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Evaluation of Relative Efficiency of Several Selection Indices for Prediction of Expected Genetic Advance in Bread Wheat Grain Yield (*Triticum aestivum* L)

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genotypes, selection index, heritability, grain yield.

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ABSTRACT

This experiment was conducted with fifteen genotypes of bread wheat introduced from ICARDA and two local varieties (Sham6 and Abu-Graib3), using three rows spacing (15, 25 and 35 cm). All genotypes were grown in 7 December, 2017 at Field Crops farm (inside Mosul University) under rain fed conditions with complementary irrigation, using split plots in randomized complete block design with three replications, for evaluation through constructing several selection indices and calculation of the expected gains of grain yield. The analysis of variance results for studied traits (grain yield, plant height, number spikes, biological yield, number of grains per spike, 1000-grain weight and harvest index) showed that mean square of genotypes were highly significant for plant height, number of grains per spike and 1000 grain weight. The selection index constructed from number of grains per spike and harvest index had high increase in the efficiency as compared with direct selection for yield. This indicate of the importance of a selection index based on combination of characters. This index in the present study considered the superior due to its highest efficiency. Using this index for genotypes evaluation revealed that the higher mean of selection index was 109.961 for genotype REYNA-12 with significant difference over Abu-Graib3 and is not with others, followed in importance by Sham6, ATTILA-7, PASTOR-2/BOCRO-2 and HUBARA-5/3/SHA3/SERI//SHA4LLIRA. The local varieties of bread wheat included in this study, (Sham6 and Abu-Graib3) locates at the sequences 2 and 17 respectively.

INTRODUCTION

Wheat is one of the most important and essential strategic crops for the population in most countries of the world (Rauf et al., 2007), and ranks first among the grain crops in Iraq. The goal of increasing crop yield per unit area is a constant prerequisite to meet the need due to the population growth in many countries of the world (Hamam, 2008). In Iraq, productivity per unit area is still much lower compared to many other countries in the world. Sail et al. (2005) and Memon et al. (2007) have explained the reasons for the decrease in wheat productivity in general to factors related to environmental conditions, especially the wide variations in temperature, drought and salinity, as well as biological factors, most importantly disease and insect infections. In order to overcome the consumer pressure resulting from global population growth, crop breeders have focused their efforts on improving their production capacity by developing new varieties through appropriate and efficient breeding methods. The selection process is the main way of developing different field crops, and

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plant breeders usually focus their attention to improve any crop through breeding programs because of its short time, efforts and costs. In such cases, the selection index technique is used to distinguish and differentiate between different genotypes to choose the suitable ones for a particular environment, and then recommend those with higher values of the selection index, which is estimated through the selection of an electoral an index that has the lowest number of traits, and characterized by higher relative efficiency compared to direct selection of grain yield alone (Taha, 2007). Hazel and Lush (1942) pointed out that when multiple traits affect the net output of an organism, it is necessary to determine the importance of these traits in appropriate proportions to maximize the progress required from selection. Smith (1936), Hazel (1943), Lerner et al. (1947) provided a method of estimating the optimal relative importance of various selection programs. Robinson et al. (1951) provided methods for estimating genetic and phenotypic variances and covariance's required to establish selection indices. Numerous studies have been carried out by researchers in this field, dealing with the selection indices in wheat and some other self-fertilized crops, among them were, Wells and Kofoid (1986), Ahmad and Hamdo (2000), Al-Jubouri et al. (2006), Taha (2007), Laghari et al. (2010), Ahmed et al. (2011), Dawod et al. (2012), Raiyani et al. (2015), Sahar et al. (2016) and Ghaed-Rahimi et al. (2017), whose results indicated that some election indices, consisting of several traits, outweighed the direct selection of the yield alone, some were characterized by a high relative efficiency and expected genetic improvement as a result of selection.

The aim of the present study is to construct selection indices in all possible ways between seven traits of bread wheat and compare its efficiency with the direct selection for grain yield in order to select a simple and useful selection index, to use it in evaluating 17 genotypes used in this study.

MATERIALS AND METHODS

The experiment was carried out in the field of Field Crops Dept. (inside Mosul University campus), and included the cultivation of 15 genotypes of bread wheat (introduced from the International Center for Agricultural Research in the Dry Areas) 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).

Table 1: Genotypes of bread wheat used in the study and their selection history.

Seq	Name	Selection history
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

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.

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

At maturity, data were recorded on the traits of plant height (cm), number of spikes per m^2, biological yield (gm per m^2), number of grains per spike, 1000 grains weight, harvest index (%), and grain yield per 1 m^2 (gm). The data of genotypes of all traits were analyzed according to the experimental design method used (Al-Zubaidy and Al-Falahy, 2016). Phenotypic and genotypic variances (σ^2_P and σ^2_G respectively) and covariance's ($\sigma P_x P_y$ and $\sigma G_x G_y$ respectively) were estimated through the relationship between the estimated and expected mean squares in the variance and covariance analysis table, the following estimates were made (Al-Zubaidi and Al-Jabouri, 2016):

(1) Genetic and phenotypic correlations (rG and rP respectively) between the traits under study from the following two equations:

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

(2) Inheritance in the broad sense heritability (H^2) from the ratio between $\sigma^2 G / \sigma^2 P$.

(3) The expected genetic advance (GA) from selection in the next generation for each trait GA = (k) (H^2) (σP), where k means the selection intensity and equal to 2.06 when selecting 5% of plants, σP = phenotypic standard deviation, as well as the expected genetic advance was estimated as a percentage of the trait mean ($\bar{Y}..$) from the equation: GA% = (GA/ $\bar{Y}..$)(100).

(4) The expected changes in grain yield (response to selection) (CRx) as a result of the selection of any other traits from the equation: CRx = (k) (Γ_G) ($\sqrt{H^2 x}$) ($\sqrt{H^2 y}$) (σPx), as well as the expected change in yield as a percentage of the mean of grain yield ($\bar{Y}..$) from the equation: CRx% = (CRx / $\bar{Y}..$) (100).

(5) The method of constructing the selection indices suggested by Miller et al. (1958) was used, and the selection indices were constructed in all possible ways between the traits under study. The format of the index: $I = b_1x_1 + b_2x_2 + ... + b_nx_n$, where: x_1, x_2 ... x_n indicate the phenotypic values of the traits, and b_1 and b_2 ..... b_n are the relative weights of the traits, and the values of (b) are obtained from the following equation (by applying matrices) $b = P^{-1} g$, P^{-1} means the inverse of the phenotypic variances and covariance's matrix, and g (g_{1y}, g_{2y}, ... g_{ny}) the genetic covariance's of each trait with the grain yield.

(6) The expected genetic advance when adopting selection through selection indices was estimated from the equation:

$$GA = k\sqrt{b_1 g_{1y} + b_2 g_{2y} + \ldots\ldots\ldots + b_n g_{ny}}$$

(7) The values of the selection index for each genotype in each replicate were estimated by adopting the best selection index, then variance analysis of these data was carried out and the Duncan's Multiple Range Test was used to compare its means.

SAS (Statistical Analysis System, Minitab, and Microsoft office Excel 2003 available programs were used in analysis of data and make all above estimates.

RESULTS AND DISCUSSION

Table (3) shows the analysis of variance results of the data of the genotypes grown at three spaces between the rows for grain yield and some of its components in bread 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 consistent with the findings of Ahmad et al. (2011) and dawod et al. (2012) for these three traits. The mean square of spaces was significant for grain yield, number of spikes/m^2 and biological yield, while that related to the spaces x genotypes interaction was significant for biological yield only.

Table 3: The results of analysis of variance for grain yield and some of its components.

SOV	**df**	**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 of the variance analysis of the traits under study and covariance between them were used to estimate the phenotypic and genetic variances for these traits and their results are shown in Table (4), and these components were adopted in the calculations of phenotypic and genetic correlations, broad sense heritability, construction of selection indices in all possible ways and estimation of the expected genetic advance in the next generation.

Table (5) shows the values of the genetic and phenotypic correlation coefficients between yield and its components of other traits, It is noted that the genetic and phenotypic correlations were close in their strength and direction for most cases, and that genetic correlations increase in value over phenotypic most of cases. It is clear that the grain yield in the unit area positively and significantly correlated genetically and phenotypically with plant height, biological yield, number of grains per spike, 1000 grains weight and harvest index, and phenotypically with number of spikes per unit area, indicating that the first five traits are genetically correlated with the grain yield, and the negative genetic correlation between grain yield and number of spikes per unit area did not reach the significant limit. 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, the number of spikes per unit area with the number of grains per spike, the number of grains per spike with 1000 grains weight and phenotypically for number of spikes per unit area with both plant height and 1000 grains weight and for number of grains per spike with 1000 grains weight. This independent association of these traits with the grain yield per unit area is generally beneficial to crop breeder, This is because if any of these traits are heavily selected in early generations, there is less possibility of excluding good offspring if they are negatively correlated.

Table 4: genetic variances and covariance's (values up) and phenotypic variances and covariance's (values down) for different traits in bread wheat.

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**
Yield (gm/m^2)	99.189 383837	6.930	-3.437	61.342	26.017	11.329	28.549
Plant height (cm)	31.814	7.875 11.869	-7.458	4.281	-0.052	3.435	0.161
Number spikes/m^2	202.773	7.476	61.438 239.965	-66.564	0.201	-13.409	10.239
Biological yield	614.326	51.708	339.125	174.38 1389.431	-145.359	-151.478	44.922
Number grains/spike	53.576	.473	17.073	-96.219	8.887 14.168	-0.175	5.733
1000 grains weight (gm)	23.259	4.645	-3.907	-128.019	1.052	7.374 8.290	11.329
Harvest index	56.619	3.078	31.347	81.129	10.002	23.259	4.371 11.039

Table 5: Genetic correlations (upper) and phenotypic correlations (lower) between grain yield and Some of its components in bread wheat

Traits	**Yield (gm/m^2)**	**Plant height (cm)**	**Number spikes /m^2**	**Biological yield (gm/m^2)**	**Number grains/ 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**	0.025
Number spikes/m^2	0.668**	0.141	1	-0.643**	0.009	-0.629**	0.625**
Biological yield	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	-0.0216	0.919**
1000 grains weight	0.412**	0.468**	-0.088	-1.193**	0.097	1	1.996**
Harvest index	0.870**	0.269**	0.609**	0.655**	0.799**	2.431**	1

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

Estimates of variance components (genetic, environmental, phenotypic), inheritance, and expected genetic advance in the next generation (GA) for the traits under study that are used as a criterion for selection are shown in Table 6. It is generally noted that the broad sense heritability ranged from 12.55% for the biological yield to 88.95% for the 1000 grains weight, as it was high for plant height, number of grains per spike and 1000 grain weight, moderate for grains yield, number of spikes per unit area and harvest index and low for biological yield. The results also showed moderate amount of expected genetic advance as a percentage of mean in the next generation (GA%) for the number of grains per spike and 1000 grains weight (15.313% and 12.947% respectively) and low for other traits, and from a previous study, Dawod et al. (2012) obtained high heritability for number of grains per spike, 1000 grains weight and grain yield, followed by an expected genetic advance in the next generation moderate or high. In the same table, the expected gain values in the field of grain yield improvement through the selection of any of its components from other traits expressed as a percentage of the grain yield mean (CRx%). It is noted that the expected response of grain yield if the selection was practiced for the number of grains per spike and harvest index at 5% selection intensity was 12.421% and 15.429% respectively from the original mean of grain yield and it is moderate values. The selection for plant height, biological yield and 1000 grains weight caused little changes in grain yield by 3.612%, 4.979% and 7.066% respectively, while the selection for number of spikes per unit area showed a negative result of -0.398%. Direct selection is very important when assessing the primary trait is difficult, and the secondary trait has a high heritability and correlates significantly with the desired trait.

Table 6: Mean and genetic parameters for grain yield and some of its components in bread wheat.

parameters	**Traits**						
	Yield (gm/m^2)	**Plant height (cm)**	**Number spikes /m^2**	**Biological yield (gm/m^2)**	**Number grains/ spike**	**1000 grains weight**	**Harvest index**
Mean	97.453	77.359	133.424	259.097	26.982	34.617	36.739
Genetic V.	99.189	7.785	61.438	174.380	8.887	7.374	4.371
Environmental V.	213.706	3.669	178.527	680.630	4.710	0.872	6.101
Interactional V.	70.942	0.325	0.000	534.421	0.571	0.044	0.567
Phenotypic V.	383.837	11.879	239.965	1389.431	14.168	8.290	11.039
Heritability	0.258	0.663	0.256	0.126	0.627	0.889	0.396
GA	8.859	3.999	6.941	8.187	4.132	4.482	2.302
GA%	9.092	9.017	5.202	3.197	15.313	12.947	6.266
CR_x	----	3.520	-0.388	4.852	12.096	6.886	15.037
CR_x%	----	3.612	-0.398	4.979	12.412	7.066	15.429

The selection indices was constructed in all possible ways (some of which include and without grain yield) and were tested in an attempt to identify traits that are catalysts for future selection and evaluation of genotypes used in this study. Table (7) shows the expected improvement in grain yield based on different selection indices as compared with the direct selection for grain yield in a set of indices (including weights values b). Selection indices that is less efficiency than direct selection for grain yield only is excluded. It is noted from Table 6 that the expected improvement in the grain yield of the selection indices at 5% selection intensity ranged from (0.388) for the index in sequence 3 to (17.320) in the index in sequence 16 compared to the expected improvement of (8.859) from the direct selection for grain yield. The selection improvement expressed by the relative efficiency of the 27 selection index presented in table (7) ranged from (4.379%) to (170.979%), and it is noteworthy that 30% of these indices (which have a relative efficiency higher than the selection for the grain yield only) does not include the grain yield, and this result is incompatible with Al-Juboury et al (2006), Taha (2007) and Dawod (2012), they pointed out that the selection indices that
They were obtained, which did not include grain yields, were all with less relative efficiency than the case of direct selection for grain yield. It is clear that the selection index in sequence 11 (I_{57}), which includes the two traits, number of grains per spike and harvest index had a relative efficiency of (69.726%) higher than the case of direct selection for grain yield alone, indicating that this index is superior in the selection for high grain yield as compared to direct selection for grain yield or about the case of using any other selection indices which constructed in this study. The choice of this index because it does not include the grain yield trait, although the two indices in the sequences 16 and 24 achieved (95.495%) and (70.979%), respectively, higher than the selection status for grain yield alone, and neither of them was selected as having 3 and 5 traits respectively, including grain yield. The reason for the superiority of these three selection indices may be due to the significant correlations between some of the traits they contain as well as their correlations with the grain yield. Other researchers, including Ahmad and Hamdo (2000), Taha (2007) and Dawod et al. (2012), have pointed to the importance of selection indices that includes grain yields and some of its components in wheat.

Table 7: Expected genetic advance for yield and relative efficiency from some selection indices.

sq	Index	Traits							Genetic advance	Relative efficiency
		Yield (gm/m^2)	Plant height (cm)	Number spikes /m^2	Biological yield (gm/m^2)	Number grains/ spike	1000 grains weight	Harvest index		
		b_1	b_2	b_3	b_4	b_5	b_6	b_7		
1	I_1	0.259							8.859	100
2	I_2		0.584						3.520	39.734
3	I_3			-0.014					0.388	4.379
4	I_4				0.044				2.878	32.488
5	I_5					1.836			10.435	114.783
6	I_6						1.367		6.886	77.727
7	I_7							2.586	10.147	114.525
8	I_{35}			-0.159		2.027			12.775	144.191
9	I_{36}			0.008			1.370		6.889	77.765
10	I_{23}		0.605	-0.033					3.631	40.984
11	I_{57}					0.029		2.559	15.037	169.726
12	I_{67}						1.199	0.059	6.843	77.239
13	I_{34}			-0.117	0.073				3.859	43.563
14	I_{135}	0.243		-0.312		1.298			13.438	151.672
15	I_{136}	0.518		-0.457			-0.303		12.319	139.043
16	I_{157}	-0.510				0.228		4.996	17.320	139.043
17	I_{467}				0.070		0.683	0.630	9.593	108.277
18	I_{167}	0.212					0.698	0.025	9.538	107.661
19	I_{457}				0.029	1.013		1.450	14.599	164.776
20	I_{123}	0.553	-0.608	-0.463					12.652	142.805
21	I_{134}	0.829		-0.396	-0.225				14.611	164.910
22	I_{1457}	-0.514			0.002	0.281		4.959	17.319	195.481
23	I_{1467}	0.095			0.042		0.669	0.383	9.659	109.029
24	I_{4567}				0.084	1.743	-0.271	0.964	15.148	170.979
25	I_{14567}	0.562			-0.103	-0.391	0.819	-0.914	8.296	93.638
26	I_{234567}		-1.797	-1.253	0.389	4.333	-1.559	3.141	14.902	168.200
27	$I_{1234567}$	0.771	-0.936	-0.402	-0.068	-0.305	0.763	-0.797	11.759	132.732

Based on the selection index selected as the best, which includes both the number of grain per spike and harvest index ($I_{57} = 0.02976\ X_5 + 2.55907\ X_7$), the values of the selection index for each genotype in each replicate was estimated, and these genotype data were then statistically analyzed according to the method of randomized complete block design (Table 8), and the F test showed that the mean square of the genotype was significant at a 1% probability level, indicating significant differences between the mean of index values for the genotypes. These differences were tested using Duncan multiple range test method (Table 9), from which it is evident that the highest index value was (109.961) for genotype in sequence 5 by a non-significant difference from most other genotypes, followed by genotypes in sequences 16, 9 and 1 with (107.591), (103.62) and (103.559) values respectively. The two registered varieties in Iraq, Cham 6 and Abu Ghraib 3 in terms of the value of the index, were in sequences 2 and 17 respectively, This means that one introduced genotype surpassed the best one of the two local variety (Cham 6), and the other genotypes were similar, while all genotypes outperformed Abu Ghraib 3.

It was suggested from the above that the best introduced genotypes were in sequences 1, 3, 4 and 5, respectively ATTILA-7, PASTOR-2/BOCRO-2, HUBARA-5/3/SHA3/ SERI//SHA4LLIRA and REYNA-1, and these genotypes, particularly the introduced one REYNA-12, which surpassed the best local varieties Cham 6 can be used in breeding programs to improve the grain yield of bread wheat and in the development of new varieties of wheat characterized by production specifications and good quality and suit the environmental conditions in Iraq.

Table 8: Analysis of variance results for selection index values in genotypes used in this study.

Source	Degrees of freedom	Sum Square	Mean Square	Computed F
Reps.	2	2148.805	306.061	
Genotypes	16	3360.285	123.039**	1.71
Error	32	3937.241		

(**) significant at 1% probability level.

Table 9: The trade-off between genotypes according to the values of the selection index

genotype	Mean of selection index	Trade-off sequence	genotype	Mean of selection index	Trade-off sequence
1	103.559 a	(4)	10	92.297 ab	(11)
2	88.069 ab	(16)	11	89.276 ab	(13)
3	93.463 ab	(9)	12	93.933 ab	(8)
4	90.134 ab	(12)	13	96.126 ab	(7)
5	109.961 a	(1)	14	97.229 ab	(6)
6	93.113 ab	(10)	15	89.110 ab	(14)
7	89.080 ab	(15)	16	107.591 a	(2)
8	99.740 a	(5)	17	75.676 b	(17)
9	103.620 a	(3)			

- Means followed by the same letter do not significantly different.

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تقييم الكفاءة النسبية لعدد من أدلة الانتخاب للتنبؤ بالتحسين الوراثي المتوقع في حاصل حبوب الحنطة الناعمة (*Triticum aestivum* L.)

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المستخلص

اجريت هذه التجربة باستخدام 15 تركيب وراثي من الحنطة الناعمة مدخلة من المركز الدولي للبحوث الزراعية في المناطق الجافة وصنفين محليين (شام6 وابو غريب3) عند ثلاث مسافات زراعة بين الخطوط (15 و25 و35سم). زرعت جميع التراكيب الوراثية في 7 كانون اول 2017 في حقل قسم المحاصيل الحقلية (داخل حرم جامعة الموصل) تحت الظروف المطرية مع اعطاء ريات تكميلية وباستخدام نظام الالواح المنشقة بتصميم القطاعات العشوائية الكاملة بثلاثة مكررات، بهدف تقييمها من خلال إنشاء أدلة انتخاب متعددة وتقدير الزيادة المتوقعة في حاصل الحبوب. أظهرت نتائج تحليل التباين للصفات المدروسة (حاصل الحبوب وارتفاع النبات وعدد السنابل بالمتر المربع والحاصل الحيوي وعدد الحبوب بالسنبلة ووزن 1000حبة ودليل الحصاد) أن متوسط مربعات التراكيب الوراثية كان معنوياً عالياً لصفات ارتفاع النبات وعدد الحبوب بالسنبلة ووزن 1000 حبة. تميز الدليل الانتخابي المتضمن صفتي عدد الحبوب بالسنبلة ودليل الحصاد بزيادة كبيرة في الكفاءة مقارنة بالانتخاب المباشر لحاصل الحبوب، دلالة على أهمية الانتخاب باعتماد الدليل الانتخابي لعدة صفات. واعتبر هذا الدليل في الدراسة الحالية هو الأفضل لتميزه بكفاءته العالية، وباعتماده في تقييم التراكيب الوراثية تبين أن أعلى متوسط للدليل بلغ 109.961للتركيب الوراثي (REYNA-12) بفارق معنوي عن الصنف ابو غريب3 وغير معنوي عن التراكيب الوراثية الأخرى، تليه في الاهمية الصنف شام6 والتراكيب الوراثية ATTILA-7 وPASTOR-2/BOCRO-2 و HUBARA-5/3/SHA3/SERI//SHA4LLIRA. كان تسلسل الصنفين المحليين شام6 وابو غريب3 المعتمدين في الدراسة من حيث الأداء 2 و17 على التوالي.

الكلمات المفتاحية: تراكيب وراثية، دليل الانتخاب، التوريث، حاصل الحبوب