TÜRK TARIM ve DOĞA BİLİMLERİ DERGİSİ



TURKISH JOURNAL of AGRICULTURAL and NATURAL SCIENCES

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Heritability, Variance Components and Genetic Advance of Yield and Some Yield Related Traits in Barley Doubled Haploid Lines

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Abstract

A total of 23 doubled haploid lines of winter malting barley were grown in two successive seasons of 2011 and 2012 to study variability, heritability and genetic advance for grain yield and 5 yield related characters - spike length, spikelet number per a spike, grain number per a spike, grain weight per a spike and 1000 grains weight. Significant differences were observed among the doubled haploid lines regarding all the traits studied. Genotypic and phenotypic coefficients of variability were higher in grain yield and grain weight per a spike than other traits. Estimates of heritability ranged from 73,0 % for spikelet number per a spike to 81,6 % for 1000 grains weight, while grain yield showed 78,3% heritability. Heritability coupled with high genetic advance was observed for 1000 grains weight indicating the importance of this trait in yield improvement of winter malting barley.

Keywords: barley, variability, heritability, genetic advance

Introduction

Information on the nature and magnitude of variability and irritability is one of the prerequisites for a successful breeding program in selecting genotypes with desirable characters (Dudly and Moll, 1969). It is, therefore, of great importance for breeders to know the heritability of the agronomic characters to improve the yield of the crop effectively. According to Falconer and Mackay (1996), heritability is defined as the measure of the correspondence between breeding values and phenotypic values. Thus, heritability plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value (Tazeen et al., 2009). There is a direct relationship between heritability and response to selection, which is referred to as genetic advance. High genetic advance with high heritability estimates offer the most effective condition for selection (Larik et al., 2000). The utility of heritability therefore increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection pressure. Thus, genetic advance is another important selection parameter that aids breeder in a selection program.

The objective of this study was to assess the variability, heritability and genetic advance of grain

yield and some of its related components to select a more desired trait that may contribute for the improvement of winter barley.

Materials and Methods

This research was conducted in the 2011 and 2012 growing seasons in the experimental field of the Institute of Agriculture – Karnobat, Southeastern Bulgaria. The soil of experimental field was slightly acid (pH is 6.2) leached chernozemsmolniza. Long term average precipitation for this region was 203.1 mm per growing season. The amount of precipitation in the first year growing period was lower (141.1 mm) than that in the second year (193.4 mm).

The experiments were organized in a Block Design with 4 replications on plots of $10\ m^2$. Standard agronomic and plant protection practices were used.

Twenty three double haploid lines (DH lines) from winter malting barley breeding program of the Institute of Agriculture – Karnobat, obtain via anther culture were studied.

The characters studied included spike length (cm), spikelet number per a spike, grain number per a spike, grain weight per a spike (g) and 1000 grains weight (g) measured on ten plants sampled from the middle of the plot of each genotype in

each replication. The plot yield was converted to t.ha⁻¹.

Heritability in broad sense (h²) was estimated according to Falconer (1989):

$$h^2 = \sigma^2 g / \sigma^2 ph$$

where: $\sigma^2 g$ - genotypic variance and $\sigma^2 ph$ - phenotypic variance. Genotypic $(\sigma^2 g)$ and Phenotypic variances $(\sigma^2 ph)$ were obtained from the analysis of variance table according to Comstock and Robinson (1952).

The mean values were used for genetic analyses to determine Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV), according to Singh and Chaudhury (1985):

GCV (%) =
$$\frac{\sqrt{\sigma^2 \mathbf{g}}}{\mathbf{x}} \cdot 100$$

PCV (%) = $\frac{\sqrt{\sigma^2 \mathbf{ph}}}{\mathbf{x}} \cdot 100$

where: $\sigma^2 g$ - genotypic variance, $\sigma^2 ph$ - phenotypic variance, X - sample mean.

Genetic advance (GA) was calculated with the method suggested by Allard (1960) and Singh and Chaudhury (1985):

GA= K.h²

where: K- constant = 2.06 at 5% selection intensity, $\sigma^2 ph$ - phenotypic variance, h^2 - heritability in broad sense.

Analysis of variance was computed for all the traits evaluated using the computer software system of SPSS 16.00 for Windows 16.0 (SPSS Inc., 2007).

Results and discussion

The results from analyses of variance over two years for the investigated characteristics are presented in Table 1. Effects of genotype, year and interaction of genotype by year were found to be significant for all the traits. The significant differences among barley DH lines in the investigation indicate the presence of genetic variability in the material used and provide a good opportunity for yield improvement. The presence of genotype by environment interaction can reduce gains from selection and complicate identification of superior genotypes.

Table 1. Mean squares for grain yield and some yield related traits for 23 barley DH lines /2011-2012/

Traits	Genotype	Year	Interaction
Spike length	4,375*	7,632*	0,817*
Spikelet number per a spike	17,326*	140,273*	4,673*
Grain number per a spike	16,241*	66,841*	3,632*
Grain weight per a spike	0,113*	0,078*	0,025*
1000 grains weight	136,308*	748,065*	25,097*
Grain yield	1,818*	12,031*	0,395*

^{*}Significant at 0.01 % level of probability;

The mean values of the traits studied are shown in Table 2. Spike length ranged from 7,58 to 10,59 cm. Maximum spikelet number per a spike of 29,49 was exhibited by A9/16 whereas minimum spikelets per a spike of 23,61 was recorded for the DH line A8/3. Grain number per a spike ranged from 22,03 to 28,51. Grain weight per a spike varied from 1,13 for A8/7 to 1,57 g for A9/16. Data for 1000-grain weight ranged between 44,07 and 57,92 g, maximum 1000-grain weight was recorded for A8/25 whereas minimum was recorded for A8/6. Maximum grain yield of 6,15 was exhibited by A8/39 whereas minimum grain yield of 4,35 was recorded for the DH line A8/12. Genotypic variance, phenotypic variance, genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), broad sense heritability and genetic advance for studied traits are presented in Table 3. The estimates of phenotypic and genotypic variances ware the highest for 1000 grains weight (σ 2g=13.901; σ 2ph=17,039) and the lowest for grain weight per a spike (σ 2g=0.011; σ 2ph=0,014). As expected, phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the characters. Phenotypic coefficient of variation and genotypic coefficient of variation ware the highest for grain yield (PCV=9.35%; GCV=8.27%), followed by grain weight per a spike (PCV =9.09%; GCV=8.04%). Low variability was recorded for the spikelet number per a spike and grain number per a spike.

Heritability is the proportion of genetic variance in phenotypic variance, expressed as a

percentage. In the present study heritability was high (above 70%) for all studied characters. The highest estimate of heritability was observed for 1000 grains weight (81.6%), followed by spike length (81.3%). High heritability indicated that the characters were less influenced by the

environment. High heritability for different characters in barley was also reported by Vimal and Vishwakarma (1998), El-Bawab (2003), Wang et al. (2006), Singh (2011) and Al-Tabbal and Al-Fraihat (2012).

Table 2. Means for grain yield and some yield related traits for 23 barley DH lines /2011-2012/

-	Spike length	Spikelet	Grain number	Grain weight	1000 grains	Grain yield
DH lines		number per a	per a spike	per a spike	weight	
	(cm)	spike		(g)	(g)	(t.ha ⁻¹)
A8/1	8,44	27,43	24,93	1,22	49,21	5,08
A8/3	7,58	23,61	22,03	1,22	54,13	5,74
A8/6	8,66	27,22	25,48	1,18	44,07	4,76
A8/7	8,66	26,69	25,05	1,13	45,25	4,71
A8/8	8,40	27,30	25,28	1,17	45,99	4,53
A8/11	8,31	25,07	23,24	1,29	55,16	4,83
A8/12	9,36	28,29	26,51	1,39	52,42	4,35
A8/13	8,69	26,00	23,99	1,21	51,15	5,38
A8/16	8,67	28,48	25,45	1,24	48,98	5,63
A8/18	9,30	27,38	26,11	1,41	54,93	4,53
A8/19	8,08	25,02	23,72	1,32	55,90	4,81
A8/25	9,88	27,97	25,30	1,48	57,92	4,84
A8/27	8,71	26,70	24,86	1,29	50,01	4,53
A8/28	9,65	27,46	25,98	1,43	55,05	5,53
A8/33	8,56	26,73	25,21	1,17	46,38	5,41
A8/35	9,00	26,94	25,66	1,27	50,74	5,19
A8/36	8,96	26,57	25,22	1,33	53,63	5,06
A8/39	9,69	28,33	26,59	1,50	57,12	6,15
A9/8	9,37	28,37	25,91	1,33	49,91	5,01
A9/10	7,75	24,19	22,93	1,30	56,64	6,13
A9/12	10,59	28,88	27,25	1,44	53,39	5,09
A9/15	9,33	27,61	26,05	1,21	46,49	4,83
A9/16	10,09	29,49	28,51	1,57	54,75	5,29
Mean	8,94	27,03	25,27	1,31	51,70	5,10
Minimum	7,58	23,61	22,03	1,13	44,07	4,35
Maximum	10,59	29,49	28,51	1,57	57,92	6,15

Since high heritability does not always indicate a high genetic gain, heritability with genetic advance considered together should be used in predicting the ultimate effect of selecting superior varieties (Ali et al., 2002). Genetic advance was the highest for 1000 grains weight (6.94%). 1000 grains weight spike showed high heritability coupled with high genetic advance. Vimal and Vishwakarma (1998) observed high heritability along with high genetic advance for the length of spike, spikelets per spike and grain yield

per plant in barley. Panse (1957) stated that high heritability coupled with high genetic advance indicates the additive gene effects while high heritability coupled with low genetic advance indicates the non-additive gene effects for control of the particular character. The present study indicated that 1000 grains weight showing high heritability and high genetic advance is important character to be considered for selection and improvement of winter malting barley.

Table 3. Estimates of variance and genetic parameters for spike traits in 23 spring barley genotypes

Traits	$\sigma^2 g$	σ²ph	h² /%/	GCV /%/	PCV /%/	GA
Spike length	0,445	0,547	81,3	7,460	8,272	1,239
Spikelet number per a spike	1,582	2,166	73,0	4,653	5,445	2,214
Grain number per a spike	1,576	2,030	77,6	4,968	5,638	2,279
Grain weight per a spike	0,011	0,014	78,3	8,042	9,086	0,192
1000 grains weight	13,901	17,039	81,6	7,212	7,984	6,938
Grain yield	0,178	0,227	78,3	8,269	9,347	0,769

 σ 2g - genotypic variance; σ 2ph - phenotypic variance; h^2 - heritability in broad sense; GCV - genotypic coefficient of variation; PCV - phenotypic coefficient of variation; GA - genetic advance;

Conclusion

Significant differences were observed among the DH lines regarding all the traits studied. Genotypic and phenotypic coefficients of variability were higher in grain yield and grain weight per a spike than other traits. Estimates of heritability ranged from 73,0 % for spikelet number per a spike to 81,6 % for 1000 grains weight, while grain yield showed 78,3% heritability. Heritability coupled with high genetic advance was observed for 1000 grains weight indicating the importance of this trait in yield improvement of winter malting barley.

References

- Ali, A., Khan, S., Asad, M.A., 2002. Drought tolerance in wheat: Genetic variation and heritability for growth and ion relations. Asian J. Plant Sci., 1: 420-422.
- Allard, R.W., 1960. Principles of plant breeding. John Wiley and Sons, New York.
- Al-Tabbal, J.A., Al-Fraihat, A.H., 2012. Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. J. Agric. Sci. 4(3),193-210.
- Comstock, R.R., Robinson, H.F., 1952. Genetic parameters, their estimation and significance, proc. 6th international Grassland Congress.Vol. 1, Nat. publ. Co. Wash., D.C., U.S.A., pp: 248-291.
- Dudly, J.W., Moll, R.H., 1969. Interpretation and use of estimates of heritability and genetic variance in plant breeding. Crop Sci. 9: 257-267.
- El-Bawab, A.M.O., 2003. Genetic studies on some characters in barley. Egyptian J. Agric. Res., (2): 581-593.

- Falconer, D.S., 1989. Introduction to quantitative genetics. (3rd Ed) Logman Scientific and Technical, Logman House, Burnt Mill, Harlow, Essex, England.
- Falconer, D.S., Mackay, F.C., 1996. Introduction to Quantitative Genetics. Longman, New York. p. 464.
- Larik, A.S., Malik, S.I., Kakar, A.A., Naz, M.A., 2000.

 Assessment of heritability and genetic advance for yield and yield components in *Gossypium hirsutum L.* Scientific Khyber 13: 39-44.
- Panse, V. G., 1957. Genetics of quantitative characters in relation to plant breeding. Indian J. Genet. Pl. Br., 28: 225-229.
- Singh A.P., 2011. Genetic variability in two-rowed barley (*Hordeum vulgare* L.). Indian J. Sci.Res.2 (3): 21-23.
- Singh, R.K., Chaudhary, B.D., 1985. Biometrical Methods in Quantitative Analysis. Kalayani Publishers. New Delhi.
- SPSS Inc., 2007. SPSS for Windows. Release 16.0. SPSS Inc. Chicago, IL. USA.
- Tazeen, M., Nadia, K., Farzana, N.N., 2009. Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. J. Food. Agric. Environ. 7(3&4): 278 282.
- Vimal, S.C., Vishwakarm, S.R., 1998. Heritability and genetic advance in barley under partially reclaimed saline-sodic soil. Rachis, (1-2): 56-57.
- Wang, J., Zhou, M., Huang, Z., Lu, C., Xu, R., 2006. Genetic analysis of quantitative traits of a doubled haploid population in barley. J. Yang Zhou Univ. Agr. Life Sci., (3): 65-69.