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GENOTYPE BY YIELD*TRAIT BIPLOT FOR GENOTYPE EVALUATION IN WINTER BARLEY

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ABSTRACT

Genotype selection in winter barley, considering multiple traits over several years, often faces challenges due to unpredictable rainfed conditions. The aim of this study was to utilize the genotype by yield*trait (GYT) biplot methodology for selecting genotypes using multi-trait data and analyzing trait profiles in winter barley under rainfed conditions in Southeast Bulgaria. In the experimental field of the Institute of Agriculture – Karnobat, Bulgaria 5 varieties and 15 advanced breeding lines of winter barley were evaluated in a complete block design with four replications in three growing seasons (2019/2020, 2020/2021, and 2021/2022). The GYT biplot method was used for ranking the genotypes based on their levels in combining grain yield with important grain quality traits. The variety Zemela (G5) demonstrated the most favorable combination of grain yield and grain quality. The advanced breeding line M102/10 (G20) outperformed not only the standard variety Veslets (G1), but also newly developed feed varieties like Bojin (G3), Bori (G4), and Zemela (G5), as indicated by the superiority index. These results highlight the potential usefulness of the GYT biplot for selecting genotypes with both desirable grain yield and crucial grain quality traits in winter barley, particularly under rainfed conditions.

Keywords: *winter barley, genotype by yield*trait biplot, multi-traits, superiority index, rainfed condition.*

INTRODUCTION

As barley is one of the most grown cereal in the world, it is crucial to develop high-yielding barley varieties with suitable grain quality to meet the specific end-use requirements. In Bulgaria, barley cultivation primarily relies on rainfed conditions, making the development of varieties with high and stable yield and tolerance to abiotic stresses one of the main challenges for barley breeding.

The simultaneous improvement of multiple traits of interest is one of the main hurdles in plant breeding. Improving a single trait is relatively straightforward however, it is unlikely to result in the development of a useful new variety. This task becomes particularly difficult when negative correlations exist between different traits, which may be attributed to gene linkage, pleiotropic effects, or population genetic structure.

The economic value of any trait in a barley genotype depends on the level of the main target trait, namely, grain yield (Yan et al., 2019). Therefore, the primary objective of multiple trait selection is to combine desirable traits with high grain yield within a single genotype. Various breeding approaches, such as independent culling, tandem selection, and index selection, have been employed to select genotypes with optimal combinations of grain yield and other agronomic traits, under both favorable and stress-inducing environmental conditions (Godshalk et al., 1988; Simmonds and Smartt, 1999; Bos and Caligari, 2007). However, these approaches often involve subjective decisions, as breeders assign weights or truncation points to each trait based on their judgment and the economic importance of the trait (Yan and Frégeau-Reid, 2018).

Recently, the genotype-by-yield trait (GYT) biplot approach, proposed by Yan and Fregeau-Reid (2018), has emerged as a valuable method for selecting superior genotypes based on multiple traits. The GYT biplot ranks genotypes according to their combination of yield with other target traits, such as grain quality and disease resistance. It provides multiple views that not only rank genotypes based on yield-trait combinations but also reveal the trait profiles of each genotype, highlighting their strengths and weaknesses. The GYT biplot approach has been effectively utilized for genotype selection across various cereal crops, including bread wheat (Hamid et al., 2019; Merrick et al., 2020), durum wheat (Kendal, 2019; Mohammadi, 2019; Faheem et al., 2022), and barley (Kendal, 2020; Karahan and Akgun, 2020; Hudzenko et al., 2021; Bakhshi & Shahmoradi, 2022).

The aim of this study was to utilize the genotype by yield*trait (GYT) biplot methodology for selecting genotypes using multi-trait and multi-year data and analyzing trait profiles in winter barley under rainfed conditions in Southeast Bulgaria.

MATERIAL AND METHODS

A total of twenty genotypes of 6-rowed feed winter barley were included in this study. The genotypes consisted of five varieties, namely Vaslets (G1), Izgrev (G2), Bojin (G3), Bori (G4), and Zemela (G5), and fifteen advanced mutant lines: M56/3 (G6), M56/9 (G7), M93/2 (G8), M93/5 (G9), M93/11 (G10), M93/14 (G11), M93/19 (G12), M100/2 (G13), M100/4 (G14), M100/7 (G15), M100/12 (G16), M102/1 (G17), M102/3 (G18), M102/5 (G19), and M102/10 (G20).

The study was conducted in three growing seasons 2019/2020, 2020/2021, and 2021/2022 at the experimental field of the Institute of Agriculture - Karnobat, Southeast Bulgaria (42°39' N, 26°59' E). The soil of the experimental field was slightly acid (pH is 6.2) Pellic Vertisol. The experiments were organized in a Complete Randomize Block Design with 4 replications on plots of 10 m^2 with sowing rate 450 seeds/m^2.

Protein content, % (Keldal's method); lysine content, % (ninhydrin method); fat content, % (Soxhlet method); ash content, % (after burning in a muffle furnace at

550 °C for 3 h); fiber content, % (Weende method), β-glucan content, % (Megazyme kit K-BGLU 07/11), 1000-grains weight, g were analyzed.

The data underwent graphical analysis using the Genotype × Yield × Trait (GYT) biplot method, following the approach outlined by Yan and Frégeau-Reid (2018). A superiority index (SI) combining all yield-trait interactions was calculated based on the standardized GYT data so that the mean for each trait or yield-trait combination was 0 and the variance a unit (Yan and Frégeau-Reid, 2018).

The GYT biplots were carried out in RStudio, R version 4.2.1 by using "metan" R package (Olivoto and Lúcio, 2020).

RESULTS AND DISCUSSION

Accordingly, Yan and Frégeau-Reid (2018) the GYT data was generated by the combination of each trait and grain yield (Table 1). This approach involves applying positive selection through multiplication or negative selection through division for a particular trait. Consequently, the selection outcomes in GYT biplot analysis strongly rely on the included traits. Therefore, Yan and Frégeau-Reid (2018) recommend incorporating only essential traits for the success of a variety in GYT biplot analysis. In present study 5 varieties and 15 advanced breeding lines of winter feed barley were tested. In addition to grain yield, which is of the utmost significance for feed barley, other essential grain quality traits were employed to assess the tested genotypes. Therefore, the GYT table was obtained as follows: for the protein, starch, lysine, fat, ash content, and 1000-grains weight the values for each trait was multiplied (*) with the yield. While for traits fiber and β-glucan content, in which the high values are undesirable, the value for each trait was divided (/) by the yield. The GYT biplot graphically displays the standardized GYT data (Table 1), and the different views of the GYT biplot (Figs 1, 2, and 3) allow the data to be investigated from different angles. The GYT biplot represented 82.23% of total variation by plotting first two principal components.

The Superiority Index (SI) enables the assessment and ranking of genotypes based multiple traits. In this study, the superiority index identified Zemela as exhibiting the most favorable combination of grain yield and quality among the tested varieties. Furthermore, when comparing the advanced breeding lines to the standard variety Veslets (G1), the line M102/10 (G20) overperformed not only the standard variety but also the newly developed feed varieties such as Bojin (G3), Bori (G4), and Zemela (G5), as indicated by the superiority index.

Table 1. Standardized genotype by yield*trait (GYT) data and superiority index for the genotypes

Genotypes	GY*P	GY*L	GY*A	GY*F	GY/Fb	GY/G	GY* TGW	SI
G1	0.54	0.17	-0.36	1.22	0.15	0.13	-0.48	1.37
G2	-1.30	-0.82	-1.40	-0.91	-0.73	-1.17	-1.39	-7.73
G3	1.01	1.45	1.18	0.02	2.08	1.46	0.72	7.92
G4	0.88	0.88	0.63	-0.09	-1.00	1.28	-0.08	2.51
G5	1.15	1.50	0.93	1.40	1.60	1.10	0.60	8.28
G6	0.01	0.26	0.98	0.54	1.41	-0.20	0.32	3.32
G7	0.70	-0.06	0.25	0.24	-0.24	0.25	0.47	1.61
G8	0.32	0.21	0.39	-0.13	0.00	0.54	-0.13	1.19
G9	-0.78	-1.09	-0.56	-1.55	-1.51	-0.89	-1.08	-7.46
G10	-0.72	-0.11	-0.89	0.00	-0.32	-0.70	0.11	-2.63
G11	-1.35	-1.35	-1.46	-0.93	-0.78	-1.30	-0.69	-7.86
G12	-2.38	-2.29	-2.25	-2.48	-1.55	-2.19	-2.48	-15.63
G13	-0.27	-0.14	-0.37	0.19	-0.51	-0.46	-0.47	-2.03
G14	0.25	-0.13	0.08	0.18	0.07	0.00	0.23	0.68
G15	0.36	0.38	0.50	0.43	0.23	0.56	0.86	3.32
G16	-0.14	-0.63	-0.06	-0.22	-0.16	0.10	-0.41	-1.52
G17	0.37	0.98	1.16	1.22	1.01	0.03	1.25	6.04
G18	-0.54	-0.65	-0.36	-0.07	-0.62	-0.47	0.19	-2.53
G19	-0.11	-0.23	-0.07	-0.69	-0.26	0.01	0.22	-1.13
G20	1.99	1.65	1.69	1.64	1.14	1.93	2.22	12.27

P - protein content, %; L - lysine content, %; F - fat content, %; A - ash content, %; Fb - fiber content, %; G - β-glucan content, %; TGW - 1000-grains weight, g; GY – grain yield, t/ha; SI - Superiority Index

Due to the fact that all yield-trait combinations in the GYT biplot included grain yield as a component, most of them were positively associated as exhibited by the acute angles in the biplot (Figure 1). Nevertheless, some of the strong associations between traits, such as the negative correlation between fiber and β-glucan content, can be observed in the GYT biplot, as indicated by the magnitudes of angles between GY/G and GY/Fb. (Figure 2).

Figure 3 presents the polygon view, also known as the "which-won-where" analysis, illustrating the relationship between different yield-traits combinations and genotypes. This visualization technique allows us to identify genotypes that exhibit superior performance in combining grain yield with other desirable traits.

Upon analyzing the figure, it is evident that genotype G17 stands out as it possesses the largest value for GY/G, indicating an exceptional combination of high grain yield and low β-glucan content. This suggests that G17 is a promising variety for achieving both high yield and reduced levels of β-glucan, which is desirable for feed barley.

Furthermore, genotype G4 demonstrates a favorable combination of high grain yield and low fiber content in the grain. This characteristic is valuable as low fiber content is often associated with improved feed grain quality.

Another noteworthy genotype is G20, which exhibits high levels across most of the studied yield-traits combinations. This implies that G20 possesses a well-rounded profile, excelling in both high yield and grain quality simultaneously.

Ranking of the genotype by yield*trait biplot in Figure 3 ranks the genotypes based on their overall superiority. The ATA axis separates genotypes that perform better than the average (placed on its right) from those that perform poorer than the average (placed on the left side) (Yan & Frégeau-Reid, 2018). Based on this ranking, the best-performing genotypes in terms of yield-trait combinations are G20, G5, G7, and G3, while genotypes G12, G2, G9, and G11, positioned on the far-left side of the biplot, are ranked as the worst performers.

Genotypes placed close to the ATA axis tend to exhibit balanced trait profiles, suggesting they have relatively equal strengths and weaknesses across the studied traits (Yan & Frégeau-Reid, 2018). In this case, G20, G5, and G7 demonstrate balanced trait profiles.

Furthermore, genotypes positioned above the ATA axis, such as G7, G3, G6, G10, and G11, showed a relatively better combination of 1000-grain weight (TGW) and lower β-glucan content (G). Conversely, genotypes placed below the ATA axis, including G4, G1, G15, G16, and G9, exhibit a better combination of grain yield, higher protein content (P), and lower fiber content (Fb).

The results showed that the GYT biplot approach allows the selection of high-yielding barley genotypes with good agronomic characteristics and it may be used to assist the development of new barley varieties with high economic value for the rainfed conditions of Bulgaria.

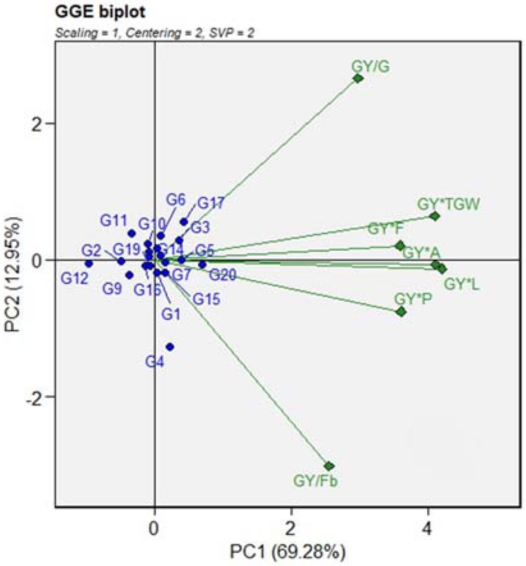

Figure 1. The Tester Vector view of the genotype by yield*trait (GYT) biplot

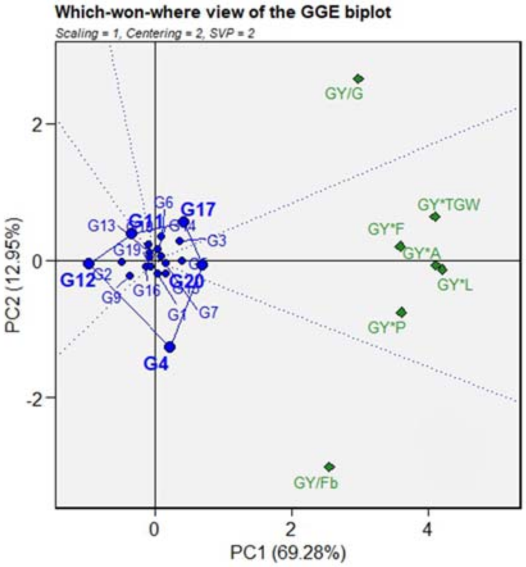

Figure 2. The which-won-where view of the genotype by yield*trait (GYT) biplot

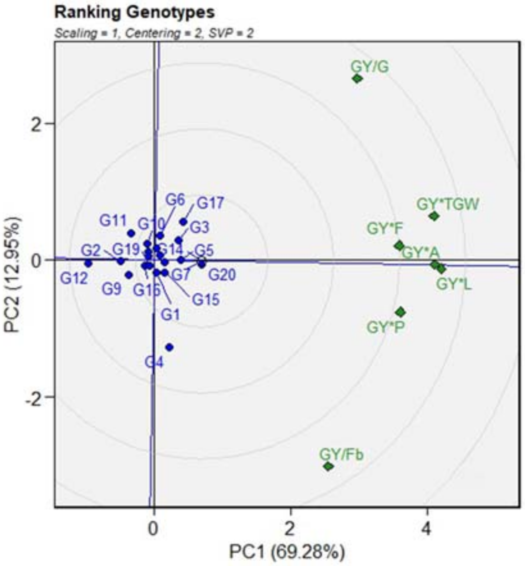

Figure 3. Ranking of the genotypes by yield*trait (GYT)

CONCLUSIONS

The results of this study provide valuable insights into the assessment and selection of winter feed barley genotypes based on grain yield and feed grain quality traits using the GYT biplot analysis. Among the tested genotypes, Zemela (G5) exhibited the most favorable combination of grain yield and quality. The advanced breeding line M102/10 (G20) displayed superior performance not only compared to the standard variety Veslets (G1) but also outperformed newly developed feed varieties, including Bojin (G3), Bori (G4), and Zemela (G5), as indicated by the superiority index. The results highlight the potential of the GYT biplot approach in selecting high-yielding barley genotypes with desirable agronomic characteristics. This methodology can support the development of new barley varieties that possess high economic value, particularly suitable for rainfed conditions in Bulgaria.

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