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CORRELATION AND PATH COEFFICIENT ANALYSIS IN BREAD WHEAT

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ABSTRACT

Fifteen genotypes of bread wheat in addition to the two local varieties (Sham6 and Abu-Graib3) were planted inside Mosul University under three spaces between rows (15, 25 and 35cm) using split plots system in randomized complete block design with three replications to evaluate grain yield and some of its components (plant height, number spikes, number of grains/spike, biological yield, 1000 grain weight and harvest index), and genotypic and phenotypic path coefficient analysis among grain yield and its components. The results showed that 15 cm row space gave highest means for biological yield, number spikes and grain yield. The grain yield at this row space was 59.378% and 123.422% higher than that at 25 and 35 cm row space respectively. Some genotypes significantly outperformed for larger number of traits including grain yield, came in the forefront of it MEXIPAK 65/ASFOOR-7, and Sham6 followed by the genotypes PBW343, NESMA*2/14-2//2*SAFI-3 and BT1735/ACHTAR//ASFOOR-1. It was shown that the yield/unit area had significant positive genotypic and phenotypic correlations with plant height, biological yield, number of grains/spike, 1000 grain weight and harvest index, and phenotypically with number of spikes per unit area. It was revealed from path coefficient analysis that number of grains/spike and harvest index had higher genetic and phenotypic direct effects and indirect effects through some other traits on grain yield, followed in importance by biological, this is useful in the reliability of these three traits as selection criteria for higher yield performance in breeding programs.

Key words: bread wheat, path coefficient, correlations

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INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is an important strategic crop in most countries of the world, and the process of developing new varieties of the crop characterized by high production specifications and good quality characteristics of the most important objectives sought by plant breeders. It is possible to improve crop yield using available genetic resources and by recognizing the nature and importance of genetic variations in the population, and that estimating genetic differences is a prerequisite for planning an appropriate breeding method. A careful look at the importance of genetic variations in crop species is also of paramount importance in that it provides a fundamental basis for an effective selection process, and to practice an effective selection prosses, determining the outcome of the crop is desirable. Correlations between traits are a measure of the strength of their relationship, and their knowledge between traits is important in plant breeding. If two traits are positively correlated, one can be indirectly improved by improving the other. The correlation coefficient would be useful if indirect selection of the secondary trait would be

Part of M.Sc. Thesis for the first researcher used to improve the essential trait beneficial (Hussain et al., 2010). The estimation of the correlation coefficient is necessary to develop a selection index, and in order to create a sense for correlation, Wright (1921) developed a path coefficient analysis method which was used to develop criteria for selecting complex traits in many crop (Dewey and Lu, 1958; Diz et al., 1994; Kang et al., 1983; Pandey and Torrie, 1973). This analysis provides effective means by estimating the direct and indirect causes of correlations (Kale et al., 2007). The method of analyzing the path coefficient in wheat was adopted by many researchers, Dutamo et al. (2015) from an experiment carried out in one location and from its use of the path coefficient analysis indicated that the two traits, harvest index and biological yield showed direct and indirect effects on the yield, and reliable In the selection for high yielding, but the final conclusion can only be judged once the experiment is repeated at multiple locations. Khan and Dar (2016) concluded that the analysis of path coefficient showed the higher importance of positive direct effect on grain yield by the number of spikes/plant followed by number of grains/spike and 100 grains weight., Desheva (2016) reported from his study that the number of grains/spike and 1000 grains weight through the grains weight/spike had the highest positive indirect effect on the grain yield per plant, and this relationship can be used as a selectoral index in breeding studies to improve high-yielding varieties. The results of Sapi et al. (2017), Ayer1 et al. (2017) and Kamani et al. (2017) showed that the direct positive effect on the grain yield/plant was higher through biological yield and harvest index.

The aim of the study is to evaluate the yield and some of its components for fifteen introduced genotypes in addition to the two registered and certified in Iraq, Sham 6 and Abu Ghraib 3 at different spaces between rows and to partition the genetic and phenotypic correlation coefficients of grain yields with some of its components to direct and indirect effects.

MATERIALS AND METHODS

The experiment was carried out in the field of Field Crops Dept. (inside University of Mosul campus), and included the cultivation of 15 genotypes of bread wheat introduced from the International Center for Agricultural Research in the Dry Areas (ICARDA) in addition to the two registered and certified varieties in Iraq Sham 6 and Abu Ghraib 3 (their names and selection history are shown in table 1). The planting date was on December 7, 2017 with the adoption of a seeding rate of 100 kg per hectare under rainy conditions, with supplementary irrigation simulating rain due to its receding during the season (Their quantities and dates are shown in Table 2), at three spaces of cultivation between rows (15, 25 and 35 cm) using a split plot system by randomized complete block design with three replicates (planting spaces were distributed within each block in the main plots and genotypes in the split plots within each main plot, each block included 51 experimental units and each unit contained two lines with a length of 1.5 m for the line with no spaces between the experimental units. DAP fertilizer containing (46% P_2O_5 and 18% N) was added at a rate 200 kg per hectare during the preparation of the land for cultivation, and urea fertilizer (46% N) was added at a rate of 300 kg per hectare twice, the first after 45 days of planting and the second month after. At maturity, data were recorded on the traits of plant height (cm), number of spikes/m^2, biological yield (gm per m^2), number of grains per spike, Table (1): Genotypes of bread wheat used in the study and their selection history.

Seq	Name	Pedigree
1	ATTILA-7	CM85836-50Y-0M-OY-3M-0Y-0SY-0AP
2	HAAMA-2/QAFZAH-16	ICW03-0184-13AP/0TS-0AP-0AP-8AP-0AP
3	PASTOR-2/BOCRO-2	ICW03-0203-12AP/0TS-0AP-0AP-1AP-0AP
4	HUBARA-5/3/SHA3/SERI//SHA4LLIRA	ICW03-0041-10AP/0TS-0AP-0AP-3AP-0AP
5	REYNA-12	ICW00-0634-3AP-0AP-0AP-39AP-0AP-0DZ/0
6	SEKSAKA-7/3/SHUHA-2//US732/HER	ICW01-00054-0AP-11AP-0AP-0AP-14AP-16AP
7	ANGI-5/ZEMAMRA-8	ICW03-0132-10AP/0TS-0AP-0AP-29AP-0AP
8	PBW343	CM85836-4Y-0M-0Y-8M-0Y-0IND-0AP
9	HUBARA-3*2/SHUHA-4	ICW04-20024-10AP-0AP-0AP-0AP-2AP-0AP
10	UNIQUE 96/FLAG-1	ICW02-00330-11AP/0TS-0AP-030AP-1KUL-0
11	HUBARA-3*2/SHUHA-4	ICW04-20024-28AP-0AP-0AP-0AP-2AP-0AP
12	DAJAJ-5/4/CMH82A.1294/2*KAUZ/MUNIA/CHT	ICW04-20101-17AP-0AP-0AP-0AP-3AP-0AP
13	NESMA*2/14-2//2*SAFI-3	ICW00-0801-1AP-0AP-0AP-40AP/MOR-0AP
14	MEXIPAK 65/ASFOOR-7	ICW04-0359-8AP-0AP-0AP-4AP-0AP
15	BT1735/ACHTAR//ASFOOR-1	ICW01-00164-0AP-11AP-0AP-0AP-2AP-110AP
16	Sham6	Registered and certified in Iraq
17	Abu-Graib3	Registered and certified in Iraq

1000 grains weight, harvest index (%), and grain yield per/1 m^2 (gm). The data of genotypes of the traits under study were analyzed according to the experimental design used and the differences between the means of the cultivation spaces between rows and the genotypes were compared by Duncan's multiple rang test method (Al-Zubaidy and Al-Falahy, 2016), and then phenotypic and genotypic variances (σ^2_P and σ^2_G) and phenotypic and genotypic covariance's ($\sigma P_x P_y$ and $\sigma G_x G_y$) were estimated through the relationship between estimated and expected mean squares in the variance and Covariance analysis table, and then phenotypic and genotypic correlations were estimated between the traits under study from the following equations (Al-Zubaidi and Al-Jabouri, 2016).

Table (2): The amount of rainfall and supplementary irrigation for the agricultural season 2017-2018

Month	The amount of rain falling (mlm)	sprinkled water (mlm)		Total
		The amount	Its date	
December	7.81	20	14/12/2017	47.81
		20	21/12/2017	
January	12.69	20	11/1/2018	52.69
		20	31/1/2018	
February	32.56	20	8/2/2018	52.56
March	4.58	10	8/3/2018	34.58
		20	29/3/2018	
April	14.04	20	5/4/2018	34.04
May	13.79	----	----	13.79
Total	85.47	150	----	235.47

$$rP = \sigma P_x P_y / [\sqrt{(\sigma^2 P_x)(\sigma^2 P_y)}] \; ; \quad rG = \sigma G_x G_y / [\sqrt{(\sigma^2 G_x)(\sigma^2 G_y)}]$$

The path coefficient analysis established by Wright (1921) was approved to partition the coefficients of correlation (genetic and phenotypic) between the grain yield and some of its components to the two types of effects (direct and indirect) in the manner described by Dewey and Lu (1959) and then explained by Al-Rawi (1987) in detail to test the model which included six independent variables: Plant height (x_1), number of spikes m^2 (x_2), biological yield gm/m^2 (x_3), grains number/spike (x_4), 1000 grain weight (x_5) and the harvest index (x_6) as illustrated in the Figure (1). Direct effects (phenotypic and genetic) were estimated using correlation matrices as follows: $P_{iy} = R^{-1}$ r, Where, P_{iy} = direct effects vector, R^{-1} = inverse matrix of correlation coefficients between all possible pairs of traits and r = correlation coefficient vector between grain yield and other traits. Following the

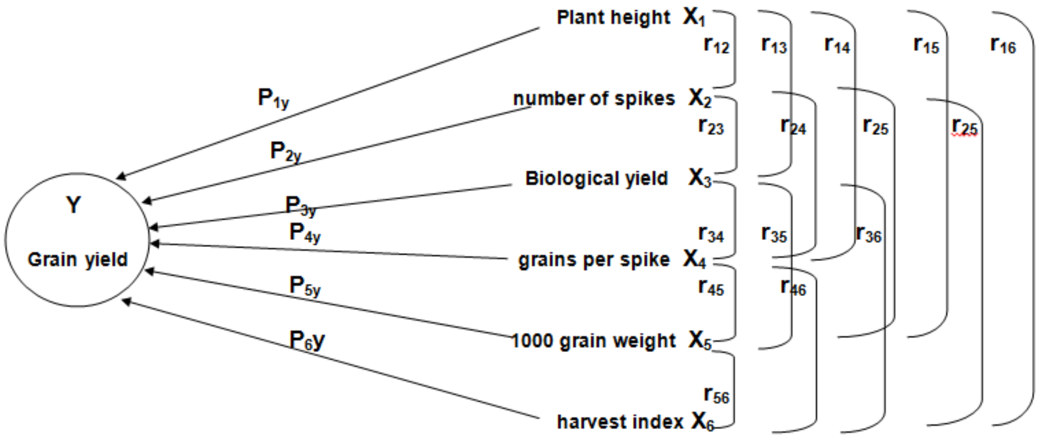

Figure 1: diagram of path way relationship for plant height (X_1), number of spikes (X_2), biological yield (X_3), Number of grains per spike (X_4), 1000 grain weight (X_5), and harvest index (X_6) affecting the grain yield (Y)

path way shown in Figure 1, the direct and indirect effects (genetic and phenotypic) were estimated.

The significance of direct and indirect effects was determined according to the grading mentioned by Al-Zubaidy and Al-Jaboury (2016) as follows (from 0,00 - 0.09 neglected), (from 0.10 - 0.19 few), (from 0.20 - 0.29) moderate, (from 0,30 - 0,99) high and (more than 1,00) very high.

RESULTS AND DICUSSION

Table (3) shows the results of analysis of variance from the data of genotypes grown at three spaces between the rows for yield and some other traits in wheat. It is noted that the mean square of the genotypes was significant at a 1% probability level for plant height, number of grains per spike and 1000 grains weight only, and not significant for the other traits. This result is similar to what found by Ahmad et al. (2011) and Dawod et al. (2015) for these three traits.

Table (3): The analysis of variance results for grain yield and some other traits.

S. O. V.	d.f.	Traits						
		Yield (gm/m^2)	Plant Height (cm)	Number spikes $/m^2$	Biological yield (gm/m^2)	Number grains per spike	1000 grains weight (gm)	Harvest index
Reps.	2	47615.8	336.49	32409.01	273492.5	861.05	78.23	477.74
Spaces	2	80367.1	26.63	128825.2	599622.0	76.09	34.34	113.27
Error (a)	4	8441.1*	153.08	4153.31*	82265.6*	214.95	86.94	200.44
Genotypes	16	2816.1	103.89**	2159.68	7695.1	122.38**	74.21**	94.24
S x G	32	2561.8	35.952	1605.41	10935.5*	47.53	8.24	60.02
Error (b)	96	1923.4	33.025	1606.74	6125.7	42.39	7.85	54.90

- (**) and (*) significant at 1% and 5% respectively.

The mean squares data from the variance analysis of the traits under study and covariance between them were used to estimate the phenotypic and genetic variances of these traits, then these components were adopted in the calculations of genetic and phenotypic correlations as shown in Table 6. Table (4) shows the means of cultivation spaces between the rows as average of genotypes, and it is noted that the space 15 cm had highest means for the biological yield, spikes number and yield with a significant difference from the other two spaces, while the means of spaces for the rest of the traits were close and without significant differences between them, and the grain yield at 15 cm was higher than at 25 and 35 cm by 59.378% and 123.422% respectively. The means of genotypes for the different traits are shown as an average of the cultivation spaces in Table (5). The results of the Duncan's multiple range test show that there are significant differences between them for all traits except the biological yield (although F was not significant in the results of analysis of variance for grain yield, number of spikes and harvest index). The highest mean values for grain yield, plant height, number of spikes, biological yield, number of grain per spike, 1000 grain weight and harvest index were 126.88, 51.111, 134, 298.5, 33.621, 40.454 and 42.578 in genotypes 16 (i), 14, 16 (ii) and 13 (i), 5 (i), 13 (ii) and 5 (ii), respectively, while the lowest mean values were 60.33, 38.222, 97.19, 196.08, 17.022, 29.590 and 29.374

Table (4): Means of planting spaces between rows for grain yield and its components.

Spaces	Traits						
	Yield (gm/m^2)	Plant Height (cm)	Number spikes $/m^2$	Biological yield (gm/m^2)	Number grains per spike	1000 grains weight	Harvest index
15 cm	140.89 a	45.176 a	188.67 a	377.09 a	26.028 a	34.257 a	36.749 a
25 cm	88.40 b	43.804 a	121.18 ab	223.48 ab	28.359 a	34.038 a	38.225 a
35 cm	63.06 b	44.098 a	90.42 b	167.72 b	26.560 a	35.556 a	35.244 a

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

Table (5): Means of genotypes for grain yield and its components.

Genotypes	Traits						
	Yield (gm/m^2)	Plant Height (cm)	Number spikes $/m^2$	Biological yield (gm/m^2)	Number grains per spike	1000 grains weight	Harvest index
1	112.7 ab	44.111b-e	150.29 ab	282.78 a	25.91 b	34.846cde	40.166 ab
2	82.79abc	44.389b-e	122.34abc	230.56 a	25.548 b	32.203 ef	34.177 bc
3	112.5 ab	46.778abc	138.91abc	288.86 a	31.02 ab	33.132 de	36.162abc
4	98.95abc	41.722cde	125.79abc	262.75 a	27.53 ab	33.290 de	34.901abc
5	114.7 ab	41.500cde	152.27 ab	272.05 a	33.621 a	32.648 de	42.578 a
6	91.00abc	44.611bcd	134.90abc	237.79 a	27.04 ab	31.989 ef	36.071abc
7	74.62 bc	38.222 e	115.49 bc	226.72 a	24.46 ab	33.143 de	34.525abc
8	107.8 abc	44.722bcd	125.51abc	273.65 a	28.89 ab	38.184 ab	38.639 ab
9	109.1 abc	41.889cde	135.60abc	262.00 a	31.32 ab	33.507 de	40.127 ab
10	73.17 bc	45.556a-d	97.19 c	196.08 a	24.535 b	38.199 ab	25.781abc
11	90.09abc	48.611 ab	124.46abc	250.43 a	25.311 b	37.244 bc	34.592abc
12	89.80abc	42.111cde	127.60abc	242.10 a	27.36 ab	35.430bcd	36.388abc
13	114.06 ab	44.889bcd	138.55abc	298.58 a	24.065 b	40.454 a	37.283abc
14	98.97 abc	51.111 a	131.47abc	257.83 a	27.64 ab	35.576bcd	37.672abc
15	99.24 abc	45.722abc	264.35 a	264.35 a	27.73 ab	31.838 ef	34.499abc
16	126.88 a	45.944 ab	269.672 a	269.48 a	29.67 ab	37.225 bc	41.698 ab
17	60.33 c	39.222 de	210.65 a	210.65 a	17.022 c	29.590 f	29.374 c

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

in genotypes 17 (i), 7, 10 (i), 10 (ii), 17 (ii), 17 (iii) and 17 (iv), respectively, and It is evident that some genotypes gave distinct results for the most number of traits, including grain yield, in the foreground, Genotypes 14 and 16, followed by genotypes 8, 13 and 15, and these results indicate the possibility of utilizing these distinct genotypes in hybridization breeding programs in the future in order to transfer desirable traits to local varieties that adapted to environmental conditions, as well as in the development of new varieties of bread wheat. From previous studies, other researchers obtained significant differences between the means of genotypes for grain yield and their components in wheat, including

Kalapana et al. (2014), Esmail et al. (2016) and Bhattarai et al. (2017). Table (6) shows the values of genetic and phenotypic correlation coefficients between pairs of traits. It is noted that both types of correlations were similar in strength and direction for most cases, and that genetic correlations increase in value over most of the phenotypic one, and It is evident that grain yield/unit area correlated positively and significantly (genetically and phenotypically) with plant height, biological yield, number of grains/spike, weight of 1000 grains and harvest index, and phenotypically with number of spikes/unit area, indicating that the first five traits are genetically associated with the grain yield. The genetic correlation (which was negative) between yield and number of spike/unit area did not reach the significant level. On the other hand, no significant genetic correlations (whether negative or positive) were shown for plant height with both the biological yield and number of grains per spike, for the number of spikes per unit area with the number of grains per spike and for the number of grains per spike with 1000 grain weight, and phenotypically for number of spikes per unit area with both plant height and weight of 1000 grain and for number of grains/spike with the weight of 1000 grains. This independent association of these traits with the grain yield per unit area is generally beneficial to crop breeders, this is because if any of these traits are heavily selected in early generations, there is less possibility of excluding offspring that yielded well, if they are negatively correlated.

Table (6): Genetic correlations (above) and phenotypic (below) between the grain yield of bread wheat and some of its components.

Traits	Yield (gm/m^2)	Plant height (cm)	Number spikes $/m^2$	Biological yield (gm/m^2)	Number grains per spike	1000 grains weight	Harvest index
Yield (gm/m^2)	1	0.248*	-0.044	0.786**	0.876**	0.419**	1.371**
Plant height (cm)	0.471**	1	-0.339**	0.116	-0.006	0.451**	0.028
Number spikes/m^2	0.668**	0.140	1	-0.643**	0.009	-0.629**	0.625**
Bio. yield (gm/m^2)	0.841**	0.403**	0.587**	1	-3.692**	-4.224**	1.627**
Number grains/spike	0.722**	0.268**	0.293**	-0.686**	1	-0.022	0.919**
1000 grains weight	0.412**	0.468**	-0.088	-1.193**	0.097	1	1.996**
Harvest index (%)	0.869**	0.269**	0.609**	0.655**	0.799**	2.431*	1

- (**) and (*) significant at 1% and 5% respectively.

In order to determine the most influential traits in the grain yield for use in breeding programs for selection of high yield, the simple correlation coefficients (genetic and phenotypic) of yield with the other traits were hashed to the direct and indirect effects through the adoption of path analysis technique, and it was noted from genetic path analysis (Table 7), that the direct effect of plant height in yield was low, while the indirect effect through number of spikes was highly positive and through 1000 grain weight highly negative, and not important through other traits. The direct effect of number of spikes in the grain yield was negative and high, whereas the indirect effects through 1000 grains weight and harvesting index were positive and high and through the biological yield highly negative and not important through other traits. The direct genetic effect of the biological yield was positive and high in the grain yield, and the indirect effects were positive high through the number of spikes and very high through 1000 grains weight and harvest index, Table (7): Genetic path analysis for traits affecting grain yield

Traits	Plant height (cm)	Number spikes /m^2	Biological yield (gm/m^2)	Number grains per spike	1000 grains weight	Harvest index	Correlation with yield
plant height (cm)	(0.176)	0.317	0.055	-0.009	-0.326	0.035	0.278*
No. spikes/m^2	-0.059	(-0.936)	-0.307	0.013	0.456	0.791	-0.044
Bio. yield (gm/m^2)	0.021	0.602	(0.478)	-5.432	3.059	2.059	0.786**
No. grains/spike	-0.001	-0.008	-1.765	(1.471)	0.016	1.164	0.876**
1000 grains weight	0.079	0.589	-2.019	-0.032	(-0.724)	2.525	0.419**
Harvest index (%)	0.005	-0.585	0.778	1.353	-1.445	(1.265)	1.371**

- (**) and (*) significant at 1% and 5% respectively.

and negative very high through the number of grains per spike, but not important through plant height. The direct effects of number of grains/spike and harvesting index in the yield was positive and very high and it reached 1.4709 and 1.2651 respectively, and at the same time, the correlation of these two traits with the yield was highly significant and close to one, while the indirect effect of the number of grains per spike was positive very high through the harvest index, as well as the indirect effect of the harvest index was positively high through the biological yield and very high through the number of grain per spike. Finally, the direct genetic effect of the weight of 1000 grains in the yield get negative and very high, while the indirect effect was highly positive through the number of spikes and very high through harvest index. From the results of the phenotypic pathway analysis shown in Table (8), it is noticed that the direct effects on grain yield were negative low for plant height, and high for the number of spikes and 1000 grains weight, while the indirect effect of plant height was moderately positive through the number of grains per spike and harvest index and high through the biological yield, and the indirect one of the spikes number is positive, medium through the number of grains per spike and high through the biological yield and harvest index, while the indirect effect of 1000 grains weight was

Table (8): Phenotypic path analysis for traits affecting grain yield

Traits	Plant height (cm)	Number spikes /m^2	Biological yield (gm/m^2)	Number grains per spike	1000 grains weight	Harvest index	Correlation with yield
Plant height (cm)	(-0.118)	-0.098	0.376	0.252	-0.174	0.233	0.471**
No. spikes/m^2	-0.017	(-0.700)	0.548	0.276	0.033	0.529	0.668**
Bio. Yield(gm/m^2)	-0.048	-0.411	(0.933)	-0.645	0.444	0.569	0.841**
No. grains/spike	-0.032	-0.205	-0.639	(0.941)	-0.036	0.694	0.723**
1000 grains weight	-0.055	0.062	-1.113	0.092	(-0.372)	2.109	0.723**
Harvest index (%)	-0.032	-0.427	0.611	0.753	-0.904	(0.868)	0.869**

- (**) significant at 1%.

positive very high through harvest index. The direct phenotypic effect of the other traits (biological yield, grains number/spike and the harvest index) was highly positive, and respectively, reaching 0.933, 0.941 and 0.868, whereas the indirect effect of the biological yield was positive and high through the weight of 1000 grains and index harvest, and the indirect one of grains number/spike was positive and high through the harvest index, while the indirect effect of the harvest index was positive and high through the biological yield and number of grains per spike.

It is noted from the foregoing that the highest direct and indirect effects through other traits in grain yield (genetically and phenotypically) were for the number of grains per spike and harvest index, followed in importance by biological yield, and it is therefore possible to rely on these three traits as selection indices for the high grain yield in breeding programs. From previous studies, Ayerl et al. (2017), Sapi et al. (2017) and Kamani (2017) concluded that path analysis explain the significance of the direct effect on yield/plant which appeared higher through biologic yield and index harvest. Dutamo et al. (2015), from their experiment that carried out in one location, indicated that despite the direct and indirect effects of the harvest index and biological yields, and the possibility of their adoption in the selection of high grain yield, but this is not a final conclusion only after repeated implementation of the experiment in multiple locations. Khan and Dar (2010) indicated that the significance of the positive direct effect on grain yield was higher by the spikes number/plant, followed by the grains number/spike and weight of 100 grains, while the study of Desheva (2016) showed that the two traits, number of grains per spike and 1000 grains weight through grain weight per spike had the highest positive indirect effect on grain yield per plant, and this relationship can be used as a selection index in breeding programs to improve high-yielding varieties.

الارتباط وتحليل معامل المسار في حنطة الخبز

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الخلاصة

تم زراعة 15 تركيب وراثي من حنطة الخبز بالإضافة الى الصنفين المعتمدين في العراق (شام6 وابو غريب3) داخل حرم جامعة الموصل عند ثلاث مسافات للزراعة بين الخطوط (15 25 و35سم) باستخدام نظام الالواح المنشقة بتصميم قطاعات عشوائية كاملة بثلاثة مكررات لتقييم صفات حاصل الحبوب وبعض مكوناته من الصفات الأخرى (ارتفاع النبات وعدد السنابل وعدد الحبوب بالسنبلة والحاصل الحيوي ووزن 1000حبة ودليل الحصاد) وتحليل معامل المسار الوراثي والمظهري بين الحاصل ومكوناته. أظهرت النتائج ان المسافة 15سم اعطت اعلى المتوسطات لصفات الحاصل الحيوي وعدد السنابل وحاصل الحبوب، وكان حاصل الحبوب عندها اعلى مما هو عليه عند المسافتين 25 و35سم بنسبة 59.378٪ و123.422٪ على التوالي. تفوقت بعض التراكيب الوراثية معنوياً لأكثر عدد من الصفات بضمنها حاصل الحبوب، جاء في مقدمتها التركيبين الوراثيين MEXIPAK

65/ASFOOR-7 وشام6 تلاهما التراكيب الوراثية PBW343 و-NESMA*2/14-2//2*SAFI و3BT1735/ACHTAR//ASFOOR-1، ظهر لحاصل الحبوب في وحدة المساحة ارتباطاً موجباً معنوياً وراثياً ومظهرياً مع صفات ارتفاع النبات والحاصل الحيوي وعدد الحبوب بالسنبلة ووزن 1000 حبة ودليل الحصاد ومظهريا مع صفة عدد السنابل في وحدة المساحة. تبين من خلال تحليل معامل المسار أن اعلى التأثيرات المباشرة وغير المباشرة من خلال الصفات الاخرى في الحاصل وراثياً ومظهرياً كانت لصفتي عدد الحبوب بالسنبلة ودليل الحصاد وتلتهما في الاهمية صفة الحاصل الحيوي، وعليه بالإمكان الاعتماد على هذه الصفات الثلاث كأدلة انتخابية للحاصل العالي في برامج التربية.

الكلمات الدالة: حنطة الخبز، معامل المسار، الارتباطات

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