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Genetic Gain through Selection Indices in Hulless Barley

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ABSTRACT

In order to study selection indices for improving hulless barley grain yield and its components, 75 F₂ plants resulting from the two crosses ICNBF93-369×ICNBF-582 and SB91925×ICB-102607 were evaluated regarding plant height, number of tillers per plant, spike length, number of grains per spike, grain weight per spike, thousand grain weight, days to maturity, harvest index and grain yield per plant. High estimates of heritability in broad sense were recorded for days to maturity, plant height and number of tillers in both populations. Path analysis showed that number of tillers in both crosses and harvest index in cross ICNBF93-369×ICNBF-582 had the most positive direct effects and plant height in both crosses had the highest negative direct effects on grain yield. Assessment of seven different selection indices based on Smith-Hazel and Brim-Williams indices showed that the most genetic advance in grain yield and traits such as number of tillers and plant height was accomplished through a completely new index in which economic values were calculated via multiplication of broad-sense heritability values and values of direct effects of path analysis. The results also indicated that taking advantage of Smith-Hazel and Brim-Williams indices led to almost similar genetic advance in the traits under study. Hence, using the Brim-Williams index is recommended due to simplicity of calculations and interpretation of results, so as to improve the grain yield and its components. © 2011 Friends Science Publishers

Key Words: Hulless barley; Selection index; Smith-Hazel index; Brim-Williams index; Heritability; Path analysis

INTRODUCTION

Hulless barley (*Hordeum vulgare* L.) has almost equal nutritional value to wheat and corn. Because of possessing higher amounts of protein and starch, less fiber and adaptation to short growth season, this crop can be an appropriate alternative for corn in the nourishment of poultry and other monogastric animals. Furthermore, considering its amounts of protein, lysine contents and beta glucan compared to barley, it is suitable for human nutrition as well (Bhatti, 1999; Griffey, 1999). On the other hand, many vitamins and minerals, which are lost in the process of barley's threshing are completely preserved in hulless barley. Nonetheless, the breeding programs in previous years have been mostly concentrated on barley and its yield has been lower compared to hulled barley, wheat and corn.

Yield in crops has a very complex control mechanism and direct selection is not much effective on it. Therefore, the most desirable approach to improve characteristics such as grain yield is simultaneous selection based on related traits (Bos & Caligari, 2007; Hayes, 2007; Brown & Caligari, 2008; Mahpara *et al.*, 2008). Selection can be carried out in several ways. In tandem selection method, each trait is individually selected in sequential generations. In other words, a trait is chosen to reach a desired level and then another trait is selected. The other technique is the

method of independent culling levels in which the selection is simultaneously and independently performed for all the traits. In this method, a specific level is considered for each trait and all the plants, which do not reach this level are removed regardless of other traits. The method, which is expected to result in the fastest advance in increasing the economic value of a population, called selection index, is to perform simultaneous selection on all traits or the most significant ones. In selection index, a suitable score or weight is assigned to each trait depending on its relative economic importance.

Taking advantage of selection indices was first proposed by Smith (1936) in order to improve the plants. Hazel (1943) extended the index procedure for the selection of individuals in animal populations. They made use of the idea by Fisher (1936), who had suggested the concept of discrimination function and said that since genetic values cannot be determined, but it is possible to approximate its values using a linear function of observable phenotypic values. This method was afterwards developed by Baker (1986) and widely used in different breeding programs. Williams (1962) labeled the Smith-Hazel index as an estimated index since phenotypic and genetic parameters are never known and thus the index has to be derived by use of sample estimates. Sampling errors associated with estimation from a small data set could affect the reliability

of the index (Lin, 1978). Brim *et al.* (1959) pointed out that inaccurate estimation of population parameters could bias estimates of theoretical gains. They suggested an alternative index such that each trait is weighted according to its relative economic value. Williams (1962) called this the base index. Selection indices have been used in numerous studies in order to determine the most valuable genotypes as well as the most suitable combination of traits with the intention of indirectly improving the yield in different plants (Siahpoosh *et al.*, 2001; Asif *et al.*, 2003; Singh & Balyan, 2003; Chandra *et al.*, 2003; Rabiei *et al.*, 2004; Sabouri *et al.*, 2008; Rezaei & Yousefi Azar, 2008; Imani *et al.*, 2009). This method has also been utilized for barley with different breeding goals. The relative efficiency of various single F_2 plant selection criteria was evaluated by Chandramony and Sharma (2008) in five F_2 populations of hulless barley. They showed that selection of individual plants in F_2 generation based on number of tillers followed by grain yield proved most effective.

Jaradat *et al.* (2004) employed selection indices to investigate the reaction of barley cultivars to salinity. They related that a multivariate-based selection criterion for high forage yield at tillering stage under salinity stress, based on simultaneous selection for low temporal variation in germination and high shoot dry weight identified highly salt tolerant accessions.

In another study, Omrani *et al.* (2008) compared selection indices for barley yield improvement under nitrogen stress and non-stress conditions, using 49 F_{13} recombinant inbred lines. Smith-Hazel and Pesek-Baker (Pesek & Baker, 1969) indices based on 4 traits (days to heading, harvest index, growth rate & nitrogen harvest index) and also direct and correlated response of these traits were calculated. The result of response to selection and correlated response indicated that the selection based on higher harvest index and nitrogen harvest index under both conditions screens high yielding lines.

The purpose of present study was to determine of genetic relationships among yield and agronomic traits in hulless barley populations and its application in selection of most appropriate indices so as to reach the highest genetic advance for grain yield and its components.

MATERIALS AND METHODS

Plant material under study included parents ICNBF93-369, ICNBF-582, SB91925 and ICB-1026 as well as F_1 and F_2 generations resulted from the two crosses ICNBF93-369 \times ICNBF-582 and SB91925 \times ICB-1026. All parents were obtained from ICARDA, Aleppo, Syria. F_1 and F_2 generations were produced during two cropping seasons and all the four generations were grown together during the same cropping season (2007-2008) in a randomized block design with three replications at the Moghan region. Row length was always two meters but the number of rows varied as follows: three rows for the non-segregating P_1 , P_2

and F_1 and 10 rows for the F_2 generations since the non-segregating generations represented the homogeneous population, while the segregating generations denoted the heterogeneous population. The sample size (i.e., number of plants analyzed) varied as follows: 10 plants for the P_1 , P_2 and F_1 generations and 75 plants for the F_2 generations. The traits assessed were plant height, number of tillers per plant, spike length, number of grains per spike, grain weight per spike, thousand grain weight, days to maturity, harvest index and grain yield per plant.

Phenotypic variance-covariance matrix of all properties was assessed for parents, F_1 and F_2 generations. To calculate the genetic variance-covariance matrix of F_2 generation, the environment variance-covariance matrix was first calculated via the following formula:

$$E = P_1 + P_2 + 2F_1/4$$

Where P_1 , P_2 and F_1 are phenotypic variance-covariance matrix of parents and F_1 plants, respectively. Afterwards, the genetic variance-covariance matrix of F_2 population was calculated from the formula:

$$G = P - E$$

Where P and G are phenotypic and genetic variance-covariance matrices of F_2 population. These matrices were then used in the evaluation of selection indices in F_2 populations. The genetic correlation coefficient was calculated for each pair of traits based upon the method proposed by Falconer (1989).

Broad-sense heritability values calculated using the following formula:

$$h_{bs}^2 = \{[VF_2 - (VP_1 + VP_2 + 2VF_1)/4]/VF_2\}$$

(Mather & Jinks, 1982).

$$h_{bs}^2 = \{[VF_2 - (VP_1 \times VP_2)^{1/2}]/VF_2\}$$

(Mahmud & Kramer, 1951).

$$h_{bs}^2 = \{[VF_2 - (VP_1 + VP_2 + VF_1)/3]/VF_2\}$$

(Allard, 1960).

$$h_{bs}^2 = \{[VF_2 - (VP_1 \times VP_2 \times VF_1)^{1/3}]/VF_2\}$$

(Warner, 1952).

$$h_{bs}^2 = \{[VF_2 - (VP_1 + VP_2)/2]/VF_2\}$$

(Allard, 1960).

Important characters associated with grain yield were determined by using the multiple stepwise regression analysis (Steel & Torrie, 1982). Path analysis based on genetic correlations was carried out in order to study the direct and indirect effect of traits entered into the step wise regression analysis. The direct and indirect causes of grain yield were analyzed as described by Dewy and Lu (1959).

With each selection index score (I) was calculated from the formula (Baker, 1986):

$$I = \sum b_i P_i$$

Where P_i is the phenotypic value of each trait and the weights (b_i) were calculated as follows. Using matrix notation:

$$b = P^{-1}Ga$$

Smith-Hazel index (Smith, 1936; Hazel, 1943);

$$b = a$$

Brim-Williams index (Brim *et al.*, 1959; Williams, 1962).

The phenotypic (P) and genotypic (G) variance-covariance matrices were estimated from analyses of variance and covariance for single traits and pairs of traits, respectively. Also (a) is relative economic values for each trait.

In the present study, three different criteria were utilized for assessment and comparison of the indices.

1- Expected genetic advance for each trait (ΔG):

$$\Delta G = i \cdot \sum \sum a_i b_i G_{ij} / (\sum \sum b_i b_j P_{ij})^{1/2}$$

2- Expected genetic advance for all studied traits (ΔH):

$$\Delta H = \sum a_i \Delta G$$

3- Correlation coefficient between genotypic worth and index (R_{IH}):

$$R_{IH} = (a'Ga)^{1/2} / (b'Ga)^{1/2}$$

RESULTS AND DISCUSSION

The mean values of under study traits for parents, F_1 plants and F_2 populations are given in Table I. As is observed, in cross ICNBF93-369 \times ICNBF-582 the parent ICNBF93-369 has relative superiority in all traits except plant height and number of grains per spike. However, the parent ICNBF-582 was precocious and more long-legged and also had higher number of grains per spike. In cross SB91925 \times ICB-1026, the parent SB91925 was more short-legged and serotinous and it had also more tillers, longer spike, heavier grains per spike, higher thousand grain weight, as well as better harvest index and grain yield per plant. On the other hand, the parent ICB-102607 was higher in height and had more grains per spike.

Heritability: Broad sense heritability was estimated through different formula (Table II). Calculating the mean heritability of traits for F_2 generation indicated that in cross ICNBF93-369 \times ICNBF-582, the properties with highest heritability values were days to maturity (0.96) and then number of tillers and plant height (both with 0.87), while grain yield per plant with value of 0.43 gained the lowest heritability value. Although in cross SB91925 \times ICB-1026 the heritability values were less for all traits except number of grains per spike, Grain weight per spike and grain yield in plant compared to cross ICNBF93-369 \times ICNBF-582 (Table II), the properties days to maturity, plant height and number of tillers obtained the highest heritability values with 0.94, 0.81 and 0.71, respectively. In this cross, spike length had

Table I: Mean comparison between sub-main plots (genotypes) for various traits of the cross ICNBF93-369 \times ICNBF-582 (cross I) and cross SB91925 \times ICB-102607 (cross II) of hulless barley

Traits	P ₁		P ₂		F ₁		F ₂	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
Plant height	77.32 \pm 1.6	79.52 \pm 2.21	86.82 \pm 1.4	88.41 \pm 1.95	83.2 \pm 1.5	85.2 \pm 2.1	85.4 \pm 4.25	88.31 \pm 4.72
Number of tillers	6.41 \pm 0.31	6.52 \pm 0.32	4.51 \pm 0.32	5.02 \pm 0.2	6.88 \pm 0.32	6.25 \pm 0.26	6.58 \pm 0.91	6.2 \pm 0.5
Spike length	8.8 \pm 0.22	9.5 \pm 0.23	8.5 \pm 0.28	8.13 \pm 0.23	7.98 \pm 0.26	8.7 \pm 0.23	9.00 \pm 0.37	11.2 \pm 0.3
Number of grains/spike	60.37 \pm 1.1	59.2 \pm 0.45	57.06 \pm 1.23	55.12 \pm 0.51	58.82 \pm 1.17	60.12 \pm 0.55	59.04 \pm 1.63	63.11 \pm 0.81
Grain weight / spike	2.81 \pm 0.1	2.51 \pm 0.14	2.22 \pm 0.1	1.78 \pm 0.15	2.29 \pm 0.11	2.41 \pm 0.17	2.79 \pm 0.15	2.9 \pm 0.22
Thousand grain weight	32.8 \pm 1.52	37 \pm 0.88	40.44 \pm 1.1	43.4 \pm 0.84	40.8 \pm 1.31	40.04 \pm 0.85	40.08 \pm 2.43	47.4 \pm 1.14
Days to maturity	203.2 \pm 1.5	203.1 \pm 1.87	196.2 \pm 1.3	194.4 \pm 1.61	198.3 \pm 1.45	195.4 \pm 1.82	196.2 \pm 7.53	197.2 \pm 7.1
Harvest index	38.3 \pm 0.67	41.4 \pm 0.55	37.7 \pm 0.66	39.8 \pm 0.45	38.7 \pm 0.65	40.7 \pm 0.51	41.3 \pm 0.92	44.6 \pm 0.69
Grain yield / plant	9.71 \pm 0.22	9.93 \pm 0.45	8.27 \pm 0.17	7.67 \pm 0.59	9.64 \pm 0.2	40.7 \pm 0.51	11.3 \pm 0.27	8.87 \pm 0.73

Table II: Estimates of the heritability by different methods for various traits of the cross ICNBF93-369 \times ICNBF-582 (Cross I) and cross SB91925 \times ICB-102607 (Cross II) of hulless barley

Traits	Broad sense heritability											
	Mather and Jinks (1982)		Mahmud and Kramer (1951)		Allard (1960)		Warner (1952)		Allard (1960)		Mean	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
Plant height	0.87	0.80	0.87	0.81	0.87	0.80	0.88	0.83	0.87	0.80	0.87	0.81
Number of tillers	0.88	0.72	0.88	0.74	0.88	0.72	0.85	0.65	0.88	0.71	0.87	0.71
Spike length	0.52	0.41	0.55	0.41	0.53	0.41	0.39	0.21	0.54	0.41	0.51	0.37
Number of grains/spike	0.49	0.59	0.49	0.65	0.49	0.61	0.50	0.56	0.49	0.65	0.49	0.61
Grain weight / spike	0.51	0.48	0.55	0.57	0.52	0.51	0.25	0.30	0.55	0.56	0.48	0.48
Thousand grain weight	0.70	0.44	0.72	0.43	0.70	0.43	0.73	0.42	0.70	0.43	0.71	0.43
Days to maturity	0.96	0.94	0.96	0.94	0.96	0.94	0.97	0.94	0.96	0.94	0.96	0.94
Harvest index	0.49	0.46	0.48	0.48	0.48	0.46	0.44	0.39	0.48	0.47	0.47	0.45
Grain yield / plant	0.46	0.50	0.49	0.50	0.46	0.49	0.27	0.43	0.47	0.48	0.43	0.48

the lowest heritability, with value 0.37. High heritability values for days to maturity, plant height and number of tillers shows that genetic variance justifies a great amount of phenotypic variation and the environment's contribution to existing variety has been low for these properties. It should be noticed that in experiments carried out in one year and environment, genotype \times environment interaction is added to genetic variance, which may lead to over-estimation of heritability for days to maturity, plant height and number of tillers. Nevertheless, almost similar results have been obtained in both crosses, which can confirm the validity of heritability values for these traits. Previously, Singh *et al.* (1999), Verma *et al.* (2007), Arabi *et al.* (2008) and Eshghi and Akhundova (2010) reported high heritability and additive gene effects for number of tillers and plant height in barley and hulless barley samples.

Path analysis: Correlation values can indicate the degree of genetic relationship between two or more properties. Three significant factors may influence the correlation of agronomical traits, namely linkage of genes controlling those properties, pleiotropic effects of genes for two or more traits and environmental effects (Steel & Torrie, 1982). It should not however be forgotten that correlation coefficient has only a mathematical interpretation and does not always imply cause and effect relationships. Therefore, in most cases, path analysis is employed in order to identify and understand the cause and effect relationships among different traits. For this purpose, stepwise regression analysis was initially performed (data not shown). In cross ICNBF93-369 \times ICNBF-582, harvest index, number of tillers, plant height, number of grains per spike and spike length could justify 78.3% of the changes in grain yield. In cross SB91925 \times ICB-1026, 83.7% of the observed variety for grain yield was justified by number of tillers, plant height, thousand grain weight, days to maturity and harvest index. Path analysis based on regression results in cross ICNBF93-36 \times ICNBF-582 (Table III) indicated that harvest index and number of tillers had the highest direct and positive effect on grain yield (0.348 & 0.331, respectively). In both of these traits, the most indirect effects on grain yield were through plant height, with values 0.148 and 0.188, respectively. Besides these traits with highest positive genetic correlation with grain yield, plant height showed the highest negative direct effect on grain yield (-0.281). The highest indirect effect of this trait was via harvest index and number of tillers and was in negative direction. Correlation of this trait with grain yield in plant was high and negative (Table III). Direct effects of number of grains per spike and spike length were less than other traits and were almost equal (0.197 & 0.166, respectively). The highest indirect effects of these traits on yield were in positive direction through harvest index (Table III). In total, these findings show that most of the increase in grain yield in cross ICNBF93-369 \times ICNBF-582 has been resulted from increase in harvest index, number of tillers and decrease in plant height. Nevertheless, since the heritability of harvest

Table III: Direct and indirect effects of the components of grain yield based on genetic correlation coefficients in cross ICNBF93-369 \times ICNBF-582

Traits	H.I	N.T	P.H	N.G.S	S.L	C.G.Y
H.I	0.348	0.068	0.148	0.089	0.089	0.742**
N.T	0.071	0.331	0.188	0.038	0.02	0.648**
P.H	-0.184	-0.221	-0.281	-0.03	0.018	-0.698**
N.G.S	0.158	0.063	0.042	0.197	0.094	0.554**
S.L	0.188	0.039	-0.031	0.111	0.166	0.473**

P.H: Plant height, N.T: Number of tillers per plant, S.L: Spike length, N.G.S: Number of grains per spike, H.I: Harvest index, C.G.Y: Correlation between traits and grain yield per plant

Table IV: Direct and indirect effects of the components of grain yield based on genetic correlation coefficients in cross SB91925 \times ICB-102607

Traits	N.T	P.H	T.G.W	D.M	H.I	C.G.Y
N.T	0.367	0.252	0.082	0.024	0.019	0.744**
P.H	-0.27	-0.345	-0.008	-0.031	-0.052	-0.704**
T.G.W	-0.143	-0.014	-0.212	0.027	0.012	-0.330**
D.M	0.048	0.059	-0.032	0.183	0.026	0.284**
H.I	0.055	0.138	-0.019	0.037	0.129	0.340**

P.H: Plant height, N.T: Number of tillers per plant, T.G.W: Thousand grain weight, D.M: Days to maturity, H.I: Harvest index, C.G.Y: Correlation between traits and grain yield per plant

index in this cross was almost equal to grain yield, it should not be expected that considerable genetic advance would occur in grain yield via selection of this property. In contrast, number of tillers and to some extent plant height had high direct effects on the yield and had high heritability, so they can be considered as appropriate indices for improving grain yield per plant, such that the maximum value of grain yield in population F_2 resulted from cross ICNBF93-369 \times ICNBF-582 is reachable through selection of plants with maximum number of tillers and minimum plant height. Path analysis in cross SB91925 \times ICB-1026 indicated that number of tillers had the highest direct effect on grain yield in plant (0.367). The highest indirect effect of this trait on grain yield was via plant height (Table IV). Indirect effect of this property through other traits was insignificant. Besides number of tillers, the highest genetic correlation ($r = -0.704$) as well as the highest direct effect (-0.345) on grain yield pertained to plant height. The highest indirect effect of this trait on grain yield belonged to number of tillers, in negative direction (Table IV). Direct effect of thousand grain weight on yield was negative (-0.212) and number of tillers had a considerable role in causing the indirect effects of this property. In this cross, direct effect of days to maturity and harvest index on grain yield positive; nonetheless in total, considering the values of direct effects and also less than 0.5 correlation values of thousand grain weight, days to maturity and harvest index, these traits cannot be recommended as valid indices for improving grain yield. This is while in this cross, similar to cross ICNBF93-369 \times ICNBF-582, plant height and number of tillers with highest effects on grain yield as well as high heritability can be the most suitable indices for grain yield indirect selection.

Table V: Relative economic values of the properties used in generation of selection indices

Traits	Economic values													
	1		2		3		4		5		6		7	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
Plant height	1	1	-0.281	-0.345	-0.281	-0.345	0.87	0.81	0.87	0.81	0.87	0.81	-0.244	-0.279
Number of tillers	1	1	0.331	0.367	0.331	0.367	0.87	0.71	0.87	0.71	0.87	0.71	0.288	0.260
Spike length	1	0	0.166	0	0.166	0	0.51	0.37	0.51	0	0.51	0	0.085	0
Number of grains/spike	1	0	0.197	0	0.197	0	0.49	0.61	0.49	0	0.49	0	0.096	0
Grain weight/spike	0	0	0	0	0	0	0.48	0.48	0	0	0	0	0	0
Thousand grain weight	0	1	0	-0.212	0	-0.212	0.71	0.43	0	0.43	0	0.43	0	-0.091
Days to maturity	0	1	0	0.183	0	0.183	0.96	0.94	0	0.94	0	0.94	0	0.172
Harvest index	1	1	0.348	0.129	0.348	0.129	0.47	0.45	0.47	0.45	0.47	0.45	0.163	0.058
Grain yield / plant	1	1	1	1	0	0	0.43	0.48	0.43	0.48	0	0	0.43	0.48

Table VI: Evaluation of ΔG , ΔH and R_{IH} criteria in Smith-Hazel indices. Selection intensity has been considered to be 10% ($k = 1.76$)

Traits	Expected genetic advance for each trait in each index (ΔG) [*]													
	1		2		3		4		5		6		7	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
Plant height	-2.22	-2.17	-3.43	-3.34	-4.92	-4.79	-5.6	-5.45	-6.9	-6.88	-3.77	-3.67	-7.89	-7.68
Number of tillers	6.27	2.94	9.68	4.54	13.86	6.51	15.79	7.42	17.85	8.63	10.63	4.99	22.45	10.45
Spike length	1.07	0.337	1.65	0.228	2.36	0.745	2.69	0.85	2.35	1.36	1.81	0.572	3.79	1.19
Number of grains/spike	0.69	0.217	1.06	0.374	1.52	0.479	1.73	0.546	1.52	0.878	1.17	0.367	2.45	0.77
Grain weight/spike	0.845	0.802	2.3	1.58	1.57	1.26	2.13	2.58	3.29	4.15	1.40	1.74	2.99	3.63
Thousand grain weight	-0.426	-0.341	-0.945	-0.83	-3.78	-3.19	-3.17	-1.36	-4.9	-1.22	-2.09	-0.916	-4.47	-1.92
Days to maturity	1.68	1.23	1.67	2.67	1.38	1.82	2.72	4.35	4.2	3.89	1.79	2.93	3.83	6.13
Harvest index	0.573	0.359	0.885	0.555	0.727	0.629	1.44	0.905	1.26	0.811	0.972	0.609	2.03	1.28
Grain yield / plant	0.59	2.13	0.908	3.29	0.853	3.12	1.48	5.38	1.89	6.61	0.958	3.37	2.09	7.58
ΔH	11.93	9.17	5.82	6.84	6.91	5.13	28.23	19.49	24.97	19.66	14.49	9.97	10.19	10.05
R_{IH}	0.66	0.53	0.73	0.81	0.78	0.77	0.89	0.91	0.88	0.87	0.77	0.87	0.94	0.96

Table VII: Evaluation of ΔG , ΔH and R_{IH} criteria in Brim-Williams indices. Selection intensity has been considered to be 10% ($k = 1.76$)

Traits	Expected genetic advance for each trait in each index (ΔG) [*]													
	1		2		3		4		5		6		7	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
Plant height	-2.02	-1.86	-2.85	-2.65	-3.59	-3.5	-4.45	-4.41	-6.19	-5.95	-3.1	-3.26	-7.43	-7.23
Number of tillers	5.77	2.53	8.0	3.61	10.12	4.75	12.55	6.01	17.51	7.73	8.74	4.44	21.12	9.83
Spike length	0.984	0.289	1.37	0.181	1.72	0.544	2.14	0.688	2.02	1.17	1.49	0.509	3.57	1.12
Number of grains/spike	0.635	0.186	0.881	0.311	1.11	0.35	1.4	0.442	1.26	0.755	0.962	0.327	2.23	0.724
Grain weight / spike	0.777	0.738	1.91	1.32	1.15	0.92	1.72	2.09	2.73	3.49	1.25	1.55	2.72	3.34
Thousand grain weight	-0.361	-0.314	-0.789	-0.693	-2.76	-2.33	-2.57	-1.1	-4.06	-1.03	-1.78	-0.815	-4.07	-1.77
Days to maturity	1.44	1.13	1.39	2.22	1.01	1.33	2.2	3.28	3.61	3.27	1.59	2.57	3.49	5.64
Harvest index	0.493	0.33	0.735	0.461	0.531	0.459	1.67	0.683	1.08	0.68	0.865	0.535	1.85	1.2
Grain yield / plant	0.507	1.96	0.754	2.73	0.749	2.58	1.19	4.18	1.71	6.57	0.888	3.01	1.9	7.13
ΔH	10.4	8.12	4.86	5.58	5.05	3.74	22.79	15.45	23.58	17.52	11.95	11.45	9.59	9.43
R_{IH}	0.65	0.52	0.72	0.74	0.74	0.70	0.85	0.88	0.84	0.82	0.76	0.84	0.92	0.94

*The above indices have been calculated based upon economic coefficients provided in Table V

Sun and Wang (1999), Popova and Koeva (2001), Subash *et al.* (2008) and Chandramony and Sharma (2008) showed that traits such as tillers capacity and plant height are the most significant indices for selection of cultivars with desirable grain yield.

Selection indices: In current study, seven selection indices were investigated based upon different combinations of traits and their economic values were calculated through the two methods of Smith-Hazel and Brim-Williams. The first

index was calculated based on the properties, which genetic path analysis was performed based on them. In this index, the economic values of these traits and grain yield were considered to be equally 1, while the value zero was assigned to other traits not inserted into model (Table V). Evaluation of different criteria for this index showed that in both indices i.e., Smith-Hazel index (Table VI) and Brim-Williams index (Table VII) and also for both crosses, the correlation between the index and breeding value (R_{IH}) and

total genetic advance (ΔH) was obtained to be relatively low, and compared to other indices the lowest genetic gain was observed for both crosses almost for all traits.

In the second index, only the properties inserted into regression model were utilized; however, direct effects resulted from path analysis of grain yield were considered to be economic values. Value 1 was assigned to grain yield per plant, while value zero was considered for other traits not inserted into the model (Table V). Results of data analysis with Smith-Hazel method indicated that compared to the first index, except for days to maturity in cross ICNBF93-369 \times ICNBF-582 and spike length in cross SB91925 \times ICB-1026, higher genetic gain was observed for other properties. Values of R_{IH} and ΔH showed higher efficiency of this index as well (Table VI). The results obtained from data analysis with Brim-Williams index confirmed the results of Smith-Hazel index and indicated that especially for number of tillers, grain weight in spike, thousand grain weight and grain yield per plant, a considerable genetic advance was observed compared to first index.

In the third index, the considered economic values were similar to the second index, with the difference that in the third index the value zero was assigned to grain yield with the aim that no measurement of yield would be required for improving it. Considering the comparative criteria evaluated in both Smith-Hazel and Brim-Williams methods, this index resulted in higher genetic gain compared to the second index for both crosses and for all properties except grain weight in spike, days to maturity and harvest index. From both parameters of accuracy degree (R_{IH}) and genetic advance (ΔH), this index was desirable. Furthermore, compared to the second index a similar genetic gain was observed for grain yield. Accordingly, it can be concluded that in populations under study, we can reach desirable results even without measuring grain yield and merely through studying path analysis coefficients of properties inserted in the regression model.

Yield component breeding to increase grain yield would be most effective, if the components involved were highly heritable. Hence in the fourth index the heritability values of traits were considered as economic values. In this index, all traits under evaluation were utilized and almost for all properties a remarkable genetic advance was observed compared to previous indices. This progress was obvious for plant height, number of tillers, grain weight in spike, days to maturity, harvest index and grain yield per plant, in both crosses and methods. In this index, the correlation between the index and breeding value as well as total genetic advance was desirable in both Smith-Hazel and Brim-Williams methods (Tables VI & VII).

In the fifth index, heritability values were used as economic values; nevertheless, only the properties were considered, which were inserted into regression model. Compared to the fourth index, higher genetic gain was calculated for this index in both Smith-Hazel and Brim-

Williams methods for thousand grain weight and days to maturity in cross ICNBF93-369 \times ICNBF-582, spike length and number of grains per spike in cross SB91925 \times ICB-1026 and plant height, number of tillers, grain weight in spike and grain yield in both crosses. This index was of high accuracy degree (R_{IH}). If the fourth index is employed in order to increase yield in the samples under study, since all properties are inserted into selection cycle, it is required to measure all of them which needs more time and cost. Therefore, comparing the fourth and fifth indices, it can be found out that the increase in number of properties in an index does not necessarily mean that the index is useful.

In the sixth index, economic values were considered similar to the fifth index, with the exception that zero economic value was considered for grain yield. Compared to the fifth index, although the correlation value between the sixth index and breeding value was calculated to be lower in cross ICNBF93-369 \times ICNBF-582 in both Smith-Hazel and Brim-Williams methods, the correlation in cross SB91925 \times ICB-1026 was equal to or more than that of the fifth index. Less genetic gain was, however observed for all traits under study in this index for both crosses in both Smith-Hazel and Brim-Williams methods. Since in the populations under study removal of grain yield drastically decreased the efficiency of index, it is thus recommended to consider grain yield in selection, if heritability values are intended to be used as economic values. In addition, based on these results, it can be concluded in order to improve grain yield in hulless barley populations, using heritability values of traits as economic values is superior to the coefficients path analysis.

In the seventh index, for the first time we took advantage of a new combinatorial economic value, based upon multiplication of the values of direct effects, which were resulted from genetic path analysis and heritability values. The obtained values were considered as economic values. The economic value of grain yield was also considered equal to its heritability value (Table V). Higher genetic advance was observed for all traits in both populations and in both Smith-Hazel and Brim-Williams methods, especially for plant height, number of tillers and grain yield per plant. Correlation of this index with breeding value (index accuracy degree) as well as expected genetic advance for each trait was very desirable. Therefore, it is recommended to utilize this index with lowest number of traits in index equation and maximum genetic gain, so as to improve grain yield.

A glance on Smith-Hazel indices (Table VI) and comparing them with Brim-Williams indices (Table VII) leads to the conclusion that although the coefficients of index correlation with breeding value (R_{IH}), values of genetic advance for each trait (ΔG) and also expected values of genetic gain for all properties (ΔH) were lower in Brim-Williams indices compared to those of Smith-Hazel indices, this difference was not much great. It should be considered that in Brim-Williams method, there is no need to evaluate

genetic parameters and the results obtained from it can be simply interpreted. So it is superior to Smith-Hazel index from this regard.

In independent studies, Eta-Ndu and Openshaw (1992) on maize and Rabiei *et al.* (2004) and Fazlalipour *et al.* (2008) on rice have reported similar results. In these studies the base index of Brim-Williams has been identified as an appropriate index regarding its efficiency, simplicity of calculation and its freedom from errors of parameter estimation.

In conclusion, comparison of different selection indices is only possible through their application and their comparison via the calculated criteria is only theoretical and these indices only evaluate the expected values. As a result, application of these indices is necessary to confirm the obtained results.

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