Expected genetic gains ƒrom mono trait and index-based selection in advanced bread wheat (*Triticum aestivum* L.) populations

Ganancia genética esperada en la selección basada en rasgos únicos e índices en una población avanzada de trigo pan (*Triticum aestivum* L.)

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ABSTRACT

Keywords:
Drought
Genetic gain
Index
Simultaneous selection
Yield

This study aimed at evaluating the expected gains from selection obtained based upon direct, indirect, and index-based selection in a set of 599 bread wheat lines. The experiment was carried out at the experimental field of INRAA institute, Setif research unit (Algeria), in a Federer augmented block design including three controls. A wide range of genetic variability was observed among lines for the eleven traits assessed. The results indicated that index-based selection and selection based on grain yield expressed higher expected genetic gain than direct and indirect mono-trait-based selection. The best 15 selected lines exhibited higher grain yield than the control varieties, and they were clustered in three groups that contrasted mainly for the flag-leaf area, thousand-kernel weight, biomass, and harvest index. The index-based selection appears as a useful tool for the rapid selection of early filial generations, enriching selected breeding materials with desirable alleles and reducing the number of years required to combine these traits in elite varieties.

RESUMEN

Palabras clave:
Sequía
Ganancia genética
Índice
Selección simultánea
Rendimiento

Este estudio investigó los beneficios esperados de la selección obtenida en base al índice directo, indirecto y basado en la selección en un conjunto de 599 líneas de trigo panadero. El experimento se llevó a cabo en el campo experimental del instituto INRAA, unidad de investigación de Setif (Argelia), en un diseño de bloques aumentados Federer que incluye tres controles. Se observó un gran rango de variabilidad genética entre las líneas para los once rasgos evaluados. Los resultados indicaron que la selección basada en índices y la selección basada en el rendimiento de grano expresaron una mayor ganancia genética esperada que la selección directa e indirecta basada en rasgos individuales. Las 15 primeras líneas seleccionadas exhibieron un mayor rendimiento de grano que los controles y se agruparon en tres grupos que divergieron de manera eficiente para el área de la hoja bandera, el peso de mil granos, la biomasa, el rendimiento de grano y el índice de cosecha. La selección basada en índices aparece como una herramienta útil para la selección rápida de las primeras generaciones filiales; enriqueciendo materiales de reproducción seleccionados con alelos deseables y reduciendo el número de años necesarios para combinar estos rasgos en variedades de élite.

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In cereal crops, artificial selection has rapidly evolved, covering a wide range of technical and scientific activities, with the objective of developing varieties, with high yield potential, good adaptation, and end-use quality. Selection can be mono or multi-traits, early or late. Mono-trait selection is based on simply inherited traits such as earliness, plant height, and disease resistance. It is usually carried out early on F_2, F_3 up to F_4 filial generations. For complex traits such as yield, accumulated biomass, and tillering capacity, it is practiced in advanced generations that are somehow fixed and have been subjected to single-trait selection in early generations for highly inherited traits. Selection effectiveness is largely dependent on the existing genetic variability among individuals making up the population under selection. Only the genetic part of the variability is transmissible to the offspring and is useful for selection. Selection efficiency is also dependent on the degree of genetic determination, which measures the proportion of genetic variability within the total phenotypic variability (Acquaah, 2007). Heritability represents the breeder's ability to recognize the difference between individuals for a given trait and, therefore, the possibilities to improve this trait. High heritability values allow breeders to have a grip on the selected trait (Fellahi *et al.*, 2017). In addition to phenotypic variability and heritability, selection efficiency also depends on the relationships among the traits. A better understanding of the existing relationships between traits is interesting and necessary to identify those which could serve as selection criteria and what are their effects on traits not targeted in the selection process. Yield is a complex quantitative trait whose variation is under polygenic control, predominantly of non-additive nature. It exhibits low heritability, instability and presents significant genotype×environment interaction (Purshase *et al.*, 2000; Annicchiarico *et al.*, 2005; Montesinos-López *et al.*, 2018, Laala *et al.*, 2018). Look for alternative methods and selection criteria to improve this trait efficiently is necessary (Bouzerzour, 1998). Indirect selection is an analytical method based on the use of morpho-physiological traits and yield components that are predictive of yield potential and good abiotic stress tolerance (Fleury *et al.*, 2010; Reynolds and Langridge, 2016). Kumar and Bahl (1992) noted that indirect selection might be more efficient when the secondary trait is highly correlated with the primary trait (usually grain yield) and is easily measurable.

This method involves several steps ensuring enough knowledge of the physiological mechanisms of drought tolerance followed by the genetic study of these traits before moving to their use as selection criteria in the breeding scheme. Index-based selection is currently used to make the selection more efficient (Carvalho *et al.*, 1999). The index is, by itself, an additional trait, established through an optimal combination of several measured characteristics, for which simultaneous selection is sought, to improve overall population phenotypic values (Cruz *et al.*, 2006). Several indices were developed, and are currently employed in various cultivated crops such as wheat (Ghaed-Rahimi *et al.*, 2017; Fellahi *et al.*, 2018), cotton (Ribeiro *et al.*, 2018), popcorn (Lima *et al.*, 2018), snap bean (Gomes *et al.*, 2018), soybean (Bizari *et al.*, 2017), potato (Silva G *et al.*, 2018a), sugarcane (de Azeredo *et al.*, 2017), and strawberry (Vieira *et al.*, 2017). The use of index-based selection in genetic improvement of field crops helps breeders for selecting genotypes that combine high yield potential and other desirable characteristics. This research aims at investigating the variation in expected genetic gains generated in response to mono-traits and index-based selection and to compare the efficiency of these selection strategies in advanced bread wheat (*Triticum aestivum* L.) populations.

MATERIALS AND METHODS
Plant materials and experimental design
The experiment counted with 602 genotypes, including 599 F_4-breeding lines and three standard varieties. Breeding lines were developed through pedigree selection method, from 20 bi-parental crosses made between nine bread wheat genotypes. Controls were Rmada (Vee's/Bow's// Alondra's/Pavon's), Hidhab (HD1220/3*Kal/Nac), and El-Wifak (K134/4/Tob/ Bman/Bb/3/Cal/5/Bucc), which are registered as varieties. Plant material was grown, during the 2014-2015 cropping season, in the experimental field of the Algerian National Institute of Agronomic Research (INRAA), Research Unit of Setif (INRAA-UR Setif, 36°15'N; 5°87'E; 1,081 masl). The experiment was arranged in a Federer augmented block design (Federer, 1955). Each of the three blocks contained 200 breeding lines and three controls. The experimental plot is a single 1-m long row, spaced 0.2 m apart, having 0.2 m^2 area. Land preparation was carried out according to the recommended practices for the area. Before sowing, 100 kg ha^{-1} of 46%

superphosphate fertilizer was applied. Granstar [Tribenuron methyl] herbicide was used to control weeds, and, when necessary, weeds were removed manually to keep the crop clean. At the tillering stage, plots were fertilized with 75 kg ha^{-1} of 35% urea. As April rainfall was almost nil (6.8 mm), and to avoid crop failure, the experiment was irrigated thrice during the May –June period, adding 60.0 mm irrigation water to the 343.6 mm rainfall received during the crop cycle (September-June).

Measurements

The following traits were assessed: Flag leaf chlorophyll content (CHL, Spad) was measured at the heading stage with SPAD-502 chlorophyll meter (Minolta Camera Co., Osaka, Japan). Canopy temperature (CT, °C) was determined at the same growth stage in each plot, between 11:00 h and 14:00 h, using a Sixth Sense LT300 infrared thermometer, following the procedure described by Pask *et al.* (2012). Flag leaf area (FLA, cm^2) was determined according to the procedure established by Spagnoletti-Zeuli and Qualset (1990) as **FLA(cm^2)=L(cm)xl(cm) x0.607**, where L and l refer to the flag leaf length and width, respectively; 0.607 is the regression coefficient relating leaf area determined by the gravimetric method to leaf area determined by the L×l product. Heading date (HD, d) was recorded as the number of calendar days from January first to the date when 50% of the spikes were half-way out from the flag leaf sheath. Plant height (PH, cm) was measured at maturity from ground level to terminal spikelet tip, awns excluded. Above-ground biomass (BIO, g m^{-2}) was estimated from a hand-harvested area of one row, 0.5 m long×0.2 m inter-row spacing. This sample also served, after mechanical threshing, to determine grain yield (GY, g m^{-2}) and the number of spikes (SN, # of spikes per m^2). Thousand kernel weight (TKW, g) was derived from the count and weight of a seed sample of 250 grains. The number of grains per spike (NGS, #) was derived from estimated values of grain yield, number of spikes and thousand kernel weight as **NGS=NGP/SN** where: NGP is the number of grains per plant, calculated by the equation: **NGP=1000 (GY/TKW)**. Harvest index (HI, %) was obtained by the formula: **HI(%)=100(GY/BIO).**

Statistical analysis

Data collected were subjected to an analysis of variance (ANOVA) following the procedure outlined by Cruz (2006). The linear model for the analysis of the augmented block is: $\mathbf{Y_{ij}=\mu+c_i+g_{ij}+\beta_j+\epsilon_{ij}}$ where: Y_{ij} is the treat mean value for the ith treatment, which can be broken down into c_i which is the effect of the ith control and g_{ij} which is the effect of the ith genotype in the jth block; β_j is the effect of the jth block and ϵ_{ij} is the residual associated with the ith treatment in the jth block. Fisher's least significant difference test at 5% probability level (LSD$_{5\%}$) was calculated according to Steel and Torrie (1960). The phenotypic (σ^2_p), genotypic (σ^2_g), and environmental (σ^2_e) variances were calculated for each trait based on the expected mean squares derived from the ANOVA table. These variances served to calculate genetic and environmental parameters, including the variation index, which is the ratio **Cv$_g$/Cv$_e$**, where Cv$_g$ is the genetic coefficient of variation, and Cv$_e$ is the residual coefficient of variation. Broad-sense heritability was calculated according to Cruz (2006)**: $H^2_{bs}=100(\sigma^2_g/\sigma^2_p)$** where: σ^2_g and σ^2_p as defined above.

Selection strategies and expected genetic gains

Three selection approaches were employed to estimate direct and indirect expected genetic gains among the F$_4$ lines displayed through mono-trait and indices-based selection. Direct selection expected gain was calculated according to Cruz (2006): $\mathbf{\Delta G_i=H_i^2 x S_i=H_i^2 x}$ $\mathbf{(\overline{X}_{si}-\overline{X}_{0i})}$ where ΔG_i refers to the expected gain, H_i^2 is the broad-sense heritability; S_i is the selection differential, $\overline{X}_{si}$ is the mean value of the selected lines and $\overline{X}_{0i}$ is the mean estimate of the base population for the ith trait. Direct selection gain, was expressed as the percentage of the population mean, as follow: $\mathbf{\Delta G_i\% = (\Delta G_i x100)/\overline{X}_{0i}}$. Selection was done in the sense of increased values for each one of the measured traits, except for canopy temperature and days to heading for which decreasing mean value was targeted. Indirect selection gain was estimated as outlined by Cruz (2006): $\mathbf{GS_{j(i)}=H_j^2 x(\overline{X}_i-\overline{X}_{0j})=H_i^2 xDS_{j(i)}}$, where: $GS_{j(i)}$ refers to the jth trait gain, when the selection was based on the ith trait; $\overline{X}_{j(i)}$ is the mean value of the jth trait for the selected lines based on the ith trait; $\overline{X}_{0j}$ is the mean value of the jth trait; $\overline{X}_j^2$ is the broad-sense heritability of the jth trait and is to the selection differential of the jth trait, in which the selected lines showed the best performance for the ith trait. Indirect selection gain is converted as the percentage of the population mean as follow: $\mathbf{GS_{j(i)}\%=(GS_{j(i)} x100)/\overline{X}_{0i}}$. Expected gain was also calculated using Smith and Hazel (1943), Williams (1962), Pesek and Baker (1971),

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Subandi *et al.* (1973), Mulamba, and Mock (1978) and Cruz (2006) indexes. A value of one was adopted as the economic weight for all selection strategies applied. Among the 599 evaluated lines, the top15 breeding lines, for each selection approach, were identified. The coincidence coefficient was obtained through the ratio of double coincident lines between two selection approaches and the total of selected lines, in percentage. A high coincidence coefficient, between two selection approaches, indicated concordance of their results (Gomes *et al.*, 2018). Statistical data analysis was done using Genes software (Cruz, 2013).

RESULTS AND DISCUSSION
Genetic variability and heritability
Even though the overall mean somewhat hid variability present among breeding lines, results of the analysis of variance revealed a significant genotype effect for plant height, above-ground biomass, grain yield, and harvest index at a 5% probability level. The residual coefficient of variation values (Cv_e) was below 17%, indicating a relatively good experimental precision (Table 1). Comparisons of range magnitude with critical value for yield components, and related agronomic traits, provide evidence of the presence of appreciable genetic variability among the breeding lines, suggesting that selection within these populations could lead to the identification of potentially useful breeding lines. Chlorophyll content varied from 33.5 to 58.3 Spad, canopy temperature ranged from 20.4 to 29.9 °C, heading date from 125.0 to 139 days, and flag leaf area from 7.3 to 42.7 cm. Plant height ranged from 45.0 to 121.0 cm, the number of spikes from 110.0 to 920.0 spikes per m², while thousand-kernel weight varied from 30.0 to 61.0 g and the number of grains per spike from 10.8 to 63.6 grains (Table 1). Above-ground biomass ranged from 320.0 to 3,440.0 g m⁻², grain yield from 102.0 to 1,434.0 g m⁻² and harvest index from 14 and 61.3%.

Table 1. Analysis of variance results, overall mean, range, least significant difference ($LSD_{5\%}$), broad-sense heritability (H^2_{bs}), coefficients of genetic (Cv_g), and experimental (Cv_e) variation and the ratio of genetic to the residual coefficient of variation (Cv_g/Cv_e) for the measured traits.

| Traits | Source of variation | | Cv_e (%) | Overall mean | Range | | $LSD_{5\%}$ | H^2_{bs} (%) | Cv_g (%) | Cv_g/Cv_e |
	Treatment (601)	Error (4)			min	max				
CHL	14.1	11.2	7.7	43.5	33.5	58.3	5.4	23.7	4.3	0.6
CT	3.8	3.7	7.6	25.1	20.4	29.9	3.1	24.0	4.3	0.6
HD	3.9	1.6	1.0	127.6	125	139	2.0	79.5	2.0	2.0
FIA	30.3	10.2	16.5	19.4	7.3	42.7	5.1	77.4	30.6	1.9
PH	95.0 *	15.4	5.1	76.9	45.0	121.0	6.3	86.5	12.9	2.5
SN	17,391.4	7,466.7	16.9	510.5	110	920.0	138.6	56.8	19.5	1.1
TKW	20.1	3.8	4.2	46.3	30.0	61.0	3.1	91.8	14.1	3.4
NGS	27.8	12.7	12.6	28.2	10.8	63.6	5.7	80.3	25.5	2.0
BIO	236,652.1 *	22,377.8	9.7	1,536.4	320	3,440.0	239.9	91.0	31.0	3.2
GY	51,580.9 **	2,941.4	8.1	667.5	102	1,434.0	87.0	94.8	34.9	4.3
HI	31.1 *	4.7	5.0	43.4	14	61.3	3.5	85.9	12.3	2.5

CHL: Chlorophyll content (Spad), CT: Canopy temperature (°C), HD: Heading date (d), FLA: Flag leaf area (cm²), PH: Plant height (cm), SN: Number of spikes, TKW: Thousand kernel weight (g), NGS: Number of grains per spike, BIO: Above ground biomass (g m⁻²), GY: Grain yield (g m⁻²), HI: Harvest index (%). ∗ and ∗∗: significant effect at 5% and 1% probability, respectively.

Broad-sense heritability estimates varied from 23.7 to 94.8% (Table 2). High H^2_{bs} values were recorded for grain yield (94.8%), thousand kernel weight (91.9%), biomass (91.0%), plant height (86.50%), harvest index (85.9%), number of grains per spike (80.3%), heading date (79.5%), flag leaf area (77.4%), and number of spikes (56.8%). This behavior suggests that the traits mentioned above are highly heritable, being less subjected to environmental variation. This is supported by the Cv_g/Cv_e, ratio values which are greater than one, suggesting a

good correlation between predicted and observed mean values for these traits, and favorable selection conditions for achieving high genetic gains. Chlorophyll content (23.7%) and canopy temperature (24.0%) showed low $H^2_{b\,s}$ estimates associated with Cv_g/Cv_e ratio values below unity, indicating that both traits were subjected to a significant environmental effect. Genetic coefficient of variation (Cv_g) values varied from 2.0% to 34.9%. High values were observed for flag leaf area (30.6%), spikes fertility (25.5%), biomass (31.0%), and grain yield (34.9%); indicating that these traits showed enough variability, which could be exploited through selection.

Expected genetic gains

Expected genetic gains, expressed as a percent of the base population mean, are presented in Table 2. Total expected genetic gains varied from -19.6% for selection based on the number of days to heading to 248.0% for selection based on the Subandi index. Expected genetic gains exhibited by direct selection for CHL, CT, and HD were lower than 5.0% for CHL (4.9%), CT (-4.2%), and HD (-3.1%, Table 2). CHL selection improved FLA indirectly by 10.7%, HI by 8.4%, and reduced BIO by -8.6%. CT selection caused significant improvement in FLA, SN, TKW, BIO, and GY, which increased by 12.2, 13.7, 11.1,

Table 2. Estimates of expected genetic gain as a percentage of base population mean, generated from direct and indirect selections based on individual measured traits and indices.

Selection criterion	Traits											Sum
	CHL	CT	HD	FLA	PH	SN	TKW	NGS	BIO	GY	HI	
CHL	4.90	1.20	-0.40	10.70	-0.20	-1.10	2.30	-1.30	-8.60	-1.30	8.40	14.50
CT	0.50	-4.20	0.30	12.20	4.30	13.70	11.10	-4.70	32.30	30.70	-2.00	94.20
HD	-0.10	-0.60	-3.10	-5.70	-2.90	3.20	9.00	-14.90	-5.70	-1.70	2.90	-19.60
FLA	-0.10	-0.60	0.60	70.10	11.00	3.30	1.90	8.30	17.30	17.20	-0.30	128.60
PH	-0.80	0.40	1.40	17.10	28.90	2.30	0.80	4.00	20.80	7.70	-9.20	73.40
SN	0.40	-1.00	-0.60	-0.70	8.40	37.20	4.20	-1.30	60.10	65.60	2.20	174.60
TKW	-0.20	-1.20	-1.70	-1.40	0.20	2.40	30.00	-28.70	1.30	-1.70	-2.50	-3.40
NGS	0.00	0.60	1.40	-11.80	-0.80	1.70	-7.40	49.00	37.20	48.40	6.30	124.60
BIO	0.40	-1.50	1.90	10.50	8.60	29.50	1.20	19.30	81.40	80.40	-1.20	230.60
GY	0.60	-1.50	0.80	4.90	4.30	28.80	-0.80	27.30	73.60	88.90	7.40	234.30
HI	1.70	-1.70	-0.40	8.80	-4.10	-1.90	4.10	11.90	-10.30	13.40	27.80	49.10
SHI	0.70	-1.70	0.70	5.90	4.40	26.90	1.20	26.30	72.00	87.30	7.30	230.90
MMI	2.00	-0.50	1.00	39.80	6.80	16.00	-0.10	25.50	43.10	61.90	11.90	207.70
WI	0.40	-1.30	1.40	6.20	8.60	30.60	-0.40	23.20	79.80	85.50	2.60	236.70
SI	1.30	-1.70	1.50	45.70	8.30	23.60	-0.70	26.10	59.50	75.30	9.10	248.00
PBI	1.50	1.70	1.40	27.40	22.60	-0.80	6.80	6.10	15.00	11.50	-2.70	90.50
CI	2.00	-1.50	1.40	47.50	8.20	18.50	-0.40	26.90	49.10	66.80	11.10	229.60

CHL: Chlorophyll content (Spad), CT: Canopy temperature (°C), HD: Heading date (d), FLA: Flag leaf area (cm^2), PH: Plant height (cm), SN: Number of spikes, TKW: Thousand kernel weight (g), NGS: Number of grains per spike, BIO: Above ground biomass (g m^{-2}), GY: Grain yield (g m^{-2}), HI: Harvest index (%). ISH: Smith & Hazel Index, MMI: Mulamba & Mock Index, WI: Williams Index, SI: Subandi Index, PBI: Pesek & Backer Index, CI: Cruz Index. Sum: Total expected genetic gain per selection criterion.

32.3, and 30.7%, respectively. HD selection induced significant changes in TKW, which gained 9.0%, NGS, FLA, and BIO, which decreased by 14.9, 5.7, and 5.7%, respectively. CH, CT, and HD expected genetic gains derived from indirect selection for FLA, PH, SN, NGS, BIO, GY, and HI were almost nil, being less than 2.0% and were lower than expected genetic gains caused by

direct selection (Table 2). CHL and CT have low broad-sense heritability, while HD showed relatively weak variability, as suggested by its low Cv_g value (Table 1). These results corroborated with those of Bárbaro *et al.* (2007), who found that larger gains are generated from characters exhibiting greater genetic variation while lower gains are expected from selection for traits

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showing lower genetic variability. Based on the mono-trait selection and among the three traits cited above, CT, with total gains of 94.2%, comes out as a surrogate trait to improve indirectly and simultaneously FLA, SN, TKW, BIO and GY without any significant changes for the other measured traits. Mono trait selection for any one of the following variables FLA, PH, SN, NGS, TKW, BIO, GY, and HI, generated higher direct expected genetic gains than indirect selection. In fact, the expected genetic gains from direct selection against the best expected genetic gains of indirect selection were 70.1% vs 47.5% via CI, for FLA; 28.9% vs 22.6% via PBI for PH; 37.2% vs 30.6% via WI for SN; 30.0% vs 11.1% via CT for TKW; 49.0% vs 27.3% via GY for NGS; 81.4% vs 79.8% via WI for BIO; 88.9% vs 87.3% via WI for GY; and 27.8% vs 11.1% via CI for HI (Table 2). These results corroborated those reported by Bizari *et al.* (2017), who found that gains from direct selection were superior to those for indirect gains, for all the characters. Cargnin *et al.* (2007) compared three selection indices in 240 F$_{2:4}$ wheat families derived from eight segregating wheat populations and reported that the highest gains were estimated by direct selection.

The advantage of multi-trait selection is analyzed based on total expected genetic gains. As total gains obtained from SHI, MMI, WI, SI, and CI selection indices were of the same magnitude as those generated through selection based on GY (Table 2).

Therefore, the comparison of mono vs. multi-trait selection efficiency was made relatively to selection based on GY. Analysis of indirect gains of mono-trait selection based on CHL, CT, HD, and FLA relative to GY based selection showed a strong negative effect of this selection strategy on GY, SN, NGS, and BIO (Figure 1). In fact, 49.0, 32.0, 49.0, and 39.0% reduction in GY expected genetic gain was observed when mono trait selection was based on CHL, CT, HD, and FLA, respectively. Observed declines in BIO expected genetic gains were 50.0, 25.0, 48.0 and 34.0% for the same selection criteria; NGS expected genetic gain was reduced also by 27.0, 30.0, 39.0 and 18.0%; while SN expected gain declined by 35.0, 18.0, 30.0, and 30.0%, respectively. These decreases indicated the inefficiency of these traits as a selection criterion, relatively to GY selection (Figure 1).
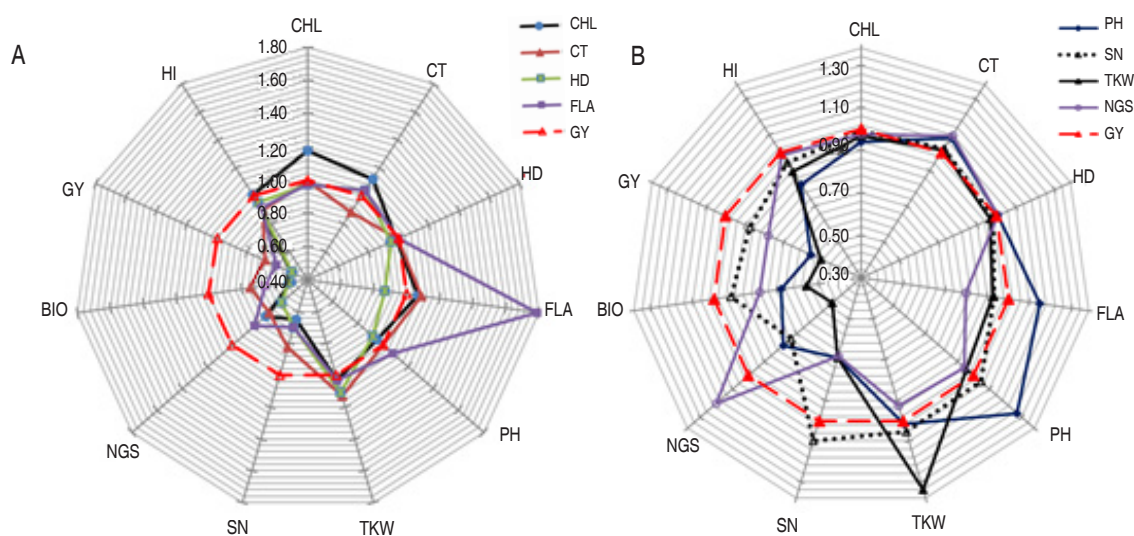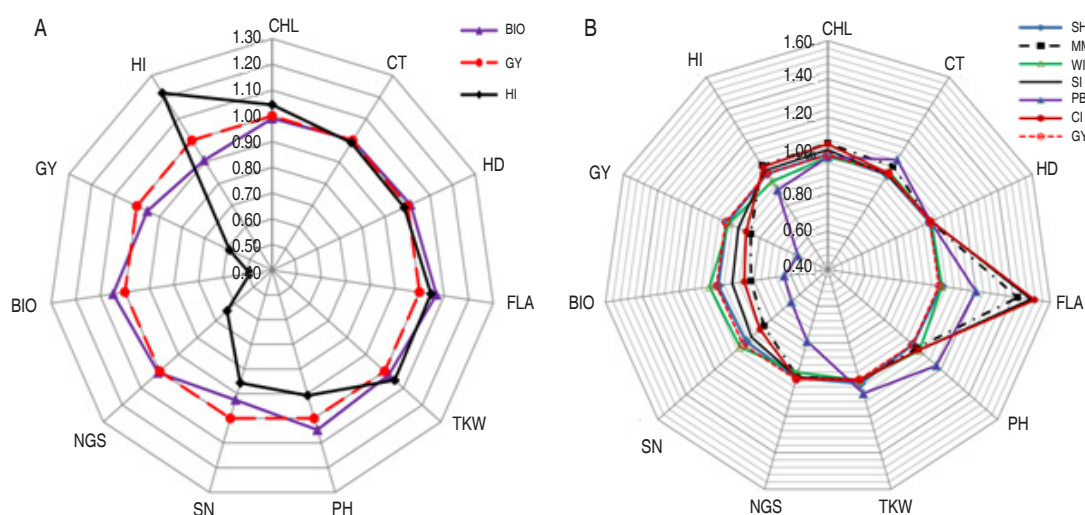

Figure 1. Direct and indirect gains of mono-trait selection based on A. CHL, CT, HD, and FLA; B. based on PH, SN, TKW, NGS, relatively to GY based selection.

Besides, their direct gain which was greater (27.0%, 10.0%, 34.0%, and 20.0% for PH, SN, TKW, and NGS, respectively) than indirect gain due to GY based selection, analysis of indirect gains exhibited by these traits indicated a sizeable negative effect on GY, BIO, and

HI (Figure 1). Indirect gain due to selection based on PH declined GY, BIO, and HI by 44.0, 32.0, and 18.0%, respectively, and caused 31.0 and 22.0% reduction in NGS and NS, respectively. The indirect gain for TKW, caused by PH based selection was almost zero.

Selection based on SN declined GY, BIO, and HI by 13.0, 8.0, and 6.0 %, respectively, and caused a 27.0% reduction in NGS. Indirect gains for PH and TKW, due to SN based selection, were below 5.0%. Selection based on TKW declined GY, BIO, and HI by 49.0, 44.0, and 11.0%, respectively, and caused a 52.0% reduction in NGS and 31.0% in SN (Figure 1). The indirect gain for PH due to TKW based selection, was low, having a 4.0% value. Selection based on NGS declined GY and BIO by 22.0% and caused a 32.0% reduction in SN and 7.0% in TKW. Indirect gains for HI, PH, and TKW from indirect selection based on NGS were 1.0, 6.0, and 7.0%, respectively (Figure 1). Because of negative indirect expected genetic gains, selection based on these traits appears to be inefficient when compared to indirect gains induced through GY based selection. Selection based on BIO resulted in almost similar direct and indirect gains

as GY based selection, but HI based selection caused a significant gain decrease in NGS (14.0%), SN (36.0%), BIO (0.51.0%), and GY (41.0%, Figure 2). Analysis of the effect of index-based selection suggested that SHI and WI expressed equivalent results as GY based selection. Compared to GY based selection, MMI, SI, PBI, and CI index-based selection caused significant indirect gain increases, 20.0% to 52.0%, in FLA. MMI induced 15.0, 16.0, and 15.0% gain a decrease in SN, BIO, and GY, respectively. SI caused gain decrease value of 9.0 and 7% for BIO and GY while application of PBI appeared as the least efficient selection strategy among index-based selection, as it induced negative indirect gains in NGS (210%), SN (34.0%), BIO (36.0%), GY (42.0%) and HI (10.0%). CI-based selection, compared to GY based selection, decreased indirect genetic gain in SN (12.0%), BIO (15.0%), and GY (12.0%, Figure 2).

Figure 2. Direct and indirect gains of mono-trait selection based on A. BIO and HI; B. based on indices, relatively to GY based selection.

Globally, it can be said that index-based selection appeared to be more efficient than individual trait-based selection, but equivalent to GY based selection. In this context, Costa *et al.* (2008) reported that SHI and PBI indices were advantageous over direct selection for soybean grain yield. Index-based selection generated gains that are evenly distributed among all traits. This is useful since, in stressed environments, genotypes, bearing a combination of physiological and morphological traits known to influence positively plant performance, are desirable. In this study, SHI and WI expressed equivalent results as GY based

selection, with positive gains for all traits included in the index. Using index-based selection Silva and Viana (2012), as well as Vasconcelos *et al.* (2010), found greater and well-distributed gains for the main characters of the passion fruit and alfalfa. In this study, the PBI index was the least efficient among the six evaluated indices. This index resulted in genetic variation loss in several important desired traits, exhibiting negative indirect gains. This contrasted with the results of Cargnin *et al.* (2007), who demonstrated that PBI exhibited the highest expected genetic gains. These authors reported that gains expected through indices selection for

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grain yield were larger than those obtained by the direct and indirect mono-trait selection, except for yield-based selection. Mahdy (1988) found that the selection-based index was more efficient for yield improvement compared to single-trait selection in a segregating population of wheat. Silva B *et al.* (2018) found that SHI provided high predicted gains for all the assessed traits in elephant grass. Ribeiro *et al.* (2018) found that MMI was the most suitable index for selecting high yielding genotypes with good fiber technological components in upland cotton. Bhering *et al.* (2012) reported that SI was promising for selection, providing balanced predicted gains for several traits of interest. According to Valério *et al.* (2009), as well as Fellahi *et al.* (2018), differences in the results of direct, indirect selection and index-based selection depend on crosses background, targeted selected traits and genotype×environment interaction.

The results of the present study indicated, so far, that SHI and WI index-based selection was advantageous to obtain sizeable gains distributed among several desired traits, without significant gain loss in the principal trait. This selection strategy is useful when a breeder focused on developing plant ideotype. The results indicated that high expected genetic gains were observed from single trait selection. This is useful to identify genotypes carrying interesting genes, like those related to stress tolerance (i.e., canopy temperature), which are often weakly associated with the principal trait (i.e., grain yield). Such genotypes could be used in biparental crosses to increase genetic variability and

to accumulate favorable genes in elite advanced breeding lines. The coefficients of coincidence values ranged from 0 to 86.7%, being low for direct selection based on CHL, HD, FLA, and PH, which resulted in few lines selected simultaneously, and high for yield, yield components, and index-based selections, excluding PBI index. None of the lines selected for GY were found among those selected for CHL, HD, FLA, PH, and PBI. The highest coincidence coefficients were recorded for WI (86.7%), SHI (80.0%), and BIO (66.7%), suggesting outcomes likeness of selection based on GY, SHI, WI and to lesser extend on BIO.

## Characterization of the potentially high yielding breeding lines

In order to identify the most promising genotypes for grain yield, all the selected lines through different methods were scored according to their appearance frequency. The scoring results indicated an absolute frequency ranging from one to eight. The top 15 breeding lines (Lines number 11, 55, 59, 60, 99, 150, 159, 160, 180, 182, 189, 285, 300, 521, and 558), with a score equal or greater than 4, were retained. These lines descended from nine out of twenty bi-parental populations studied by Fellahi *et al.* (2018). Compared to the average of the control varieties, the relative changes brought by the top 15 lines are shown in Figure 3. Significant improvements were achieved for FLA (26.22%), PH (14.62%), NGS (20.31%), BIO (38.99%), GY (44.04%), and CT (-14.53%). These differences were 1 to 4 times higher than $LSD_{5\%}$. These results indicated that the effective selection of superior
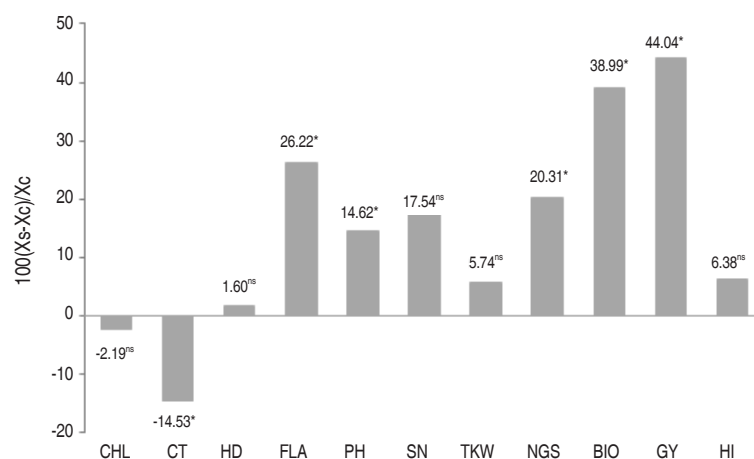

Figure 3. Relative deviation of the average of the 15 retained lines (X_S) from the average (X_C) of the three control varieties [$100\times(X_S-X_C)/X_C$] for the assessed traits.

individuals within this plant material contributes certainly to the improvement of yield and its related traits under conditions in the semi-arid regions of the Algerian high plateaus. Based on the Euclidian distance, Ward's method, these breeding lines formed three clusters (Figure 4). Lines 11, 59, 90, 150, 180, and 558 clustered apart (cluster 1). Lines 55, 99, and 182 formed cluster 2; while lines 160, 285, 521, 159, 189, and 300 grouped in cluster 3. The average values per cluster (absolute value and expressed as % of maximal value) indicated that FLA, BIO, GY, and TKW and HI discriminated efficiently between clusters (Figure 5, Table 3).
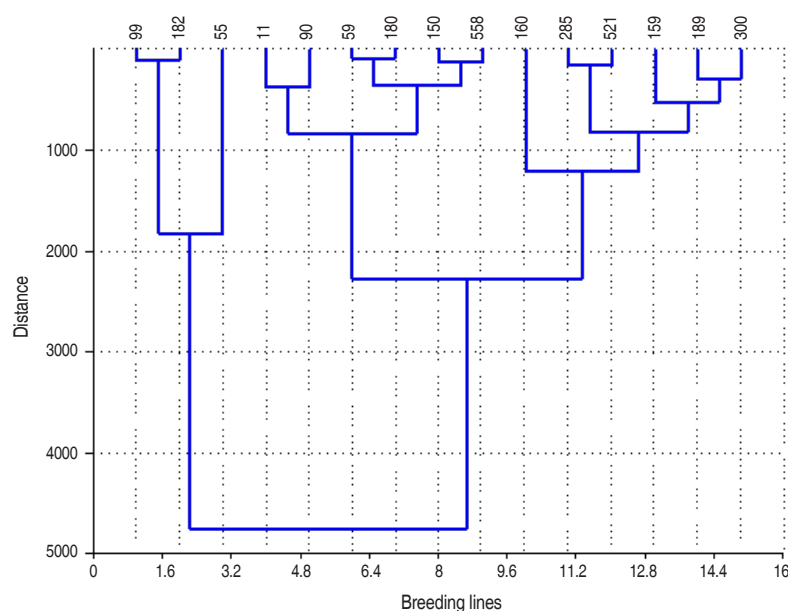
Figure 4. Genotypes clustering based on the eleven measured traits in the top 15 selected lines.
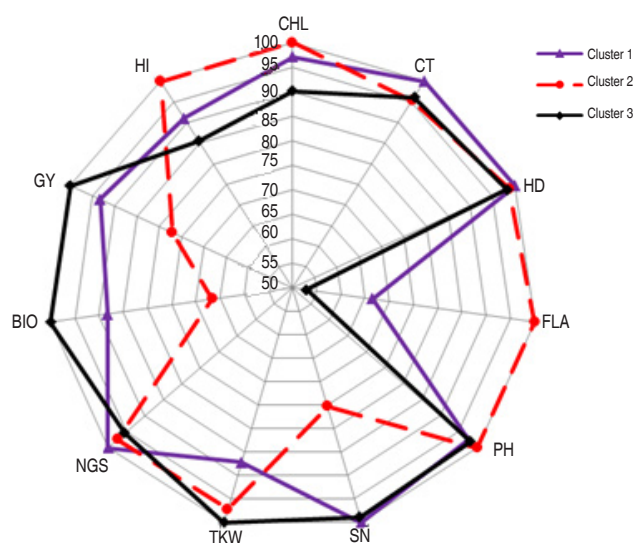
Figure 5. Behavior of the three clusters for the eleven measured traits in the top 15 selected lines.

Table 3. Cluster average values for the measured traits.

Clusters	CHL	CT	HD	FLA	PH	SN	TKW	NGS	BIO	GY	HI
1	46.4	23.6	130.9	26.4	81.8	774.4	43.9	37.6	2667.8	1242.4	47.2
2	47.8	22.5	129.2	39.7	83.9	583.3	48.9	36.6	2014.4	1024.9	51.8
3	43.1	22.7	128.5	21.0	82.3	765.6	50.3	35.9	3023.3	1330.8	44.3

CHL: Chlorophyll content (Spad), CT: Canopy temperature (°C), HD: Heading date (days), FLA: Flag leaf area (cm^2), PH: Plant height (cm), SN: Number of spikes, TKW: Thousand kernel weight (g), NGS: Number of grains per spike, BIO: Above ground biomass (g m^{-2}), GY: Grain yield (g m^{-2}), HI: Harvest index (%).

Genotypes belonging to cluster 3 had the best values in terms of yield performance, biomass and grain weight with a short vegetative cycle, low chlorophyll content, small leaves, and lower spike fertility compared to the genotypes of clusters 1 and 2. Lines of cluster 2, which had larger leaves with high chlorophyll content and decreased canopy temperature, were taller, less performing with increased harvest index. On the other hand, genotypes of cluster 1 were later, shorter with increased canopy temperature and fertile tillers. They were also characterized by low grain weight compared to the genotypes of clusters 2 and 3 (Figure 5).

CONCLUSION

Heritability estimates were sufficient for the prediction of next-generation means when the plant material selected is under the same environmental and management conditions. The results pointed out that those high expected genetic gains were observed from single trait selection, suggesting possibilities to identify genotypes carrying interesting genes, which are often weakly associated with grain yield. However, index-based selection was more efficient over the above approaches employed. Indeed, Smith and Hazel index and William index expressed equivalent results as grain yield based selection and provided the most satisfactory gains in all traits studied. The coefficients of coincidence values were low for direct selection based on chlorophyll, heading date, flag leaf area, and plant height, which resulted in few lines selected simultaneously, and high for yield, yield components, and index-based selections, excluding Pesek and Baker index. Cluster analysis grouped the 15 best-selected lines in three divergent groups that discriminated clearly for flag leaf area, thousand kernel weight, biomass, and harvest index.

REFERENCES

Acquaah G. 2007. Principles of plant genetics and breeding. Second Edition. Blackwell publishing, Oxford. 569 p.

Annicchiarico P, Bellah F and Chiari T. 2005. Defining sub regions and estimating benefits for a specific-adaptation strategy by breeding programs. Crop Science 45(5): 1741–1749. doi: 10.2135/cropsci2004.0524

Bárbaro IM, Da Cruz Centurion MAP, Di Mauro AO, Unêda-Trevisoli SH and Costa MM. 2007. Comparação de estratégias de seleção no melhoramento de populações F5 de soja. Revista Ceres 54(313): 250–261.

Bhering LL, Laviola BG, Sanchez CFB, Salgado CC, Rosado TB and Alves AA. 2012. Genetic gains in physic nut using selection indexes. Pesquisa Agropecuaria Brasileira 47(3): 402–408.

Bizari EH, Val BHP, Pereira EDM, Di Mauro AO and Unêda-Trevisoli SH. 2017. Selection indices for agronomic traits in segregating populations of soybean. Revista Ciência Agronômica 48(1): 110–117. doi: 10.5935/1806-6690.20170012

Bouzerzour H. 1998. Sélection pour le rendement, la précocité, la biomasse et l'indice de récolte chez l'orge en zones semi-aride (Doctoral dissertation). Université Constantine, Algeria.

Cargnin A, de Souza MA, Machado CG and Pimentel AJB. 2007. Genetic gain prediction for wheat with different selection criteria. Crop Breeding and Applied Biotechnology 7(4):334–339. doi: 10.12702/1984-7033.v07n04a01

Carvalho SPD, Cruz CD and de Carvalho CGPD. 1999. Estimating gain by use of a classic selection index under multicollinearity in wheat (*Triticum aestivum*). Genetics and Molecular Biology 22(1): 109–113. doi: 10.1590/s1415-47571999000100021

Costa MM, Di Mauro AO, Uneda-Trevisoli SH, Arriel NHC, Bárbaro IM, da Silveira GD and Muniz FRS. 2008. Analysis of direct and indirect selection and indices in soybean segregating population. Crop Breeding and Applied Biotechnology 8: 47–55. doi: 10.12702/1984-7033.v08n01a07

Cruz CD. 2006. Programa GENES:Biometria (Vol. 1). First Edition. Editora UFV, Viçosa. 382 p.

Cruz CD. 2013. Genes: a software package for analysis in experimental statistics and quantitative genetics. Acta Scientiarum 35(3): 271–276. doi: 10.4025/actasciagron.v35i3.21251

de Azeredo AAC, Bhering LL, Brasileiro BP, Cruz CD, Silveira LCI, Oliveira RA, Bespalhok Filho JC and Daros E. 2017. Comparison between different selection indices in energy cane breeding. Genetics and Molecular Research 16(1): gmr16019535. doi: 10.4238/gmr16019535

Federer WT. 1955. Experimental design: theory and application.

Macmillan Co., New York and London. 544 p.

Fellahi ZEA, Hannachi A, Bouzerzour H, Dreisigacker S, Yahyaoui A and Sehgal D. 2017. Genetic analysis of morpho-physiological traits and yield components in F$_2$ partial diallel crosses of bread wheat (*Triticum aestivum* L.). Revista Facultad Nacional de Agronomía Medellín 70(3): 8237–8250. doi: 10.15446/rfna.v70n3.61927

Fellahi ZEA, Hannachi A and Bouzerzour H. 2018. Analysis of Direct and Indirect Selection and Indices in Bread Wheat (*Triticum aestivum* L.) Segregating Progeny. International Journal of Agronomy 2018: 11. doi: 10.1155/2018/8312857

Fleury D, Jefferies S, Kuchel H and Langridge P. 2010. Genetic and genomic tools to improve drought tolerance in wheat. Journal of experimental botany 61(12): 3211–3222. doi: 10.1093/jxb/erq152

Ghaed-Rahimi L, Heidari B and Dadkhodaie A. 2017. Construction and Efficiency of Selection Indices in Wheat (*Triticum aestivum* L.) under Drought Stress and Well-Irrigated Conditions. Plant Breeding and Biotechnology 5(2): 78–87. doi: 10.9787/pbb.2017.5.2.078

Gomes ABS, Oliveira TRA, Cruz DP, Gravina GA, Daher RF, Araújo LC and Araújo KC. 2018. Genetic gain via REML/BLUP and selection indices in snap bean. Horticultura Brasileira 36(2): 195–198. doi: 10.1590/s0102-053620180208

Hazel LN. 1943. The genetic basis for constructing selection indexes. Genetics 28(6): 476–490.

Kumar J and Bahl PN. 1992. Direct and indirect selection for yield in chickpea. Euphytica 60: 197–199. doi: 10.1007/BF00039398

Laala Z, Benmahammed A, Oulmi A, Fellahi ZEA and Bouzerzour H. 2018. Response to F3 Selection for Grain Yield in Durum Wheat [*Triticum turgidum* (L.) *Thell. ssp. turgidum conv. durum* (Desf.) Mac Key] under South Mediterranean Conditions. Annual Research & Review in Biology 21(2): 1–11. doi: 10.9734/arrb/2017/37923

Langridge P and Reynolds MP. 2015. Genomic tools to assist breeding for drought tolerance. Current Opinion in Biotechnology 32: 130–135. doi: 10.1016/j.copbio.2014.11.027

Lima VJ, Junior SPF, Souza YP, Silva CS, Farias JEC, Souza RF, Chaves MM and Feitosa JV. 2018. Genetic gain capitalization in the first cycle of recurrent selection in popcorn at Ceará's Cariri. Revista Brasileira de Ciências Agrárias 13(3): e5556.V. doi: 10.5039/agraria.v13i3a5556

Mahdy EE. 1988. Single and Multiple Traits Selection in a Segregating Population of Wheat, *Triticum aestivum* L. Plant Breeding 101(3): 245–249. doi: 10.1111/j.1439-0523.1988.tb00293.x

Montesinos-López OA, Baenziger PS, Eskridge KM, Little RS, Martínez-Crúz E and Franco-Perez E. 2018. Analysis of genotype-by-environment interaction in winter wheat growth in organic production system. Emirates Journal of Food and Agriculture 30(3): 212–223. doi: 10.9755/ejfa.2018.v30.i3.1643

Mulamba NN and Mock JJ. 1978. Improvement of yield potential of the ETO blanco maize (*Zea mays* L.) population by breeding for plant traits [Mexico]. Egyptian Journal of Genetics and Cytology 7(1): 40–51.

Pask AJD, Pietragalla J, Mullan DM and Reynolds MP. 2012. Physiological Breeding II: A Field Guide to Wheat Phenotyping. CIMMYT, Mexico, D.F. 132 p.

Pesek J and Baker RJ. 1971. Comparison of predicted and observed responses to selection for yield in wheat. Canadian Journal of Plant Science 51(3): 187–192.doi: 10.4141/cjps71-038

Purchase JL, Hatting H and Van Deventer CS. 2000. Genotype×environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. South African Journal of Plant and Soil 17(3): 101–107. doi: 10.1080/02571862.2000.10634878

Reynolds M and Langridge P. 2016. Physiological breeding. Current Opinion in Plant Biology 31: 162–171. doi: 10.1016/j.pbi.2016.04.005

Ribeiro LP, Carvalho LPD, Farias FJC, Rodrigues JIDS, Teodoro PE and Bhering LL. 2018. Genetic gains in agronomic and technological traits of elite cotton genotypes. Bragantia 77(3): 466–475. doi: 10.1590/1678-4499.2017329

Silva MGM and Viana AP. 2012. Alternativas de seleção em população de maracujazeiro-azedo sob seleção recorrente intrapopulacional. Revista Brasileira de Fruticultura 34(2): 525–531. doi: 10.1590/s0100-29452012000200026

Silva GO, Pereira AS, Azevedo FQ, Carvalho ADF and Pinheiro JB. 2018. Selection of potato clones for tuber yield, vine maturity and frying quality. Horticultura Brasileira 36(2): 276–281. doi: 10.1590/s0102-053620180222

Silva VBD, Daher RF, Menezes BRDS, Gravina GDA, Araújo MDSBD, Carvalho Júnior ARD, Cruz DP, Almeida DO and Tardin FD. 2018. Selection among and within full-sib families of elephant grass for energy purposes. Crop Breeding and Applied Biotechnology 18: 89–96. doi: 10.1590/1984-70332018v18n1a12

Smith HFA. 1936. A discriminant function for plant selection. Annals of Eugenics 7(3): 240–250. doi: 10.1111/j.1469-1809.1936.tb02143.x

Spagnoletti-Zeuli PL and Qualset CO. 1990. Flag leaf variation and the analysis of diversity in durum wheat. Plant Breeding 105(3): 189–202. doi: 10.1111/j.1439-0523.1990.tb01196.x

Steel RGD and Torrie JH. 1960. Principles and procedures of statistics, McGraw-Hill Books, New York. 481 p.

Subandi W, Compton A and Empig LT. 1973. Comparison of the efficiencies of selection indices for three traits in two variety crosses of corn. Crop Science 13(2): 184–186. doi: 10.2135/cropsci1973.0011183X001300020011x

Valério PI, de Carvalho IF, Costa de Oliveira A, Benin G, Silveira GD, Manmann Schmidt DA, Stumpf MT and Woyann LG. 2009. Seleção efetiva para o caráter número de afilhos em populações segregantes de trigo. Bragantia 68(4): 885–899. doi: 10.1590/s0006-87052009000400008

Vasconcelos ES, Ferreira RP, Cruz CD, Moreira A, Rassini JB and Freitas AR. 2010. Estimativas de ganho genético por diferentes critérios de seleção em genótipos de alfafa. Revista Ceres 57:205–210.

Vieira SD, de Souza DC, Martins IA, Ribeiro GHMR, Resende LV, Ferraz AKL, Galvão AG and de Resende JTV. 2017. Selection of experimental strawberry (*Fragaria* x *ananassa*) hybrids based on selection indices. Genetics and Molecular Research 16(1): gmr16019052. doi: 10.4238/gmr16019052

Williams JS. 1962. The evaluation of a selection index. Biometrics 18(3): 375–393. doi: 10.2307/2527479

Rev. Fac. Nac. Agron. Medellín 73(2): 9131-9141. 2020

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