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Efficiency of index-based selection for potential yield in durum wheat [*Triticum turgidum* (L.) ssp. *turgidum convar. durum* (Desf.) Mackey] lines

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Highlights

- *The predicted genetic gains were estimated from direct, indirect and index-based selection in 418 F4–derived lines of durum wheat.*
- *Wide genetic variation with moderately high broad-sense heritability were found among progenies for yield components.*
- *The Smith & Hazel (SHI) and Williams (WI) selection indices, provided a more balanced gains distribution to the set of measured traits.*
- *The index selection with the highest responses was found to be useful tool in improving efficiency considering all traits simultaneously.*
- *The simultaneous selection for agronomic traits identified L34, L24 and L15 as the most promising lines in this breeding program.*

Abstract

Wheat is a socioeconomically important crop in Algeria. Improving genetic gain of quantitative traits through selection is at the core of every successful breeding program. Selection is usually performed on grain yield, but other agronomically related characteristics can also help increase genetic gain through indirect or multi-trait selection. The objective of this work was to quantify genetic parameters and compare the efficiency of direct, indirect and simultaneous selection methods in terms of predicted genetic values of wheat progenies. For this purpose, 418 F4-derived lines were evaluated for six agronomic traits including heading date, flag leaf area, plant height, number of spikes, thousand kernel weight and grain yield in an augmented block design with three check varieties. Wide genetic variation with moderately high broad-sense heritability were observed for the recorded traits, except for heading date. The results from genetic gain revealed variation in gains for assessed traits and breeding methods employed. The classic index of Smith and Hazel (SHI) demonstrated a similar genetic gain in grain yield compared to gain from direct selection. Generally, the selection-based index showed the highest responses considering all traits simultaneously with a slight inferiority of the SHI index. The coincidence rates among the evaluated indices were higher than those obtained between the measured traits. Based on the comparisons between the selected lines, the SHI index and the selection base index of Williams were similar to grain yield and can reach up to 79.51% coincidence of breeding lines identified by these selection criteria. Breeding lines L252, L34, L24, L130 and L413 were the most common individuals identified according to number of coincidences from the different selection methods used. Of these, L34 and L24, and to a lesser extent L15 can be considered promising wheat lines for improving grain yield.

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Introduction

Durum wheat [*Triticum turgidum* (L.) ssp. *turgidum* convar. *durum* (Desf.) MacKey] is the most important cereal crop in Algeria before barley (*Hordeum vulgare* L.) and bread wheat (*Triticum aestivum* L.). This crop species is widely cultivated in a rainfed agricultural system in the northern national territory from the Tunisian frontier in the East to Morocco in the West. Globally, it is grown over 1.49 million hectares with a total production of 2.57 million tons in 2019-2020 and an average yield during the 2000-2020 period of 1.70 t ha^{-1} (MADRP-DSASI, 2020; Kourat *et al*., 2022; Martínez-Moreno *et al*., 2022). Algerian production fails to meet the needs of the country, estimated at 8.5 million tons per year (Benbelkacem, 2022). The low average productivity largely explains the insufficient production since the area of land allocated to this crop has been comparatively stable through time (Mekaoussi *et al*., 2021). This ascertainment of yield stability is due to several natural (soil and climate), technical (seeds and cultural practices) and human constraints (organization and training of producers) (Chabane and Boussard, 2012). However, low yield has largely been caused by the occurrence of biotic (diseases and pests) and particularly abiotic stresses (drought, heat and frost), which cause a strong irregularity of produced wheat grain (Beres *et al*., 2020; Benbelkacem, 2022).

Breeding potential genotypes that have the capacity to produce better yields under a such growth conditions seems to be the most societally acceptable, cheapest and rapidly adopted approach to ameliorate the total production (Lamara *et al*., 2022). Grain yield is a polygenic complex trait and is highly influenced by the environmental fluctuations. Hence, the direct selection of wheat genotypes based solely on grain yield would not be reliable in many cases. The ineffectiveness of this selection method is explained by the presence of the genotype x environment interaction (Haddad *et al*., 2016; Laala *et al*., 2021). Breeders are looking for other traits of interest that could be more predictive in the selection process of breeding programs. Candidate traits for indirect selection should have a large genetic variability, be highly heritable and strongly correlated with grain yield, both under stress and non-stress conditions (Richards *et al*., 2002).

Use of a selection based-index is another strategy that has been found to be more efficient compared to direct and indirect mono-trait selection for grain yield (Fellahi *et al*., 2018, 2020). In the literature, many indices have been proposed for the selection of promising genotypes in different environments to obtain stable, high-yielding and stress-tolerant genotypes (Cruz *et al*., 2014). Development of a selection based-index can be performed using various methods to assist breeders for simultaneous selection of multiple traits related to grain yield that aims to obtain high-genetic gains in each selection cycle (Candido *et al*., 2020). Among the available indices, we cite the classical index proposed by Smith (1936) and Hazel (1943) and the selection base index of Williams (1962) as parametric indices. The free weights and parameters index suggested by Elston (1963), the index of desired gains of Pesek and Baker (1971), the multiplicative index of Subandi *et al.* (1973), the index of sum of ranks proposed by Mulamba and Mock (1978) and the genotype-ideotype distance index developed by Cruz (2006) are non-parametric indices. Each index has certain particularities in its calculation and application is often laborious due to the necessity to assign appropriate economic weights to each measured trait. According to Cruz *et al.* (2014), these indices provide optimal linear combinations between the sets of information from the experimental unit and offer the opportunity to carry out efficient simultaneous selection of several traits, enhancing the chance of success in the breeding program.

The aim of this study was to evaluate and define the most appropriate selective strategy for the improvement of yield and yield-related traits in durum wheat breeding lines, by comparing direct and indirect selection, and selection based-indices methods in the assessment of expected genetic gains for traits of economic interest.

Materials and Methods

Population development and experimental design

The experiment was conducted under field conditions at the National Agronomic Research Institute of Algeria (INRAA-Setif, 36°15’N, 5°87’E, 1081 m above sea level) during the 2014-2015 cropping season. The plant material consisted of 421 durum wheat genotypes including 418 F_4–derived lines belonging to 15 biparental populations developed by the pedigree selection method (Hannachi *et al*., 2013), and also three check varieties named Waha (*Plc/Ruff//Gta’s/3/Rolette*), Ofanto (*Adamelo/Appulo*) and GTA dur (*Gaviota/durum*). Waha is a variety selected from the ICARDA[1]-CIMMYT[2] breeding program, Ofanto is an Italian cultivar, and GTA dur is a CIMMYT variety (Hannachi *et al*., 2013). The pedigree of durum wheat populations, names of check varieties and the number of breeding lines selected per family in each developed population are indicated in Table 1.

The experiment was set up using Federer’s augmented block design, with three blocks (Federer, 1955) wherein the first block was composed of 139 plots containing 136 different wheat breeding lines and three plots containing the check varieties which were randomly distributed in three plots within this block. Similarly, the second block was composed of another 139 breeding lines and three plots reserved for check varieties. Finally, the third block contained the remaining 140 lines in addition to the three check cultivars. It should be noted that the breeding lines of each population remained in the same order but the order of the 15 popula-

Table 1. Pedigree of durum wheat populations, names of check varieties and the number of breeding lines selected in each developed population.

N.	Pedigree/names	No. of lines
1	Waha//ZB/Fg	26
2	Waha/Mexicali$_{75}$	30
3	Waha/Ofanto	27
4	Waha/Gta dur	28
5	Waha/Guemgoum Rkhem	27
6	ZB/Fg//Mexicali$_{75}$	30
7	ZB/Fg//Ofanto	28
8	ZB/Fg//Gta dur	27
9	ZB/Fg//Guemgoum Rkhem	26
10	Mexicali$_{75}$/Ofanto	29
11	Mexicali$_{75}$/Gta dur	29
12	Mexicali$_{75}$/Guemgoum Rkhem	30
13	Ofanto/Gta dur	28
14	Ofanto/Guemgoum Rkhem	30
15	Gta dur/Guemgoum Rkhem	23
16	Waha	Check variety
17	Ofanto	Check variety
18	GTA dur	Check variety

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[1] International Center for Agricultural Research in the Dry Areas.

[2] International Maize and Wheat Improvement Center.

tions within the blocks was completely randomized. The experimental plot consisted of a single 2-m long row, with 0.2 m spacing between rows. Seeding was performed manually in the first half of December 2014, adopting a seeding density of 300 seeds m^{-2}. Agronomic practices and crop management followed technical recommendations for wheat species. According to Chennafi *et al*. (2006), Setif is located in the semi-arid Mediterranean climate region, which is characterized by hot and dry summers, and cold and rainy winters. Rainfall accumulated during the crop cycle was 343.6 mm. The open-air mean temperature in central Setif region varied from 3.7°C in January to 21.3ºC in June.

Progeny evaluation and statistical data analyses

Heading date (HD, days) was taken as the number of calendar days from January 1st to the date when 50% of the spikes in the experimental plot had emerged from the flag leaf sheath. Flag leaf area (FLA, cm^2) was determined at heading stage using the procedure described by Spagnoletti Zeuli and Qualset (1990) as follows:

$$FLA\ (cm^2) = L\ (cm) \times l\ (cm) \times 0.607$$

where: L and l are the flag leaf length and width, respectively.

Plant height (PH, cm) was measured just before harvest from the soil surface to terminal spikelet tip, excluding awns. Grain yield (GY, g m^{-2}) and the number of spikes (SN, m^{-2}) were calculated after mechanical threshing of the hand-harvested plots. Thousand kernel weight (TKW, g) was determined from the count and weight of a seed sample of 250 grains.

The data collected were subjected to analysis of variance (ANOVA) using F-test at $P \leq 0.05$ according to the procedure outlined by Cruz (2006). The mean squares obtained from the ANOVA table served to obtain the phenotypic (σ^2_p), genotypic (σ^2_g) and environmental (σ^2_e) variances for each trait. These variances were thereafter used to calculate the genetic (CV_g), phenotypic (CV_p) and environmental (CV_e) coefficients of variation, variation index (VI) and broad-sense heritability (h^2_{bs}) as described by Cruz (2006). Means comparison was based on least significant difference at 5% probability level ($LSD_{5\%}$). The adjusted means obtained after running the ANOVA were used to investigate the relationships between measured traits using Pearson's correlation coefficients according to Steel and Torrie (1982). They served also to calculate the genetic gains estimations considering the selection of 2.4% of top progenies for the direct and indirect selection methods, and the selection-based index. The selection criteria were applied to reduce the heading date and increase the remaining traits.

The expected gains from direct and indirect selection for each evaluated trait were estimated according to Cruz *et al*. (2012). Gains from direct selection for the ith trait (GS_i) were expressed by:

$$GS_i = (X_{si} - X_{oi})\, h_i^2 = DS_i\, h_i^2$$

where: X_{si} is the mean of lines selected for the ith trait; X_{oi} is the mean of the original population; DS_i is the population selection differential; and h_i^2 is the heritability of the ith trait.
Gains from indirect selection (GS_i) were calculated as outlined by Cruz *et al*. (2012) using the following expression:

$$GS_{j(i)} = DS_{j(i)}\, h_i^2$$

where: $DS_{j(i)}$ is the indirect selection differential from the mean of individuals' traits whose superiority had been highlighted by annother trait to which the direct selection was applied; and h_i^2 is the heritability of the ith trait.

The multiplicative index (I_{Ei}) of Subandi *et al*. (1973) is assumed to be directly or inversely proportional to the variable analyzed, according to the breeder's criteria. The index is given by:

$$I_{Ei} = log \prod_{j=i}^{m} (X_{ij} - k_j = \log[(X_{i1} - K_1)(X_{i2} - K_2) \ldots (X_{in} - k_n)$$

where: X_{ij} is the mean of the jth trait measured in the ith genotype; K_j refers to the lowest possible value:

$$K_j = \frac{n(min.X_{ij}) - max.X_{ij}}{n-1}$$

where: n is the number of genotypes; $min.X_{ij}$ and $max.X_{ij}$ are the jth trait lowest and highest means, respectively.

The classic index of Smith (1936) and Hazel (1943) comprises a linear combination of assessed traits of economic importance, through the selection index (I) and the aggregate genotype (H), as follows:

$$I = b_1y_1 + b_2y_2 + \cdots. + b_ny_n = \sum_{i_1}^{n} b_i\, y_i = y'b$$

$$H = a_1g_1 + a_2g_2 + \cdots a_ng_n = \sum_{i-1}^{n} a_i\, g_i = g'a$$

where: n is the number of traits evaluated; b is the vector of dimension $1 \times n$ of the weighting coefficients of the selection index to be estimated; y dimension matrix $n \times p$ (plants) of phenotypic values of the traits; a is the vector of dimension $1 \times n$ of previously established economic weights; and g is the $n \times p$ matrix of unknown genetic values of the n traits considered. The vector (b) used was:

$$b = P^{-1}\, G_a$$

where: P^{-1} is the inverse of the matrix, of dimension $n \times n$ of phenotypic variance and covariance between traits. G_a is the $n \times n$ dimension matrix of genetic variance and covariance between traits.

The expected gain for the jth trait ($\Delta_{gj(I)}$) with selection based on index I was calculated by:

$$\Delta_{gj(I)} = DS_{j(I)}\, h^2_j$$

where: $DS_{j(I)}$ is the selection differential for the jth trait, with selection based on index I; and h^2_j is the heritability of the jth trait evaluated.
Mulamba and Mock's sum of ranks (1978) index (I) classifies the genotypes for each trait in an order which is favorable for breeding. The different orders of each genotype are then summed, resulting in the selection index as follows:

$$I = r_1 + r_2 + \ldots + r_n$$

where: r_j is the classification of an individual in relation to the jth trait; n refers to the number of traits considered in the index.

The method can assign different weights to sort the variables rank. Thus, the economic weights were given by:

$$I = P_1r_1 + P_2r_2 + \ldots + P_jr_n$$

where: P_j is the economic weight assigned to the jth trait.

Elston's (1963) free weights index involves the product of the phenotypic values (P) less the minimum observed value for each trait. Given P traits, for each genotype, the Elston index (I_E) is calculated as follows:

$$I_E = \prod_{i=1}^{P} (X_i - K_i)$$

where: X_i is the value of the genotype for i^{th} trait; and K_i is some lower bound. Two options for K:

$$K = \min X_i$$

$$K = \frac{n \min X_i \ - \max X_i}{n - 1}$$

The base index of Williams (1962) proposes the establishment of indices by the linear combination of the mean phenotypic values of the traits weighted directly by their respective economic weights. The Williams' base index (I) is given by:

$$I = a_1 y_1 + a_2 y_2 + \cdots + a_n y_n = \sum_{i-1}^{n} a_i y_i = y'a$$

where: y is the mean; and a is the economic weight for the traits studied.

The genotype-ideotype distance index (Cruz, 2006) allows the optimal values for each variable to be set, as well as the range of values considered to be favorable for breeding. For each variable, the maximum, minimum and mean values are calculated. X_{ij} is considered as the mean phenotypic value of the i^{th} genotype in relation to the j^{th} trait; Y_{ij} is the transformed mean phenotypic value; and C_j a constant relative to depreciation of the mean value for the genotype where this does not fall within the standards required by the breeder. Therefore, LI_j is the lower limit to be presented by the genotype for the j^{th} trait, according to the standard desired by the breeder; LS_j is the upper limit presented by the genotype; and VO_j refers to the optimal value presented by the genotype under selection.

If $LI_j \leq X_{ij} \leq LS_j$, then $Y_{ij} = X_{ij}$

If $Y_{ij} < X_{ij}$, then $Y_{ij} = X_{ij} + VO_j - LI_j - C_j$

If $X_{ij} > LS_j$, then $Y_{ij} = X_{ij} + VO_j - LS_j - C_j$

It was considered that $C_j = LS_j - LI_j$

The C_j value guarantees that X_{ij} value within the interval variation around the optimal value resulted in Y_{ij} value with magnitude close to the optimal value (VO_j), in opposition to X_{ij} values outside this interval. Thus, X_{ij} transformation was conducted to ensure the depreciation of phenotypic values outside the interval.

The Y_{ij} values obtained by the transformation were eventually standardized and weighed by the weights attributed to each trait, which provided Y_{ij} values according to the following specifications:

$$Y_{ij} = \sqrt{a_j} \times \frac{Y_{ij}}{S(Y_i)}$$

where: $S(Y_i)$ is the standard deviation of the transformed mean phenotypic values; and a_j is the trait economic weight.

The VO_{ij} was standardized and weighted as well, as follows:

$$VO_{ij} = \sqrt{a_j}\,\frac{VO_j}{S(Y_i\ )}$$

Then, the values of the index were calculated and expressed by the distance between the genotype and the ideotype from the following expression:

$$I_{DGI} = \sqrt{\frac{1}{n}\sum_{j=1}^{n} (Y_{ij} - VO_j)^2}$$

The various parametric and non-parametric selection indices evaluated in the present investigation to obtain genetic gains were calculated using an economic weight equivalent to 1 for all measured traits.

At the above-mentioned amount of selection of 2.4%, the optimal values for each variable were defined, the best 10 breeding lines were identified for each selection approach. Selection efficiency was examined via the coincidence index calculated between each pair of selection criterion according to Hamblin and Zimmermann's (1986) method as:

$$IC = \frac{(A - C)}{(M - C)} \times 100$$

where: A is the number of lines coinciding in both strategies; M is the number of selected lines, in this case 10; and C is the number of random coincidences assigned-in this case, 2.4% of M.

The higher coincidence coefficient between two selection approaches, the better the concordance of their results.

All statistical analyses were performed via Genes software (Cruz, 2013) and a Microsoft Excel© spreadsheet.

Results and Discussion

Variance components and genetic parameters

Means, range values, variances, genotypic coefficient of variation, variation index and broad-sense heritability of the measured traits are reported in Table 2. Adjusted means give the true genotype values eliminating environmental variations. When compared to the least significant difference, there were significant differences between maximal and minimal values observed for all measured traits, days to heading excluded. Heading date ranged from 125.00 to 128.67 days, flag leaf area varied from 5.54 to 46.94 cm^2, plant height from 38.22 to 94.22 cm. The number of spikes ranged from 20.00 to 693.30 spikes per m^2, while thousand kernel weight varied from 31.67 to 64.33 g and grain yield from 33.30 to 1176.70 g m^{-2}.

Grain yield followed by spike number m^{-2} and flag leaf area showed the highest genotypic variation ($CV_g \geq 20\%$). Plant height showed an intermediate level of variability ($10\% \leq CV_g < 20\%$) whereas heading date and thousand kernel weight exhibited the lowest variability level with CV_g values below 10% ($CV_g < 10\%$). Broad-sense heritability (h^2_{bs}) estimates varied between 11.86% for days to heading and 92.28% for plant height. Based on the classification outlined by Acquaah (2012), flag leaf area, plant height, thousand kernel weight and grain yield were considered to be as highly heritable traits (h^2_{bs}≥60%). Spike number was just intermediate (30%≤h^2_{bs}<60%) while heading date demonstrate low heritability (h^2_{bs}<30%). These results are supported by the variation index (*VI*) calculated as the ratio of genetic and environmental coefficients of variation (CV_g/CV_e). According to Cruz *et al.* (2014), traits exhibiting *VI* values superior to the unit are considered ideal for selection. In this study, heading date, and to a lesser extent spike number per unit area, were the most affected by the environment fluctuations. These findings suggest the possibilities to make significant improvements in wheat genotypes through selection in the F_4 filial generation based on these highly heritable traits. Nevertheless, sampling a greater number of replicates across a wider range of environments over future generations would improve the response to selection.

Relationships among measured traits

Significant to highly significant phenotypic correlations were observed between the six measured traits in wheat populations, except for thousand kernel weight which demonstrated weak even though significant or weak statistically significant relationships with flag leaf area, spikes number and grain yield (Figure 1). Significant positive correlations were observed for grain yield with flag leaf area, plant height and spike number. In contrast, significant negative correlation was found between grain yield and heading date, suggesting that high plant stature, larger leaves and increased spikes number per plot were advantageous for the grain yield of the investigated durum wheat populations, while earliness is somewhat advantageous for yield potential and spike number as well. So, indirect improvement of grain yield should be targeted through these characters that had also high positive relationships among each other.

Predicted selection gain from direct and indirect selection

Considering the selection of 2.4% of top progenies, 10 individuals were selected for each trait. Direct and indirect selection displayed positive total gains ranging from 41.69 to 160.33% (Table 3). The highest direct gains were obtained for grain yield followed by flag leaf area and spike number with 96.00, 58.90 and 55.04%, respectively. Even though direct selection generated significant gains, indirect selection gains were also important in some cases.

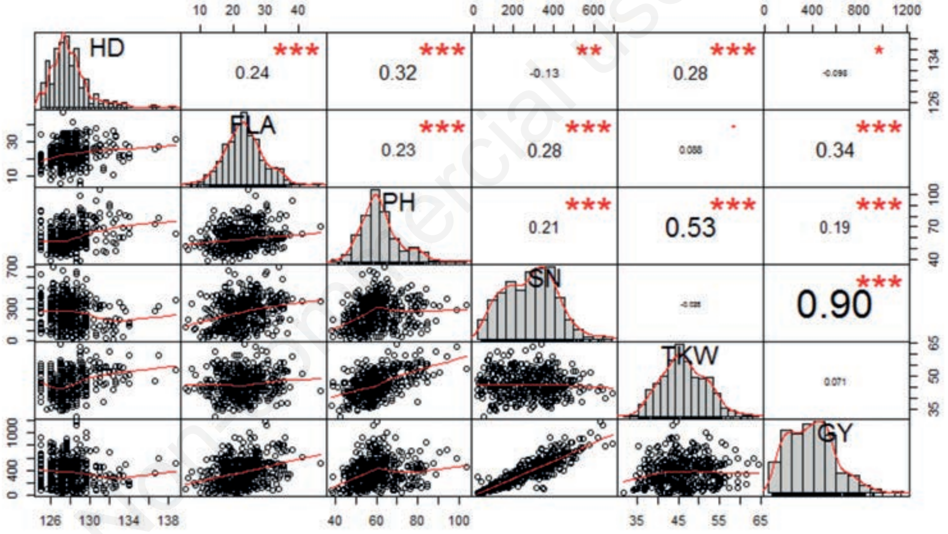

Figure 1. Pearson's linear correlation among the six traits measured in 418 durum wheat breeding lines. *, **, and *, significant correlation coefficient at 0.05, 0.01 and 0.001 levels of probability, respectively; HD, heading date; FLA, flag leaf area; PH, plant height; SN, spikes number; TKW, thousand kernel weight; GY, grain yield.**

Table 2. Adjusted means, range, variances, genetic, phenotypic and environmental parameters for durum wheat traits of 418 breeding advanced lines.

Traits	$LSD_{5\%}$	Means	Range	σ^2_p	σ^2_g	σ^2_e	CV_g (%)	VI	h^2_{bs} (%)
HD	4.03	127.99	125.00-128.67	3.59	0.43	3.17	0.51	0.37	11.86
FLA	4.60	22.89	5.54-46.94	38.11	33.88	4.23	25.40	2.83	88.90
PH	6.39	60.17	38.22-94.22	102.96	95.01	7.94	16.19	3.46	92.28
SN	229.09	274.19	20.00-693.30	19208.67	9002.50	10206.16	34.65	0.94	46.87
TKW	8.07	46.19	31.67-64.33	33.80	21.13	12.67	9.95	1.29	62.53
GY	279.76	383.09	33.30-1176.70	47139.35	31906.05	15233.30	46.73	1.45	67.68

HD, heading date; FLA, flag leaf area; PH, plant height; SN, spikes number; TKW, thousand kernel weight; GY, grain yield; $LSD_{5\%}$, least significant difference at 5% probability level; σ^2_p, phenotypic variance; σ^2_g, genotypic variance; σ^2_e, environmental variance; CV_g (%), genetic coefficient of variation; VI, variation index; h^2_{bs} (%), broad-sense heritability.

For example, selection for flag leaf area resulted in desirable indirect gains of -14.76 and 21.70% for heading date and grain yield, respectively. Similarly, selection based on plant height generated an indirect gain of 28.75% for thousand kernel weight which was larger than the direct selection gain obtained via direct selection on thousand kernel weight itself (19.70%). The direct selection for grain yield increased the indirect gains in all remaining traits such as flag leaf area (26.66%), plant height (20.89%), spikes number (88.01%) and thousand kernel weight (11.47%). The direct gain of heading date was expected to be at least low, or negative; however, when individuals were selected for grain yield, there was an undesirable indirect selection for longer crop cycle (44.64%). This, in despite of the range of variability for the characteristic days to heading which was very narrow within the studied population (Table 2). Under the growth conditions of Algerian semi-arid regions, wheat genotypes with shorter cycle are less subject to drought and early heat stress (Rabti *et al*., 2020; Haddad *et al*., 2021).

In the literature, the efficiency of direct and indirect mono-trait selection has generated significant controversy. Fellahi *et al*. (2020) concluded that gains from direct selection were superior to those for indirect gains for all wheat traits. Despite this, direct selection may result in undesirable changes in related traits as noted by Guimarães *et al*. (2021). The presence of some indirect gain that surpassed the direct gains was also observed by Costa *et al*. (2008). This may be attributed to higher heritability of the auxiliary trait compared to the main trait under selection and the strong genetic correlation between the traits of interest (Falconer and Mackay, 1996). The intensity of selection, the genetic properties of the population, and the environmental conditions are the most important factors that interfere, directly or indirectly, in the selection gain (Silva *et al*., 2020a). This gain is therefore directly attributed to the difference in the mean among selected individuals and that of the base population. The more heterogeneous a population, the better the possibilities of obtaining higher gains through selection. But the application of a high selection pressure risks considerably decreasing the genetic variability, which can jeopardize gains in subsequent cycles (Hamawaki *et al*., 2012). The results of this study evidence the complexity of simultaneous improvement for multiple traits through direct and indirect selection. Therefore, the use of indices-based selection becomes an interesting and easier strategy to identify genotypes with positive selection gain values for grain yield, flag leaf area, plant height, spikes number and thousand kernel weight, and negative value for heading date.

Predicted selection gain from index-based selection

In wheat breeding programs, it is recommended to create potential genotypes that possess a number of desirable attributes such as tolerance to abiotic and biotic stresses, end-use quality, good yield and yield stability. So that none of these characteristics are left aside, the option offered to the breeder is to adopt the simultaneous selection of these traits through the use of indices. The selection based-index is a good alternative to single trait direct and indirect selection. It is based on the combination of multiple values of the different traits analyzed, so that the selection is made in a single value involving all the variables of economic interest (Ramalho *et al*., 2012; Cruz *et al*., 2014). In the present study, expected genetic gains obtained by the different selection indices are presented in Table 4. The highest total gain was observed for the index of

Table 3. Selection gain estimates obtained for the six measured traits, by direct (diagonal) and indirect (off diagonal) selection, for the durum wheat breeding lines.

Traits	GS (%)					
	HD	FLA	PH	SN	TKW	GY
HD	-0.28	0.13	0.14	-0.12	0.24	-0.05
FLA	-14.76	58.90	12.99	5.22	9.18	21.70
PH	-9.20	13.56	46.22	1.62	28.75	-1.36
SN	23.88	5.55	5.78	55.04	-1.70	44.02
TKW	-2.59	2.79	11.41	-1.88	19.70	0.02
GY	44.64	26.66	20.89	88.01	11.47	96.00
Total	41.69	107.59	97.43	147.89	67.64	160.33

HD, heading date; FLA, flag leaf area; PH, plant height; SN, spikes number; TKW, thousand kernel weight; GY, grain yield; GS (%), selection gain.

Table 4. Selection gain estimates obtained for the six traits measured, by selection-based index, for the durum wheat breeding lines.

Indices	GS (%)					
	SI	SHI	MMI	EI	WI	CI
HD	0.08	-0.10	0.12	0.03	-0.07	0.09
FLA	35.58	27.18	31.53	55.60	15.95	39.39
PH	18.57	1.20	10.55	14.23	-1.86	23.94
SN	36.61	41.02	41.02	29.43	52.04	31.78
TKW	6.24	-2.78	3.85	5.25	0.42	6.34
GY	81.80	88.04	85.39	61.54	94.74	74.23
Total	178.88	154.56	172.46	166.08	161.22	175.77

HD, heading date; FLA, flag leaf area; PH, plant height; SN, spikes number; TKW, thousand kernel weight; GY, grain yield; GS (%), selection gain; SI, Subandi index; SHI, Smith and Hazel index; MMI, Mulamba and Mock index; EI, Elston index; WI, Williams index; CI, Cruz index.

Subandi (SI) followed by Cruz index (CI) and the Mulamba and Mock's sum of ranks (MMI) with 178.88, 175.77 and 172.46%, respectively. Although the Williams' base index (WI) displayed the second lowest total selection gain estimate after the Smith and Hazel index (SHI), selection on the basis of these two last indices resulted in the highest gains of 94.74 and 88.04% for grain yield, and 52.04 and 41.02% for spike number, respectively.

Considering the recorded traits, there was an important difference between indices in terms of total genetic gains, being higher than those obtained from direct and indirect selection. This is likely due to the fact that the traits in question were included primarily in the values of the indices, so the selection was principally based on these traits. According to de Santiago *et al.* (2019), the use of selection indices is an effective strategy since there are simultaneous gains for various important agronomic and economic traits. Different results for the evaluation of index efficiency were reported in the literature. This sort of controversy could be related to the number and type of traits included and the use or not of economic weights, in addition to the population size, level of homozygosity and selection pressure (Bernardo, 2002). Cargnin *et al*. (2007) studied 240 $F_{2:4}$ families of wheat over two sowing dates and pointed out that the use of selection indices was advantageous in improving selection efficiency for heat tolerance in central Brazil. The use of selection indices in wheat improvement programs would allow a yield increase under semi-arid regions of Algeria through the identification of potential varieties with specific adaptability to water stress as reported by Fellahi *et al.* (2018, 2020). These authors also showed that SHI and WI indices produced better performance when used to select important characteristics of bread wheat, without significant gain loss in the main trait. In another study, Mahdy *et al.* (2022) showed good results using the index of desired gains of Pesek and Baker (PBI) in simultaneous improvement of several involved traits in wheat families. Peixoto *et al.* (2021) noted that the classical index proposed by Smith and Hazel (SHI) and the sum of ranks index by Mulamba and Mock (MMI) were advantageous to produce sizeable gains distributed among several desired traits of biofortified lettuce, similar to that observed in Guimarães *et al.* (2021) with rice and Ramos *et al.* (2022) with peanut. The selection base WI afforded the highest total gain, desired gains all assessed traits, balanced genetic gains and considerable direct gain on GY of sweet corn (Silva *et al*., 2020b). In carrot, the genotype-ideotype CI provided sizeable genetic gains with an economic weight equal to the coefficients of genetic variation (Carvalho, 2022).

Coincidence between selection methods and selected lines

Direct and indirect selection together with selection-based indices identified a total of 52 individuals among the 418 durum wheat breeding lines composing the base population evaluated in the present study. Table 5 shows the coincidence rates between the different selection criteria used as well as the number of common selected genotypes among these selected lines. Accordingly, it is possible to notice that the selection based on GY identified the same genotypes as SHI and WI (*i.e.* 8 individuals out of 10 lines selected by each trait/index) with a high coincidence percentage equal to 79.51% among these selection criteria. Fellahi *et al.* (2020) with bread wheat, also observed a high level of coincidence between GY-based selection and the selection indices WI and SHI. Similarly, there were higher coincidence index levels in the selection of wheat breeding lines of SI with MMI and CI indices (*i.e.* 8 individuals out of 10 lines selected by each index). A high coincidence percentage allows in principle, the breeder to use these indices to assist selection in favor of multiple traits as reported by Smiderle *et al.* (2019). The coincidence index of indirect selection on SN and WI-based selection was equal to 69.26% (*i.e.* 7 individuals out of 10 lines by each trait/index) considering the selection of 2.4% best performing progenies from the base population understudy. The coincidence between the breeding lines identified through direct selection on GY and multi-traits selection based on SI and MMI indices was also important (59.02%) for which 6 individuals were common out of 10 lines selected via these selection criteria. Similar number of lines with equal coincidence index value (59.02%) were also observed in the WI-based selection relative to SI, SHI and MMI; and CI-based selection compared to MMI and EI indices. FLA *vs* EI index, SN *vs* GY and SHI index, GY *vs* CI index, SI *vs* EI, and SHI *vs* CI index exhibited an intermediate coincidence rate value of 48.77% with 5 common individuals out of 10 lines selected among the traits/indices assessed.

Table 5. Coincidence index (above diagonal) and number of common selected genotypes (below diagonal) among the 52 durum wheat breeding lines identified based on direct, indirect and index-based selection.

Selection criteria	HD	FLA	PH	SN	TKW	GY	SI	SHI	MMI	EI	WI	CI
HD		-2.46	-2.46	7.79	-2.46	7.79	-2.46	7.79	7.79	-2.46	-2.46	-2.46
FLA	0		7.79	-2.46	7.79	7.79	7.79	18.03	7.79	48.77	-2.46	28.28
PH	0	1		-2.46	28.28	-2.46	28.28	-2.46	7.79	7.79	-2.46	28.28
SN	1	0	0		-2.46	48.77	28.28	48.77	38.52	7.79	69.26	28.28
TKW	0	1	3	0		-2.46	7.79	-2.46	7.79	7.79	-2.46	18.03
GY	1	1	0	5	0		59.02	79.51	59.02	28.28	79.51	48.77
SI	0	1	3	3	1	6		38.52	79.51	48.77	59.02	79.51
SHI	1	2	0	5	0	8	4		38.52	38.52	59.02	48.77
MMI	1	1	1	4	1	6	8	4		38.52	59.02	59.02
EI	0	5	1	1	1	3	5	4	4		28.28	59.02
WI	0	0	0	7	0	8	6	6	6	3		38.52
CI	0	3	3	3	2	5	8	5	6	6	4	

HD, heading date; FLA, flag leaf area; PH, plant height; SN, spikes number; TKW, thousand kernel weight; GY, grain yield; SI, Subandi index; SHI, Smith and Hazel index; MMI, Mulamba and Mock Index; EI, Elston index; WI, Williams index; CI, Cruz index.

In general, the coincidences between the wheat lines selected indirectly via HD, FLA, PH, SN and TKW were not high, their coincidence rates with GY were also very low, except for GY with SN. This result could lead to the inferreance that the same individuals may not be identified by two or more selection criterion and that indirect selection through these recorded traits was less efficient. Conversely, the strategies of direct selection for GY and indices-based selection were more efficient, which was demonstrated by higher coincidence index values in comparison to single-trait indirect selection, and individuals with similar performances were identified. According to Pedrozo *et al*. (2009), the higher the coincidence percentage between two indices, the higher the agreement of the results of selection between them. When working with selection indices of different economic weight in wheat families grown in two sowing dates, Cargnin *et al.* (2007) observed a high coincidence between the indices SHI and WI, reaching a 100% coincidence percentage in the same environment but independent of the economic weight adopted. These results were in line with those reported by Costa *et al.* (2008) in soybean. It was demonstrated earlier that each trait/index identified the 10 top individuals considering the selection of 2.4% of top progenies. The number of common individuals among the 52 lines selected through direct, indirect and index-based selection varied between 0 and 8. Figure 2 shows the wheat breeding lines and their ranking obtained based on the number of selections using the three selection strategies. Accordingly, 30 lines were identified by only one selection criterion out of the 12 traits/indices used in this study, 8 lines *i.e.* L407, L173, L196, L199, L223, L241, L288 and L337 were maintained by two selection criteria, while 1 line (L410) only was selected by 3 traits/indices. Similarly, 4 lines which are L208, L15, L304 and L333 were selected by 4 criteria and the same number of lines *i.e.* L408, L21, L343 and L406 were identified by 5 selection traits/indices. Moreover, 1 line named L413 was selected by 6 traits/indices, whereas 3 lines *i.e.* L130, L24 and L34 were recognized by 7 selection criteria. Finally, the breeding line L252 was identified as being among the 10 best lines retained by 8 out of the 12 selection traits/indices evaluated in this study. Considering the selection of 10% of best progenies, breeding lines L252, L34, L24, L130 and L413 can be considered as the most commonly selected individuals among the 52 durum wheat lines retained from the base population via the three selection criteria employed in the current investigation.

Yield performance, in ascending order, of the 52 wheat breeding lines retained by the different selection criteria is shown in Figure 3. Grain yield varied between 113.30 g m^{-2} in L334 and 1176.70 g m^{-2} in L34 with an average estimate of 592.7 g m^{-2}. The mean yield of the base population composed of 418 lines was 383.09 g m^{-2}, whereas the average yield of the controls was relatively higher at 420.00 g m^{-2}. The 5 most frequently selected lines according to the number of coincidences from the different selection methods had, in average, a seed yield of 914.02 g m^{-2}. According to the presented results it was observed that the mean yield of controls exceeded the average yield of the base population understudy, but their performance was largely below the average yield of the plant material previously retained by the mono- and multi-trait selection. Of these lines, 27 entries recorded above average yields whereas the rest of lines yielded lesser. The high yielding lines appeared to be desirable entries as they exhibited better yield performances when compared to other wheat genotypes including control checks. Of these entries, 3 lines including L34, L24 and L15 were the best performers, showing significantly higher yields relative to the mean yield of the 5 most selected lines according to number of coincidences from direct, indirect and index-based selection. These breeding lines may give opportunities for wheat breeders to exploit their potential for breeding purposes.

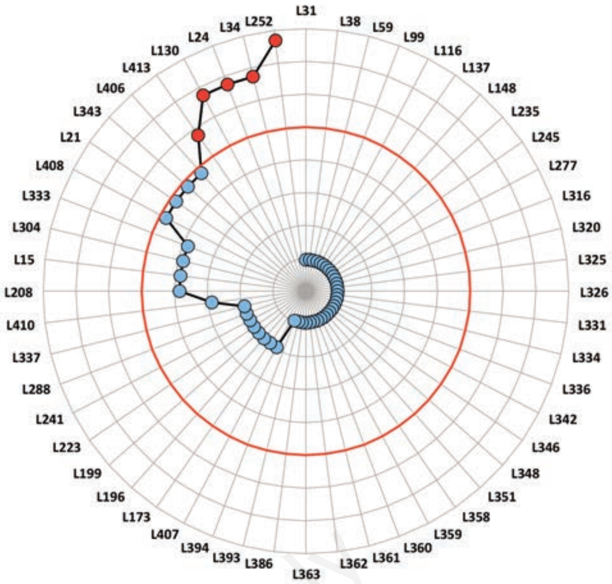

Figure 2. Breeding lines ranking in ascending order obtained through coincidence index from direct, indirect and index-based selection. The selected genotypes are shown in red dots. The red circle represents the cutpoint considering the selection of 10% of best progenies.

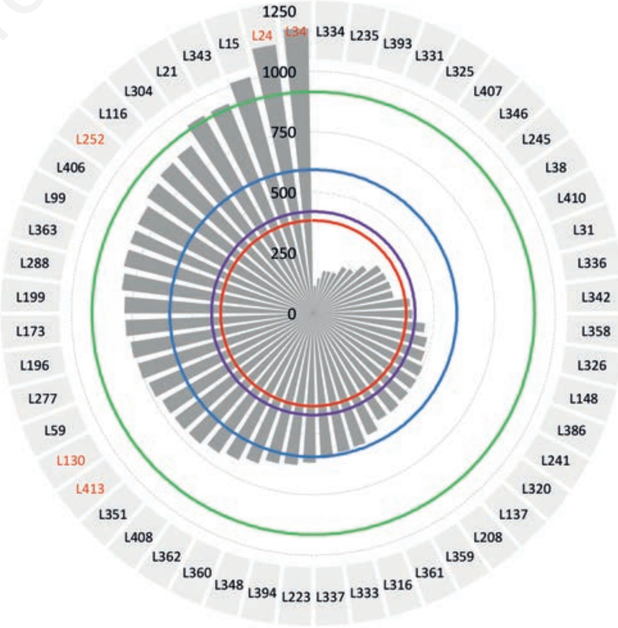

Figure 3. Grain yield (g m^{-2}), in ascending order, for the 52 lines selected from direct, indirect and index-based selection. The red circle represents the overall average yield of the base population. The blue circle represents the average yield of the 52 lines identified according to the three selection methods considering the selection of 2.4% of best progenies. The green circle represents the average yield of the 5 most selected lines according to number of coincidences from direct, indirect and index-based selection considering the selection of 10% of best progenies. The purple circle represents the average yield of the check varieties.

Conclusions

The gains achieved by direct selection were higher than the indirect response in most recorded traits. Nevertheless, some indirect predicted gains surpassed the direct gains that were observed. Our results showed that the total gains obtained by the indices surpassed the direct gains, except for SHI index. On the contrary, SHI exhibited a similar selection gain in GY compared to gain from direct selection, whereas the gains observed in GY through the other indices were slightly lower to gain obtained from GY-based selection. In general, the coincidences between the lines selected via the recorded traits were low; those observed between GY and indices and among indices were much higher, providing evidence for the advantage of the use of selection indices in improving selection efficiency in this breeding program. Based on the comparisons between the selected lines, there was a certain similarity between GY versus SH and WI indices, reaching 79.51%. Considering all selection methods (*i.e.* direct selection, indirect selection and indices-based selection) and coincidence percentage among selection criteria, individuals L34 and L24 along with L15 appear to be the most promising breeding lines. The selected lines showed significant differences in grain yield, with higher performance compared to the other plant material including the check varieties. It is worth noting that, while index selection can be a useful tool in this durum wheat breeding program, it is not the only selection method used and should be used in conjunction with other methods to achieve the desired results.

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