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Genetic gain and selection criteria effects on yield and yield components in barley (*Hordeum vulgare* L.)

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Abstract

Background and Purpose: *The objective of this study was to evaluate the efficiency and applicability of different selection criteria on grain yield and grain yield components for the purposes of optimizing barley breeding program.*

Materials and Methods: *The experimental material of the cross Timura/Osk.4.208'2-84 included 150 and 26 lines of* F_4 *generation developed by single seed descent (SSD) and pedigree method, respectively. Trial was set up as a randomized block design with three repetitions. The following traits were analyzed: stem length, number of spikes per plant, grain weight per primary spike, grain number per primary spike, grain yield per plant, single grain weight, harvest index and grain yield per plot.*

Results: *Genetic gain estimates showed that pedigree method was efficient for shorter stem, higher number of spikes per plant, and single grain weight and grain yield per plant while single seed descent method was superior for grain yield per plant. Direct genetic gain for grain yield per plot was 33.0% while indirect genetic gain varied from –18.99% to 21.7 %, depending on the applied selection criteria. The most efficient indexed selection criteria for improving grain yield were Q12, Q15, Q8 and Q13.*

Conclusion: *The study indicated that the highest efficiency in grain yield per plot was accomplished by »Q« index multi-trait selection approach. Furthermore, plant selection could be directed to a specific traits but it should be carefully exerted due to unfavorable correlations that could cause gain losses in selection.*

INTRODUCTION

Breeding for quantitative traits in early generations is impeded by several factors such as polygenic nature and low heritability of a trait (grain yield, number of spikes per plant, etc.), linkage, non-additive gene effects and environmental effects. In order to overcome these difficulties it is necessary to get as much as possible information about genetic structure of breeding population undergoing selection. This means identifying the gene effects that control the inheritance of a trait of interest and contributing to the exploitable genetic variance of the population.

SSD and Pedigree methods of selection are very common selection techniques in self-pollinated crops. SSD is the method where single seed is collected from each plant from F2 segregating generation, and the same selection procedure is applied till advanced generations (from F5 and so on). This method preserves genetic variability in advanced generations, but the major drawback is that it can cause genetic drift in a population due to loss of some genotypes. Pedigree method represents the procedure where an individual plant is selected successively through generations (F2-Fn) by monitoring selected offspring till the formation of homozygous lines.

Both of these methods have drawbacks due to high costs of record keeping, utilization of manpower, genetic drift and loss of desirable genes.

Besides that, effective selection is influenced by the usage of breeding method for population development and availability of reliable selection criteria for the identification of the most productive genotypes, which represents a critical point in breeding programs (*1*).

Undesirable between-trait relations are often present additional nuisance in breeders' work. According to the previous experience, this type of limitations should be approached by simultaneous multi-trait selection. Mahdy (*2*) demonstrated that indexed selection criteria were more efficient for grain yield improvement as compared to the single seed descent method and freely termed »the better genotype« selection method. Numerous advantages of indexing genotype traits by simple numeric value were pointed out (*3*).

The objective of this paper was to evaluate the efficiency and applicability of different selection criteria based on the assessment of variability, heritability, phenotypic and genotypic correlations and the selection method effects on grain yield and grain yield components in winter barley cross Timura/Osk.4.208'2-84.

The objective of this research was to compare the efficiency of SSD and Pedigree methods of selection together with the criteria of choosing either single or the combination of many different traits, considering the heritability of individual traits.

MATERIAL AND METHODS

Material. Experimental material included the parents Timura and line Osk.4.208´2-84, 150 lines of the F_4 generation developed by the SSD method and 26 lines developed by the pedigree method. Timura is a German two-rowed winter barley cultivar originating from the cross Igri/Weihenstephan 1911, and Osk.4.208´2-84 is two-rowed winter barley line selected at the Agricultural Institute Osijek from the cross Osk.4.10´1 /1/ Alpha /2/ Osk.4.5´9 /3/ Union /4/ Sladoran. For the development of populations (generations F1-F4) used in the research we chose parents with significant differences in plant height, lodging resistance, coefficient of tillering, grain yield per plant and date of heading.

Experiment. The field trial was set up as a randomized block design with three repetitions at the field of the Agricultural Institute Osijek in one-year experiment. The main plot was a square, 25 x 25 cm, on which 36 kernels were planted, which corresponds to the planting density of 400 kernels/m^2. Laboratory measurements were made on five randomly selected plants per plot in three repetitions, excluding border and non-competitive plants.

The following traits were measured and weighed:

1) Stem length till the base of spike (cm),

2) Number of spikes per plant,

3) Grain weight per primary spike (g),

4) Grain number per primary spike,

5) Grain yield per plant (g),

6) Single grain weight (mg) of the primary spike calculated by the ratio of grain weight on the primary spike and grain number per primary spike and

7) Harvest index (%) calculated as ratio between grain yield per plant and total above-ground biomass, and

8) Grain yield per plot (g).

Data analysis. Data were analyzed by the variance analysis. Based on the phenotypic (V_p) and environmental (V_e) variances estimated from each replication, phenotypic (CV_p), environmental (CV_e), and genotypic variation coefficients (CV_g) were calculated. The genotypic correlation coefficients were only calculated for the lines developed by the SSD method.

Heritability in a broad sense (h^2) and its errors were calculated according to the formula (*4, 5*): $h^2 = (V_p - V_e)/V_p$ and $SE(h^2) = [(2/_{n1+2}) + (2/n_{2+2})]/(1 - h^2)$, where n_1 and n_2 stand for degrees of freedom for the lines and error sources of variation.

The genetic correlation coefficients (r_g) among traits were estimated (*6, 7*): $r_g = Cov_gXY/\tilde{o}_gX^*\tilde{o}_g$, where Cov_gXY is genetic covariance between traits x and y, and $\tilde{o}_gX^*\tilde{o}_gY$ is the product of the square root of genetic variance for traits x and y.

Expected genetic gain from the selection (R) was estimated for the proportion of 10% selected lines (*8, 9*): $Gs = i^*h^{2*}\tilde{o}_P$, where i is standardized selection differential, h^2 is the heritability in a broad sense and $\tilde{o}_P$ is the phenotypic standard deviation.

The correlated response realized from the selection (CRy) was estimated for the 10% proportion of selected lines *(9):* $CRy = i_* h_x h_{y*} r_{g*} \tilde{o}_{PY}$ where i – the standardized selection differential for traits x, h_x and h_y – the square roots of heritability of traits x and y, r_g is genetic correlation between x and y and $\tilde{o}_{PY}$ is the phenotypic standard deviation for y.

Lalić and Kovačević (*3*) developed 15 selection criteria, applying Q index selection *(10, 11)* with their appropriate weights presented in Table 1.

The unit value of one for weight simply means that direct selection for individual trait was applied only for that trait. For indirect selection Q index weights were obtained based on path coefficient analysis among analyzed traits.

All statistical analyses were performed using statistical software *(23)*.

TABLE 1

Indexed selection criteria (Q1-Q15) with their appropriate weights.

Indexed selection criteria	Stem length	Grain weight per spike	Single grain weight	Grain number per spike	Number of spikes per plant	Harvest index	Grain yield per plant	Phenotype preference	Visual character of grain	TOTAL
Q1	–	–	–	–	–	–	–	1	–	1
Q2	1	–	–	–	–	–	–	–	–	1
Q3	–	1	–	–	–	–	–	–	–	1
Q4	–	–	–	–	–	–	1	–	–	1
Q5	–	–	–	–	1	–	–	–	–	1
Q6	–	–	–	–	–	1	–	–	–	1
Q7	–	0.12	–	0.19	0.03	0.29	0.37	–	–	1
Q8	–	0.09	–	0.10	0.19	0.42	0.20	–	–	1
Q9	–	0.20	–	0.17	0.17	0.20	0.26	–	–	1
Q10	–	0.20	–	0.12	0.19	0.22	0.27	–	–	1
Q11	–	–	–	0.23	0.39	0.38	–	–	–	1
Q12	–	–	0.26	0.24	0.38	0.12	–	–	–	1
Q13	–	–	–	0.20	0.49	0.31	–	–	–	1
Q14	–	–	0.23	0.33	0.32	0.12	–	–	–	1

RESULTS

Coefficients of phenotypic variability presented in Table 2 were similar, irrespective of the method of population development (SSD or Pedigree method). Traits that showed low phenotypic variation were single grain weight, harvest index and stem length. Intermediate level of variation was found for grain weight and grain number per spike, and high values were observed for the number of spikes per plant, grain yield per plant and grain yield per plot. This trend holds true for genotypic coefficients of variation. Based on the estimates of heritability in a broad sense (h^2), stem length, grain weight and grain number per spike can be classified as highly heritable, while for other traits heritability values varied around intermediate level (Table 2).

When we look at the relationship among traits at the phenotypic level, the highest values of linear correlations were found between grain weight per spike and grain number per spike ($r=0.83^{**}$), grain yield per plant and the number of spikes per plant ($r=0.76^{**}$) and grain yield per plant and grain yield per plot ($r=0.65^{**}$) (Table 3). This relationship is even more pronounced at the genotypic level. The lack of or weak correlations were observed between: harvest index, on one side, and stem length and grain weight per spike, on the other side. The similar trend was observed between single grain weight and other traits, except grain weight per spike. The only significant negative genotypic correlation was found between single grain weight and harvest index, while others were positive, but not always significant (Table 3).

TABLE 2

Coefficients of phenotypic (C_{VP}) and genotypic (C_{VG}) variability, heritability (h^2) in a broad sense for grain yield and grain yield components for pedigree and single seed descent methods (SSD).

Method	Stem length (cm)	Grain weight per spike (g)	Single grain weight (g)	Grain number per spike	Number of spikes per plant	Grain yield per plant (g)	Harvest index	Grain yield per plot (g)
C_{VP}(%)								
F_4 SSD	9.04	14.80	6.69	12.83	31.64	36.60	9.51	39.32
F_4 Pedigree	6.66	11.76	6.65	9.99	28.22	32.66	8.59	36.04
C_{VG}(%)								
F_4 SSD	7.24	11.77	4.59	10.04	21.07	24.73	6.55	26.72
h^2								
F_4 SSD	0.64**	0.64**	0.47**	0.61**	0.44**	0.46**	0.47**	0.46**

TABLE 3

Phenotypic and genotypic correlation coefficients for the lines of the F_4 generation developed by the SSD and pedigree methods.

Correlation coefficients	Method	Grain weight per spike	Single grain weight	Grain number per spike	Number of spikes per plant	Grain yield per plant	Harvest index	Grain yield per plot
with stem length								
Phenotypic	SSD	0.51**	0.13**	0.55**	0.33**	0.44**	0.10*	0.44**
	Pedigree	0.50**	0.29**	0.39**	0.31**	0.31**	0.03	0.37**
Genotypic	SSD	0.76**	0.05	0.66**	0.55**	0.61**	–0.04	0.49**
with grain weight per spike								
Phenotypic	SSD		0.58**	0.83**	0.41**	0.58**	0.12**	0.37**
	Pedigree		0.55**	0.81**	0.51**	0.63**	0.08	0.37**
Genotypic	SSD		0.53**	0.89**	0.55**	0.76**	0.09	0.24**
with single grain weight								
Phenotypic	SSD			0.06	0.08*	0.16**	0.03	0.09*
	Pedigree			–0.02	0.09	0.30**	0.01	0.08
Genotypic	SSD			0.23**	0.11*	0.20**	–0.28**	0.01
with grain number per spike								
Phenotypic	SSD				0.45**	0.60**	0.13**	0.40**
	Pedigree				0.54**	0.54**	0.04	0.37**
Genotypic	SSD				0.60**	0.80**	0.23**	0.27**
with number of spikes per plant								
Phenotypic	SSD					0.76**	0.24**	0.57**
	Pedigree					0.91**	0.27**	0.63**
Genotypic	SSD					088**	0.27**	0.64**
with grain yield per plant								
Phenotypic	SSD						0.31**	0.65**
	Pedigree						0.31**	0.65**
Genotypic	SSD						0.37**	0.66**
with harvest index								
Phenotypic	SSD							0.25**
	Pedigree							0.20*

It is evident that direct selection for a certain trait per se, measured by expected genetic gain, was efficient for the improvement of that trait, except for grain weight per spike and single grain weight (Table 4).

The greatest expected genetic gains were found for grain yield per plot (33.0 %), grain yield per plant (30.57 %) and the number of spikes per plant (26.37 %).

However, it is reasonable to assume that direct selection for one trait could have negative effect for other traits. It was found that direct selection for shorter stem length had negative effect on grain yield per plot (–18.99 %) and the number of grains per spike (–7,41 %). Another situation that was observed is that direct selection for higher grain yields per plot as a consequence had increase the stem length (negative effect) and harvest index (positive effect), while the values for other traits remain unchanged (Table 4).

As results suggest, index selection can be helpful to balance out such negative effects of direct selection.

By all applied selection criteria, excluding selection for shorter stem, grain yield improvement was accomplished (Figure 1). Furthermore, it was found that multi-trait approach and indexed selection criteria (Q) were more reliable for grain yield per plot and harvest index improvement. Significantly higher grain yields per plot were realized by applying indexed selection criteria Q8, Q12, Q13 and Q15 as compared to better parent values. Among these criteria Q12 also improved the number of spikes per plant (4%), grain yield per plant (3%), grain weight per spike (1%) and harvest index (1 %). For the other applied selection criteria (Q7, Q9, Q10, Q11 and Q14) there was not significant improvement when compared to the better parent (Figure 1).

TABLE 4

Direct and indirect genetic gain from selection based on the selection intensity of 10% and relative (%) to better parent value.

	Stem length	Grain weight per spike	Single grain weight	Grain number per spike	Number of spikes per plant	Grain yield per plant	Harvest index	Grain yield per plot
Stem length, %	–9.49*	6.59**	0	5.49	3.82	4.28	0	3.93
Grain weight per spike, %	–0.01	0.02	0.01	0.01	0.01	0.01	0	0
Single grain weight, %	0	5.48	5.83	0	0	0	0	0
Grain number per spike, %	–7.41	10.25	0.00	12.81	5.62	7.50	0	0
Number of spikes per plant, %	–0.02	0.01	0	0.02	26.37	0.02	0.01	0.02
Grain yield per plant, %	–0.02	24.10	0.01	25.56	24.81	30.57	0.02	0.02
Harvest index, %	0	2.29	0	3.29	3.95	5.19	7.87	5.29
Grain yield per plot, %	–18.99	9.33	0	11.57	19.68	21.71	19.39	33.00

* Diagonal elements – Direct genetic gain (%)
** Off-diagonal elements – Indirect genetic gain (%)

By this type of selection criteria, selection of plants could be directed to single a or group of traits, keeping in mind that optimal balance among traits will preserve population from losing its grain yield genes.

DISCUSSION

Single trait selection concept is most reliable way to improve single trait *(12, 13, 14, 15)*. This is confirmed by our results when selection for shorter stem, grain yield per plant, number of spikes per plant, grain weight per spike and harvest index was applied. We concluded that selection for grain yield improvement should be conducted by simultaneous selection for many traits such as grain weight per spike, number of spikes per plant, grain yield per plant and harvest index.

We have found undesirable influence of direct selection for shorter stem to grain yield and its components (Table 2, 4; Figure 1) most probably due to shortening of stem length below optimum. It is rather questionable to decrease stem length even more when the stature of modern barley is now within the range that would optimize yield *(16)*. Any further decrease of plant height should be accompanied by appropriate selection for other traits, especially grain yield per plant, single grain weight and harvest index. This can be explained by the influence of the experimental material, environment and the interaction of the genotype x environment as

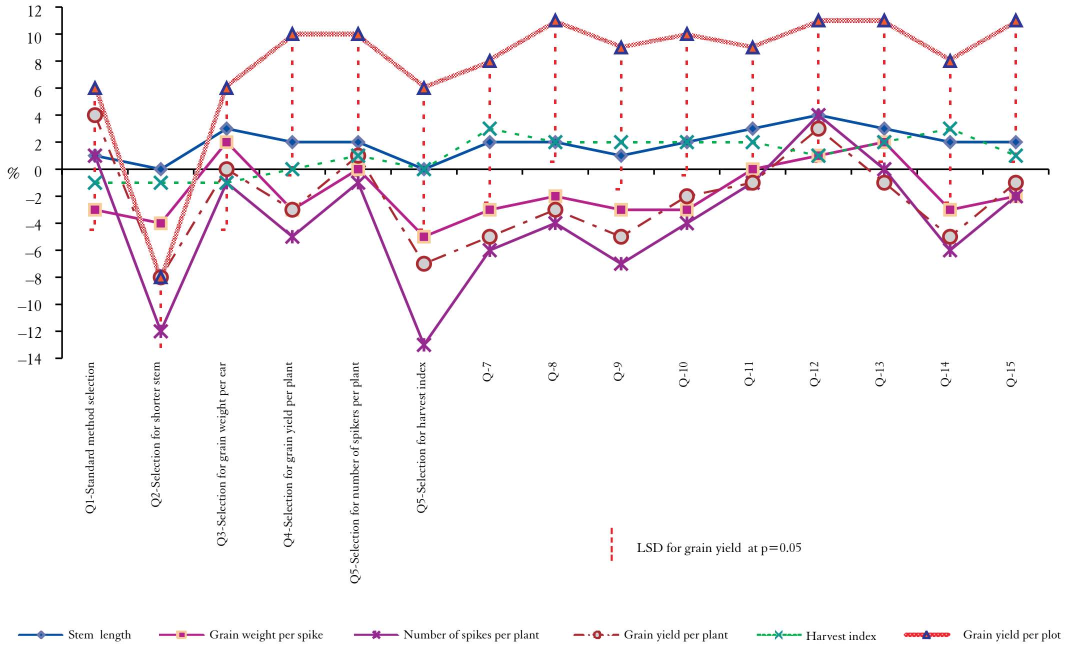

Figure 1. *Effect of indexed selection criteria relative to better parent value.*

suggested by the results of QTL analysis for plant height and other agronomic traits *(17, 18, 19, 20)*.

According to our research it was observed that harvest index can be very useful selection criteria in barley breeding for biomass enlargement which is in agreement with reports of some other authors *(21)*. However, selection for higher harvest index undesirably affected grain yield per plot and grain yield per plant *(14)*.

Some authors pointed out that the genotypes selected based on higher harvest index do not show any improvement due to masked effect of environment *(14, 15)*. It should be pointed out that indexed selection criteria which included more traits identified more efficiently top-yielding genotypes (Q8, Q12 and Q15). This result suggests that for practical breeding purposes such approach can be useful not only for identifying promising genotypes but also it can be very helpful in selection of parents used for creation of genetic variability.

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