Research Article

Analysis of Direct and Indirect Selection and Indices in Bread Wheat (*Triticum aestivum* L.) Segregating Progeny

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Three selection methods including direct and indirect selection along with selection index based on the phenotypic values of eleven traits of agronomic interest were assessed for their application in F_4 bread wheat progenies. Significant genetic variation existed among parents and crosses for the traits measured. The following were the most efficient indices for simultaneous selection of superior lines for yield and its components: base index of Williams, followed by the sum of ranks index of Smith and Hazel. The selection-based index provided the highest grain yield gains as compared to the other selection criteria, except for flag leaf area, indicating that the direct and indirect monotrait selection were not appropriate in the situation analyzed in this work. PCA identified Ain Abid $\times$ Mahon-Demias, Ain Abid $\times$ Rmada, and Ain Abid $\times$ El-Wifak as the most promising populations. At 5% selection intensity, the top 30 lines selected were distinguished, in comparison with the standard check Hidhab, by significant improvements in yield and yield components.

1. Introduction

In Algeria, most of wheat producing areas are located in the High Plateaus which are characterized by cold winters, insufficient and erratic rainfall, frequent spring frosts, and late-season sirocco occurrence [1, 2]. In addition to these climatic stresses, there are some other technical constraints that essentially arise from the use of unproductive varieties and often bad agronomic practices. Selection for a better adaptation to environmental stresses is, therefore, more promising outcome in the field of wheat breeding. Breeders are continually seeking to improve the selection methods in order to develop superior wheat varieties with high grain yield, good end-use quality, and tolerance to biotic and abiotic stresses.

Direct selection based on grain yield is mainly practiced in wheat breeding programs without considering the adaptive traits that are crucial production regulators under variable environments [3–5]. In these environments, the presence of

genotype $\times$ environment interactions reduces the efficiency of using grain yield as the sole selection criterion and, thus, complicates the efforts of selection [6, 7]. In addition to the environmental effects, other factors such as polygenic nature, low heritability of grain yield, linkage, and nonadditive gene action may make the selection less efficient mainly in early segregating generations.

In order to overcome these difficulties, breeders are focusing on other traits that can be used in parallel or independently of yield in a multitraits approach. Indirect selection uses some yield components that are more heritable than yield itself and more stable in relation to genetic and environmental factors affecting them. When these components are measured without error and expressed in appropriate units, their product is yield. This has created new opportunities for plant breeders to use certain morphological, physiological, and biochemical traits during selection for grain yield. In the literature, several authors have reported the use of many of

these traits to improve grain yield in diverse environments [8–10].

Selection-based index is another approach, certainly complex, but can avoid the limits of the single-trait selection, particularly the undesirable between-trait relations that present an additional nuisance in breeders' work [11]. Selection-based index approach targets the simultaneous improvement of several traits at the same time, including the grain yield [12, 13]. The indices allow the use of a single value in the selection process, since the analysis is carried out by means of linear combinations of phenotypic data of different traits of agronomic interest with the genetic properties of a population [14]. The objective is to guarantee the improvement of the population genotypic values and consequently the efficiency of the selection process, maximizing the expected genetic gain. In this purpose, many selection indices have been used as an effective selection criterion in plant breeding programs on different crops [15]. However, the conditions determining the usefulness of an appropriate selection index may vary with individual plant breeder. The objective of this research paper was to evaluate the efficiency and applicability of different selection criteria based on the estimation of genetic gain in F_4 segregating populations of bread wheat evaluated under semiarid conditions.

2. Materials and Methods

2.1. Plant Material and Experimental Design. This experiment had 609 genotypes, comprising 20 F_4 -derived families and their 9 parents. The history of these families is that, after the initial crosses in 2010/11 [18], 30 F_2 lines were selected in each family by using pedigree method and were evaluated during the 2012/13 cropping season [19]. A total of 600 lines were planted and harvested in bulk during two consecutive growing seasons 2013/14 and 2014/15. The F_4 lines along with their parents were planted in Sétif Research Unit (36°15'N; 5°87'E; 1081 masl) of the Algerian National Institute of Agronomic Research (INRAA) in a modified randomized complete block design with three replications. The experimental unit consisted of a single row plot of 2 m length with rows spaced 0.2 m apart. The plots were fertilized with 100 kg ha⁻¹ of 46% superphosphate, before sowing, and 75 kg ha⁻¹ of 35% urea, at tillering stage. Weed control was performed chemically using 12 g ha⁻¹ of the Granstar [*tribenuron methyl*] herbicide. According to Chennafi et al. [20], the climate of the region is a semiarid type, continental with cold winter and hot and dry summer. Total annual rainfall is around 350 mm. The soil used was classified as a silty clay with high CaCO₃ content [20].

2.2. Measurements. The following traits were measured as per plot basis. Chlorophyll content (CHL, Spad) was determined at heading stage using the SPAD-502 chlorophyll meter (Minolta Camera Co., Osaka, Japan). Flag leaf area (FLA, cm²) was obtained using the formula described by Spagnolletti Zeuli and Qualset [21]: FLA (cm²) = L (cm) $\times$ l (cm), where L is the flag leaf length and l refers to the flag leaf width. Heading date (HD, days) was recorded as the number

TABLE 1: The skeleton of the analysis of variance.

Source of variation	df	MS	F-test
Block	$b - 1$	$M1$	$M1/M6$
Genotype	$g - 1$	$M2$	$M2/M6$
Parents	$P - 1$	$M3$	$M3/M6$
F_4	$n - 1$	$M4$	$M4/M6$
Parents vs. F_4	1	$M5$	$M5/M6$
Residual	$(g - 1)(b - 1)$	$M6$	--
Total	$bg - 1$	--	--

of calendar days from January first to the date when 50% of the spikes were half way out from flag leaf. Plant height (PH, cm) was measured at maturity from the soil surface to the top of the spike, awns excluded. Above ground biomass (BIO, g m⁻²) was estimated from a harvested area of 0.5 m long $\times$ 0.20 m interrow spacing, which served also to obtain the grain yield (GY, g m⁻²), number of spikes (SN, m⁻²), and spikes weight (SW, g m⁻²). 1000-kernel weight (TKW, g) was obtained from the count and weight of 250-kernel. The number of grains per spike (GN) was derived from estimated values of grain yield, number of spikes, and 1000-kernel weight. Harvest index (HI, %) was estimated by the ratio between grain yield and above ground biomass.

2.3. Data Analysis. Data collected were subjected to analysis of variance following the procedures described by McIntosh [22]; the skeleton of the analysis of variance is shown in Table 1. The statistical model used considered the complete randomized block design as $Y_{ij} = \mu + g_i + b_j + \epsilon_{ij}$, where Y_{ij} is the observation of the i th genotype, evaluated in the j th replicate; μ is the overall mean of the experiment; g_i is the effect of the i th genotype; b_j is the effect of the j th block; and ϵ_{ij} is the effect of the ij th plot.

In case F -test was significant, standard error and critical differences were calculated by using the least significant difference test at 0.05 probability level (LSD0.05) according to Steel and Torrie [23]: $LSD0.05 = t_{0.05} \sqrt{2\sigma_e^2/b}$, where $t_{0.05}$ is the tabulated value of the t -test at 0.05 probability level for $(g - 1)(b - 1)$ residual degrees of freedom; σ_e^2 is the residual variance; and b refers to the number of replications or blocks.

The genotypic variance (σ_g^2) and residual variance (σ_e^2) were calculated and served to determine the following genetic and nongenetic parameters for each trait. The coefficient of experimental variation (CV) was calculated by $CV (\%) = \sqrt{\sigma_e^2/\bar{X}}$, where σ_e^2 is the residual variance and $\bar{X}$ is the general mean of the trait. The coefficient of genetic variation (CV_g) was calculated by the following equation: $CV_g (\%) = \sqrt{\sigma_g^2/\bar{X}}$, where σ_g^2 is the genotypic variance and $\bar{X}$ is the general mean of the trait. The variation index was determined as the ratio of CV_g/CV_e . Broad-sense heritability of average progenies (h_{bs}^2) was estimated by the expression [24]: $h_{bs}^2 (\%) = 100 \times [\sigma_g^2/(\sigma_g^2 + \sigma_e^2)]$. Narrow-sense heritability of individuals within families (h_{ns}^2) was determined based on the parent-offspring

regression. To do so, two methods were used: the first was by the linear regression of F_4 on the parental F_3 individual values [16], while the second approach was performed with standardized data of offspring (F_4) versus standardized of the corresponding parent (F_3) according to Frey and Horner [17].

The selection gains were estimated among families based on three selection criteria: direct selection, indirect selection, and selection-based index considering the selection intensity of 5% of top families. The expected gains by direct selection for each trait evaluated were estimated by the expression [25]: $\Delta G_i = h^2_i \times S_i = h^2_i \times (\bar{X}_{si} - \bar{X}_{0i})$, where ΔG_i is the gain with the direct selection carried for the i th trait; h^2_i is the heritability of the i th trait; S_i refers to the differential selection of the i th trait; $\bar{X}_{si}$ is the mean of the i th trait for the selected individuals; and $\bar{X}_{0i}$ is the mean of the i th trait in the base population. The expected gain of direct selection, expressed as a percentage of the population mean, is given by $\Delta G_{ii}\% = (\Delta G_i \times 100) / \bar{X}_{0i}$.

Gains from indirect response to selection were calculated using the following expression [25]: $GS_{j(i)} = h^2_j \times (\bar{X}_{ij} - \bar{X}_{0j}) = h^2_j \times DS_{j(i)}$, where $GS_{j(i)}$ is the gain on the j th trait, with selection based on the i th trait; $\bar{X}_{sj}$ is the mean of the j th trait for the selected individuals based on the i th trait; $\bar{X}_{0j}$ is the mean of the j th trait; h^2_j is the heritability of the j th trait; and $DS_{j(i)}$ refers to the differential selection of the j th trait, in which the selected lines presented the best performance for the i th trait. The expected gain of indirect selection, expressed as a percentage of the population mean, is given by $GS_{j(i)}\% = (GS_{j(i)} \times 100) / \bar{X}_{0i}$.

For the selection-based index, the following methodologies were used for gains estimation: the classic index proposed by Smith [26] and Hazel [27], the base index of Williams [28], the free weights and parameters index of Elston [29], the index of desired gains of Pesek and Baker [30], the multiplicative index of Subandi et al. [31], the sum of ranks index of Mulamba and Mock [32], and the genotype-ideotype distance index proposed by Cruz [25]. Each index displays certain particularities in its calculations and, as such, application is generally laborious due to the need to assign adequate economic weights to each trait. Based on the different analytical procedures of selection, the best populations were identified and the gains from selection were calculated. All statistical analyses were carried out using Genes software [33] and a Microsoft Excel[®] spreadsheet.

3. Results and Discussion

3.1. Genetic Variability and Heritability. The analysis of variance revealed significant genotype effect for almost all the traits under study except for flag leaf area and grain yield, which were not significant at 0.05 probability level (Table 2). This provides evidence of the presence of sufficient genetic variability among parents and hybrids that can be exploited in wheat breeding program through selection. Partitioning the genotype effect indicated significant differences between all parents for HD, PH, SN, TKW, SW, GN, BIO, and HI, and significant interpopulation differences for HD, PH, and GN. The contrast “Parents versus F_4 ,” was highly significant

for HD, PH, and SN, while the F_4 populations exhibited significant differences for nearly all the observed quantitative phenotypic traits, except for CHL, FLA, GN, and HI, which were not significant at the 5% probability level. The results of this study corroborate those of Abd El-Shafi [34], who reported significant and highly significant differences among genotypes (families + parents) and families for all studied traits across three segregating generations F_2 , F_3 , and F_4 . This author, also, reported that greater response to selection can be expected from selection in cross having greater phenotypic and genotypic variances.

The coefficient of variation (CV) presented values between 0.7 and 26.8% for heading date and grain yield, respectively (Table 2). The CV above 20% is considered high, indicating high dispersion of the experimental data, which may have been caused by the genetic and phenotypic differences between the studied materials. High CV estimate obtained for grain yield can be explained by the fact that it is quantitative trait, governed by several genes and highly influenced by the environment.

The variances values, coefficient of variation, and genetic parameters estimates for wheat traits studied are presented in Table 3. Broad-sense heritability is the proportion of total phenotypic variation due to all genetic effects. The knowledge of the genotypic determination coefficient (h^2_{bs}) allows establishing an estimate of the genetic gain to be obtained and defines the best strategy to be used in the plant breeding program [35]. In this study, the estimated broad-sense heritability varied from 0.00 to 91.80%. The highest values were found for heading date (91.80%) followed by plant height (80.82%), 1000-kernel weight (72.90%), biomass (65.33%), and number of grains per spike (61.64%), indicating that these traits are highly heritable among the genotypes evaluated. These results can be confirmed with the values obtained by the CV_g/CV_e ratio that were close to or greater than 1 for these traits, suggesting satisfactory conditions for selection [36]. Moderate estimates of h^2_{bs} occurred for the number of chlorophyll contents (40.31%), number of spikes (52.00%), spikes weight (54.85%), and harvest index (40.67%). On the other hand, the lowest values of h^2_{bs} were found for the flag leaf area (0.00%) and grain yield (19.39%). These traits exhibited also low CV_g/CV_e ratio values, indicating the dominant effect of the environment on crop.

Generally, literature indicates widely varying narrow-sense heritability estimates. Mesele et al. [37] reported high heritability values for days to heading, days to maturity, and 1000-kernel weight; moderate estimates for grain filling period, spike length, number of spikelets per plant, grains per spike, and harvest index; and low values for number of tillers per plant, biomass yield and grain yield. Evaluating seven F_2 populations derived through cross combinations of five parental varieties/lines of bread wheat, Saleem et al. [38] found low to high broad-sense heritability values ranging from 4.75% to 92.6% depending on the trait and the cross. The findings of Yaqoob [39] showed that heritability estimates were low for number of tillers per plant (20%), grains per spike (26.81%), days to maturity (30.13%), spike length (36.66%), and 1000-kernel weight (38.68%), moderate for plant height (45.79%), and high for heading date (84.73%)

TABLE 2: Analysis of variance of different bread wheat traits studied.

SV	Bloc	Genotypes	Parents	F ₄	Parents versus F ₄	Error	CV (%)
df	2	28	8	19	1	56	
CHL	8.6	19.0**	9.5 ^{ns}	23.8**	3.6 ^{ns}	8.6	6.6
HD	1.5	9.0**	18.3**	2.5**	58.7**	0.7	0.7
FLA	89.4	11.1 ^{ns}	6.9 ^{ns}	6.6 ^{ns}	0.1 ^{ns}	14.9	20.4
PH	9.1	86.3**	103.0**	80.0**	72.6*	16.6	6.3
SN	1183.1	11187.5**	26092.4**	2657.8 ^{ns}	53994.5**	5371.1	15.9
TKW	33.5	28.2**	39.4**	12.7 ^{ns}	232.1**	7.7	7.4
SW	117034.6	44873.6**	74490.4**	18248.8 ^{ns}	313746.3**	20259.8	20.9
GN	36.6	44.7**	61.3**	37.0*	41.0 ^{ns}	17.1	16.8
BIO	81189.5	131077.4**	243142.1**	43601.7 ^{ns}	896559.2**	45440.8	18.5
GY	34149.2	15727.9 ^{ns}	26835.4 ^{ns}	11096.5 ^{ns}	56205.9*	12677.8	26.8
HI	122.2	62.3*	136.6**	36.1 ^{ns}	21.4 ^{ns}	37	16.8

CHL: chlorophyll content (Spad), HD: heading date (days), FLA: flag leaf area (cm²), PH: plant height (cm), SN: number of spikes, TKW: 1000-kernel weight (g), SW: spikes weight (g m⁻²), GN: number of grains per spike, BIO: above ground biomass (g m⁻²), GY: grain yield (g m⁻²), HI: harvest index (%), and ns, *, and **: nonsignificant and significant effect at 0.05 and 0.01 probability.

TABLE 3: Genetic and nongenetic parameters of different bread wheat traits studied.

Traits	σ_p^2	σ_e^2	σ_g^2	h_{bs}^2	h_{ns}^2 (SK)	h_{ns}^2 (FH)	CV _g (%)	CV _g /CV _e
Chl	3.36	2.00	1.35	40.31	28.55	30.13	2.64	0.47
HD	3.01	0.25	2.76	91.80	16.69	34.32	1.31	1.93
FLA	3.68	4.98	0.00	0.00	0.00	0.00	0.00	0.00
PH	28.78	5.52	23.26	80.82	27.27	27.27	7.43	1.19
SN	3729.17	1790.37	1938.79	52.00	0.00	0.00	9.59	0.60
TKW	9.41	2.55	6.86	72.90	31.64	25.99	6.98	0.95
SW	14957.91	6753.25	8204.67	54.85	8.66	10.70	13.19	0.64
GN	14.67	5.63	9.04	61.64	16.70	7.14	12.28	0.73
BIO	43692.45	15146.93	28545.52	65.33	3.37	5.93	14.48	0.79
GY	5242.64	4225.92	1016.71	19.39	10.13	12.31	7.58	0.28
HI	20.76	12.31	8.45	40.67	14.10	14.97	8.03	0.48

CHL: chlorophyll content (Spad), HD: heading date (days), FLA: flag leaf area (cm²), PH: plant height (cm), SN: number of spikes, TKW: 1000-kernel weight (g), SW: spikes weight (g m⁻²), GN: number of grains per spike, BIO: above ground biomass (g m⁻²), GY: Grain yield (g m⁻²), HI: harvest index (%), h_{bs}^2 : broad-sense heritability, h_{ns}^2 (SK): narrow-sense heritability according to Smith and Kinman [16], and h_{ns}^2 (FH): narrow-sense heritability according to Frey and Horner [17].

and grain yield (99.83%). His results also indicated that most of these traits exhibited low heritability under drought stress conditions, suggesting the presence of high genotype $\times$ environment interactions that affected the crop behavior.

Narrow-sense heritability is the proportion of the total phenotypic variation that is due to the additive effects of genes. This component of variation is important because it is the only variation that natural selection can act on. Hence, h_{ns}^2 determines the resemblance of offspring to their parents and the population's evolutionary response to selection. There can be considerable nonadditive genetic variance, but this does not contribute to the resemblance between parents and offspring, or the response to selection. Low to moderate narrow-sense heritability values were recorded in this study. Chlorophyll content, heading date, plant height, 1000-kernel weight, and number of grains per spike recorded the highest estimates. These traits were less influenced by the environmental factors and would respond positively to a selection

pressure in the current breeding program. The low heritability values can be explained by the change occurring in the segregating lines behavior from the precedent to the current generation. This change may be due to nonadditive gene action and/or high environmental factors effects.

Means of the variables measured showed that the best values varied depending on the cross and the trait, and the few populations had the best performances for several traits at the same time (Table 4). The best grain yielding population (557.5 g) was Ain Abid $\times$ El-Wifak which had also the highest average for the number of grains per spike (31.47 grains), spikes weight (857.3 g), above ground biomass (1350.3 g), and harvest index (41.3%). Ain Abid $\times$ Hidhab cross combination had the longest vegetative cycle with an average of 127.8 days and presented the highest mean for the flag leaf area (21.0 cm²). Acsad₁₀₆₉ $\times$ El-Wifak had the highest average for the chlorophyll content (54.0 Spad). Acsad₁₀₆₉ $\times$ Mahon-Demias was the tallest (75.23 cm), while Acsad₁₁₃₅ $\times$ Rmada

TABLE 4: Means of the measured traits for 20 F₄ bread wheat populations.

Population	CHL	HD	FLA	PH	SN	TKW	SW	GN	BIO	GY	HI
Acsad ₉₀₁ × Mahon-Demias	43.0	126.0	20.1	73.7	448.3	38.6	634.0	22.0	1135.0	379.2	33.4
Acsad ₉₀₁ × Rmada	44.5	125.2	19.9	60.8	442.4	34.6	633.6	28.1	1049.7	425.5	40.5
Acsad ₉₀₁ × Hidhab	42.5	125.9	19.8	65.7	426.7	33.4	616.7	23.0	1098.3	325.5	29.6
Acsad ₉₀₁ × El-Wifak	45.1	124.9	20.4	70.4	467.3	33.2	684.3	30.4	1149.0	460.4	40.1
Acsad ₈₉₉ × Mahon-Demias	43.7	125.7	16.9	70.8	476.0	36.4	626.0	20.5	1151.7	366.8	31.9
Acsad ₈₉₉ × Rmada	43.4	125.0	16.6	59.5	479.7	37.8	625.7	20.0	1032.7	368.8	35.7
Acsad ₈₉₉ × Hidhab	44.4	126.9	18.2	56.6	406.0	35.0	598.0	22.8	997.0	336.0	33.7
Acsad ₈₉₉ × El-Wifak	45.4	125.0	18.1	63.1	414.7	35.5	566.7	24.2	965.7	357.7	37.0
Acsad ₁₁₃₅ × Mahon-Demias	41.6	126.1	17.0	68.1	456.7	39.8	604.0	21.0	1073.7	383.4	35.7
Acsad ₁₁₃₅ × Rmada	42.2	125.2	16.8	61.5	503.7	36.9	685.3	24.0	1113.7	440.4	39.6
Acsad ₁₁₃₅ × Hidhab	41.5	127.0	17.5	68.8	477.0	39.5	744.7	23.2	1268.7	450.9	35.5
Acsad ₁₁₃₅ × El-Wifak	45.5	125.2	17.0	64.6	397.0	34.6	489.3	22.1	879.0	309.9	35.3
Acsad ₁₀₆₉ × Mahon-Demias	43.8	125.8	18.2	75.2	439.0	39.2	623.3	21.7	1193.7	371.3	31.1
Acsad ₁₀₆₉ × Rmada	44.2	125.0	17.3	61.7	414.7	34.8	581.0	24.5	961.7	360.8	37.5
Acsad ₁₀₆₉ × Hidhab	46.7	125.9	18.5	60.5	411.3	35.0	617.0	26.6	976.7	395.3	40.5
Acsad ₁₀₆₉ × El-Wifak	54.0	125.0	18.4	66.5	423.3	34.6	611.0	27.9	994.0	403.3	40.6
Ain Abid × Mahon-Demias	42.0	127.7	20.0	72.7	454.7	38.8	747.3	27.2	1286.7	481.8	37.5
Ain Abid × Rmada	40.3	126.3	20.5	65.8	435.7	36.5	699.3	28.2	1171.7	458.1	39.1
Ain Abid × Hidhab	43.2	127.8	21.0	60.2	405.0	36.8	693.3	30.4	1130.7	462.8	40.9
Ain Abid × El-Wifak	43.6	126.9	20.3	65.1	469.3	37.7	857.3	31.5	1350.3	557.5	41.3
Parents Range	39.1 52.2	125.0 132.0	8.7 39.1	53.0 82.0	270.0 800.0	30.0 49.0	320.0 1260.0	9.7 39.4	530.0 2330.0	185.0 809.0	14.1 63.6
F ₄ Range	33.4 53.8	124.0 136.0	7.6 36.4	42.0 100.0	80.0 850.0	19.0 51.0	80.0 1480.0	9.3 56.8	150.0 2420.0	43.0 921.0	12.6 70.0
LSD0.05	4.8	1.4	6.3	6.7	119.7	4.5	235.2	6.8	353.2	185.1	9.9

CHL: chlorophyll content (Spad), HD: heading date (days), FLA: flag leaf area (cm²), PH: plant height (cm), SN: number of spikes, TKW: 1000-kernel weight (g), SW: spikes weight (g m⁻²), GN: number of grains per spike, BIO: above ground biomass (g m⁻²), GY: grain yield (g m⁻²), and HI: harvest index (%).

exhibited the highest average for the number of spikes (503.7 spikes). For 1000-kernel weight, Acsad₁₁₃₅ × Mahon-Demias was the best population with an average of 39.8 g.

As the contrast “Parents versus F_4 ” was significant for PH, SN, TKW, SW, BIO, and GY, and, compared with the least significant difference (LSD0.05), significant differences existed between the parents and hybrids values for these measured traits. These differences were 1 to 3 times higher than the LSD0.05 and were in favor of some F_4 lines, indicating that they perform better than the parents and suggesting the possibilities of making significant changes through effective selection. These findings were in harmony with those obtained by Abd El-Shafi [34], Löffler and Busch [40], and Alexander et al. [41].

3.2. Genetic Gain from Direct and Indirect Selection and Selection-Based Index. The gains of direct and indirect selection are shown in Table 5. The results showed a big variation in the percentages of gains among the measured traits. The total sum of gains per selection varied from −36.11% for heading date to 34.75% for flag leaf area. Generally, the direct selection based on chlorophyll content, heading date, spikes weight, grain yield, and harvest index resulted in negative total gains. On the other hand, flag leaf area, plant height, number of spikes, 1000-kernel weight, number of grains per spike, and biomass recorded positive total gains.

The gains obtained by direct selection were higher than those of indirect selection. But, sometimes the indirect selection may be more efficient, especially if the secondary trait is highly correlated with yield and is easily measurable [42]. The number of grains per spike (15.86%) followed by above ground biomass (12.30%), plant height (12.10%), and number of spikes (10.84%) exhibited the greatest gains from direct selection. Inversely, heading date (−1.13%), spikes weight (−4.99%) and harvest index (−3.81%) showed negative gain values. Negative gain for heading date is desired in the case of this study as the Algerian wheat breeding program designed for semiarid regions; precocity is a crucial criterion adopted for selection. It is related to the ability of plants to shorten their cycle, so as to decrease their exposure to the late-season sirocco weathering.

The direct selection for chlorophyll content resulted in negative indirect gains for nearly all the other traits, except for the flag leaf area, number of grains per spike, and harvest index that showed positive responses. For heading date, the indirect selection gains were only positive for chlorophyll content, number of spikes, and harvest index. The correlative effects of the selection based on the flag leaf area were desirable for grain yield, although the indirect gain for the remaining traits was practically negative.

The direct selection for plant height resulted in positive indirect gains for heading date, number of spikes, 1000-kernel weight, and spikes weight. In addition, positive responses of the selection based on yield and yield components were observed for grain yield itself, heading date, 1000-kernel weight, and spikes weight. However, negative indirect gains were exhibited for other traits including chlorophyll content, flag leaf area, and number of grains per spike, indicating that indirect selection for one variable for gain in another

is unfeasible, because there will be a loss in the indirectly selected variable. In cases of negative gains, the model is considered inappropriate for selection in this plant material.

The highest correlated responses for grain yield were generated through indirect selection on the base of the flag leaf area (8.04%, i.e., 33.87 g m^{−2}), followed by the spike fertility (3.65%, i.e., 15.39 g m^{−2}), 1000-kernel weight (3.63%, i.e., 15.31 g m^{−2}), and above ground biomass (2.74, i.e., 11.54 g m^{−2}). These results indicated that the indirect selection was to be more effective in improving the primary trait than the indirect selection based on other traits and/or on the direct selection based on the grain yield itself.

Several authors have estimated the genetic gains of traits involved in yield determination. The results are often inconsistent and scarce. Our results were consistent with those of DePauw and Shebeski [43] and Inagaki et al. [44], who mentioned that direct selection on the basis of yield is ineffective in early generations. Benmahammed et al. [45] reported the same findings in barley crop. Their results showed that biomass-based direct selection appeared more discriminating than yield-based selection in their plant material. However, the results of this study do not corroborate findings reported by Lalić et al. [11], Mitchell et al. [46], Lungu et al. [47], and El-Morshidy et al. [48] and who observed the effectiveness of the direct selection on grain yield. The difference in the results may be attributed to differences of breeding material and to genotype × environments.

The gains of selection-based index are shown in Table 6. The total sum of gains from the selection-based index ranged from −9.37% to 42.86%. Five out of seven used indices showed positive total gains. The base index of Williams recorded the highest total gain (42.86%) followed by the classic index of Smith and Hazel, the index desired gains of Pesek and Baker (27.46%), and the genotype-ideotype distance index of Cruz (22.07%). The sum of ranks index of Mulamba and Mock had a very low gain of 3.74%. Subandi's and Elston's indices exhibited negative total gains.

The base index of Williams yielded positive responses for all measured traits, except for chlorophyll content, flag leaf area, and harvest index, which showed negative gains. This index also achieved the highest grain yield response (6.27%, i.e., 26.41 g m^{−2}) compared to the other indices employed in this study. The classic index of Smith and Hazel ranked second followed by the index of desired gains of Pesek and Baker, the genotype-ideotype distance index proposed by Cruz, and the sum of ranks index of Mulamba and Mock with selection responses of 36.93%, 27.46%, 22.07%, and 3.74%, respectively. The single-trait responses varied from one index to another with, a more or less, balanced distribution of positive and negative estimates among the traits. This shows that the monotrait selection was inadequate because it led to a higher final product when considering the grain yield and generated unfavorable responses in other traits. These results indicated that methods that combine favorable expected gains should be used in the evaluation of these progenies. The gains expected through indices for grain yield per se were larger than those obtained by direct and indirect monotrait selection, except for the flag leaf area (Tables 5 and 6). Mahdy [49] mentioned that selection-based index was predicted to be

TABLE 5: Selection gain estimates (GS%) obtained from direct (diagonal) and indirect (of diagonal) selection in different bread wheat traits.

Traits	X_o	X_s	Chl	HD	FLA	PH	SN	TKW	SW	GN	BIO	GY	HI	Total
CHL	43.7	46.4	6.15 (2.69)	-0.07 (-0.09)	1.60 (0.30)	-3.25 (-2.11)	-4.06 (-18.62)	-0.49 (-0.19)	-4.12 (-28.31)	2.14 (0.52)	-7.14 (-83.30)	-1.10 (-4.63)	5.77 (2.09)	-4.58
HD	126.5	125.0	1.43 (0.63)	-1.13 (-1.43)	-7.74 (-1.44)	-4.69 (-3.05)	1.76 (8.09)	-2.35 (-0.88)	-10.98 (-75.43)	-4.95 (-1.21)	-12.33 (-143.86)	-3.76 (-15.84)	8.63 (3.13)	-36.11
FLA	18.6	19.4	-1.51 (-0.66)	0.54 (0.68)	4.30 (0.80)	-0.65 (-0.42)	-4.72 (-21.69)	-0.71 (-0.27)	8.76 (60.15)	14.00 (3.43)	6.40 (74.63)	8.04 (33.87)	0.31 (0.11)	34.75
PH	64.9	72.8	-1.30 (-0.57)	0.36 (0.45)	-4.57 (-0.85)	12.10 (7.86)	9.33 (42.85)	7.14 (2.68)	5.63 (38.69)	-15.79 (-3.86)	12.38 (144.36)	-1.23 (-5.17)	-11.08 (-4.01)	12.98
SN	459.2	508.9	-0.88 (-0.38)	0.10 (0.13)	-8.17 (-1.52)	4.58 (2.97)	10.84 (49.76)	4.22 (1.58)	5.52 (37.90)	-12.15 (-2.98)	8.15 (95.01)	1.14 (4.80)	-4.37 (1.58)	8.97
TKW	37.5	41.3	-0.70 (-0.30)	0.96 (1.22)	-4.77 (-0.89)	3.87 (2.52)	11.19 (51.38)	9.93 (3.73)	10.84 (74.42)	-14.46 (-3.54)	14.04 (163.76)	3.63 (15.31)	-7.41 (-2.68)	27.14
SW	686.8	652.5	-1.26 (-0.55)	0.40 (0.50)	-3.36 (-0.62)	-0.17 (-0.11)	-7.18 (-32.95)	3.59 (1.35)	-4.99 (-34.25)	-0.13 (-0.03)	-4.07 (-47.44)	-5.05 (-21.27)	-1.50 (-0.54)	-23.71
GN	24.5	28.4	2.05 (0.89)	0.53 (0.67)	3.85 (0.72)	-5.84 (-3.79)	-10.50 (-48.20)	-0.99 (-0.37)	0.70 (4.80)	15.86 (3.88)	-4.14 (-48.30)	3.65 (15.39)	6.87 (2.49)	12.04
BIO	1166.4	1309.9	-1.22 (-0.53)	0.63 (0.80)	-3.58 (-0.67)	7.93 (5.15)	7.44 (34.18)	6.15 (2.31)	7.36 (50.55)	-8.94 (-2.19)	12.30 (143.50)	2.74 (11.54)	-7.44 (-2.69)	23.39
GY	421.4	422.2	-2.07 (-0.90)	0.69 (0.87)	-1.48 (-0.27)	-0.95 (-0.62)	-6.49 (-29.82)	3.40 (1.27)	-1.38 (-9.45)	4.37 (1.07)	-2.47 (-28.84)	0.20 (0.85)	2.10 (0.76)	-4.08
HI	36.2	34.8	-0.91 (-0.40)	0.45 (0.57)	0.30 (0.06)	-2.08 (-1.35)	-5.74 (-26.35)	2.72 (1.02)	0.60 (4.09)	-0.80 (-0.19)	0.14 (1.63)	-3.54 (-14.90)	-3.81 (-1.38)	-12.67

CHL: chlorophyll content (Spad), HD: heading date (days), FLA: flag leaf area (cm^2), PH: plant height (cm), SN: number of spikes, TKW: 1000-kernel weight (g), SW: spikes weight (g m^{-2}), GN: number of grains per spike, BIO: above ground biomass (g m^{-2}), GY: grain yield (g m^{-2}), HI: harvest index (%), X_o : trait mean value of the base population, and X_s : trait mean value of the selected populations; values between parentheses correspond to the genetic gain in terms of percent mean for yield and yield-related traits.

TABLE 6: Selection gain estimates (GS%) obtained from selection-based index in different bread wheat traits.

Indices	CHL	HD	FLA	PH	SN	TKW	SW	GN	BIO	GY	HI	Total
Smith & Hazel	1.95 (0.85)	0.97 (1.23)	-0.93 (-0.17)	8.74 (5.68)	4.28 (19.65)	9.53 (3.57)	10.20 (70.02)	-8.04 (-1.97)	13.60 (158.63)	3.94 (16.59)	-7.30 (-2.64)	36.93
Mulamba & Mock	-2.71 (-1.18)	0.03 (0.04)	-0.02 (-0.00)	4.05 (2.63)	-1.60 (-7.35)	2.08 (0.78)	-2.35 (-16.11)	1.50 (0.37)	-0.58 (-6.77)	1.56 (6.57)	1.78 (0.65)	3.74
Williams	-0.43 (-0.19)	1.56 (1.98)	-0.37 (-0.07)	5.71 (3.71)	0.85 (3.91)	8.44 (3.17)	12.43 (85.35)	0.00 (0.00)	14.78 (172.43)	6.27 (26.41)	-6.40 (-2.32)	42.86
Subandi	-1.37 (-0.60)	0.78 (0.99)	0.06 (0.01)	3.27 (2.12)	-9.31 (-42.75)	4.62 (1.73)	-3.18 (-21.85)	2.53 (0.62)	-1.10 (-12.84)	-3.08 (-12.99)	-2.58 (-0.93)	-9.37
Elston	-2.07 (-0.90)	0.69 (0.87)	-1.48 (-0.27)	-0.95 (-0.62)	-6.49 (-29.82)	3.40 (1.27)	-1.38 (-9.45)	4.37 (1.07)	-2.47 (-28.84)	0.20 (0.85)	2.10 (0.76)	-4.08
Pesek & Baker	2.23 (0.97)	0.78 (0.99)	4.38 (0.81)	-5.11 (-3.32)	0.33 (1.51)	5.88 (2.21)	8.72 (59.89)	-0.31 (-0.08)	7.91 (92.23)	5.42 (22.83)	-2.76 (-1.00)	27.46
Cruz	-1.46 (-0.64)	0.95 (1.20)	2.24 (0.42)	0.15 (0.10)	-7.99 (-36.69)	3.82 (1.43)	3.63 (24.95)	10.49 (2.57)	1.59 (18.50)	5.76 (24.27)	2.88 (1.04)	22.07

CHL: chlorophyll content (Spad), HD: heading date (days), FLA: flag leaf area (cm^2), PH: plant height (cm), SN: number of spikes, TKW: 1000-kernel weight (g), SW: spikes weight (g m^{-2}), GN: number of grains per spike, BIO: above ground biomass (g m^{-2}), GY: grain yield (g m^{-2}), and HI: harvest index (%); and values between parentheses correspond to the genetic gain in terms of percent mean for yield and yield-related traits.

TABLE 7: Differences of the F₄ selected lines relatively to the standard check Hidhab for the measured traits.

Traits	F ₄ selected lines mean	Hidhab	Difference	Difference in % of Hidhab	LSD0.05
Chl	42.26	43.30	-1.05	-2.41	4.80
HD	126.57	129.67	-3.10*	-2.39	1.40
FLA	19.15	19.40	-0.24	-1.26	6.31
PH	68.67	62.33	6.33	10.16	6.67
SN	615.67	463.33	152.33*	32.88	119.67
TKW	39.97	38.33	1.63	4.26	4.53
SW	1147.67	823.33	324.33*	39.39	235.17
GN	31.57	24.83	6.75*	27.18	6.75
BIO	1833.67	1376.67	457.00*	33.20	353.15
GY	758.13	441.33	316.80*	71.78	185.10
HI	41.78	32.23	9.55	29.63	9.94

CHL: chlorophyll content (Spad), HD: heading date (days), FLA: flag leaf area (cm²), PH: plant height (cm), SN: number of spikes, TKW: 1000-kernel weight (g), SW: spikes weight (g m⁻²), GN: number of grains per spike, BIO: above ground biomass (g m⁻²), GY: grain yield (g m⁻²), and HI: harvest index (%).

*Significant effect at 0.05 probability.

superior for yield improvement as compared to the monotrait selection method.

The first three axes of the Principal Component Analysis (PCA) explained more than 77.93% of the total variation available in the data subjected to analysis. Heading date (0.386*), flag leaf area (0.308*), spikes weight (0.923*), biomass (0.853*), and grain yield (0.866*) correlated significantly to PCA1. PCA2 was mainly related to the chlorophyll content (0.276*), 1000-kernel weight (0.440*), number of grains per spike (0.655*), and harvest index (0.547*) (Figure 1). The number of spikes (0.333*) was related to PCA3 (Figure 2). The PCA biplots showed that the populations Acsad₈₉₉ × Hidhab (P7), Acsad₈₉₉ × El-Wifak (P8), Acsad₁₁₃₅ × Hidhab (P11), Acsad₁₁₃₅ × El-Wifak (P12), Acsad₁₀₆₉ × Rmada (P14), Ain Abid × Mahon-Demias (P17), Ain Abid × Rmada (P18), and Ain Abid × El-Wifak (P20) were well represented on the plane formed by the first axis PCA1 (Figure 1).

Ain Abid × Mahon-Demias (P17), Ain Abid × Rmada (P18), and Ain Abid × El-Wifak (P20) had positive coordinates with this axis. They were characterized by a long vegetative cycle and high biomass, spikes weight, and grain yield values. The last two populations Ain Abid × Rmada (P18) and Ain Abid × El-Wifak (P20) were also distinguished by high values of chlorophyll content, flag leaf area, spikes fertility, and harvest index, relatively to PCA2 but were associated with low number of ears, relatively to PCA3 (Figures 1 and 2). On the other hand, Ain Abid × Mahon-Demias (P17) was distinguished, relatively to PCA2, by high estimates of the 1000-kernel weight and plant height, and associated with high number of spikes, relatively to PCA3 (Figures 1 and 2). From these results, it could be concluded that effective selection of superior individuals within this population certainly contributes to the improvement of yield and yield components, in a semi-late genetic background.

3.3. Selection of Superior Genotypes for Grain Yield. Genotypes were first ranked according to grain yield, then the 5% highest yielding lines were selected, and their mean yield estimated. The 30 lines thus selected are derived from 15 out of 20 F₄ populations studied. Half part of these lines was equitably

FIGURE 1: Principal Component Analysis (PCA) projections on axes 1 and 2, accounting for 63.56% of total variation, for 20 F₄ populations of bread wheat.

derived from Acsad₁₁₃₅ × Hidhab (P11), Ain Abid × Hidhab (P19), and Ain Abid × El-Wifak (P20) crosses. The population Ain Abid × Mahon-Demias (P17), previously identified among the promising populations, contributed with four lines. Acsad₁₀₆₉ × Rmada (P14) and Ain Abid × Rmada (P18) participated with two lines each. Seven other populations contributed by one line each. Relative to the standard check Hidhab, which is the most cultivated variety in Algeria, the top 30 lines selected were characterized by significant improvements in yield components, including the number of spikes (152.33 spikes m⁻²), spikes weight (324.33 g m⁻²), spikes fertility (6.75 grains spike⁻¹), above ground biomass (457.00 g m⁻²), and grain yield (316.80 g m⁻²) (Table 7). Besides, they were distinguished by significant reduction of the duration in the vegetative phase with 3.10 days (Table 7).

4. Conclusion

The results of this study indicated appreciable genetic variability among the evaluated populations. Selection based-index was more efficient to improve grain yield compared to direct

FIGURE 2: Principal Component Analysis (PCA) projections on axes 1 and 3, accounting for 53.65% of total variation, for 20 F_4 populations of bread wheat.

and indirect single-trait selection. The analytical procedures of the different selection methods showed possibilities of applications in advanced generations of breeding being superior when compared with direct and indirect selection. Williams's index was predicted to be more effective than the other selection indices for improving multiple traits at time. It brought the highest total genetic gain and the best yield gain per se associated with positive correlated responses for most of yield components. Compared to the check cultivar Hidhab, the 30 F_4 selected lines, at 5% selection intensity, were characterized by significant increase in grain yield and yield related traits.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this article.

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