000 grains, reaching (0.456, 0.804, 0.353) respectively, and notes that the phenotypic correlations

reflect genetic correlations, which confirms the possibility of the components of the crop, which gave a higher genetic and phenotypic correlation and a higher direct effect on the grain yield, as for the indirect effects, positive and negative, were taken in the interaction between medium, few and neglected. This result agreed with [10] [26], [27].

Table (9) Direct (diagonal) and indirect phenotype effect for some traits on grain yield in bread wheat

Genotype	Days 75% flowering	No. of active tillers plant ⁻¹	No. of spikelet's spike ⁻¹	No. of grains. spike ⁻¹	grains 1000 weight
Days 75% flowering	-0.030	-0.094	-0.009	0.122	0.114
No. of active tillers plant ⁻¹	0.006	0.456	0.014	-0.052	-0.062
No. of Spikelet's spike ⁻¹	0.003	0.082	0.079	0.276	-0.077
No. of grains. spike ⁻¹	-0.005	-0.029	0.027	0.804	-0.012
1000 grains weight	-0.010	-0.080	-0.017	-0.027	0.353

Conclusion

From the foregoing, it is concluded that parent 2 excelled in grain yield and its components and early in flowering, and the hybrid 2 * 6 in which he participated gave the highest grain yield and its components (the number of spikelet's spike⁻¹, the number of grains spike⁻¹, and the weight of 1000 grains), and this hybrid had the heterosis deviation from the average of the parents and the best of them are significant and in the desired direction in the number of active tillers plant⁻¹, the number of grains spikes⁻¹ and grain yield, and the genetic and phenotypic correlation was positive for the significant number of active tillers plant⁻¹, the number of spikelet's spike⁻¹ and the number of grain spike⁻¹, and significant positive for the weight of 1000 grains with the grains yield plant⁻¹, and the highest genetic and phenotypic correlation value of the number of grains spike⁻¹ was 0.8** and 0.785**, respectively with grain yield, and when the correlations were divided into direct and indirect effects, the number of spikes had the highest direct effect, which confirms the possibility of adopting it as a selective indicator to improve grain yield.

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قوة الهجين، الارتباطات ومعامل المسار لمكونات حاصل الحبوب في حنطة الخبز

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• تاريخ استلام البحث 2023/07/01 وتاريخ قبوله 2023/07/23

• البحث مستل من رسالة ماجستير الباحث الأول.

المستخلص

استخدمت سبعة أصناف من حنطة الخبز (*Triticum aestivum* L.) وهي (Sk 95، Side 14، Side 12، Sk 94، 9، Giemiza 7، Giemiza) (الفياض) وهجنها الـ 21 وفق نظام التهجينات التبادلية النصفية، وزرعت في محطة البحوث الزراعية التابعة لكلية الزراعة - جامعة كركوك، وفق تصميم القطاعات العشوائية الكاملة وبثلاث مكررات من أجل دراسة قوة الهجين، والارتباطات الوراثية والمظهرية وتحليل معامل المسار لمكونات حاصل الحبوب. ويلاحظ من النتائج ان الهجين (6x2) قد اظهر انحرافاً كبيراً عن متوسط الابوين وأفضلها في الاتجاه المرغوب في صفة عدد الاشطاء الفعالة. النبات¹⁻ وعدد الحبوب. السنبلية¹⁻ وحاصل الحبوب، وكان الارتباط الوراثي والمظهري عالياً وموجباً لصفة عدد الاشطاء الفعالة. النبات¹⁻ وعدد السنيبلات. السنبلية¹⁻ ووزن 1000 حبة مع حاصل الحبوب، وعلى قيم ارتباط وراثي ومظهري كانت لصفة عدد الحبوب. السنبلية¹⁻ وبلغ (*0.8) و (*0.785)، على التوالي مع حاصل الحبوب. وعندما تم تقسيم الارتباطات الى تأثيرات مباشرة وغير مباشرة، كان لعدد الحبوب. السنبلية¹⁻ أعلى تأثير مباشر، مما يؤكد إمكانية اعتماده كمؤشر انتخابي لتحسين محصول الحبوب.

الكلمات المفتاحية: قوة الهجين، الارتباطات، معامل المسار، حنطة الخبز.