


Construction of some selection procedures for improvement of grain yield in durum wheat

Ibrahim S.M. Abdel-Latif^{1*} , Mohamed N.T. Abd EL-Kader¹ and Mousa S. Salous¹

Address:

Wheat Research Department, Field Crops Research Institute, Agriculture Research Center, Egypt

*Corresponding author: **Ibrahim S.M. Abdel-Latif**, e-mail: i.sabri4848@gmail.com



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ABSTRACT

The purpose of this study was to estimate and compare the genetic gain obtained from the Smith-Hazel index model of selection index with direct selection to enhance the selection efficiency of superior promising families in early segregating generations of the durum wheat population. Two methods of selection were evaluated, namely, direct selection and indirect selection, by the selection index in the yield and its components. A comparison of mean performances for different traits among the four generations (F₂, F₃, F₄, and F₅) revealed an increase in mean values for most traits with advanced generations from F₂ to F₅, with some exceptions due to environmental factors. PCV and GCV were generally larger in magnitude for all studied traits in the F₂ generation as compared with the advanced generations F₃, F₄, and F₅, indicating that the magnitude of the genetic variability persisting in this material was sufficient for providing a rather substantial amount of improvement through the selection of superior progeny. High heritability values over 50% for most studied traits across generations indicate a high magnitude of genetic variability and possible success in selection in early generations. Nine out of eleven selection indices were more efficient than direct selection for improving GY/P in the F₂ population. The highest predicted genetic gain from F₂ generation for GY/P was observed when selection index (I_{w123}) was followed by selection index (I_{w2}) and by selections for (I_{w12}), (I_{w23}), (I_{w1}), and (I_{w3}). Selection index (I_{w123}), followed by I_{w12} and direct selection (I_{xw}), gave the highest actual genetic gains from the third generation for trait GY/P. Most indices showed a high discrepancy between predicted and actual genetic gain as GY/P; this was due to the interaction between genetic effects and large effects of environmental factors. The maximum predicted genetic advance from F₃ and F₄ generations for GY/P was achieved when selecting directly (I_{xw}) in F₃ followed by selection indices (I₁₂₃). While maximum actual genetic advance from F₃ and F₄ generations for GY and P was achieved when using selection indices (I₁₂₃), followed by (I_{w2}), and then direct selection (I_{xw}). Deviations of the actual genetic advance from the predicted advance from the F₃ and F₄ generations showed positive and large values in most procedures.

Keywords: *Triticum durum*, PCV, GCV, Heritability, Selection procedures, Selection index.

INTRODUCTION

The kind and degree of genetic diversity present in the population heavily influences the selection techniques chosen for wheat genetic improvement. In order to create superior wheat varieties with large yields, favorable quality, and tolerance to biotic and abiotic stress, wheat breeders are always working to improve the selection processes. Because grain yield is a complex trait that is greatly influenced by environmental factors, direct selection based solely on grain yield is challenging to implement in wheat breeding. However, the presence of genotype-environment interactions reduces the effectiveness of using grain yield as the sole selection criterion and further complicates selection efforts (Fellahi *et al.*, 2018).

In addition to the effects of the environment, selection may be less effective, especially in early segregating generations, due to factors such polygenicity, low heritability, linkage, and non-additive gene action. Grain yield in wheat, as in other cereal crops, is a complex trait that is influenced by some yield-contributing traits. For planning a yield improvement program, knowledge of the relationship between yield and yield-contributing traits is important. The study of the correlation coefficient between the traits has importance in selection practice because it helps construct selection indices and also permits the prediction of correlated responses. Thus, direct selection for yield is not expected to be effective. Therefore, breeders avoid selection for yield and prefer to select for its components individually (Ferdous *et al.*, 2010; Lali *et al.*, 2010). When single trait selection is practiced and the correlation of that trait with others is high and unfavorable, an undesirable correlated response may occur for those traits not

considered in selection criteria (Bos and Caligari, 1995; Patel *et al.*, 2019). In order to get through these obstacles in a multi-trait approach, breeders are concentrating on additional traits that can be employed concurrently with or independently of yield (Habib *et al.*, 2007). A breeding program's likelihood of success is increased by simultaneously selecting features that are important from an economic perspective (Sayd *et al.*, 2019).

The selection index, which is typically used to distinguish between selection units by taking into account both the genetic and statistical structure of the population from which the genotype originated as well as the economic importance of the traits, is used for this purpose. It is a multiple regression of genotypic values on phenotypic values of several traits. It is therefore projected to produce offspring with better economic value when solely evaluating such individuals (Jesus *et al.*, 2006). A selection index is preferable for enhancing complicated features. Additionally, selection indexes sought to locate the most advantageous genotypes and the best set of features that would increase overall yield in various plants (Shah *et al.*, 2016). A review of the literature revealed that less effort has been put into index-based selection and that most studies of plant selection have frequently concentrated on single trait or multiple trait selection without taking into account the interrelationship, heredity, and weight of characteristics. The use of indices as selection criteria produced somewhat better outcomes, according to certain comparisons of the indices with direct selection.

Determining the genetic gain from the Smith (1936) and Hazel (1943) index model of selection index with direct and indirect selection to increase the selection efficiency of superior families, as well as estimating the correlated response to selection, are the goals of the current investigation into wheat's genetic variability.

MATERIALS AND METHODS

The local cultivar (Sohag-3) of durum wheat (*Triticum durum*, Desf.) is more adapted in Egypt and has high yielding ability; however, the local line (Line#1) is early. Therefore, this line was crossed with the Egyptian cultivar in order to enlarge the variability for selection in the breeding program for the heading date, yield and its component. The pedigree and origin of these parents are presented in Table (1).

Table 1. The pedigree and origin of the parents of the cross population.

Parents	Pedigree	Origin
(P ₁) Sohag-3	MEXI"s"/MGHA/51792//DURUM6	Egypt
(P ₂) Line#1	14-Sohag1/4/CMN79.1168/Mexi75//CMN77. 774/3/omrabi-5.	Egypt

The present investigation was carried out at the Agricultural Research Station of El-Mattana in Upper Egypt, Agric. Res. Center, Ministry of Agriculture, Egypt, during the four successive growing seasons from 2017/2018 to 2020/2021.

In the 2017–2018 season, the F₂ generation with the original parents was grown in a non-replicated row with 3.0 m length, 30 cm width, and 15 cm between plants. The data was recorded on 500 inner individual plants. After harvest, single plants (500) were ranked using a selection intensity of 2.5% with eleven selection indicators and four direct selections, and 50 F₂ plants were selected based on their performance. The plants with the highest performance in each procedure were saved.

In the 2018-2019 season, the 50 F₃ families' progeny were evaluated with the original parents and a bulked random sample (a mixture of an equal number of seeds from each plant to represent the generation mean) in a randomized complete blocks design with three replicates. The experimental plot consisted of one row like that carried out in 2017–2018. The different selection procedures include direct selection for each selected trait and a classical selection index in which all studied traits are applied. The superior progeny of each selection procedure was selected using a 2.5% selection intensity. This gave a total of 20 selected families.

Selection procedures were as follows:

NO	Indices		Indicate that involving traits
1	lw123	=	Selection index involving grain yield/plant, number of spikes/plant, number of grains/spike and 100kernel weight.
2	lw12	=	Selection index involving grain yield/plant, number of spikes/plant and number of grains/spike
3	lw13	=	Selection index involving grain yield/plant, number of spikes/plant and 100kernel weight.
4	lw23	=	Selection index involving grain yield/plant, number of grains/spike and 100kernel weight
5	l123	=	Selection index involving number of spikes/plant, number of grains/spike and 100kernel weight.
6	lw1	=	Selection index involving grain yield/plant and number of spikes/plant.
7	lw2	=	Selection index involving grain yield/plant and , grains/spike
8	lw3	=	Selection index involving grain yield/plant and 100kernel weight.
9	l12	=	Selection index involving number of spikes/plant and grains/spike
10	l13	=	Selection index involving number of spikes/plant and 100kernel weight
11	l23	=	Selection index involving grains/spike and 100kernel.
12	lxw	=	Selection for grain yield/plant.
13	lx1	=	Selection for number of spikes/plant.
14	lx2	=	Selection for number of grains/spike
15	lx3	=	Selection for 100kernel weight.

In 2019/2020 season, the 20 selected families were evaluated with the original parents and F₃ bulked same like in 2018/2019, then 10 selected families were saved in F₄ generation by superiority of these families for the better parent and F₄ bulked, F₄ families and point start of F₂ plants mean for evaluation in the F₅- generation in season 2020/2021.

The ordinary practices of wheat cultivation were applied. Data were recorded on inner individual plants basis for each entry in F₂, F₃, F₄ and F₅ families for heading date (HD), duration of grain filling period (DGFP), grain production rate (GPR), plant height (PH), number of spikes/plant (#S/P), number of grains/spike (#G/S), 100-kernel weight(100-KW), grain yield/plant (GY/P) and biological yield/plant (BY/P).

Statistical procedure:

The phenotypic (PCV) and genotypic (GCV) coefficients of variation were estimated according to Kearsy and Pooni (1996). Also, according to Walker (1960), heritability in broad sense was calculated as follows:

$$h_b^2 \text{ (in } F_2 \text{ generation)} = \frac{VF_2 - (VP_1 + VP_2)/2}{VF_2} \times 100$$

$$h_b^2 \text{ (in } F_3 \text{ and } F_4 \text{ generation)} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where:

VF₂ = the phenotypic variance of the F₂ generation.

VP₁, VP₂= the variance of the first and second parents.

g = the genotypic variance of the F₃ and F₄ generations.

p = the phenotypic variance of the F₃ and F₄ generations.

Phenotypic and genotypic correlation coefficients between studied traits were also computed in three generations according to Falconer and Mackey (1996).

The phenotypic correlation (r_{pij}) = $\sigma_{pij} / \sqrt{\sigma_{pi}^2 \times \sigma_{pj}^2}$

The genotypic correlation (r_{gij}) = $\sigma_{gij} / \sqrt{\sigma_{gi}^2 \times \sigma_{gj}^2}$

Where;

σ_{pij} , σ_{pi}^2 and σ_{pj}^2 are the phenotypic covariance between i and j traits and phenotypic variance for i and j traits.

σ_{gij} , σ_{gi}^2 and σ_{gj}^2 are the genotypic covariance between i and j traits and genotypic variance for i and j traits.

The expected gain through direct selection (SGx) and indirect (SGy(x)) were calculated as follow:

$$SGx = i \cdot \sigma_x \cdot h_b x$$

$$SGY(x) = i \cdot \sigma_y \cdot h_b x \cdot r_g(xy)$$

According to Bos and Caligari (1995) Where:

i is selected the intensity obtained considering a selection of 2.5% among the progeny.

x = Standard deviation of the genotypic variance of trait x.

y = Standard deviation of the genotypic variance of trait y.

$h_{b.x}$ = Square root of heritability in broad sense.

$r_g(xy)$ = is the genotypic correlation between trait x and trait y.

The relative importance or economic values was calculated according to Walker (1960). Classical selection index was calculated according to Smith (1936) and Hazel (1943).

$$(b) = (P)^{-1} \cdot (G) \cdot (a)$$

Where: b = vector of relative index coefficients.

(P^{-1}) = inverse of the phenotypic variance – covariance matrix.

(G) = Genotypic variance – covariance matrix.

(a) = vector of relative economic values based on equally important = 1 for all traits.

Calculation of selection indices:

The formula suggested by Smith (1936) and Hazel (1943) was used in calculating various selection indices:

$$I = b_1 X_1 + b_2 X_2 + \dots + b_n X_n$$

Where:

I indicate a single index value of the individual unit on which selection is based.

X_1 to X_n indicates phenotypic values of characters.

B_1 to b_n indicate weighting factor given to the corresponding character; X 's.

Calculation of genetic advances:

Predicated improvement in grain yield on the basis of an index in standard measure was calculated according to the following expression:

$$\text{Selection advances (SA)} = SD \sqrt{\sum b_i \times \sigma_{giw}} \quad \text{Walker (1960)}$$

Where:

SD denotes selection differential in standard units.

b_i denotes index weights for characters considered in an index.

σ_{giw} denotes genotypic covariance of the character of yield.

The selection advance is also expressed as percentage terms of yield by dividing by the mean of the yield

$$\text{Percentage selection advance (\% SA)} = \frac{SA}{\bar{X}_w}$$

Predicted improvement in grain yield for selecting 2.5% of the families on the basis of an index was calculated from the general formula, $SG_i = 1bG/(v_i)^{1/2}$.

Where: SG_i = predicted gain from selection.

i = selection intensity.

b_i = is the index weight for the traits considering in an index.

G_i = is the row of genetic matrix.

(v_i) = is the index variance.

The predicted response in any selected and unselected traits was also computed according to Falconar (1989) as follows: $GS_k = i \cdot \sigma_{gki} / (\sigma_i)^{0.5}$

Where; i = is the selection differential in standard units.

$\sigma_{g_{ki}}$ = is the genotypic covariance of k trait and the index.

σ_i = is the variance of the index.

The actual gains were calculated as deviation of generation mean for each trait from procedure mean of the trait.

RESULTS

Segregating populations with high mean performance was relatively effective in identifying the superior recombinants. A comparison of mean performance for different traits among the four generations (F_2 , F_3 , F_4 , and F_5) Table (2) revealed increases in mean values for most traits with advanced generations from F_2 to F_5 , with some expectation due to environmental factors.

The range, an index of variability, was comparatively wider in the F_2 generation as compared with the later generations (F_3 , F_4 , and F_5) for all studied traits. At the same time, the lower limits of range were lower in the F_2 generation for all studied traits, leading to a wider spectrum of variability. However, in advanced generations (F_3 and F_4), the lower limits of range were relatively high, and the upper limits were also relatively high.

The estimates of genetic variation make the task of breeding easy, so as to make effective selection. The data in Table (2) showed that the PCV and GCV were generally larger in magnitude for all studied traits in the F_2 generation as compared with the advanced generations F_3 , F_4 , and F_5 . At the same time, the PCV was generally slightly higher than the GCV for all studied traits and in most cases.

Table 2. Means, standard deviation ($SX \pm$), range, phenotypic (PCV) and genotypic (GCV) coefficients of variation and broad sense heritability (h^2_b) for the studied traits in F_2 , F_3 , F_4 and F_5 generations in wheat population.

Generation	Traits	Mean	$SX \pm$	Min	Maxi	VP	VG	V e	h^2 b.s %	PCV%	GCV%
F2	HD	83.92	4.81	70.0	92.0	23.10**	11.51	11.59	49.83	5.73	4.04
F3		83.80	3.06	73.0	92.0	6.08**	4.40	1.67	72.46	2.94	2.50
F4		86.45	2.93	76.0	95.0	8.587**	7.22	1.37	84.05	3.39	3.11
F5		85.70	1.81	80.0	91.0	3.27**	1.96	1.31	60.04	2.11	1.63
F2	GFPD	37.51	3.28	28.0	48.0	10.74**	9.07	1.67	84.48	8.74	8.03
F3		38.77	3.02	29.0	46.0	6.02**	4.52	1.50	75.12	6.33	5.48
F4		40.08	2.90	31.0	48.0	8.407**	6.77	1.64	80.49	7.23	6.49
F5		42.47	1.30	39.0	45.0	1.683**	0.56	1.12	33.47	3.06	1.77
F2	GFR	0.47	0.24	0.1	1.3	0.06**	0.055	0.003	95.61	50.39	49.27
F3		0.91	0.18	0.6	1.6	0.02**	0.019	0.004	81.40	16.68	15.05
F4		1.00	0.20	0.6	1.6	0.041**	0.035	0.006	85.69	20.33	18.82
F5		1.06	0.23	0.6	1.6	0.0534**	0.046	0.0074	86.09	21.74	20.17
F2	PH	99.67	10.29	72.0	137.0	105.97**	100.70	5.30	95.00	10.33	10.07
F3		104.80	6.83	95.0	120.0	26.60**	16.77	9.83	63.03	4.92	3.91
F4		110.30	4.70	100.0	125.0	22.067**	12.83	9.23	58.16	4.26	3.25
F5		102.33	5.94	85.0	115.0	35.3*	30.27	5.03	85.74	5.81	5.38
F2	#S/P	6.48	2.26	2.0	11.0	5.09**	4.690	0.390	92.26	34.81	33.43
F3		9.72	2.06	5.0	16.0	2.88**	2.190	0.690	76.13	17.45	15.22
F4		9.72	2.48	4.0	17.0	6.133**	5.450	0.690	88.80	25.49	24.02
F5		15.50	0.98	13.0	18.0	0.9690	0.674	0.295	69.56	6.35	5.30
F2	#G/S	57.40	14.12	12.0	93.0	199.40**	146.7	52.65	73.60	24.60	21.10
F3		71.20	11.86	36.0	96.0	94.77**	71.30	23.47	75.24	13.67	11.86
F4		76.40	7.32	57.0	88.0	53.600**	36.93	16.67	68.91	9.58	7.95
F5		66.37	7.60	53.0	86.0	57.8000	41.27	16.53	71.40	11.45	9.68
F2	100KW	4.88	0.86	2.0	6.8	0.74**	0.540	0.190	73.99	17.57	15.12
F3		4.83	0.47	3.3	6.0	0.11**	0.050	0.060	46.34	6.84	4.65
F4		5.11	0.36	4.2	6.0	0.133*	0.070	0.070	50.38	7.13	5.06
F5		4.96	0.20	4.1	5.6	0.0413	0.020	0.021	49.27	4.10	2.88
F2	BY/P	29.13	10.70	10.4	63.7	114.49**	108.5	5.98	94.78	36.73	35.76
F3		50.99	7.59	37.8	79.1	40.47**	31.73	8.73	78.42	12.48	11.05
F4		56.89	8.87	41.7	80.2	78.733**	69.27	9.47	87.98	15.60	14.63
F5		61.40	11.11	48.4	85.3	123.36**	120.14	3.22	97.39	18.09	17.85
F2	GY/P	18.41	9.22	2.0	48.2	84.94**	80.99	3.95	95.35	50.06	48.88
F3		34.97	5.89	24.6	55.6	24.57**	19.47	5.10	79.24	14.18	12.62
F4		39.54	6.69	27.7	58.9	44.700**	38.07	6.63	85.16	16.91	15.61
F5		47.46	8.15	37.9	65.1	66.427**	65.03	1.40	97.89	17.17	16.99

*, ** Indicated significant at 0.05 and 0.01 probability levels, respectively. HD = heading date, DGFP = duration of grain filling period, GPR= grain production rate, PH = plant height, #S/P = number of spikes/plant, #G/S = number of grains/spike, 100-KW = 100-kernel weight, GY/P = grain yield/plant and BY/P = biological yield/plant.

The data shown in Table 2 showed a wide range of genetic and phenotypic differences between the traits. The degree of heritability was high, more than 50%, for most traits studied across generations. On the flip side, some traits have a low heritability value. A large part of the traits showed a change in heritability towards higher

values in the F₃ and F₄ generations; however, some traits showed a decrease in heritability in the broad sense in the F₅ generation.

The data presented in Tables 3 and 4 showed that, in most cases, genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficient values in the F₂, F₃, and F₄ generations. Data presented showed that grain yield per plant was positively and significantly associated with each of grain production rate, number of spikes per plant, 100-kernel weight, and biological yield per plant at both genotypic and phenotypic levels. At the same time, most yield contribution traits showed associations with each other. Some relations were changed over generations, from F₂ to F₄.

Table 3. The phenotypic and genotypic correlation coefficients between studied traits in F₂ generation (above diagonal) and F₃ generation (below diagonal).

Traits		HD	GFPD	GFR	PH	#S/P	#G/S	100KW	BY/P	GY/P
HD	r _p		0.176*	0.141	0.459**	0.052	0.003	0.185	0.137	0.094
	r _g		0.687**	0.127	0.864**	0.178*	-0.524**	0.734**	0.203*	0.118
GFPD	r _p	0.930**		-0.067	0.331**	-0.019	-0.076	0.208*	0.066	0.040
	r _g	0.971**		-0.041	0.285**	-0.068	0.125	0.094	0.069	0.051
GFR	r _p	-0.464**	-0.461**		0.296**	0.761**	0.594**	0.345**	0.978**	0.988**
	r _g	-0.511**	-0.490**		0.312**	0.774**	0.662**	0.413**	0.982**	0.990**
PH	r _p	-0.286*	-0.324*	0.170		0.235*	0.121	0.308**	0.381**	0.311**
	r _g	-0.429**	-0.434**	0.255		0.206*	0.240*	0.291**	0.381**	0.314**
#S/P	r _p	-0.082	-0.045	0.484**	0.013		0.131	0.023	0.817**	0.772**
	r _g	-0.140	-0.096	0.558**	0.010		0.208*	-0.026	0.816**	0.775**
#G/S	r _p	0.010	0.002	0.248	0.059	-0.481**		0.008	0.534**	0.588**
	r _g	0.022	0.015	0.233	0.142	-0.629**		0.326**	0.639**	0.689**
100KW	r _p	0.066	0.024	0.285*	0.078	-0.022	0.040		0.341**	0.358**
	r _g	-0.017	-0.015	0.417**	0.007	0.075	0.280*		0.375**	0.400**
BY/P	r _p	-0.094	-0.060	0.897**	0.058	0.544**	0.273*	0.337*		0.992**
	r _g	-0.149	-0.115	0.915**	0.106	0.608**	0.253	0.480**		0.993**
GY/P	r _p	-0.092	-0.056	0.908**	0.044	0.543**	0.266	0.329*	0.986**	
	r _g	-0.146	-0.111	0.918**	0.090	0.766**	0.286*	0.748**	0.995**	

*, ** Indicated significant at 0.05 and 0.01 probability levels, respectively. HD = heading date, DGFP = duration of grain filling period, GPR = grain production rate, PH = plant height, #S/P = number of spikes/plant, #G/S = number of grains/spike, 100-KW = 100-kernel weight, GY/P = grain yield/plant and BY/P = biological yield/plant.

The F₂ and F₃ for a population were evaluated for yield and its components to the classical selection index according to Smith (1936) and Hazel (1943). Eleven selection indices containing two or more traits simultaneously were constructed in the F₂ population besides direct selection for grain yield and other components only. Predicted and actual genetic advances from different selection procedures are presented in Table (5) and Figure (1). Furthermore, it was found that nine out of eleven selection indices were more efficient than direct selection for improving grain yield/plant in the F₂ population. The highest predicted genetic gain for grain yield/plant from F₂ generation was observed when selecting for grain yield/plant along with number of spikes/plant, number of grains/spike, and 100-kernel weight (I_{w123}), followed by selecting for grain yield/plant along with grains/spike (I_{w2}), followed by equal selections of grain yield/plant along with number of spikes/plant and grains/spike (I_{w12}), grain yield/plant with the number of grains/spike and weight of These indices gave 136.3, 133.6, 129.6, 127.8, 126.6, and 105.7% relative efficiency over selection based on grain yield alone. This was true since grain yield showed a positive correlation with the other yield-contributing traits. On contrast, the lowest predicted genetic advance for grain yield per plant in F₂ was observed when direct selection for 100-kernel weight (I_{x3}) was followed by direct selection for number of spikes per plant (I_{x1}).

The highest actual genetic gain from F₃ generation for grain yield and plant occurred when applied selection index involving grain yield and plant with each of #S/P, #G/S, and 100-KW (I_{w123}), followed by selection index involving grain yield and plant with each of #S/P and #G/S (I_{w12}), and direct selection for grain yield and plant (I_{xw}). Most indices showed a high discrepancy between predicted and actual genetic gain as grain yield/plant (Figure 1); this was due to the non-additive gene effect and the large effect of environmental factors. On the other side, some indices showed close agreement between the predicted and actual response to selection since the deviation of the actual advance from the predicted advance was positive and low.

Table 4. The phenotypic and genotypic correlation coefficients between studied traits in F₄ generation.

Traits		HD	GPDP	GPR	PH	#S/P	#G/S	100KW	BY/P
GPDP	r _p	0.927**							
	r _g	0.972**							
GPR	r _p	-0.447**	-0.530**						
	r _g	-0.546**	-0.563**						
PH	r _p	-0.413**	-0.380*	0.079					
	r _g	-0.539**	-0.531**	0.127					
#S/P	r _p	-0.105	-0.146	0.671	-0.052				
	r _g	-0.131	-0.161	0.738	-0.135				
#G/S	r _p	0.059	0.019	0.113	-0.093	-0.345*			
	r _g	-0.005	-0.011	0.107	0.015	-0.377*			
100KW	r _p	-0.055	-0.099	0.198	0.029	0.124	-0.160		
	r _g	-0.307	-0.324	0.389	0.071	0.171	-0.002		
BY/P	r _p	-0.122	-0.179	0.906**	-0.044	0.765**	0.102	0.211	
	r _g	-0.240	-0.246	0.932**	-0.054	0.833**	0.104	0.298*	
GY/P	r _p	-0.119	-0.180	0.926**	-0.068	0.741**	0.109	0.181	0.978*
	r _g	-0.239	-0.249	0.938**	-0.082	0.829**	0.080	0.319*	0.993**

*, ** Indicated significant at 0.05 and 0.01 probability levels, respectively. HD = heading date, DGFP = duration of grain filling period, GPR= grain production rate, PH = plant height, #S/P = number of spikes/plant, #G/S = number of grains/spike, 100-KW = 100-kernel weight, GY/P = grain yield/plant and BY/P = biological yield/plant.

Maximum predicted and actual genetic advance from F₃ and F₄ generation for grain yield/plant Table (6) and Figure (2) were achieved when selecting directly for grain yield/plant (*I_{xw}*) in F₃ followed by selection indices containing #S/P, #G/S and 100-KW (*I₁₂₃*). These are the main attributes of grain yield. The highest actual gains in F₄ were achieved with index selection involving #S/P, #G/S and 100-KW (*I₁₂₃*) followed by index containing GY/P with #G/S (*I_{w2}*) followed by index selection involving grain yield/plant with #S/P and 100-KW (*I_{w13}*) and direct selection for grain yield/plant (*I_{xw}*), these indices gave (16.49, 16.33 and 13.90 gm), respectively. On the other side, the lowest predicted and realized genetic gains for grain yield/plant were observed when selecting for number of grain/spikes with 100 kernel weight (*I₂₃*) by value (2.59).

Figure (2) shows that the actual genetic advance consistently deviated favorably from the expected advance from the F₃ and F₄ generations. Due to the significant influence of the (genotypic x environment) interaction, this deviation revealed huge values for some procedures; yet, this large gap between projected and actual gains did not cast doubt on the validity of the general theory of selection index.

It is important to keep in mind that single trait selection is ineffective for genetically improving wheat grain yield. This is because selection for single qualities alone is not anticipated to fully explain genotypic variation for yield since yield is a commutative effect of multiple traits. The relative effectiveness of the result index, however, is higher when two or more traits-based indices are combined than when using each trait alone, as the gains made are dispersed throughout all evaluated traits and resulted in a higher total without a major loss in the primary traits.

The data presented in Table 7 indicate that selection indices involving grain yield/plant with number of spikes/plant, number of grains per spike, and 100-kernel weight (*I_{w123}*), followed by selection indices involving GY/P with #S/P and #G/S (*I_{w12}*), and direct selection for grain yield/plant (*I_{xw}*), gave high values of realized advance for selected traits and unselected traits. There was a close agreement between grain yield and selected traits. These results indicate that advanced generations were the highest in means for three selected traits in the F₂ generation and got up fast in response to improvement through advanced progeny.

This trend was changed in F₄ generation Table (8) since the maximum actual gain was observed for most traits when applying indices involved the three selected traits #S/P, #G/S and 100-KW (*I₁₂₃*) followed by direct selection for grain yield (*I_{xw}*).

The results of the current study suggest that choosing high-yielding wheat genotypes may be improved by using a selection index based on these three qualities. For unselected qualities, the actual advance typically declines in F₄ generations compared to F₃ generations. Through advanced generations, both selected and unselected traits continued to demonstrate very high percentages of improvement. To reach a stability point and homogeneity between various families, the F₄ generation made less progress than the F₂ and F₃ generations combined.

To determine a population's true value, segregating populations can be evaluated using means, variability, and their capacity to produce superior segregates. The ten selected families were isolated in the F₅ generation based on their superiority to the better parent, F₄ families, and point start of F₂ plants, respectively. In the current study, the scope of superior segregates was isolated on the basis of several selection processes. All of

the selected families outperformed the better parent and point start of the F₂ mean, according to data shown in Table 9, however some of these families outperformed the F₅ families in terms of mean yield attributes and earliness features.

Table 5. Predicted (Pred.), actual (Act.) and comparative percentage by I_{xw} (comp.%) gain from application of different selection procedures for improving grain yield/plant in F₂ and F₃ generations.

No.	Indices	F ₂			F ₃			Differential Act. -Pred.
		Pred.	Pred. %	Comp. %	ACT.F3	ACT. %	Comp. %	
1	I _{w123}	16.6	90.4	136.3	22.4	121.7	112.4	5.8
2	I _{w12}	15.8	86.0	129.6	21.8	118.2	100.0	5.9
3	I _{w13}	15.6	84.7	127.8	19.7	107.1	90.5	4.1
4	I _{w23}	15.8	86.0	129.6	18.7	101.5	85.8	2.9
5	I ₁₂₃	15.5	83.9	126.6	19.4	105.1	88.9	3.9
6	I _{w1}	15.8	86.0	129.6	17.8	96.4	81.6	1.9
7	I _{w2}	16.3	88.6	133.6	18.5	100.3	84.8	2.1
8	I _{w3}	15.8	85.9	129.6	19.9	108.2	91.5	4.1
9	I ₁₂	11.4	61.8	93.2	18.9	102.8	86.9	7.6
10	I ₁₃	12.9	70.1	105.7	18.4	99.8	84.4	5.5
11	I ₂₃	10.7	58.1	87.6	17.2	93.6	79.2	6.5
12	I _{xw}	12.2	66.3	100.0	21.8	118.2	100.0	9.6
13	I _{x1}	5.3	28.7	43.2	18.3	99.3	84.0	13.0
14	I _{x2}	11.8	63.9	96.3	18.1	98.3	83.1	6.3
15	I _{x3}	2.2	12.0	18.1	16.8	91.4	77.3	14.6
Mean GY/P in F₂		18.41						

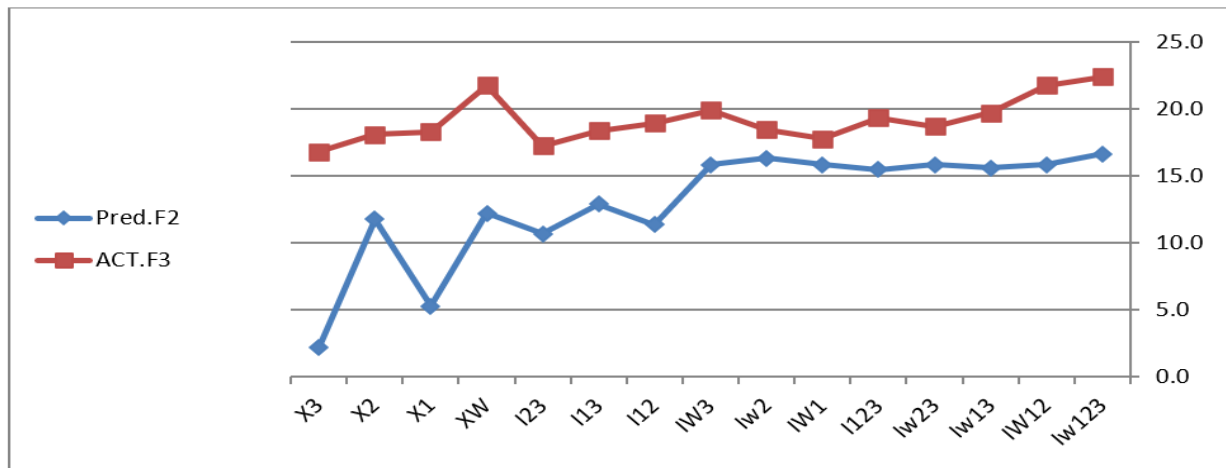


Fig. 1. The differences between improvement in grain yield /plant as a predicted genetic gain in F₂ and actual genetic gains estimated from 15 selection procedures in F₃ generation.

Table 6. Predicted (Pred.), actual (Act.) and comparative percentage by I_{xw} (comp.%) gain from application of different selection procedures for improving grain yield/plant in F₃ and F₄ generations.

NO. Indices		F ₃			F ₄							
		Pred.	Pred. %	Comp.%	Actual	Act. %	Comp.%	Act-red.	Pred.	SA %	Comp.%	
1	I_{w123}	7.08	20.24	58.32	10.96	31.35	78.86	3.88	5.37	13.59	61.56	
2	I_{w12}	7.06	20.18	58.14	7.99	22.84	57.44	0.93	5.37	13.58	61.53	
3	I_{w13}	7.28	20.82	59.98	13.90	39.76	100.00	6.62	5.46	13.80	62.53	
4	I_{w23}	7.19	20.55	59.22	12.13	34.70	87.27	4.94	5.39	13.63	61.72	
5	I_{123}	8.86	25.33	72.98	16.49	47.16	118.62	7.63	6.32	15.98	72.39	
6	I_{w1}	7.21	20.63	59.43	13.47	38.52	96.88	6.26	5.45	13.79	62.48	
7	I_{w2}	7.21	20.62	59.40	16.33	46.70	117.47	9.12	6.11	15.46	70.03	
8	I_{w3}	7.16	20.49	59.03	10.45	29.90	75.20	3.29	5.37	13.59	61.55	
9	I_{12}	5.01	14.33	41.28	7.42	21.22	53.37	2.41	2.54	6.42	29.08	
10	I_{13}	5.50	15.73	45.31	7.72	22.07	55.52	2.22	5.17	13.07	59.20	
11	I_{23}	2.35	6.73	19.40	2.59	7.39	18.60	0.24	0.94	2.38	10.78	
12	I_{xw}	12.14	34.71	100.00	13.90	39.76	100.00	1.76	8.73	22.08	100.00	
13	I_{x1}	3.12	8.92	25.70	9.35	26.73	67.23	6.23	4.23	10.69	48.45	
14	I_{x2}	6.65	19.01	54.78	11.69	33.44	84.11	5.04	1.00	2.53	11.47	
15	I_{x3}	0.46	1.32	3.82	7.34	20.99	52.81	6.88	0.17	0.43	1.95	
M GY/P in F₃		34.97							M GY/P in F₄ 39.54			

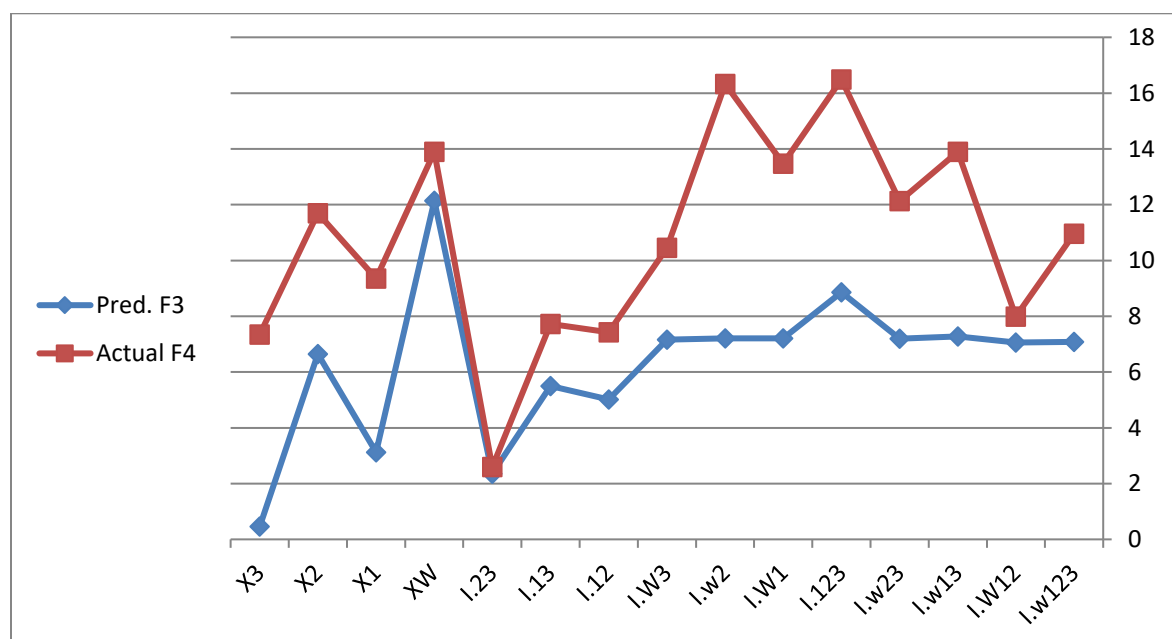


Fig. 2. The differences between improvement in grain yield/plant as predicted genetic gains in F₃ and actual genetic gains estimated from 15 selection procedures in F₄ generation.

Table 7. Actual genetic advance estimated from F₃ generation for all studied traits by using different selection procedures in wheat population.

No. Indices		HD		GFPD		GFR		PH		#S/P		#G/S		100KW		BY/P	
		Act.F ₃	Act.%	Act.F ₃	Act.%	Act.F ₃	Act.%	Act.F ₃	Act.%	Act.F ₃	Act.%	Act.F ₃	Act.%	Act.F ₃	Act.%	Act.F ₃	Act.%
1	lw123	-2.17	-2.58	-0.67	-1.79	0.70	146.97	8.25	8.27	4.48	69.11	20.05	34.94	0.17	3.52	31.98	109.79
2	lw12	-0.64	-0.76	0.66	1.76	0.59	124.67	6.86	6.88	3.69	56.89	20.32	35.40	0.17	3.54	28.55	98.01
3	lw13	-0.37	-0.44	1.02	2.72	0.52	110.75	5.42	5.44	3.57	55.13	17.75	30.93	0.07	1.49	25.87	88.82
4	lw23	-0.02	-0.02	1.38	3.68	0.49	103.14	5.33	5.35	3.53	54.52	15.01	26.14	0.08	1.54	24.54	84.24
5	l123	-0.20	-0.24	1.19	3.18	0.51	107.93	5.41	5.43	3.57	55.06	16.63	28.97	0.07	1.44	25.38	87.12
6	lw1	-0.06	-0.07	1.34	3.56	0.47	98.13	5.59	5.61	3.15	48.64	16.07	27.99	0.04	0.84	23.36	80.20
7	lw2	-0.07	-0.09	1.29	3.43	0.49	102.44	5.49	5.51	3.33	51.38	15.87	27.64	0.06	1.23	24.25	83.26
8	lw3	-0.38	-0.45	1.01	2.70	0.53	111.99	5.24	5.25	3.54	54.61	18.00	31.36	0.10	2.12	26.14	89.73
9	l12	-0.01	-0.02	1.40	3.72	0.50	104.45	5.19	5.21	3.52	54.32	15.57	27.12	0.07	1.45	24.82	85.19
10	l13	-0.03	-0.04	1.36	3.62	0.48	101.41	5.56	5.58	3.30	50.95	15.93	27.75	0.08	1.74	24.22	83.14
11	l23	0.06	0.07	1.44	3.85	0.45	94.54	5.91	5.93	3.10	47.79	14.94	26.03	0.08	1.56	22.77	78.16
12	lxw	-0.64	-0.76	0.66	1.76	0.59	124.67	6.86	6.88	3.69	56.89	20.32	35.40	0.17	3.54	28.55	98.01
13	lx1	-0.69	-0.83	0.73	1.95	0.49	103.61	6.04	6.06	4.68	72.20	7.85	13.67	-0.07	-1.48	23.92	82.12
14	lx2	0.23	0.27	1.45	3.86	0.48	100.36	6.28	6.30	2.09	32.28	25.91	45.13	0.05	1.03	23.97	82.30
15	lx3	-0.61	-0.72	0.73	1.95	0.52	109.66	5.93	5.94	3.21	49.54	15.43	26.88	0.36	7.33	25.37	87.09
M. F₂		83.92		37.51		0.47		99.67		6.48		57.40		4.88		29.13	

HD = heading date, DGFP = duration of grain filling period, GPR= grain production rate, PH = plant height, #S/P = number of spikes/plant, #G/S = number of grains/spike, 100-KW = 100-kernel weight, GY/P = grain yield/plant and BY/P = biological yield/plant.

Table 8. Actual genetic advance estimated from F₄ generation for all studied traits by using different selection procedures in wheat population.

NO. Indices		F4															
		HD		GPDF		GPR		PH		#S/P		#G/S		100KW		BY/P	
		Actual	Act.%	Actual	Act.%	Actual	Act.%	Actual	Act.%	Actual	Act.%	Actual	Act.%	Actual	Act.%	Actual	Act.%
1	w123	0.72	0.86	-0.58	-1.50	0.30	33.09	7.15	6.82	1.57	16.11	5.47	7.68	0.34	7.12	13.50	26.48
2	w12	2.47	2.94	0.76	1.96	0.19	20.91	6.87	6.55	1.95	20.03	3.67	5.15	0.19	4.02	11.02	21.61
3	w13	1.62	1.93	0.31	0.80	0.43	47.01	4.87	4.64	3.70	38.03	6.22	8.73	0.45	9.23	17.00	33.34
4	w23	0.63	0.76	-0.84	-2.17	0.42	45.73	5.97	5.69	2.95	30.32	7.43	10.44	0.42	8.77	16.88	33.10
5	123	1.20	1.43	-0.77	-1.99	0.53	58.21	4.37	4.17	4.78	49.18	6.47	9.08	0.50	10.37	22.30	43.74
6	w1	1.39	1.65	-0.18	-0.47	0.43	47.32	4.94	4.71	3.69	37.94	6.87	9.65	0.41	8.53	18.65	36.57
7	w2	1.31	1.56	-0.22	-0.56	0.51	55.64	4.20	4.01	5.06	52.03	5.36	7.52	0.47	9.68	18.50	36.28
8	w3	1.87	2.23	0.50	1.30	0.25	28.04	5.26	5.01	3.00	30.89	0.19	0.27	0.29	6.01	10.70	20.98
9	12	1.03	1.23	-0.38	-0.99	0.21	23.09	5.76	5.49	0.50	5.17	5.30	7.44	0.55	11.30	6.36	12.48
10	13	2.02	2.41	0.86	2.23	0.18	20.00	5.08	4.85	0.58	6.00	5.22	7.34	0.32	6.65	6.62	12.98
11	23	2.09	2.49	0.95	2.45	0.05	5.65	6.59	6.29	-1.28	-13.12	5.63	7.91	0.21	4.26	2.64	5.18
12	XW	1.62	1.93	0.31	0.80	0.43	47.01	4.87	4.64	3.70	38.03	6.22	8.73	0.45	9.23	19.34	37.93
13	X2	0.82	0.98	-0.49	-1.26	0.26	28.21	5.72	5.46	1.61	16.60	4.13	5.81	0.47	9.74	9.09	17.82
14	X1	1.87	2.23	0.45	1.16	0.29	31.53	5.81	5.55	2.56	26.31	4.41	6.20	0.44	9.08	12.47	24.45
15	X3	1.39	1.65	0.00	0.01	0.19	21.13	5.98	5.70	1.02	10.50	4.06	5.70	0.50	10.41	6.52	12.78
M.F3		83.80		38.77		0.91		104.80		9.72		71.20		4.83		50.99	

HD = heading date, DGFP = duration of grain filling period, GPR= grain production rate, PH = plant height, #S/P = number of spikes/plant, #G/S = number of grains/spike, 100-KW = 100-kernel weight, GY/P = grain yield/plant and BY/P = biological yield/plant.

Table 9. The best selected families resulted from different selection procedures in F₅ generation in wheat population.

Pedigree families				HD	GPDP	GFR	PH	#S/P	#G/S	100KW	BY/P	GY/P	
F ₂	F ₃	F ₄	F ₅										
36	3	2	1	89.33	41.33	1.57	100.00	17.00	80.67	4.73	84.37	64.37	
135	17	6	2	83.33	44.00	1.00	101.67	15.33	68.00	5.07	59.47	46.03	
142	18	7	3	87.67	40.00	1.00	110.00	14.67	64.00	5.03	55.63	44.33	
188	23	9	4	87.00	43.00	0.77	98.33	14.00	64.33	5.00	49.50	40.50	
214	24	10	5	85.67	42.33	0.93	90.00	16.33	59.67	4.60	51.43	39.27	
224	26	11	6	85.33	43.67	1.33	103.33	16.33	76.00	5.17	75.40	58.17	
245	28	12	7	84.67	42.67	0.90	100.00	14.33	57.67	4.87	52.60	40.23	
249	29	13	8	84.33	43.33	1.03	103.33	16.33	61.33	4.83	57.33	43.80	
256	31	15	9	85.33	43.33	1.13	110.00	15.33	71.67	5.07	63.93	48.83	
470	48	20	10	84.33	41.00	0.97	106.67	15.33	60.33	5.27	64.30	49.03	
L.S.D				0.05	3.46	3.22	0.28	6.46	2.83	14.79	0.50	15.55	11.87
				0.01	4.73	4.41	0.39	8.84	3.87	20.26	0.68	21.30	16.26
Mean F ₂				83.92	37.51	0.47	99.67	6.48	57.40	4.90	29.13	18.41	
Mean F ₃				83.80	38.80	0.90	104.80	9.70	71.20	4.80	51.00	35.00	
Mean F ₄				86.45	40.08	1.00	110.27	9.72	76.40	5.11	56.89	39.54	
Mean F ₅				85.70	42.47	1.06	102.33	15.50	66.37	4.96	61.40	47.46	
Mean P ₁				85.33	43.67	1.23	103.33	14.67	71.67	5.16	70.06	41.50	
Mean P ₂				80.67	36.00	0.81	88.33	12.00	58.67	4.22	37.90	28.93	
Bulk				80.00	42.33	1.10	103.33	16.33	76.33	5.07	82.67	38.40	
M.F ₃ - M F ₂			Act .after 1 cycle	-0.12	1.29	0.43	5.13	3.22	13.80	-0.10	21.87	16.59	
Act.%				-0.14	3.45	89.95	5.15	49.69	24.03	-2.04	75.08	90.11	
MF ₄ - MF ₃			Act. after 2 cycles	2.65	1.28	0.10	5.47	0.02	5.20	0.31	5.89	4.54	
Act.%				3.16	3.30	11.11	5.22	0.21	7.30	6.46	11.55	12.97	
MF ₅ - MF ₄			Act. after 3 cycles	-0.75	2.39	0.06	-7.94	5.78	-10.03	-0.15	4.51	7.92	
Act.%				-0.87	5.96	6.00	-7.20	59.47	-13.13	-2.94	7.93	20.03	
M.F ₅ - M.F ₂ Total actual genetic gains after three cycles from selection indices				1.78	4.96	0.59	2.66	9.02	8.97	0.06	32.27	29.05	
The total actual genetic advance Act. %				2.12	13.24	123.72	2.67	139.20	15.62	1.22	110.78	157.79	
MF ₅ - MP ₁			Act .relative P ₁	0.37	-1.20	-0.17	-1.00	0.83	-5.30	-0.20	-8.66	5.96	
Act.%				0.43	-2.74	-13.59	-0.97	5.68	-7.39	-3.94	-12.36	14.36	
MF ₅ - MP ₂			Act. relative P ₂	5.03	6.47	0.25	14.00	3.50	7.70	0.74	23.50	18.53	
Act.%				6.24	17.97	31.40	15.85	29.17	13.13	17.63	61.99	64.03	
MF ₅ - Bulk			Act .relative Bulk	5.70	0.14	-0.04	-1.00	-0.83	-9.96	-0.11	-21.27	9.06	
Act.%				7.13	0.32	-3.64	-0.97	-5.10	-13.05	-2.17	-25.73	23.59	

HD = heading date, DGFP = duration of grain filling period, GPR= grain production rate, PH = plant height, #S/P = number of spikes/plant, #G/S = number of grains/spike, 100-KW = 100-kernel weight, GY/P = grain yield/plant and BY/P = biological yield/plant.

DISCUSSIONS

A wheat breeder seeks to isolate genotypes superior in yield characteristics and quality. Thus, different selection methods were used, and the choice of selection procedure for genetic improvement of wheat is largely conditioned by the type and relative amount of genetic variance in the population, while the gain from selection in a population depends on genetic variability within a population for a given trait, heritability, and selection intensity Falconor (1989).

A comparison of mean performance for different traits among the four generations (F₂, F₃, F₄, and F₅) revealed an increase in mean values for most traits with advanced generations from F₂ to F₅, with some expectation due to environmental factors. At the same time, the lower limits of range were lower in the F₂ generation for all studied traits, leading to a wider spectrum of variability. However, in advanced generations (F₃ and F₄), the lower limits of range were relatively high, and the upper limits were also relatively high. This shift in mean values and range in the desirable direction could largely be attributed to the progress in selection from the F₂ to the F₅ generation, which was interested in improving grain yield/plant and other traits in wheat, as well as to

the possible accumulation of favorable alleles as a result of the selection procedures adapted in this study (Ferdous *et al.*, 2010; Fellahi *et al.*, 2018).

The PCV and GCV were generally larger in magnitude for all studied traits in the F₂ generation as compared with the advanced generations F₃, F₄, and F₅, indicating that the magnitude of the genetic variability persisting in this material was sufficient for providing a rather substantial amount of improvement through the selection of superior progeny. At the same time, the PCV was generally slightly higher than the GCV for all studied traits and, in most cases, indicated the influence of environment on the expression of those traits. These results indicated the feasibility of selection for these traits. Our results are in accordance with those obtained by Habib *et al.* (2007), Ferdous *et al.* (2010), Fellahi *et al.* (2018), and Rasha (2020). The reduction in PCV and GCV values in the advanced generation (F₃, F₄, and F₅) may be due to a reduction in genetic variability and heterozygosity as a result of using different selection procedures that exhausted a major part of variability.

Heritability plays a productive role in breeding, expressing the reliability of a phenotype as a guide to its breeding value. The knowledge of the genotypic determination coefficient allows establishing an estimate of the genetic gain to be obtained and defining the best strategy to be used in the plant breeding program. Allard (1960) Heritability values can be used to forecast the predicted progress made throughout the selection process. The data showed a wide range of genotypic and phenotypic variations among the characteristics. Substantial heritability levels of more than 50% for most examined variables across generations indicate a high magnitude of genetic diversity and the possibility of early-generation selection success.

On the other hand, certain traits have a low heritability value due to a decrease in genetic variety; thus, the observed decrease in heritability could be attributed to the complex nature of traits and the influence of genotypic by environment interaction. Those named Fellahi *et al.* (2018) A large proportion of characteristics showed heritability increases toward higher values in F₃ and F₄ generations, owing to an increased proportion of genetic variance to total phenotypic variance caused by cryptic genetic alterations brought about by two rounds of selection. Breeders are particularly interested in improving heritability values for these traits since it increases the possibility of improved selection responses for such traits. However, some traits showed a reduction in broad sense heritability in the F₅ generation; this is most likely due to the use of several selection procedures that exhausted genetic variability, particularly non-additive genetic variability, resulting in more homogeneity in the population and a strong effect of environmental factors. This could be because the non-additive effects were weak or non-existent, and the additive effects appeared to be overwhelming. Shiv *et al.* (2008) proposed that the number of tillers per plant, spikelets per ear, grains per ear, grain weight per ear, 100-grain weight, and biological yield could be appropriate selection indices for high yielding wheat genotypes. Bergale *et al.* (2002) proposed that while selecting better wheat genotypes, the number of spikes per plant, grains per spike, and harvest index should be prioritized over optimum plant height and days to flowering. According to Ferdous *et al.* (2010), the selection index based on three traits yielded the highest relative efficiency: plant height, grains per spike, and grain output per plant. Patel reported high efficiency in selection based on grain yield per plant, plant height, ear length, number of grains per main spike, grain weight per main spike, and harvest index, or a combination of all six traits (Patel, 2006). According to Patel *et al.* (2019), the harvest index, which is based on six variables, including grain yield per plant, plant height, ear length, number of grains per main spike, grain weight per main spike, and harvest index, has the highest genetic gain and relative efficiency. Bergale *et al.* (2002) proposed that while selecting better wheat genotypes, the number of spikes per plant, grains per spike, and harvest index should be prioritized over optimum plant height and days to flowering. According to Mahdy (2017), the best index for enhancing GY/P was Selection index5, which included GY/P, 100GW, and #G/S. According to Patel (2006), selection based on grain yield per plant, plant height, ear length, number of grains per main spike, grain weight per main spike, and harvest index, or a combination of all six traits, resulted in excellent efficiency. Our findings correspond with those of Mesele *et al.* (2015) and Saleem *et al.* (2015) and (2016).

Plant breeders must be concerned with the entire spectrum of characteristics. Thus, understanding these correlations enables assessing the degree of the association between multiple qualities and establishing which traits may be used to base selection to improve grain output. According to Mahdy (2017), the observed genetic gain of a single cycle of selection from the F₄ generation under both drought stress and regular irrigation settings was generally superior to three cycles begun from the F₂ generation. In the F₂, F₃, and F₄ generations, genotypic correlation coefficients were higher than phenotypic correlation coefficient values, indicating a suppressive influence of the environment that altered the phenotypic expression of these traits by decreasing phenotypic coefficient values. These findings are consistent with Moubarak (2018), who stated that the values of

phenotypic and genotypic correlations between most characters were positive and significant, with genotypic correlations being greater than phenotypic correlations under the three selection methods, indicating a slight effect of environment on character expression. Similarly, Ferdous *et al.* (2010) discovered a substantial and positive association between grain yield per plant and grains per spike and 100-grain weight. Grain yield per plant was found to be positively and significantly associated with grain production rate, number of spikes per plant, 100-kernel weight, and biological yield per plant at both the genotypic and phenotypic levels, implying that increasing these traits would result in an increase in grain yield. At the same time, most yield contribution features were shown to be related. Strong connections for such traits with substantial heritability indicated the possibility of improving these attributes simultaneously using different selection processes. These findings are consistent with those of Ferdous *et al.* (2010), Farshadfar *et al.* (2012)a, and Patel *et al.* (2012) and (2019). Some relationships evolved from F₂ to F₄ through generations. This was due to selection processes that altered gene frequency and increased the number of additive genes.

Data demonstrated that all selected families outperformed the F₂ mean for better parent and point start; however, some of these families outperformed the F₅ families in mean for yield and earliness features. The breeder may use such selected families in breeding programs aimed at increasing wheat grain yield. Overall, grain yield estimates were low, indicating that individual plant selection is inefficient for wheat improvement whereas aggregate trait selection results in relatively large genetic gain for grain yield (Ghaed-Rahimi *et al.*, 2017).

CONCLUSION

In this study, nine selection indices were more efficient than direct selection for improving GY/P in the F₂ population. While Selection index (I_{W123}), followed by I_{W12} and direct selection (I_{XW}), gave the highest actual genetic gains from the F₃ generation for trait GY/P. While maximum actual genetic advance from F₃ and F₄ generations for GY/P was achieved when using selection indices (I_{123}), followed by (I_{W2}), and then direct selection (I_{XW}).

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تطبيق بعض طرق الانتخاب لتحسين محصول الحبوب في قمح المكرونة

إبراهيم صبرى محمد عبد اللطيف ومحمد نوبى طه عبد القادر وموسى شوقي سلوس
قسم بحوث القمح ، معهد بحوث المحاصيل الحقلية ، مركز البحوث الزراعية.

* بريد الباحث المراسل: i.sabri4848@gmail.com

تمت هذه الدراسة بغرض تقدير ومقارنة التقدم الوراثي الذى يمكن أن يتم الحصول عليه من نموذج دليل الانتخاب لسميث-هازل مع الانتخاب المباشر لتعزيز كفاءة انتخاب العائلات الواعدة المتفوقة في الأجيال الإنعزالية المبكرة في القمح . تم تقييم طريقتين للانتخاب ، وهما الانتخاب المباشر والانتخاب غير المباشر عن طريق دليل الانتخاب في المحصول ومكوناته. أظهرت مقارنة متوسطات الأداء لصفات مختلفة بين الأجيال الأربعة من الجيل الثاني للخامس F₂ و F₃ و F₄ و F₅ عن زيادة في القيم المتوسطة لمعظم الصفات مع الأجيال التالية من الجيل الثاني F₂ إلى الجيل الخامس F₅ مع بعض الإستثناءات بسبب العوامل البيئية. وكانت قيم كل من معامل الإختلاف المظهري PCV ومعامل الإختلاف الوراثي GCV أكبر بشكل عام لجميع الصفات المدروسة في الجيل الثاني F₂ مقارنة بالأجيال المتقدمة من الثالث حتى الخامس F₃ و F₄ و F₅ مما يشير إلى أن حجم التباين الوراثي المستمر كان كافياً لتوفير قدر كبير من التحسين من خلال انتخاب نسل متفوق. تشير قيم كفاءة التوريث العالية التي تزيد عن 50٪ لمعظم الصفات المدروسة عبر الأجيال إلى الحجم الكبير للتنوع الوراثي وأعطت مؤشر لنجاح الانتخاب في الأجيال المبكرة. كان تسعة من أصل أحد عشر دليل انتخابي أكثر كفاءة متوقعة عن الانتخاب المباشر لتحسين صفة محصول الحبوب/للنبات في الجيل الثاني F₂ . كان أعلى تقدم وراثي متوقع في الجيل الثاني F₂ لصفة محصول الحبوب/للنبات عند دليل الانتخاب (I_{w123}) متبوعاً بدليل الانتخاب (I_{w2}) ثم بالانتخاب ل (I_{w12}) و (I_{w23}) و (I_{w1}) و (I_{w3}). أعطى دليل الانتخاب (I_{w123}) متبوعاً بكل من (I_{w12}) والانتخاب المباشر (I_{xw}) أعلى تقدم وراثي فعلي من الجيل الثالث F₃ لصفة المحصول GY / P. أظهرت معظم الأدلة الانتخابية تبايناً كبيراً في التقدم الوراثي المتوقع والفعلي لصفة محصول الحبوب/نبات ويرجع ذلك إلى تأثير التفاعل الوراثي مع البيئة. تحقق أقصى تقدم وراثي متوقع من جيل F₃ و F₄ لصفة المحصول GY / P عند الانتخاب المباشر (I_{xw}) في الجيل الثالث F₃ متبوعاً بدليل الانتخاب (I₁₂₃) . بينما تم تحقيق أقصى تقدم وراثي فعلي من الجيل الثالث F₃ والرابع F₄ لصفة المحصول GY / P عند الأدلة الانتخابية (I₁₂₃) متبوعة ب (I_{w2}) ثم الانتخاب المباشر (I_{xw}). أظهرت انحرافات التقدم الوراثي الفعلي عن التقدم المتوقع من أجيال F₃ و F₄ قيماً موجبة وكبيرة في معظم طرق الانتخاب.

الكلمات المفتاحية: قمح المكرونة، معامل الإختلاف المظهري PCV، معامل الإختلاف الوراثي GCV، درجة التوريث، طرق الانتخاب، الدليل الانتخابي