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GENETIC DIVERSITY IN SIX-ROWED WINTER BARLEY (*HORDEUM SATIVUM* JESS., SSP. VULGARE L.) GENOTYPES

B. DYULGEROVA, D. DIMOVA and D. VALCHEVA
Institute of Agriculture, BG - 8400 Karnobat, Bulgaria

Abstract

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Twenty-five six-rowed winter barley genotypes were assessed for nature and magnitude of genetic diversity among them based of traits related to yield and quality of feed barley. The study was conducted in the Institute of Agriculture - Karnobat, during the period 2010/2011-2011/2012. Maximum variation was found for grain weight per a spike and spike length. The results of the present study showed considerable genetic divergence among the genotypes. This suggested that adequate scope is available for selection of superior and diverse genotypes for use in a programmed aimed at enhancing grain yield potential and grain quality of winter feed barley. Considering diversity pattern and agronomic performance the cultivars Konrat, Fedor, Zimur and Dobrinya 3 and breeding lines K-3.11 and K-3.12 might be selected as promising genotypes for future hybridization program.

Key words: genetic diversity, cluster analysis, principal component analysis, barley

Introduction

Barley is an important cereal crop in Bulgaria. Most feed barley cultivars grown in Bulgaria are winter six-rowed types. One of the main objectives of winter feed barley breeding program is to produce high-yielding and better-quality lines for release as cultivars. The availability of genetic variability is a pre-requisite for any breeding program (Ifftikhar et al., 2009). Barley improvement has been and continues to be dependent on continues supply of new germplasm material as donor of various genes of breeding importance. Studies on barley genetic resources show that the right utilization of appropriate cultivars can substantially put forward and make effective the breeding work.

Analysis of variability among the traits would be of great importance in planning a successful breeding program (Mary and Gopalan, 2006). Genetically diverse parents are able to produce considerable variability, which can enhance the scope of selection. More diverse the parents, greater are the chances of obtaining broad spectrums of variability in segregating generations (Arunachalam, 1981).

Hence, the objective of the present investigation was analyzing the genetic diversity among the six-rowed winter genotypes for their further utilization in the feed barley breeding program.

Materials and Methods

The experimental work was conducted during the 2010/2011 and 2011/2012 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 chernozem-smolniza. Long-term average precipitation for this region was 424.6 per growing period. The amount of precipitation in the first year growing period was 344.5 mm and in the second year - 524.9 mm.

The experiment was set up as a randomized block design. The genotypes were evaluated for eight traits – spike length (cm), awn length (cm), spikelet number per a spike, grain number per a spike, grain weight per a spike (g), 1000 grains weight (g), hectoliter weight (kg.hl^{-1}), protein content (%) and starch content (%).

The materials studied included 25 winter six-rows genotypes: 3 Bulgarian cultivars – Veslets, Izgrev, Aheloy 2 (Institute of Agriculture - Karnobat), 10 Russian cultivars – Se-

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E-mail: bdyulgerova@abv.bg

cret, Dobrinya 3, Fedor, Zimur, Rubez, Samson, Kondrat, Mihailo, Platon and Romance (Krasnodar Lukyanenko Research Institute of Agriculture) and 12 Hungarian breeding lines – K-3.1, K-3.2, K-3.3, K-3.4, K-3.5, K-3.6, K-3.7, K-3.8, K-3.9, K-3.10, K-3.11 and K-3.12 (Fleischmann Rudolf Research Institute, Kompolt).

Two multivariate analyses - principal component and cluster analyses were utilized for the evaluation of barley genotypes. Principal component were obtained by SPSS 16.00 for Windows 16.0 (SPSS Inc., 2007). The cluster analysis was performed using the program Statistica 7.0 (StatSoft Inc., 2004) that adopts Euclidian distance as a measure of dissimilarity and the unweighted pair-group average method as the clustering algorithm. Before computing our data were standardized.

Results and Discussion

The genotypes were characterized by a substantial variability of the spike traits (Table 1). Spike length ranged from 5.75 to 10.06 cm with coefficient of variability of 20.30 per cent. Hungarian lines had significant longer spike compare with Bulgarian and Russian cultivars. Awn length varied from 8.23 to 12.92 cm. Spikelet number per a spike varied

Table 1
Mean values of studied traits of six-rowed winter barley genotypes (2010/2011-2011/2012)

Genotypes	Spike length, cm	Awn length, cm	Spikelet number per a spike	Grain number per a spike	Grain weight per a spike, *g*	1000 grains weight, *g*	Hectoliter weight, kg.hl^{-1}	Protein content, %	Starch content, %
Veslets	7.35	9.68	68.54	54.39	2.44	44.83	70.70	11.92	57.89
Izgrev	6.60	8.50	61.63	45.25	1.82	40.29	68.70	12.32	58.63
Aheloy 2	7.83	9.50	72.50	58.04	2.26	39.07	65.20	11.20	57.82
Secret	5.77	11.50	74.00	67.84	2.82	41.48	62.30	11.64	59.36
Dobrinya 3	6.07	10.96	76.00	70.13	3.26	46.41	62.20	12.52	57.85
Fedor	6.06	10.96	82.38	77.17	3.21	41.61	60.90	10.75	58.79
Zimur	6.06	12.40	80.50	72.00	3.07	42.69	63.60	12.21	58.80
Rubez	5.81	12.92	73.71	67.00	3.05	45.60	61.70	10.43	59.14
Samson	7.69	11.73	70.75	61.42	2.98	48.42	59.80	12.02	59.42
Kondrat	6.65	11.98	87.00	83.00	3.48	41.84	60.50	11.38	57.44
Mihailo	6.00	10.29	74.88	65.33	3.16	48.37	63.50	12.32	56.43
Platon	5.92	12.58	71.58	62.88	3.05	48.48	61.40	11.96	58.58
Romance	5.75	10.20	71.16	62.72	2.78	44.38	60.35	10.05	61.30
K-3.1	8.73	9.90	75.38	61.42	2.23	37.08	65.70	11.37	55.06
K-3.2	10.06	9.86	81.55	67.79	2.37	37.00	66.80	11.43	55.82
K-3.3	8.58	8.23	82.75	70.59	2.52	41.50	70.20	10.69	54.77
K-3.4	9.50	9.27	84.13	69.33	2.40	42.00	69.20	11.62	55.45
K-3.5	9.15	9.48	78.36	63.12	2.37	43.00	70.20	11.37	54.96
K-3.6	9.16	10.21	81.88	64.04	2.48	44.50	71.20	11.93	55.30
K-3.7	9.84	11.63	81.50	65.71	1.94	36.00	63.00	12.43	53.92
K-3.8	9.42	10.52	70.25	57.71	2.10	34.50	65.50	11.68	54.11
K-3.9	9.33	10.29	77.88	57.42	1.85	42.00	67.50	11.93	54.37
K-3.10	9.07	12.15	70.00	56.92	1.98	45.00	70.00	11.93	57.28
K-3.11	8.67	10.42	78.63	67.34	2.53	42.50	71.50	12.85	55.57
K-3.12	9.91	11.66	84.75	66.79	2.37	35.89	64.20	13.10	52.17
LSD 0.05	0.42	1.09	4.90	4.09	0.44	3.22	2.23	0.49	1.97
Minimum	5.75	8.23	61.63	45.25	1.82	34.50	59.80	10.05	52.17
Maximum	10.06	12.92	87.00	83.00	3.48	48.48	71.50	13.10	61.30
CV%	20.30	11.78	8.01	11.78	18.52	9.40	5.94	6.23	3.90

from 61.63 to 87.00 with a CV 8.01 per cent. Grain number per a spike ranged from 45.25 to 83.00 and CV was 11.78 per cent. Nine Hungarian lines (K-3.1, K-3.2, K-3.3, K-3.4, K-3.5, K-3.6, K-3.7, K-3.11 and K-3.12) had spikelet and grain numbers per a spike significantly higher the Bulgarian check cultivar Veslets. Grain number per a spike in all Russian cultivars was significantly higher than the check. Grain weight per a spike varied from 1.82 to 3.48 g with a CV of 18.52 per cent. Grain weight per a spike in Russian cultivars was significant higher than those of Bulgarian cultivars and Hungarian lines. Weight of 1000 grains ranged from 34.50 to 48.48 g in the genotypes evaluated. The CV observed was 9.40 per cent. Hectoliter weight showed a range of 59.80 to 71.50 kg.hl^{-1}, with a CV of 5.94 per cent. Grain protein content (%) varied from 10.05 to 13.10%. Only two Hungarian lines (K-3.11 and K-3.12) showed significantly higher protein compared to Bulgarian cultivar Izger. Minimum CV (3.90%) was observed for the starch content ranged from 52.17 to 61.30%.

The variation studied through Principal Component Analysis revealed that three principal components having greater than 1 eigenvalues contributed 81% of the total variation (Table 2). It was found that Principal Component 1 (PC1) contributed 42.48%, whereas PC2, PC3 contributed 25.18% and 13.21% respectively of the total variation. The traits, which contributed positively to PC1 were grain weight per a spike (0.889), starch content (0.797) and 1000 grain weight (0.627). Spike length (-0.880) and hectoliter weight (-0.761) contributed negatively to the first component. Maximum genetic variance to PC2 was contributed by number of spiklets (0.955) and grains per spike (0.848). Protein content contributed positively to PC3 (0.860).

Figure 1 displays a biplot in the dimension of the first and second PCs. All Russian cultivars had positive values for first PC. These cultivars are characterized by short spike, high grain weight per a spike and relatively low hectoliter weight. All of these cultivars (except cultivar Samson) belong to the var. *paralellum*. Cultivars Konrat, Fedor, Zimur and Dobrinya 3 had positive values for first and second PCs and had best combination between high grain weight per spike and 1000 grains weight with high spikelet and grain number per spike. According to spike density all Bulgarian cultivars and Hungarian lines belong to var. *pallidum* and showed long and lax spike, lower grain weight per a spike and high hectoliter weight.

The dendrogram of the evaluated barley genotypes is presented in Figure 2. The groupings indicated correspondence between the origin and clustering pattern on the basis of all traits studied. Cultivars and lines were grouped into three clusters at a distance of 15 units. Cluster I included 10 Russian cultivars. This cluster had genotypes with maximum in grain number and grain weight per a spike (Table 3). A lot of studies reported that number of grains per spike had positive correlation with grain yield and that this trait can be used as a selection criteria for barley (Al-Tabbal and Al-Fraihat 2011; Tas and Çelik, 2011; Budakli Carpici and Celik, 2012; Dyulgerova, 2012; Dimitrova-Doneva et al., 2012). The high yield potential of winter six-rowed Russian cultivars under Bulgarian agro-ecological conditions has also been reported from Michova (2011). Cluster II was constituted of 12 Hungarian breeding lines and produced highest mean for spike length and spikelet number per a spike. The cluster III composed of 3 Bulgarian cultivars and this cluster had highest mean values for hectoliter weight.

Table 2
Principal Component analysis of 25 six-rowed winter barley genotypes

Characters	PC1	PC2	PC3
Eigenvalues	3.823	2.267	1.189
Proportion of variance	42.475	25.184	13.211
Cumulative variance	42.475	67.660	80.871
	Factor loadings		
Spike length	**-0.880**	0.303	0.045
Awn length	0.572	0.262	0.579
Spikelet number per a spike	-0.068	**0.955**	-0.141
Grain number per a spike	0.463	**0.848**	-0.167
Grain weight per a spike	**0.889**	0.311	-0.009
1000 grains weight	**0.627**	-0.324	0.161
Hectoliter weight	**-0.761**	-0.172	-0.114
Protein content	-0.323	0.081	**0.860**
Starch content	**0.797**	-0.487	-0.158

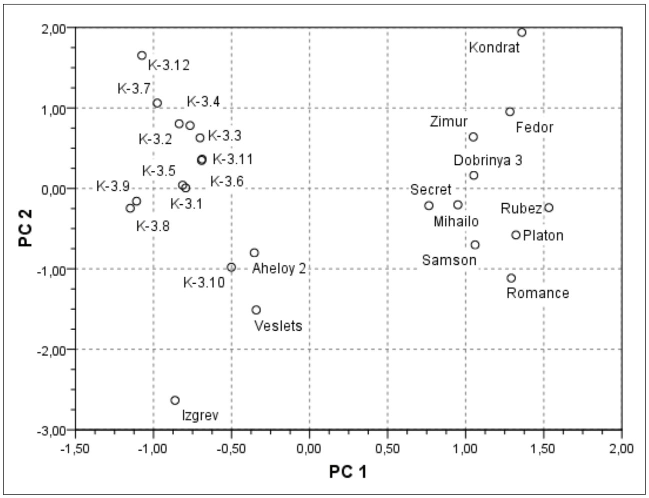

Fig. 1. Scatter diagram for PC1 and PC2 in 25 six-rowed winter barley genotypes

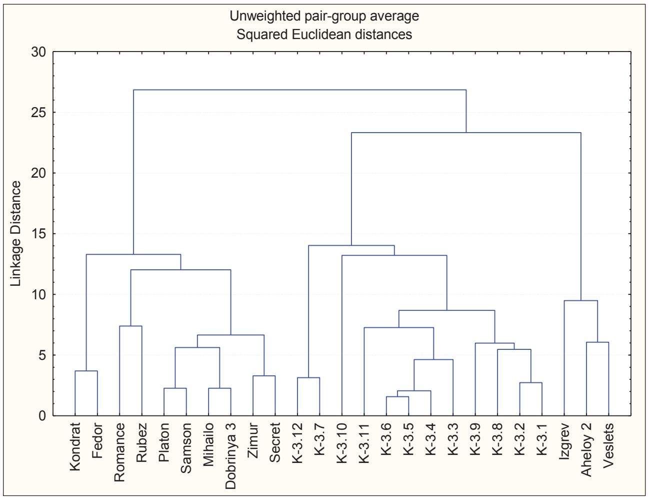

Fig. 2. Dendrogram base on 9 traits of 25 six-rowed winter barley genotypes (2010/2011-2011/2012)

Table 3

Cluster mean of characters of 25 six-rowed winter barley genotypes (2010/2011-2011/2012)

Traits	Cluster		
	I /10/	II /12/*	III /3/
Spike length, cm	6.18	9.29	7.26
Awn length, cm	11.55	10.30	9.23
Spikelet number per a spike	76.20	78.92	67.56
Grain number per a spike	68.95	64.02	52.56
Grain weight per a spike, g	3.09	2.26	2.17
1000 grains weight, g	44.93	40.08	41.40
Hectoliter weight,.kg.hl^{-1}	61.63	65.43	68.20
Protein content, %	11.53	11.72	11.81
Starch content, %	58.71	54.90	58.11

* Figures in parentheses indicate number genotypes included in cluster

Grouping of germplasm by multivariate methods in the study is of practical value to the breeders of winter feed barley. Among 9 traits under study, a considerable variation was observed for grain weight per a spike and spike length. Chand et al. (2008) reported high diversity for number of grains per spike and grain yield per plant in elite barley lines. At the same time, Abebe et al. (2008) studied the diversity of the Ethiopian barley germplasm through morphological traits and found a considerable diversity for days to heading, days to maturity, biomass, plant height and 1000-grain weight. The divergence in the present materials will offer a good scope for improvement of grain yield and quality through rational selection of parents for hybridization in breeding program of winter feed barley. Cultivars Konrat, Fedor, Zimur and Dobrinya 3 showed high values for grain weight per spike, grain number per spike and 1000 grains weight and may be used as parents in hybridization programmes to develop high-yielding feed barley cultivars. Of particular interest for feed barley breeding are materials with a combination of high protein content and yield potential as Hungarian breeding lines K-3.11 and K-3.12.

Conclusions

The multivariate methods applied revealed considerable genetic diversity for important traits of studied genotypes. Maximum variation was found for grain weight per a spike and spike length. Considering diversity pattern and agronomic performance the cultivars Konrat, Fedor, Zimur and Dobrinya 3 and breeding lines K-3.11 and K-3.12 might be selected as promising genotypes for future hybridization program.

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