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(Original Article)

Response to Direct and Indirect Selection to Improve Grain Yield of Durum Wheat

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Abstract

This study was conducted over three growing seasons (2020/21, 2021/22, and 2022/23) at Shandaweel Agric. Res. Stat., Agri. Res. Cent., Egypt. The aim of this research was to evaluate the effect of direct selection for grain yield plant^{-1} and indirect selection for each of spike number plant^{-1} and 100-kernel weight to improve grain yield and produce new high yielding durum wheat lines. Two pedigree selection cycles were applied from the F_2 to F_4 generations, focusing on grain yield plant^{-1}, spike number plant^{-1}, and 100-kernel weight, under optimal growing conditions. The findings revealed that the phenotypic variance marginally exceeded the genotypic variance, and both generally declined from (F_2) to (F_4) generation. Following two pedigree selection cycles, broad sense and realized heritability estimates for grain yield plant^{-1} attained 78.73 and 48.63%, respectively. Similarly, the heritability estimates were 97.29% and 46.14% for the spike number plant^{-1} and 91.51% and 61.90% for the weight of 100 kernels. The observed gain following two direct pedigree selection cycles were 11.12 and 8.45% for grain yield plant^{-1}, 5.23 and 2.11% with indirect selection for spike number plant^{-1} and 7.57 and 10.39% with indirect selection for 100-kernel weight in comparison with the bulk sample and the superior parent, respectively.

Keywords: *Durum wheat, Selection for grain yield plant^{-1}, Spike number plant^{-1}, 100-kernel weight.*

Introduction

Wheat, a globally vital crop cultivated across varied climates, is essential for securing food and nutritional stability worldwide (Mahdy, Rasha *et al.*, 2022). As a staple food, it serves as a primary carbohydrate source and a key component of the daily diet for millions of people around the globe (Litoriya *et al*. 2018). The Egyptian national production of wheat is still far less for fulfilling the demands of overgrowing population. In such circumstances, the government still resorts to importing large quantities of wheat with substantial purchases. The cultivated area of wheat is about 1.45 million hectares producing 9.5 million metric tons (USDA-Egypt, 2023). Durum wheat is among the predominant crops cultivated in the Mediterranean region, accounting for nearly 75% of the global cultivation area and contributing to half of the world's total production (Graziani *et al* 2014). Improving wheat yield is a big challenge faced by wheat breeders who are being asked to select potential varieties to satisfy the present and future

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demands of farmers and consumers, (Lamara *et al*, 2022). According to Singh *et al* (2001), focusing on yield-related traits through selective breeding can enhance wheat productivity. Various traits have been utilized in wheat breeding programs as indirect selection criteria to enhance high yield (Chowdhury *et al.* 2021).

Pedigree selection is a valuable approach for identifying high-performing genotypes to enhance grain yield in cultivar development programs. Numerous researchers have highlighted that this method is among the most efficient strategies for grain yield improvement (Ali, 2011a; Abd El-Rady, 2017). Some researchers prefer selection within optimal conditions (Betran *et al.*, 2003). Numerous breeders have employed pedigree selection as a method to improve grain yield (Mahdy, Rasha 2012, Hamam, 2014, and Fouad *et al.,* 2020). Grain yield selection was prioritized in advanced segregating generations rather than in the initial stages (Mahdy, Rasha, 2017). Moreover, numerous studies have investigated the relationship between yield and its associated traits. According to Ahmed *et al.* (2010), the strong connections between yield and its components indicated that focusing on these components through selective breeding can lead to significant yield improvements. Selecting for increased 100-kernel weight over two cycles produced greater grain yield relative to directly selecting for grain yield (Fouad *et al.,* 2020). Mutawe *et al.*, (2018) found that 100-kernel weight is a good selection criterion, with an improved of grain yield by 4.92%. Improving grain yield has largely been achieved by strategically modifying specific yield-related traits (Calderini and Reynolds 2000; Kobata *et al.*, 2018). Numerous investigations into wheat kernel weight, commonly measured as thousand kernel weight, along with additional kernel-related characteristics, have highlighted their critical role in enhancing yield (Yang *et al.*, 2019; Li *et al.*, 2021). Enhancing the genetic characteristics associated with kernel dimensions and shape is regarded as a key strategy for creating high-yielding wheat varieties that offer greater commercial value and adaptability to various environmental conditions (Würschum *et al.*, 2018; Brinton and Uauy, 2019).

The aims of this research were to evaluate the effectiveness of pedigree selection in enhancing grain yield plant^{-1} utilizing spike number plant^{-1}, grain yield plant^{-1}, and 100-kernel weight as selection criteria and to determine the best method of selection (direct or indirect) for producing high yielding genotypes.

Materials and Methods

This study was accomplished during three growing seasons, i.e. 2020/21, 2021/22 and 2022/23 at the experimental farm of Shandaweel Agriculture Research Station, Agriculture Research Center, Egypt. The base population was the F2 of the cross Sohag5×Altar84 (Table 1), which represent a wide range of genetic diversity. Two pedigree selection cycles were accomplished under normal conditions with selection for grain yield plant^{-1}, spike number plant^{-1}, and 100-kernel weight. This population was grown under favorable conditions, with all standard farming practices followed.

In the 1st season (2020/21), 750 F2 plants were cultivated within non-replicated plots under standard sowing date. The plot contained 30 rows, each 2.5 m in length, spaced 30 cm apart. Within the rows, plants were positioned 10 cm apart. At maturity, plants were harvested and threshed individually, and data were collected from all protected plants. For the subsequent growing season, thirty plants fulfilling every specified selection criterion were chosen and cultivated as F_3 families. In the 2nd season (2021/22), the 30 F_3 families for each selection criterion were evaluated under normal conditions. From each experiment, the top 10 plants from the most promising 10 families were chosen and preserved to be cultivated as F_4 families in the subsequent season. During the last season (2022/23) the 10 F_4 families chosen based on each selection criterion were sown under normal conditions.

Table 1. The parental lines pedigree, selection history, and origin of the studied population.

Parents	Pedigree and selection history	Origin
P_1 (Sohag5)	TRN//21563/AA/3/BD2080/4/BD2339/5/Rascon37//Tarro2//Rascon 3/6/Auk/Gull//Green CDSS00B00364T-0T0PB -0B- 2Y-0M-oY-1B-0Y-0SH	Egypt
P_2 (Altar84)	RUFF/FLAMINGO,MEX//MEXICALI-75/3/SHEARWATER CD-22344-A-8M-1Y-1M-1Y-2Y-1M-0Y	Mexico

For F_3 and F_4 generations, every family was cultivated in individual rows measuring 2.5 meters in length, spaced 30 cm apart, with 10 cm between plants within the row. The experiment followed a Randomized Complete Block Design (RCBD), replicated three times. Both parental lines and the non-selected bulk were incorporated into every replication. Selection procedures were applied both among and within families.

The examined characters included: Days to heading (DH), Days to maturity (DM), spike count plant^{-1} (S plant^{-1}), plant height (PLH), 100-kernel weight (100-KW), kernel count plant^{-1} (K P^{-1}), kernel count spike^{-1} (K S^{-1}) biological yield plant^{-1} (BY), and grain yield plant^{-1} (GY).

Statistical analysis

Analysis of variance and combined analysis were conducted following the methodology outlined in Snedecor and Cochran (1980). The MSTAT-C software was utilized within RCBD framework. Phenotypic and genotypic variances, along with heritability estimates, were computed by using EMS of the variance and covariance components across the chosen families. Genotypes' means were compared utilizing Revised Least Significant Difference (RLSD) (El-Rawi and Khalafalla, 1980). Broad sense heritability, phenotypic (σ^2p), and genotypic (σ^2g) variances were computed following Walker (1960):

The genotypic variance $\sigma 2g$ = (MS Treat–MS Error)/r.

The phenotypic variance $\sigma 2p = \sigma 2g + \sigma 2e/r$.

Broad-sense heritability: H^2 bs = $\sigma^2 g / \sigma^2 p$

Realized heritability (h^2) was determined as: $h^2 = R/S$ (Falconer, 1990), with S = selection differential and R = response to selection. The genotypic (gcv%) and phenotypic (pcv%) coefficients of variation were assessed based on the method introduced by Burton (1952).

The phenotypic correlation coefficients between the inspected attributes were computed for both the base population (F_2) and the second selection cycle (F_4), following Al-Jibouri *et al.* (1958): Phenotypic correlation $rp_{xy} = \text{cov } p_{xy} / (\sigma\ p_x \ .\ \sigma\ p_y)$.

Results and Discussions

1-Description of the base population

The traits studied in the F_2 generation and the two parents are presented in Table 2. P_1 (Sohag 5) was higher than P_2 (Altar 84) in all the studied traits. The coefficient of variability varied from 35.93% for plant height to 59.46% for grain yield in F_2 population. Similar findings were reported by Amin (2003), El-Morshidy *et al.* (2010) and Ali (2011a). Heritability estimates in the broad sense varied between 43.19% for biological yield and 70.96% for plant height. Comparable findings were reported by Zakaria *et al.* (2008).

Table 2. Means, coefficient of variability (CV), broad sense heritability (H b) and ΔG/mean% of the F_2 generation (base population)

		PLH	S plant^{-1}	100-KW	K P^{-1}	K S^{-1}	BY	GY
F_2 Population	**Means±SE**	93.33± 1.84	10.02± 0.26	4.93± 0.10	466± 14.71	48.1± 1.26	74.24± 2.23	23.32± 0.75
	CV %	35.93	48.80	36.36	57.23	47.36	54.58	59.46
	H (b) %	70.96	49.89	60.01	65.14	60.36	43.19	55.33
P_1	**Means±SE**	99.00± 1.31	10.10± 0.64	5.21± 0.08	497.01± 48.65	48.79± 2.83	80.53± 7.77	26.15± 2.83
	CV %	4.18	20.05	4.84	30.96	18.35	30.51	34.24
P_2	**Means±SE**	96.90± 0.91	8.90± 0.89	4.99± 0.10	395.09± 32.89	46.35± 3.45	68.83± 7.00	19.80± 1.87
	CV %	2.98	31.54	6.22	26.33	23.51	32.14	29.87

PLH: plant height, S plant^{-1}: spike count plant^{-1}, 100-KW: 100-kernel weight, K P^{-1}: kernel count plant^{-1}, K S^{-1}: kernel count spike^{-1}, BY: biological yield plant^{-1} and GY: grain yield plant^{-1}.

Table 3 displays the phenotypic correlation coefficients for all pairs of attributes traits in the F_2 population. Positive and strong phenotypic association was noticed between grain yield plant^{-1} and all attributes examined (0.79 for spike count plant^{-1}, 0.43 for plant height, 0.26 for 100-kernel weight, 0,98 for kernel count plant^{-1}, 0.50 for kernel count spike^{-1} and 0.86 for biological yield. Comparable outcomes were reported by Abd El-Rady (2017), found a highly significant association between grain yield and each of plant height, spike count plant^{-1}, kernel count spike^{-1}, and biological yield.

Table 3. Phenotypic correlation among the attributes traits for the base population (F_2) under favorable conditions.

Treat.	S plant^{-1}	PLH	100-KW	K P^{-1}	K S^{-1}	BY	GY
S plant^{-1}							
PLH	0.40**						
100-KW	0.13*	0.28**					
K P^{-1}	0.79**	0.39**	0.07				
K S^{-1}	-0.04	0.10	-0.07	0.54**			
BY	0.92**	0.50**	0.20**	0.84**	0.12*		
GY	0.79**	0.43**	0.26**	0.98**	0.50**	0.86**	

S plant^{-1}: spike count plant^{-1}, PLH: plant height, 100-KW: 100-kernel weight, K P^{-1}: kernel count plant^{-1}, K S^{-1}: kernel count spike^{-1}, BY: biological yield plant^{-1} and GY: grain yield plant^{-1}. * and** significant at 0.05 and 0.01 probability levels, respectively.

2-Selection for grain yield plant^{-1}:

Variability and heritability estimates

The estimates of variability and heritability are displayed in Table 4 for GY. In most cases, the phenotypic coefficient surpassed the genotypic coefficient. Owing to the similar genotypic and phenotypic variability values, the broad-sense heritability estimates were notably high across both selection cycles. The phenotypic coefficient of variability (pcv%) for GY in the F_2 generation following two pedigree selection cycles was 47.78% and decreased to 13.61 and 3.13% in F_3 and F_4 generations, respectively. The genotypic coefficient of variability (gcv%) for GY was decreased from 34,27 to 10.73 and 2.78% in F_2, F_3, and F_4 generation, respectively. The heritability revealed an increase from 55.33 to 62.11 and 78.73% for cycles F_2, F_3 and F_4, respectively. The realized heritability estimates were 10.15 in C_1 and increased to 48.63% in C_2. These findings agree with Ahmed *et al.* (2010) and Ali (2011a). Soliman and Feltaous (2020) documented that the realized heritability was 20.83 after one cycle and increased to 28.05% after the second cycles, respectively.

Table 4. Heritability and variability estimate of grain yield plant^{-1} following two selection cycles.

Selection cycle	σ^2 p	σ^2 g	P.C.V.%	G.C.V.%	Broad sense heritability	Realized heritability
(C0)	118.54	60.96	47.78	34.27	55.33	--
(C1)	6.421	3.988	13.61	10.73	62.11	10.15
(C2)	1.24	0.98	3.13	2.78	78.73	48.63

Means and observed gains

The means of grain yield plant^{-1} (GY) for the 10 evaluated F_4 families are given in Table 5. The average GY varied between 19.01 for family No. 355 and 24.12 for family No. 92, averaging 21.70 g plant^{-1}. The selection process yielded a notably significant average direct observed gain ($P<0.01$), exceeding the bulk sample by 11.12% and outperforming the superior parent by 8.45%. All the families evaluated for high grain yield plant^{-1}, except families no. 124 and 355. Significant or highly significant gains were recognized compared to the bulk sample, with increases ranging from 7.65% for family 414 to 23.50% for family 92. Out of these, seven families; number 45, 77, 92, 245, 273, 298, and 522 significantly or highly significant surpassed the better parent by an average of 8.22, 10.63, 20.53, 8.36, 13,47, 14.34, and 12.04%, respectively. According to Kheiralla *et al.* (2006), implementing two selection cycles for GY led to a 20.20% improvement over the bulk sample and 7.60% increase than the better parent. Comparable findings were reported by Ali (2011$_b$) and Mahdy *et al.* (2012).

Table 5. Means of grain yield plant^{-1} and the observed gain from the bulk sample (OG% Bulk) and from the better parent (OG% BP), for the families selected for increased grain yield following two selection cycles.

Fam. No.	Mean	OG%Bulk	OG% BP
45	21.66	10.88**	8.22*
77	22.14	13.35**	10.63**
92	24.12	23.50**	20.53**
124	19.38	-0.79	-3.17
245	21.69	11.03**	8.36*
273	22.71	16.26**	13.47**
298	22.88	17.16**	14.34**
355	19.01	-2.69	-5.03
414	21.03	7.65*	5.07
522	22.42	14.79**	12.04**
Mean	21.70	11.12**	8.45*
Parent 1	20.01		
Parent 2	19.50		
Bulk	19.53 19.53 6		
R.L.S.D.	0.05: 1.32		0.01: 1.78

* and** significant at 0.05 and 0.01 probability levels, respectively.

Average observed gain following two selection cycles aimed at enhancing grain yield plant^{-1}

The means and observed gain from selection for GY within standard conditions are given in Table 6. In C_1, the selection resulted in an 11.57% increase from the bulk sample and a 5.20% rise compared to the superior parent. In C_2, the gains were 11.11% from the bulk sample and 8.45% over the better parent.

Table 6. Average values and selection gains for high GY following two direct selection cycles, in comparison with the bulk sample and the better parent.

Cycle	Mean	GY (g)
Cycle (1)	Families mean	18.61
	Parent (1)	17.69
	Parent (2)	16.24
	Bulk sample	16.68
	OG % (Bulk)	11.57
	OG% (B. P.)	5.20
R. L.S.D. 0.05		3.69
R. L.S.D. 0.01		5.27
Cycle (2)	Families mean	21.70
	Parent (1)	20.01
	Parent (2)	19.50
	Bulk sample	19.53
	OG % (Bulk)	11.11**
	OG% (B. P.)	8.45*
R. L.S.D. 0.05		1.26
R. L.S.D. 0.01		1.85

* and** significant at 0.05 and 0.01 probability levels, respectively.

The phenotypic correlation after two selection cycles aimed at high grain yield plant^{-1}

Table 7 displays the correlation coefficients for all possible trait pairs among the F_4 families. GY revealed strong positive correlations, either significant or highly significant, with several traits: spikes per plant (0.67), plant height (0.41), 100-kernel weight (0.68), kernels per plant (0.65), and biological yield per plant (0.59). The findings demonstrated that the key factors influencing grain yield include the spike count/plant, 100-kernel weight, kernel count per plant, and biological yield per plant. Indirect selection targeting these traits could effectively enhance GY. Comparable outcomes were noted by Abd-El-Rady (2017), who observed phenotypic correlation coefficients under standard irrigation conditions. These correlations between GY and attributes like heading time, days to maturity, spike number plant^{-1}, kernel number spike^{-1}, and biological yield plant^{-1} attained 0.468, 0.441, 0.847, 0.519, and 0.930, respectively.

Table 7. Phenotypic correlation between the analyzed characteristics for the chosen families in (F_4 generation) for grain yield plant^{-1}.

Item	DH	DM	S plant^{-1}	PLH	100-KW	K P^{-1}	K S^{-1}	BY
DH								
DM	0.33							
S plant^{-1}	0.28	-0.18						
PLH	0.18	0.28	0.15					
100-KW	0.04	0.09	0.41*	-0.01				
K P^{-1}	0.40*	0.23	0.18	0.59**	-0.04			
K S^{-1}	0.17	0.14	-0.38*	0.20	-0.29	0.65**		
BY	0.47**	0.03	0.68**	0.32	0.46*	0.26	-0.17	
GY	0.36	0.14	0.67**	0.41*	0.68**	0.65**	0.24	0.59**

DH: Days to heading, DM: Days to maturity, S plant^{-1}: spike count plant^{-1}, PLH: plant height, 100-KW: 100-kernel weight, K P^{-1}: kernel count plant^{-1}, K S^{-1}: kernel count spike^{-1}, BY: biological yield plant^{-1} and GY: grain yield plant^{-1}. * and** significant at 0.05 and 0.01 probability levels, respectively.

3-Selection for spike number plant^{-1}:

Variability and heritability analysis

Data of the variability and heritability estimates for spike number plant^{-1} are presented in Table 8. The genotypic coefficient was consistently smaller than the phenotypic coefficient of variability with estimates of [5.35 and 11.34), (0.59 and 0.82), and (1.64 and 1.68)] for C_0, C_1 and C_2, respectively. The narrow gap between genotypic and phenotypic variability (except in C_1) led to high broad-sense heritability estimates across the two selection cycles. The phenotypic coefficient of variability for no. of spikes plant^{-1} in the F_2 generation was 34.62% and decreased to 10.65 and 15.27% in F_3 and F_4 generations, respectively.

The genotypic coefficient of variability for spike number plant^{-1} was 23.79, 9.03 and 15.07% in F_2, F_3 and F_4 generation, respectively.

The heritability estimates were 49.89, 71.91, and 97.29% for C_0, C_1, and C_2, respectively. The realized heritability estimates were 5.01 in C_1 and increased to 46.14% in C_2. These findings align with the results reported by El-Morshidy *et al.* (2010). Similarly, Taha *et al.* (2011) observed that the broad-sense heritability for the number of spikes plant^{-1}, following two selection cycles, was 73.19% and 78.4% for the two populations studied. Soliman and Feltaous (2020) cleared that the pcv% for spike number plant^{-1} attained 32.66, 9.17 and 9.24% for C_0, C_1, and C_2, respectively, whereas gcv% values attained 28.56, 8.86, and 9.15%, respectively.

Table 8. Variability and heritability estimates of spike count plant^{-1} following two selection cycles .

Selection cycle	σ^2 p	σ^2 g	P.C.V. %	G.C.V. %	Broad sense heritability	Realized heritability
(C0)	11.34	5.35	34.62	23.79	49.89	--
(C1)	0.82	0.59	10.65	9.03	71.91	5.01
(C2)	1.68	1.64	15.27	15.07	97.29	46.14

Means and observed gains

Table 9 presents the mean spike number plant^{-1} across the 10 assessed F_4 families. The average spikes number plant^{-1} ranged from 9.62 for family 13 to 13.82 for family 344, averaging 11.67. The selection process yielded a notable direct gain, which was significant ($P<0.05$) surpassed the bulk sample by 5.53% but it in-significant surpassed the better parent (2.11%). Among the ten families evaluated for their higher spike number plant^{-1}, significant to highly significant gains were observed compared to the bulk sample. These gains attained 5.79% for family 414 to 24.97% for family 344. Additionally, four families (66, 92, 344, and 386) demonstrated significant or highly significant improvements over the better parent, with average increases of 16.07%, 4.99%, 20.93%, and 8.19%, respectively. According to Meier *et al.* (2021), the selection gains for tiller count was 14.63%, highlighting the possibility to identify superior genotypes. Soliman and Feltaous (2020) stated that mean gain observed under standard sowing conditions was highly significant, reaching 13.53% relative to the bulk sample and 9.66% relative to the superior parent.

Table 9. Means of spike count plant^{-1} and the OG% Bulk and OG% BP for the chosen families following two selection cycles.

Fam. No.	Mean	OG%Bulk	OG% BP
13	9.62	-13.00**	-15.82**
53	10.00	-9.58**	-12.51**
66	13.27	19.95**	16.07**
92	12.00	8.50**	4.99*
103	11.37	2.77	-0.55
124	11.33	2.47	-0.85
202	11.23	1.57	-1.72
344	13.82	24.97**	20.93**
386	12.37	11.81**	8.19**
414	11.70	5.79*	2.36
Mean	11.67	5.53*	2.11
Parent 1	11.43		
Parent 2	10.83		
R.L.S.D.	**0.05: 0.52**		**0.01: 0.77**

* and** significant at 0.05 and 0.01 probability levels, respectively.

Average observed gain following two selection cycles for spike number plant^{-1}:

The means and observed gain from selection for increased spike count plant^{-1} under normal conditions are listed in Table 10. The selection for a higher spike number plant^{-1} in C_1 resulted in an observed gain of 4.16% compared to the bulk sample, while it showed a decline of 6.68% relative to the better parent. Alternatively, in C_2 it was 2.11% and 5.53 from the better parent and the bulk sample, respectively. El-Hosary *et al*. (2011) reported that the selection for higher spike count plant^{-1} gave the highest observed gain and it was more efficient as indirect selection criterion to improve grain yield followed by direct selection employing GY as a selection criterion which gave the lowest one.

Table 10. Means and observed gain from selection for increased spike count plant^{-1} after two cycles of selection from the bulk sample and the better parent.

Cycle	Mean	Spikes number plant^{-1}
Cycle (1)	Families mean	8.52
	Parent (1)	9.13
	Parent (2)	8.65
	Bulk sample	8.18
	OG % (Bulk)	4.16
	OG% (B. P.)	-6.68
R. L.S.D. 0.05		1.13
R. L.S.D. 0.01		1.62
Cycle (2)	Families mean	11.67
	Parent (1)	11.43
	Parent (2)	10.83
	Bulk sample	11.06
	OG % (Bulk)	5.53*
	OG% (B. P.)	2.11
R. L.S.D. 0.05		0.52
R. L.S.D. 0.01		0.77

*: significant at 0.05 probability level.

The phenotypic correlation following two selection cycles aimed at higher spike count plant^{-1}:

Table 11 displays the correlation coefficients for all pairwise combinations of the examined traits in the F_4 families. A strong negative and highly significant correlation (r = -0.48) was observed between the spike number plant^{-1} and the days to heading. Alternatively, spike count has positive and significant or highly significant correlation coefficients with kernel count plant^{-1}, biological yield plant^{-1}, and grain yield plant^{-1} with values (0.78, 0.80, and 0.79, respectively).

The indirect selection for no. of spikes plant^{-1} could be efficient to improve GY. Similar results were obtained by Soliman and Feltaous (2020) where found that no. of spikes plant^{-1} were significantly correlated with BY and GY with values (0.54 and 0.74, respectively).

Table 11. Phenotypic correlation between the analyzed attributes for the chosen families in (F_4 generation) for spike count plant^{-1}.

Item	DH	DM	S plant^{-1}	PLH	100-KW	K P^{-1}	K S^{-1}	BY
DH								
DM	0.64**							
S plant^{-1}	-0.48**	-0.30						
PLH	-0.07	0.08	0.22					
100-KW	-0.56**	0.62**	0.29	-0.10				
K P^{-1}	-0.16	0.04	0.78**	0.36	0.17			
K S^{-1}	0.40*	0.45*	-0.09	0.26	-0.11	0.56**		
BY	0.52**	0.42*	0.80**	0.19	0.50**	0.76**	0.16	
GY	0.38*	0.25	0.79**	0.26	0.57**	0.90**	0.37	0.82**

DH: Days to heading, DM: Days to maturity, S plant^{-1}: spike count plant^{-1}, PLH: plant height, 100-KW: 100-kernel weight, K P^{-1}: kernel count plant^{-1}, K S^{-1}: kernel count spike^{-1}, BY: biological yield plant^{-1} and GY: grain yield plant^{-1}. * and** significant at 0.05 and 0.01 probability levels, respectively.

4-Selection for high 100-kernel weight

Variability and heritability estimates

Data of the variability and heritability estimates for 100-kernel weight are listed in Table 12. The genotypic was generally smaller than the phenotypic coefficient of variability with estimates of [0.12 and 0.20), (0.06 and 0.08), and (0.0323 and 0.0353)] for genotypic and phenotypic variability coefficients in C_0, C_1 and C_2, respectively. The consistent alignment between genotypic and phenotypic variability across all selection cycles led to elevated values of broad-sense heritability. The phenotypic coefficient of variability (pcv%) for 100-kernel weight in the F_2 generation was 9.09% and decreased to 6.05 and 3.28% in generations F_3 and F_4, respectively. The genotypic coefficient of variability (gcv%) for 100-kernel weight was 6.99, 5.28, and 3.14% in F_2, F_3, and F_4 generation, respectively. The heritability estimates were 60.01, 76.10, and 91.51% for C_0, C_1, and C_2, respectively. The realized heritability estimates were 25.42 in C_1 and increased to 61.90% in C_2. Hamam (2014) observed that the G.C.V. for the 100-kernel weight was 2.53% following three selection cycles when using 100-kernel weight as the selection criterion. In contrast, the G.C.V. for the same trait in the base population was significantly higher at 14.03%.

Table 12. Variability and heritability estimates of 100-kernel weight after two cycles of selection.

Selection cycle	σ^2 p	σ^2 g	P.C.V.%	G.C.V.%	Broad sense heritability	Realized heritability
(C0)	0.20	0.12	9.09	6.99	60.01	--
(C1)	0.08	0.06	6.05	5.28	76.10	25.42
(C2)	0.0353	0.0323	3.28	3.14	91.51	61.90

Means and observed gains

Mean values of 100-kernel weight for the 10 evaluated F_4 families are listed in Table 13. The average 100-kernel weight ranged from 5.57g for family 292, to 5.97 for family 243, averaging 5.72g. The mean directly observed improvement from selection was highly significant (P<0.01), exceeding both the superior parent and the bulk sample by averages of 10.39% and 7.57%, respectively.

It is interesting that all the evaluated families selected for high 100-kernel weight revealed highly significant observed gain from each of the superior parent and the bulk sample. It could be concluded that 100-kernel weight as a selection criterion was more efficient for improving grain yield because the realized heritability of 100-kernel weight was the highest. Hamam (2014) reported increases of 11.32% and 24.25% in Pop.1, as well as 7.98% and 22.28% in Pop.2, compared to the top-performing parent and bulk population, respectively, using the weight of 100 kernels as the selection criterion.

Table 13. Means of 100-kernel weight and the OG% Bulk and OG% BP after two selection cycles.

Fam. No.	Mean	OG%Bulk	OG% BP
27	5.77	8.55**	11.40**
90	5.62	5.65**	8.43**
92	5.76	8.41**	11.26**
133	5.69	7.03**	9.85**
188	5.80	9.01**	11.87**
200	5.66	6.49**	9.29**
243	5.97	12.36**	15.32**
292	5.57	4.71**	7.46**
384	5.69	7.03**	9.85**
418	5.66	6.42**	9.21**
Mean	**5.72**	**7.57****	**10.39****
Parent 1	**5.18**		
Parent 2	**4.85**		
Bulk	**5.32**		
R.L.S.D.	**0.05: 0.13**		**0.01: 0.20**

* and** significant at 0.05 and 0.01 probability levels, respectively.

Table 14. Means and observed gain from selection for higher 100-Kernel Weight following two selection cycles from the bulk sample and the better parent.

Cycle	Mean	100-kernel weight (g)
Cycle (1)	Families mean	4.81
	Parent (1)	4.39
	Parent (2)	4.15
	Bulk sample	4.40
	OG % (Bulk)	9.32*
	OG% (B. P.)	9.57*
	R. L.S.D. 0.05	0.33
	R. L.S.D. 0.01	0.48
Cycle (2)	Families mean	5.72
	Parent (1)	5.18
	Parent (2)	4.85
	Bulk sample	5.32
	OG % (Bulk)	7.57**
	OG% (B. P.)	10.39**
	R. L.S.D. 0.05	0.13
	R. L.S.D. 0.01	0.20

* and** significant at 0.05 and 0.01 probability levels, respectively.

Average observed gain following two selection cycles for high 100-kernel weight

Table 14 presents the means and the observed selection gains for high 100-kernel weight under normal conditions. In C_1, the selection gain for high 100-kernel weight was 9.32% over the bulk sample and 9.57% relative to the better parent. Similarly, in C_2, the gains were 7.57% over the bulk sample and 10.39% compared to the better parent.

The phenotypic correlation after two cycles of selection for high 100-kernel weight

Table 15 displays the correlation coefficients among all evaluated traits for F_4 families chosen based on high 100-kernel weight. 100-kernel weight have positive and significant or highly significant correlation coefficients with heading time, maturity time, no. of spikes plant^{-1}, and biological and grain yield plant^{-1} (0.40, 0.40, 0,44, 0.47, and 0.54, respectively). These findings cleared that the indirect selection for 100-kernel weight might be effective in grain yield plant^{-1} improvement.

Table 15. Phenotypic correlation between the analyzed attributes for the chosen families in (F_4 generation) for 100-Kernel Weight.

Item	DH	DM	S plant^{-1}	PLH	100-KW	K P^{-1}	K S^{-1}	BY
DH								
DM	0.73**							
S plant^{-1}	0.33	0.23						
PLH	-0.26	-0.16	-0.31					
100-KW	0.40*	0.40*	0.44*	0.04				
K P^{-1}	0.62**	0.49**	0.12	0.13	0.34			
K S^{-1}	0.09	0.02	-0.08	-0.05	0.09	0.62**		
BY	0.19	0.24	0.58*	0.22	0.47**	0.27	0.37	
GY	0.52**	0.40*	0.71*	0.09	0.54**	0.51**	0.36	0.74**

DH: Days to heading, DM: Days to maturity, S plant^{-1}: spike count plant^{-1}, PLH: plant height, 100-KW: 100-kernel weight, K P^{-1}: kernel count plant^{-1}, K S^{-1}: kernel count spike^{-1}, BY: biological yield plant^{-1} and GY: grain yield plant^{-1}. * and** significant at 0.05 and 0.01 probability levels, respectively.

Conclusion

To improve grain yield, direct selection targeting grain yield plant^{-1} can be used or indirect selection focused on yield components such as spike count plant^{-1}, 100-kernel weight or kernel number spike^{-1}. No. of spikes plant^{-1} has a great value of correlation coefficient with grain yield, but it is also affected by environment than 100-kernel weight or kernel number spike^{-1}. Thus, it is hard to select for no. of spikes plant^{-1} because it is need high degree of experience. It is clear from the current study that targeting grain yield plant^{-1} directly and 100-kernel weight indirectly proved to be a more effective strategy compared to selecting based on the spike number plant^{-1}.

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الاستجابة للانتخاب المباشر وغير المباشر لتحسين إنتاجية الحبوب في قمح الديورم

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الملخص

تم إجراء هذه الدراسة بمزرعة محطة البحوث الزراعية بشندويل، مركز البحوث الزراعية، مصر خلال مواسم الزراعة الثلاثة 2020-21، 2021-22، 2022-23 م. الهدف من الدراسة هو مقارنة تأثير الانتخاب المباشر لمحصول الحبوب للنبات والانتخاب غير المباشر لكل من عدد السنابل للنبات ووزن الـ 100 حبة لتحسين محصول الحبوب وإنتاج سلالات جديدة من قمح الديورم عالية الإنتاجية. تم تنفيذ دورتين من الإنتخاب المنسب لصفات محصول الحبوب للنبات وعدد السنابل للنبات وكذلك وزن الـ 100 حبة من الجيل الثاني إلى الجيل الرابع تحت ظروف النمو المثلى. أظهرت النتائج أن التباين المظهري كان أعلى قليلاً من التباين الوراثي وتناقصا عموماً من الجيل الثاني إلى الجيل الرابع. كانت تقديرات معامل التوريث بالمعنى العريض وكذلك معامل التوريث المتحقق بعد دورتين من الإنتخاب المنسب 78.73، 48.63% لصفة محصول الحبوب للنبات، 97.29، 46.14% لصفة عدد السنابل للنبات، 91.51، 61.90% لصفة وزن الـ 100 حبة، على التوالي. كان التحسين المتحقق بعد دورتين من الإنتخاب المنسب المباشر 11.12، 8.45% لصفة محصول الحبوب للنبات وكان 5.23، 2.11% من الإنتخاب غير المباشر لصفة عدد السنابل للنبات، 7.57، 10.39% من الإنتخاب غير المباشر لصفة وزن الـ 100 حبة بالمقارنة بمخلوط العشيرة والأب الأفضل على التوالي.

الكلمات المفتاحية: *الانتخاب لمحصول الحبوب للنبات، عدد السنابل للنبات، قمح الديورم، وزن ال 100 حبة*