



Original article

Yield and Yield-related Traits of Advanced Lines of Winter Barley

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Abstract

A field experiment was conducted at the Institute of Agriculture – Karnobat, Southeastern Bulgaria in three growing seasons. Ten advanced lines developed by experimental mutagenesis along with parent line and standard varieties Obsor and Emon were laid out in a complete block design with 4 replications. Variability and heritability for yield-related traits and grain yield were studied. There were significant differences among advanced lines for all studied traits. Heritability in broad sense ranged from 48.51 % for grain weight per spike to 79.36 % for spike length. The grain yield of advanced lines was significantly higher compared to the parent and varied from 5.34 t/ha in M5/14 to 6.28 t/ha in M5/14. Moreover, lines M5/1, M5/3, M5/10, and M5/19 had higher grain yield than the high-yielding standard variety Emon. Hence, using these lines in the breeding program of winter barley could lead to the improvement of grain yield.

Keywords: Grain yield, Yield-related traits, Heritability, Winter barley, Advanced lines.

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INTRODUCTION

Barley is one of the major cereal crops grown in Bulgaria and worldwide. It is characterized by wide adaptation and it is cultivated successfully in different climatic conditions and soil types (Newton et al., 2011). Plant breeders are continuously working to produce high-yielding and high-quality barley lines for release as new varieties.

A sufficient amount of genetic variability is needed for a successful breeding program. Experimental mutagenesis is one of the important methods to induce genetic variation in barley breeding. Induced mutations have been playing a significant role in studying functions and mechanisms of actions of genes important for crop improvement (Chaudhary et al., 2019). A number of barley cultivars with high grain yield, increased lodging resistance, and improved tolerance to biotic and abiotic stress factors were developed through induced mutation in the world (Ohnoutkova, 2019). In recent years, four mutant varieties of winter barley - IZ Bori, Ahil, Bozin and Zemela released from the mutation breeding program of the Institute of Agriculture - Karnobat were included in the Bulgarian variety list.

The information for genetic parameters of quantitative traits of economic importance is essential for the efficiency of a plant breeding program. Heritability of a plant trait is imperative in determining the selection response because it indicates the extent of transmissibility of traits into next generations (Johnson et al., 1955). Heritability estimates along with genetic advance are usually more useful in predicting the selection gain than heritability alone (Ali et al., 2002).

Phenotypic and genotypic coefficients of variation are also important genetic parameters. The greater the difference between the values of phenotypic coefficient of variation and genotypic coefficient of variation, the greater the influence of the environment on trait expression (Malek et al., 2014).

Cluster analysis can be a useful tool for identifying the variation in the germplasm and for the selection of parents for the breeding programs (Khodadadi et al., 2011). This method of parent selection has been widely used for the selection of genetic divergent genotypes for including in barley hybridization programs (Amabile et al., 2017; Kumar et al., 2020; Al Lawati et al., 2021).

The aim of this study was to evaluate grain yield and yield-related traits of sodium azide-induced advanced mutant lines developed from a breeding line of winter barley 244D, to estimate the genetic parameters of grain yield and yield-related traits, and to select advanced lines for further breeding work.

MATERIALS and METHODS

Advanced lines were obtained after mutagenic treatment of pre-soaked for 16-hour seeds from two-rowed winter barley breeding line 244D with 2 mM sodium azide for 2 hours, prepared in a buffer solution (pH=3) at room temperature. Selection for high yield and other desirable agronomical traits was

applied from M3 to M6 generation in the period from 2012-2013 to 2015-2016. The selected 10 mutant lines along with their parent line and two local standard varieties Emon and Obzor were used as plant material in the present study.

A field trial in complete block design with 4 replications on plots of 10 m² was conducted in three growing seasons (2016-2017, 2018-2019 and 2019-2020) at the Institute of Agriculture - Karnobat, Bulgaria (42°39' N, 26°59' E).

The traits spike length (cm), spikelet number per spike, grain number per spike, and grain weight per spike (g) were measured on 20 randomly selected plants in each replication of each genotype. Grain yield (t/ha) and 1000-grain weight (g) were determined on a plot basis.

The mean values were compared by the least significant difference (LSD) at the 0.05 probability level. Phenotypic (σ^2_{ph}) and genotypic (σ^2_g) variance, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense (h^2), genetic advance (GA), and genetic advance as percent of mean (GAM) were estimated according to Singh and Chaudhary (1985). Cluster analysis using Average Linkage between Groups method with squared Euclidean distance and standardized means variables was performed. All data were processed with the program SPSS for Windows, version 20.0 (Anonymous, 2011).

RESULTS and DISCUSSION

Mean of grain yield and yield-related traits of studied lines, their parent line, and check varieties Obzor and Emon are presented in Table 1. Studied lines showed from 0.48 t/ha (M5/14) to 1.25 t/ha (M5/19) higher grain yield compared to the parent line. Furthermore, lines M5/1, M5/3, M5/10, and M5/19 had significantly higher grain yields than the high-yielding standard variety Emon. Therefore, those lines would be included in the breeding program of winter barley and those lines which had a combination of high yield and good agronomic performance could be tested as candidate varieties. The selection of mutant lines with improved grain yield had been also reported by Deniz (2007) in barley, by Laghari et al. (2012), and Öztürk et al. (2020) in wheat, and by Kato and Shimizu (2020) in rice.

Spike length among the studied lines ranged from 8.74 cm (M5/12) to 10.15 cm (M5/3). Most of the lines had significantly more spikelets (16/1-1, 16/2-7, 16/2-19, 16/2-23, and 16/3-12) and grains (M5/1, M5/3, M5/10, M5/11, M5/13, M5/14, M5/16, and M5/19) per spike than the parent line. The highest grain weight per spike was observed in line M5/10 (1.69 g), followed by M5/1 (1.67 g), M5/11 (1.63 g) and M5/3 (1.61 g). Mutant lines with higher (M5/1, M5/11, M5/12, M5/13, and M5/19), and lower (M5/19) 1000-grain weight than the parent were found.

Table 1. Mean grain yield and yield-related traits of studied advanced lines of winter barley

Genotype	GY	SL	SNS	GNS	GWS	TGW
Obzor	5.14	6.58	32.72	30.84	1.45	40.26
Emon	5.32	6.82	32.08	30.45	1.42	42.25
Parent line 244D	4.86	9.28	29.39	27.61	1.40	41.25
M5/1	5.98	9.96	34.60	30.53	1.67	43.34
M5/3	5.97	10.15	32.66	30.31	1.61	40.58
M5/4	5.64	9.01	30.68	29.16	1.52	38.51
M5/10	6.28	9.74	31.95	30.65	1.69	42.20
M5/11	5.79	9.46	30.86	29.18	1.63	42.70
M5/12	5.55	8.74	28.95	27.22	1.48	42.64
M5/3	5.72	9.38	32.58	31.01	1.56	42.78
M5/14	5.34	8.77	31.28	29.53	1.43	40.79
M5/16	5.43	9.20	32.47	29.94	1.52	41.11
M5/19	6.11	9.42	30.96	29.58	1.53	40.82
<i>LSD 0.05</i>	<i>0.51</i>	<i>0.49</i>	<i>1.54</i>	<i>1.20</i>	<i>0.14</i>	<i>1.27</i>

GY - grain yield; SL - spike length; SNS - spikelet number per spike; GNS - grain number per spike; GWS- grain weight per spike; TGW – 1000-grain weight;

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 2. The phenotypic and genotypic variances were the highest for spikelet number per spike ($\sigma^2g=1.400$; $\sigma^2ph=2.215$) and the lowest for grain weight per spike ($\sigma^2g=0.004$; $\sigma^2ph=0.008$). Phenotypic and genotypic coefficients of variation were the highest for spike length (PCV=12.11%; GCV=10.78%), followed by grain yield (PCV=7.10%; GCV=5.43%). High PCV and GCV imply the existence of high variability for these traits which is needed for their improvement by selection. The lowest values for PCV and GCV were recorded for 1000-grain weight (PCV =3.22%; GCV=2.59%). The PCV values close to the GCV values indicate a low influence of the environment on the traits and selection could be more successful for these traits. In the present study, the lowest differences between PCV and GCV values were found for grain number per spike and 1000-grain weight.

Heritability values varied from 48.51% for grain weight per spike to 47.36% for spike length. Estimates of heritability in broad sense more than 80% are considered very high, 60-79% as moderately high, 40-59% as medium, and values less than 40% as low (Singh, 2001). Considering this scaling, in the present study heritability values were moderately high for spike length, spikelet number per spike, and 1000-grain weight and medium for the grain number per spike, grain weight per spike and grain yield.

Table 2. Genetic parameters for grain yield and yield-related traits of 10 advanced lines of winter barley

Trait	σ^2g	σ^2ph	h^2	GCV	PCV	GA	GAM
Grain yield	0.093	0.160	58.35	5.43	7.10	0.19	3.41
Spike length	0.933	1.176	79.36	10.78	12.11	1.92	21.46
Spikelet number per spike	1.400	2.215	63.17	3.74	4.71	2.88	9.11
Grain number per spike	0.740	1.320	54.73	2.90	3.92	1.52	5.13
Grain weight per spike	0.004	0.008	48.51	4.18	6.00	0.01	0.55
1000-grain weight	1.150	1.782	64.51	2.59	3.22	2.37	5.71

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; GAM- genetic advance as percent of mean;

As the high heritability is not always an indicator of a high genetic gain, so it is considered that high heritability values together with high genetic advance are more appropriate for determining the effect of selection (Ali et al., 2002). The range of genetic advance as a percentage of the mean (GAM) was from 0.55% for grain weight per spike to 21.46% for spike length. In the present study, the highest heritability along with the highest genetic advance as a percentage of mean was found for spike length, followed by spikelet number per spike. Vimal and Vishwakarma (1998) reported high heritability along with high genetic advance for length of spike, spikelets per spike and grain yield per plant in barley

The studied advanced lines were grouped into three clusters (Figure 1). Cluster I included parent line and line M5/12. Cluster II comprised six lines M5/1, M5/3, M5/10, M5/11, M5/13, and M5/19 which are characterized by highest grain yield, grain number per spike, and grain weight per spike. Cluster III consisted of two standard varieties Obzor and Emon, and M5/4, M5/14, and M5/16. Grouping of mutant lines by cluster analysis confirms the effectiveness of mutation treatment for the creation of genetic variation in grain yield and yield-related traits.

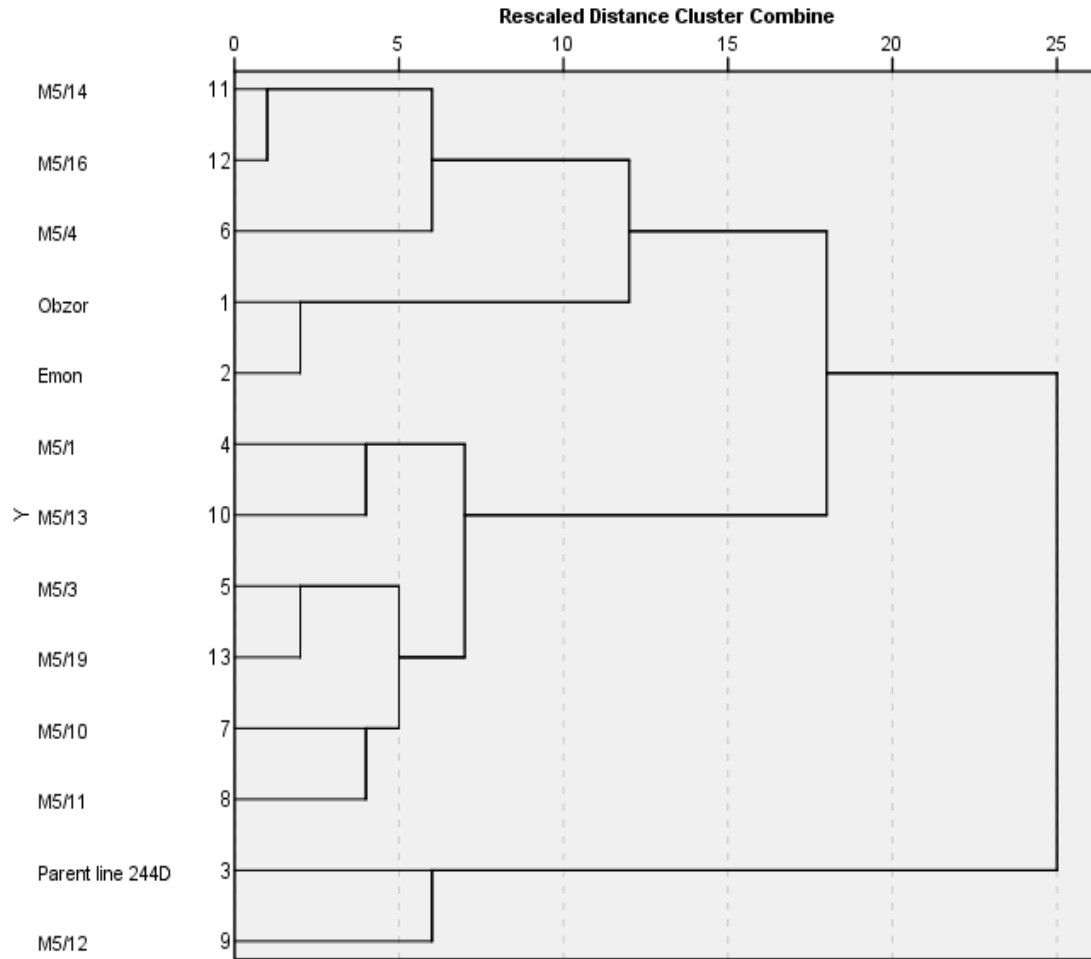


Figure 1. Dendrogram of barley advanced lines based on grain yield and yield-related traits

Conclusion

There were significant differences among advanced lines for all studied traits. Heritability in broad sense ranged from 48.51 % for grain weight per spike to 79.36 % for spike length. The grain yield of advanced lines was significantly higher compared to the parent and varied from 5.34 t/ha in M5/14 to 6.28 t/ha in M5/14. Moreover, lines M5/1, M5/3, M5/10, and M5/19 had higher grain yield than the high-yielding standard variety Emon. Hence, using these lines in the breeding program of winter barley could lead to the improvement of grain yield.

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