*Bulgarian Journal of Agricultural Science, 26 (No 6) 2020, 1198–1202*

# Agronomic and qualitative-technological traits of two-row winter barley cultivars

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## Abstract

Neykov, N. & Doneva, S. (2020). Agronomic and qualitative-technological traits of two-row winter barley cultivars. *Bulg. J. Agric. Sci., 26 (6)*, 1198–1202

Fourteen two-rowed winter barley genotypes were assessed for characteristics of main agronomic and technological traits which are important for the breeding and production.

The study was conducted in the Institute of Plant Genetic Resources – Sadovo, during the period 2014-2016. It was found that in the group with the highest yield were the cultivars Asparuh – 6490 kg/ha and Kuber – 6390 kg/ha. The traits, which contributed positively to PC1 were spike length, grain number per a spike and yield.Considering diversity pattern, agronomic and technological traits researched in this study the cultivars Aparyh, Kuber, Kristi and Potok from first cluster and Orfey, Odisey and Zagorets from second might be selected aspromising genotypes for future hybridization program.

*Keywords:* barley; cluster analysis; principal component analysis; barley; brewing qualities; yield

## Introduction

Barley is the main raw material for brewing industry and while grain growers are seeking mainly to achieve high and stable yields, brewers prefer raw materials with high quality. Breeding of new cultivars of brewing barley evolves in the direction to the creation of highly productive varieties with improved brewing-grain technological qualities-protein content below 12%, extract content about 80% with very good grain uniformity over: 90% I class (Valcheva, 2000;Valcheva et al., 2000; Popova et al., 2013; Noworolnik et al., 2014).

In the new varieties of brewing barley with the highest direct effect on the yield are the height of the plants and the length of the spike (Valcheva et al., 2013). The increase of the productive potential can also be due to increasing the tolerance of varieties to stress (drought, cold and diseases) (Richards et al., 2002; Valchev, 2007; Valcheva et al., 2010; Uhr, 2015; Bonchev, 2017).

Based on the results achieved in the period 1962-2010 (Valcheva et al., 2010) indicate that yield increases withbreweriescultivars by 30%. Breeding progress in productivity atthe brewing barley is due to the new varieties created after 2004, which have achieved a shortening of the height of the plants, length of spike, increasing the tolerance of varieties to abiotic and biotic stress (Ganusheva et al., 2005). In this regard, the need to find suitable starting forms is increasingly important. The protein content of the varieties used as raw material is a determining factor for the quality of the final product in the brewing industry (Finnie & Svensson, 2003; Vasileva & Marcheva, 2016). High protein content determines low quality of brewing products.It can vary within a broad range of 10% to 18% of the dry matter. For the territory of Bulgaria, brewing barley is inferior to European varieties in terms of protein content. This is conditioned by the continental climatic conditions, where it is difficult to reach parameters below 12% (Valcheva, 2000; Ivanova et al., 2013). One of the important

physical criteria for determining grain quality is the mass of 1000 grains. In high-quality brewing barley, the absolute mass is usually in the range of 40-49 g (Marcheva, 2006).

The aim of the study was to selectpromising cultivars with high yield and grain quality for future hybridization program.

## Materials and Methods

The experimental work was conducted during the 2014–2016 growing seasons in the experimental field of the Institute of Plant Genetic Resources – Sadovo, South Central Bulgaria.

The studied genotypes of winter barley are based on soil type Meadow Cinnamon Soil middle-ground (A + B = 60 – 80 cm). They are poorly stocked with nitrogen, on average well-stocked with phosphorus and rich in potassium. The soil response is close to neutral with pH = 6.5. Marginal humidity ranges from 24% to 26%.

The experiment was set up as a randomized block designin comparative cultivar trials in four repetitions of an area of 10 $m^2$, with sowing rate of 450 germinating seeds per $m^2$ . The genotypes were evaluated for nine traits – plant height, spike length (cm), grain number per a spike, grain mass per a spike (g), 1000 grains mass (g), hectoliter mass ($kg.hl^{-1}$), protein content (%), starch content (%) and uniformity >2.5 mm, (%). The plant material studied included 14 winter two-row genotypes.

The statistical processing of the results was done through Analysis of variance, Fit, component and cluster analyses. Statistical processing was performed with use of JMP (2002) software.

## Results and Discussion

Table 1 presents biometric data and evidence of yield differences and productivity traits average for the study period for two-row winter barley cultivars in the region of Sadovo. Asparuh and Kuber werewith the highest yields, with 6490 kg/ha and 6390 kg/ha respectively. With regard to the traits plant height, spike length and number of grains per spike there was no proven difference between genotypes. The comparative evaluation shows that grain mass per spike for Asparuh and Kuber were characterized with the highest values of 1.59 g and 1.53 g, but the difference with the average standard was not proven. With regard to 1000 grain mass, multi-directional comparative analysis showed that all cultivarsfall into one group and there was no significant difference between them, but it can be noted that Emon was characterized with high value to the trait (Table 1).

Table 2 presents data for the technological qualities of promising two-row winter barley cultivars average for the survey period. Kuber and Asparuh exhibited the highest yields in the region of Sadovo have no proven differences from the average standard for all tested technological qualities included in the study. Kuber was characterized by a high hectolitre mass of 68.10 kg. Imeon and Zagoretz were characterized by a lower crude protein content than the average standard but without significant differences between them.

**Table 1. Structural elements of productivity in two-row barley cultivars average for the period (2014-2016)**

| Cultivars | Yield kg/ha | | Plant height, cm | | Spike length, cm | | Grain number per a spike | | Grain mass per a spike, g | | 1000 grains mass, g | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Obzor | 4750 | | 67.2 | | 8.0 | | 24.9 | | 1.41 | | 41.67 | |
| Emon | 5300 | | 65.4 | | 7.9 | | 23.3 | | 1.41 | | 43.43 | |
| Kaskadyor | 4890 | | 65.7 | | 7.8 | | 22.9 | | 1.51 | | 38.23 | |
| Aver.std. | 4980 | b | 66.2 | a | 7.9 | abc | 23.7 | a | 1.44 | a | 41.11 | a |
| Lardeya | 5280 | b | 62.7 | a | 7.9 | abc | 23.2 | a | 1.37 | a | 43.17 | a |
| Orfej | 5680 | b | 60.4 | a | 7.5 | c | 23.2 | a | 1.43 | a | 39.59 | a |
| Imeon | 5740 | b | 63.8 | a | 8.1 | abc | 24.5 | a | 1.38 | a | 40.17 | a |
| Zagorets | 5820 | b | 66.7 | a | 7.9 | abc | 24.1 | a | 1.34 | a | 40.83 | a |
| Kuber | 6390 | a | 69.1 | a | 8.3 | abc | 24.8 | a | 1.53 | a | 42.53 | a |
| Asparuh | 6490 | a | 70.8 | a | 8.5 | abc | 25.2 | a | 1.59 | a | 43.33 | a |
| Odisey | 5830 | b | 64.9 | a | 7.8 | bc | 23.3 | a | 1.36 | a | 40.73 | a |
| Potok | 5480 | b | 73.4 | a | 8.3 | abc | 24.5 | a | 1.52 | a | 40.93 | a |
| Krami | 5610 | b | 74.9 | a | 8.3 | abc | 24.1 | a | 1.34 | a | 40.87 | a |
| Kristi | 5580 | b | 81.7 | b | 8.4 | abc | 24.1 | a | 1.42 | a | 40.73 | a |
| Vanesa | 5780 | b | 77.6 | a | 8.6 | a | 24.3 | a | 1.34 | a | 42.33 | a |
| $LSD_{0.05}$ | 1240 | | 10.7 | | 0.8 | | 2.1 | | 2.25 | | 5.00 | |

**Table 2. Grain quality data for two-row barley cultivars in the region of Sadovo average for the period (2014-2016)**

| Cultivar | Hectolitre mass, kg | Uniformity I class, % | Crude protein content, % | Extract content, % |
|---|---|---|---|---|
| EBCnorms | 68 | 85 | 12.5 | 78 |
| Obzor – St. | 65.40 | 94.7 | 12.10 | 79.2 |
| Emon St. | 67.80 | 97.4 | 11.55 | 79.3 |
| Kaskadyor St. | 67.70 | 94.8 | 11.65 | 79.0 |
| Avg.St. | 66.97 | 95.6 | 11.76 | 79.2 |
| Lardeya | 65.40$^{ns}$ | 90.7** | 12.05$^{ns}$ | 75.9*** |
| Orfej | 64.50* | 95.7$^{ns}$ | 11.79$^{ns}$ | 78.8ns |
| Imeon | 65.90$^{ns}$ | 94.1 $^{ns}$ | 11.17$^{ns}$ | 78.5ns |
| Zagorets | 65.10$^{ns}$ | 95.6 $^{ns}$ | 11.41$^{ns}$ | 77.6* |
| Kuber | 68.10$^{ns}$ | 95.3$^{ns}$ | 11.80$^{ns}$ | 77.9 $^{ns}$ |
| Asparuh | 65.00$^{ns}$ | 93.6 $^{ns}$ | 12.04$^{ns}$ | 78.1 $^{ns}$ |
| Odisey | 64.60* | 95.0 $^{ns}$ | 11.81$^{ns}$ | 76.6** |
| Potok | 67.10$^{ns}$ | 86.9** | 12.51$^{ns}$ | 77.0** |
| Krami | 64.70* | 94.5$^{ns}$ | 11.90$^{ns}$ | 78.7 |
| Kristi | 66.00$^{ns}$ | 94.1$^{ns}$ | 12.11$^{ns}$ | 77.7* |
| Vanesa | 65.60$^{ns}$ | 95.0$^{ns}$ | 12.24$^{ns}$ | 76.7** |
| $LSD_{0.05}$(*) | 2.20 | 2.1 | 1.7 | 1.4 |
| $LSD_{0.01}$ (**) | 4.10 | 4.0 | 2.4 | 2.0 |
| $LSD_{0.001}$ (***) | 6.30 | 6.1 | 3.3 | 2.7 |

The variation studied through Principal Component Analysis revealed that four principal components having greater than 1 eigen values contributed 81% of the total variation (Table 3). It was found that Principal Component 1 (PC1) contributed 31.41% whereas PC2, PC3 and PC4 contributed 23.16%, 13.75% and 12.65% respectively of the total variation. The traits, which contributed positively to PC1werespike length (0.501) grain number per a spike (0.464) and yield (0.403). Crude protein content (-0.048) and extract content (0.088) contributed negatively to the first component. Maximum genetic variance to PC2 was contributed by uniformity I class (0.585) and extract content (0.324). Plant height contributed positively to PC3 (0.498) and 1000 grains mass to PC4 (0.481).

Figure 1 displays a biplot in the dimension of the first and second PCs. Kuber, Asparuh, Potok, Kristi and Vanesa have positive values for first PC. These cultivars were characterized by high yield, high plant height, high spike length, high

**Table 3. Principal Component analysis of 14 two-rowed winter barley genotypes**

| Characters | PC1 | PC2 | PC3 | PC4 |
|---|---|---|---|---|
| Eigen value | 3.14121 | 2.31599 | 1.3751 | 1.26955 |
| Percent of variance | 31.412 | 23.16 | 13.751 | 12.695 |
| Cumulative percentage | 31.412 | 54.572 | 68.323 | 81.019 |
| | | Component Weights | | |
| Yield, kg/ha | 0.40395 | 0.20866 | -0.1002 | -0.2876 |
| Plant height, cm | 0.34617 | -0.2356 | 0.4980 | 0.06947 |
| Spike length, cm | 0.50133 | -0.1295 | 0.28393 | 0.13141 |
| Grain number per a spike | 0.46436 | -0.1461 | -0.0744 | -0.0777 |
| Grain mass per a spike, g | 0.31497 | 0.27301 | -0.3182 | -0.2594 |
| 1000 grains mass, g | 0.32353 | -0.0056 | -0.1228 | 0.48177 |
| Hectolitre mass, kg | 0.17423 | 0.01677 | -0.6532 | 0.32034 |
| Uniformity I class, % | 0.07464 | 0.58551 | 0.29963 | -0.0141 |
| Crude protein content, % | -0.0482 | -0.5831 | -0.0732 | 0.11131 |
| Extract content, % | -0.0889 | 0.32428 | 0.13311 | 0.68888 |

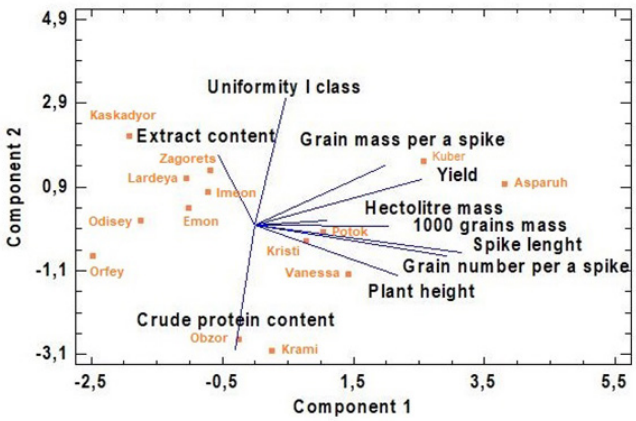


**Fig. 1. Biplot of the principal components analysisof studied traits of 14 two-Rowed winter barley genotypes (2014-2016)**

grain number per a spike, and high grain mass per a spike, high 1000 grains mass and high hectolitre mass.

The dendrogram of the evaluated barley genotypes was presented in Figure 2. Cultivars were grouped into two clusters. Cluster I (in red) have genotypes with maximum in yield, plant height, length spike, grain number per a spike, grain mass per a spike, 1000 grains mass and high hectolitre mass.

A lot of studies reported that number of grains per spike had positive correlation with grain yield and that trait can be used as selection criteria for barley (Tas & Çelik. 2011; Dimitrova-Doneva et al., 2012; Dyulgerova et al., 2016). Cluster II was constituted of 7 cultivars (in green) and produced highest extract content and uniformity I class (Figure 2).

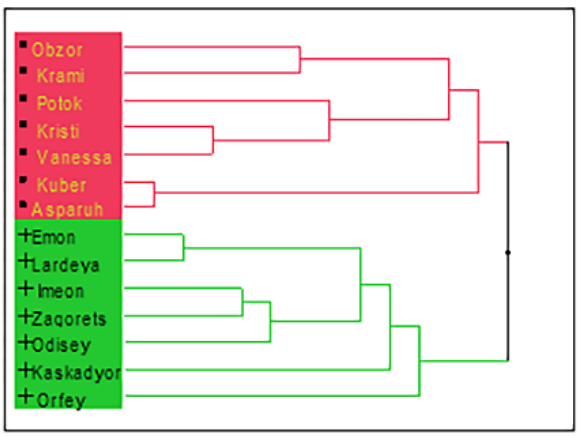


**Fig. 2. Dendrogram base on studied traits of 14 two-Rowed winter barley genotypes (2014-2016)**

## Conclusions

It was found that in the group with the highest yield were the cultivars Asparuh- 6490 kg/ha and Kuber – 6390 kg/ha.The traits, which contributed positively to PC1 were spike length, grain number per a spike and yield. Considering diversity pattern. agronomic and technological traits researched in this studythe cultivars Asparuh. Kuber, Kristi and Potok from first cluster and Orfej, Odisey and Zagorets from second might be selected aspromising genotypes for future hybridization program.

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*Received:* December, 3, 2019; *Accepted:* January, 22, 2020; *Published:* December, 31, 2020