Bulgarian Journal of Agricultural Science, 31 (No 6) 2025, 1137–1148

Genetic parameters and multiple-trait selection in winter barley genotypes

Boryana Dyulgerova[*] **and Darina Valcheva**

Agricultural Academy, Institute of Agriculture, 8400 Karnobat, Bulgaria
[*]*Corresponding author:* bdyulgerova@abv.bg

Abstract

Dyulgerova, B. & Valcheva, D. (2025). Genetic parameters and multiple-trait selection in winter barley genotypes. *Bulg. J. Agric. Sci., 31*(6), 1137–1148

This study aimed to assess the genetic potential of advanced barley genotypes using REML/BLUP and identify top-performing breeding lines by employing the multi-trait genotype–idiotype distance index (MGIDI). Twenty-one two-rowed winter barley genotypes, including six varieties and 15 advanced breeding lines, were evaluated over two growing years (2020/2021 and 2021/2022) at the Institute of Agriculture-Karnobat, Southeastern Bulgaria. Key traits such as number of spikes per m^2, plant height, dry weight of plant, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, grain weight per plant, harvest index, 1000-grain weight, and grain yield were studied. The combined analysis of variance revealed highly significant variations in genotype, year, and their interaction for all traits except harvest index, which showed no significant variation between growing seasons. Grain yield demonstrated diverse associations with different traits in each season, underscoring the impact of specific environmental conditions. Throughout both growing years, grain yield exhibited a significant correlation with ^{2}the number of spikes per m^2, emphasizing the crucial role of this trait in selecting high-yielding genotypes of winter barley. In 2021, the multi-trait genotype-ideotype distance index (MGIDI) identified 12 genotypes that outperformed the standard variety; however, only two maintained their excellence in 2022, highlighting the importance of genotype adaptability. Among the selected genotypes, the breeding line 671D-3/10 consistently demonstrated superior performance in both growing seasons, showcasing its adaptability and breeding value. The study contributes valuable insights for selecting high-yielding winter barley genotypes, providing a foundation for future breeding efforts.

Keywords: Hordeum vulgare L.; REML/BLUP; grain yield; yield-related traits; multi-trait genotype-idiotype distance index

Introduction

Barley (*Hordeum vulgare* L.) holds the position as the fourth most widely grown crop globally in terms of production volume. It stands out as a critical primary ingredient for the malting and brewing industries. Additionally, barley is a valuable source of nutrition for both humans and livestock. As the world faces increasing pressure to produce more food while adapting to a changing climate, the demand for highly productive, disease-resistant, and adaptable barley varieties has never been greater. To meet these demands, it is essential to refine the selection process for advanced barley genotypes, unlocking the full potential of this cereal crop.

The genetic improvement of barley genotypes is a gradual process that involves identifying and selecting new alleles and traits in germplasm and combining these superior alleles and traits in the desired genetic background. Mixed models are commonly used to determine the predicted genetic values for the most critical breeding objectives, thereby improving the efficiency of selection (Ramalho and Araújo, 2011). The restricted maximum likelihood (REML) and best linear unbiased prediction (BLUP) methods have been employed as practical selection approaches to estimate variance components and predict genetic values (Piepho et al., 2008).

Genetic gain, a critical measure of success in plant breeding, quantifies the improvement in selected traits between original and subsequent generations (Elsen, 2016). Breeders often aim to combine multiple desirable traits within a new genotype to achieve superior performance (Jahufer and Casler, 2015). This had led to the development of several selection indices aimed at identifying superior genotypes (Sanhueza et al., 2002; Vieira et al., 2016; Rocha et al., 2018). However, accurately expressing the economic value of traits and converting them into realistic economic weightings can pose challenges to selecting the best genotypes (Bizari et al., 2017).

To address these challenges, the multi-trait genotype–ideotype distance index (MGIDI) has been introduced as a method for genotype selection based on breeding values, considering information from multiple traits (Olivoto and Nardino, 2021). Unlike conventional ranking methods using post-hoc tests such as Fisher's least significant differences (LSD) or Tukey's honest significant difference (HSD) in ANOVA, which allow ranking for only one test, the MGIDI index can rank genotypes based on their performances across multiple traits. Furthermore, MGIDI avoids issues of collinearity by conducting indexing through factor analysis (Olivoto and Nardino, 2021). This index has been successfully utilized in various crops, including wheat (Pour-Aboughadareh and Poczai, 2021), rice (Debsharma et al., 2022; Jalalifar et al., 2023), maize (Singamsetti et al., 2023), and oat (Klein et al., 2023), among others.

This study aimed to determine the genetic potential of advanced barley genotypes using REML/BLUP and selected the best breeding lines based on the multi-trait genotype-idiotype distance index (MGIDI).

Material and Methods

***Plant material*:** Twenty-one two-rowed winter barley (*Hordeum vulgare* L.) genotypes were included in the study. Among these genotypes were four Turkish varieties – Bolayir (G13), Burgaz (G14), Harman (G16), and Hasat (G17), one Serbian variety Sladoran (G19), the Bulgarian national standard variety Emon (G15), and 15 advanced breeding lines, including lines 003D-3/13 (G1), 167D-1/05 (G2), 167D-2/05 (G3), 194D-1/15 (G4), 218D-1/15 (G5), 419D-2/08 (G6), 419D-5/08 (G7), 530D-2/09 (G8), 639D-3/10 (G9), 671D-3/10 (G10), 718D-4/10 (G11), 939D-4/13 (G12), KT337 (G18), WS270D-1/15(G20), and A9/14 (G21).

***Site characteristics, experimental design, and agronomic practices*:** The study was conducted over two growing years, 2020/2021 and 2021/2022, at the experimental field of the Institute of Agriculture-Karnobat, Southeastern Bulgaria (42°39' N, 26°59' E). The soil of the experimental field was slightly acidic (pH 6.2), Pellic Vertisol. The experiments were designed using a complete block with four replications on 10 m² plots, with a sowing rate of 450 germinated seeds per m². Standard technology for growing winter barley breeding materials at the Institute was employed, with a preceding crop of a pea–sunflower mix. In February, a one-time nitrogen (N) fertilization was applied at a rate of 30 kg/ha of active substance nitrogen. Weed control in the field trials was managed using a herbicide combination of Biathlon and Scorpio. No pesticides were used for disease or pest control, as no pathogens and pests were observed at densities surpassing economic threshold values during both growing seasons.

***Meteorological conditions*:** Table 1 provides information on average temperatures and precipitation sums during the experimental periods. Despite total precipitation during the first vegetation period (October 2020 to June 2021) exceeding the long-term average for the location by 197.4 mm, the distribution was uneven. Notably, January had the highest precipitation at 142.8 mm, a 291% increase compared to long-term values. April received 86 mm, nearly double the long-term sum, followed by a drier May. Except for March, April, and June, monthly temperatures were higher than the long-term averages. In the second cropping year (2021/2022), precipitation was close to the long-term average, with lower sums in November, January, March, and May, and more than twice the average in December. The monthly average air temperatures were higher than the long-term averages, except for October and March.

***Measurements of traits*:** The plant height (PH, cm) dry weight of plant (DWP, g), spike length (SL, cm), number of spikelets per spike (NSS), number of grains per spike (NGS), grain weight per spike (GSW, g), grain weight per plant (GWP, g) were measured on 20 randomly selected plants in each replication of each genotype. The number of spikes per *square meter (SPM) was determined by counting spikes before harvest in* a *0.25 m² area from the middle of* the *plots and then converted to 1 m².* Grain yield (GY, t ha^{-1}) and 1000-grain weight (TGW, g) were determined on a plot basis. Barley grain was harvested mechanically with a plot harvester in each year at full grain maturity (BBCH 89). After harvesting, the grain yield per unit area was determined and given as t ha^{-1}.

***Statistical analyses*:** Data analysis and graph construction were performed using R (version 4.3.0) within the RStudio integrated development environment. Two-way analysis

Table 1. Average air temperature, monthly sums of precipitation and long-term average data in Karnobat, Southeastern Bulgaria during barley vegetation (2020/2021- 2021/2022)

Months	2020/2021		2021/2022		LT	
	T, °C	P, mm	T, °C	P, mm	T, °C	P, mm
X	15.8	70.7	11.1	79.1	12.5	44.3
XI	7.4	25.5	8.7	31.7	7.1	53.7
XII	6.6	94.5	4.5	105.7	2.6	51.2
I	3.7	142.8	2.4	8.0	0.6	36.5
II	4.9	22.1	4.4	39.7	2.2	35.8
III	4.9	47.4	3.5	12.3	5.3	34.1
IV	9.5	86.0	11.2	48.2	10.5	45.3
V	16.6	15.6	15.9	36.3	15.6	58.5
VI	19.3	117.4	21.0	86.8	19.6	65.2
T, °C	9.9		9.2		8.4	
P, mm		622.0		447.8		424.6

T – average air temperature; P – sum of precipitation; LT – long-term average air temperature and sum of precipitation (1931–2022)

Source: Authors' own elaboration

of variance (ANOVA) was used to identify significant differences among the genotypes and growing seasons using the package. Calculations of Pearson correlation coefficients with p-values, genetic parameters, the best linear unbiased prediction (BLUP) for genotypes, and the multi-trait genotype-ideotype distance index (MGIDI) were performed as proposed in R using the 'metan' package (https://github.com/TiagoOlivoto/metan, 24 January 2024) (Olivoto and Lúcio, 2020). Heritability is classified as high when it has a value greater than 80%, moderate when it ranges between 40% and 80%, and low when it is less than 40% (Singh, 1990). Accuracy is classified as very high – greater than or equal to 0.90, high – from 0.70 to 0.89, moderate – from 0.50 to 0.69, and low – below 0.50 (Resende and Duarte, 2007). The BLUPs were used for hierarchical heatmap clustering based on Ward's method, implemented using the R package "*pheatmap*" (Kolde and Kolde, 2015).

Results

Analysis of variance, heritability, and phenotypic variation

The result of the combined analysis of variance (Table 2) revealed highly significant variation ($p < 0.001$) between genotype, year, and (GxY) interaction for all studied traits (SNM, PH, DWP, SL, SNS, GNS, GWS, GWP, TGW, and GY), except for HI, where no significant variation was observed between growing seasons.

The estimates of phenotypic variance (Vph) were lowest for HI and highest for SNM (Table 3). Broad-sense heritability (H2) estimates were moderate for DWP (0.52), GWP (0.47), and TGW (0.46). However, the remaining traits exhibited low heritability, ranging from 0.01 (SNS) to 0.27 (HI). Traits associated with spike productivity, as spike length (SL), spikelet number per spike (SNS), grain number per spike (GNS), and grain weight per spike (GWS), displayed exceptionally low heritability. Notably, SL, SNS, and GNS demonstrated remarkably high values for the coefficient of determination of the interaction effects (GEIr2). Heritability on the mean basis (h^2_{mg}) was low for SNM, PH, SL, SNS, GNS, GWS, and GY, while DWP, GWP, TGW, and HI showed moderate values for h^2_{mg}. The accuracy of selection (Ac) was low for SL, SNS, GNS, and GWS, moderate for SNM, PH, and GY, and high for DWP, GWP, HGW, and HI. Genotype-environment correlation (rge) exhibited high values for all studied traits, with extremely high values noted for SNM, SL, SNS, GNS, TGW, and GY. SNM, GWP, and DWP were characterized by the highest coefficient of variation for genotype (CVg). The CVg/CVr ratio, which determines the coefficient of variation, offers insight into potential improvement possibilities within the evaluated population for the studied trait. The highest relative variation was observed for TGW (8.19), followed by SPM (4.91).

Variation in yield-related traits and grain yield between the growing seasons (2021 and 2022) is also illustrated in Figure 1, as well as BLUPs. During the 2022 growing season, the conditions were conducive to higher mean values for spike number per square meter (SNM), plant height (PH), dry weight of plant (DWP), and grain weight per plant (GWP) in the studied breeding lines and varieties. Conversely, spike length (SL), spikelet number per spike (SNS), grain number per spike (GNS), grain weight per spike (GWS), and 1000-grain weight (TGW) were higher in the 2021 growing season. There was minimal variation observed between

Table 2. Combined analysis of variance for yield-related traits of 21 barley genotypes assessed for two growing seasons

Traits	GEN	ENV	GEN x ENV	Residuals
SNM	93491.563***	810509.292***	58132.498***	3.599
PH	76.633***	288.095***	55.658***	0.051
DWP	4.870***	111.443***	1.434***	0.037
SL	2.032***	52.674***	1.352***	0.052
SNS	19.462***	498.560***	17.037***	0.031
GNS	19.735***	483.652***	16.477***	0.008
GWS	0.055***	1.522***	0.036***	0.037
GWP	1.351***	19.701***	0.702***	0.036
TGW	29.993***	207.326***	9.858***	0.000
HI	0.003***	0.001ns	0.004***	0.044
GY	2.961***	26.299***	1.955***	3.599

*** significant level at $p \leq 0.001$; ns – not significant; SNM – spike number per m^2; PH – plant height, cm; DWP – dry weight of per plant, g; SL – spike length, cm; SNS – spikelet number of per spike; GNS – grain number of per spike, GWS – grain weight per spike, g; GWP – grain weight per plant, g; HI – harvest index; 1000- grain weight – TGW, g; GY – grain yield, t ha^{-1}

Source: Authors' own elaboration

Table 3. Estimation of variance components and genetic parameters for yield-related traits in 21 winter barley genotypes

Traits	V_{ph}	H^2	GEIr2	h^2_{mg}	Ac	r_{ge}	CVg	CVr	CV ratio
SNM	19091.00	0.23	0.76	0.38	0.62	0.99	8.84	1.80	4.91
PH	19.20	0.14	0.68	0.27	0.52	0.79	1.65	1.93	0.86
DWP	0.83	0.52	0.42	0.71	0.84	0.87	5.92	2.08	2.84
SL	0.53	0.02	0.91	0.04	0.21	0.93	1.26	2.32	0.55
SNS	4.88	0.01	0.99	0.01	0.10	0.99	0.58	0.85	0.68
GNS	4.78	0.04	0.96	0.07	0.27	0.99	1.67	0.70	2.37
GWS	0.02	0.09	0.48	0.23	0.48	0.52	3.00	6.81	0.44
GWP	0.25	0.47	0.39	0.69	0.83	0.72	6.84	3.84	1.78
TGW	5.15	0.46	0.53	0.63	0.80	0.99	3.11	0.38	8.19
HI	0.01	0.27	0.32	0.56	0.75	0.44	3.55	4.40	0.81
GY	0.65	0.19	0.74	0.34	0.58	0.92	4.97	2.92	1.70

V_{ph} – phenotypic variance; H^2 – heritability in broad sense; **GEIr2** - coefficient of determination of the interaction effects; h^2_{gm} – heritability on the mean basis; Ac – accuracy of selection; r_{ge} – genotype-environment correlation, **CVg-** genotypic coefficient of variation; **CVr** – residual coefficient of variation; **CV ratio** - ratio between genotypic and residual coefficient of variation; SNM – spike number per m^2; PH – plant height, cm; DWP – dry weight of per plant, g; SL – spike length, cm; SNS – spikelet number of per spike; GNS – grain number of per spike, GWS – grain weight per spike, g; GWP – grain weight per plant, g; HI – harvest index; TGW – 1000- grain weight, g; GY – grain yield, t ha^{-1}

Source: Authors' own elaboration

the two growing years for mean harvest index (HI), with no significant differences in the genotype BLUP values for this trait. Grain yield (GY) was significantly higher in the 2022 growing season compared to 2021. The mean GY for 2022 was 7.52 t ha^{-1}, with a range of 6.39 to 8.62 t ha^{-1}. In contrast, the mean GY for 2021 was 6.73 t ha^{-1}, exhibiting a wider range from 5.15 to 8.55 t ha^{-1}.

To further explore the phenotypic variation of the studied set of winter barley, the BLUPs of the genotypes are presented in Figure 2. The standard variety Emon (G15) exhibited a BLUP value for SNM approximately around the mean value. Seven breeding lines exceeded the mean SNM, demonstrating their superior performance in this regard. The lowest PH was recorded for G4 and GF16. Emon (G15) also demonstrated the highest BLUP value for DWP. The standard variety possessed a shorter SL but combined with the highest SNS, GNS, and GWS. Above-average SNS and GNS were observed in breeding lines G5, G10, G6, G21, G2, and G20, as well as in the variety Burgaz (G14). Low SL, SNS, and GNS characterized line G1. Only line G7 exhibited a higher BLUP for GWP compared to the standard variety. Very high BLUP values for TGW (exceeding 50 g) were identified in G21, G13, G7, G12, G6, G18, G16, and G5. The BLUP values for GY ranged from 6.75 t ha^{-1} for G16 (Harman) to

7.57 t ha^{-1} for G5 (218D-1/15). All studied varieties and line 419D-2/08 (G6) had GY below that of the standard Emon (G15), while the rest of the breeding lines showed GY values above the standard.

Phenotypic correlation coefficients of yield-related traits

The phenotypic correlations between various studied traits across two growing seasons, 2021 and 2022, are illustrated in Figure 3. In the 2021 cropping year, GY demonstrated a significant and positive correlation with several traits, including SNM (0.51), HI (0.49), GWP (0.39), SL (0.34), TGW (0.29), and PH (0.28). However, in the subsequent growing season of 2022, GY had a significant and positive correlation solely with SNM (0.53).

In 2021, GWP showed significant and positive correlations with DWP, HI, SNS, and GNS. In 2022, GWP displayed significant and positive correlations with HI, DWP, and TGW.

TGW also displayed varying patterns of correlation

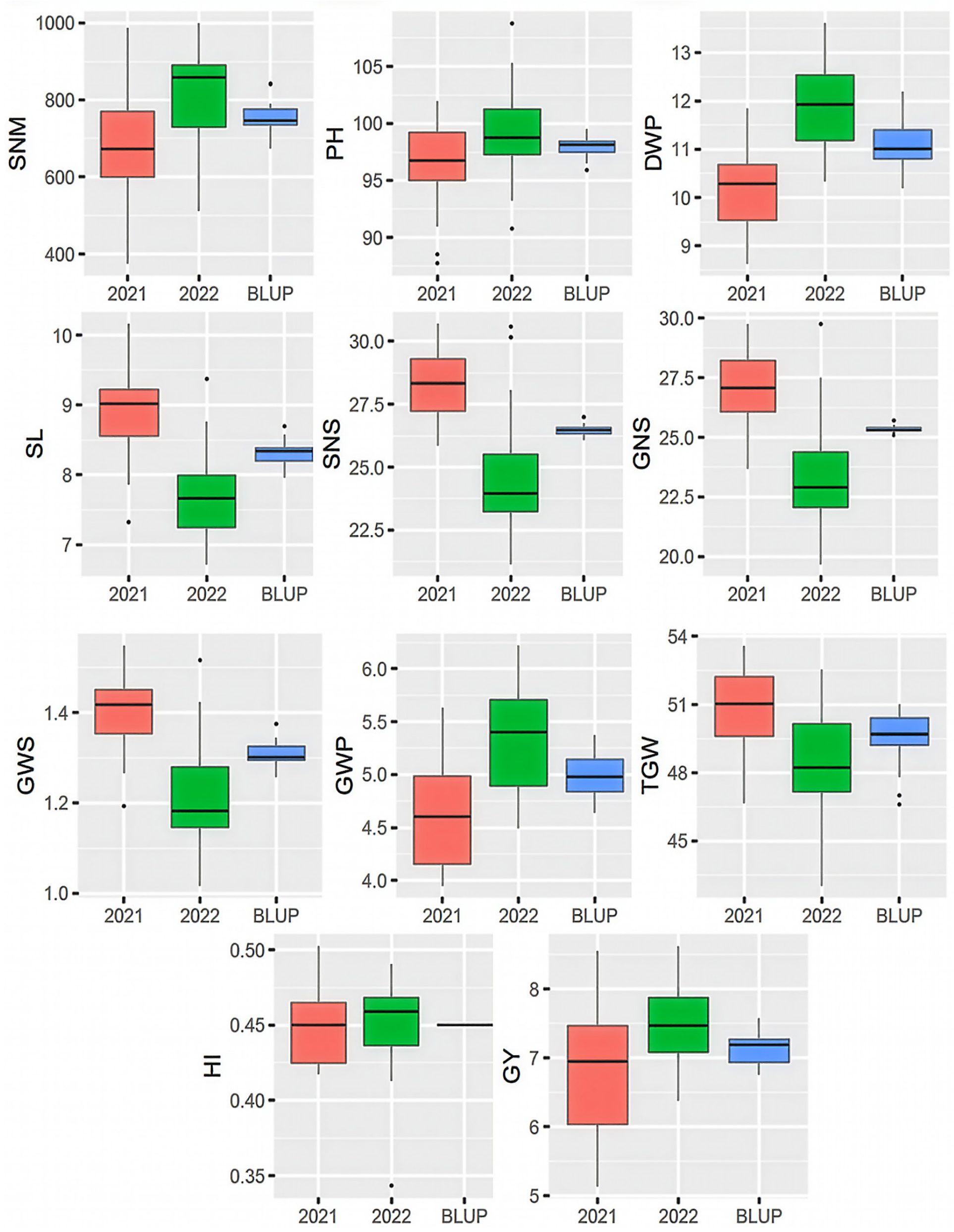

Fig. 1. Variation in yield-related traits and grain yield between the growing seasons (2021 and 2022) and BLUPs for spike number per m^2 (SNM), plant height, cm (PH), dry weight of per plant, g (DWP), spike length, cm (SL), spikelet number of per spike (SNS); grain number of per spike (GNS), grain weight per spike, g (GWS), grain weight per plant, g (GWP) ; harvest index (HI); 1000-grain weight, g (TGW), grain yield, t ha^{-1} (GY)

Source: Authors' own elaboration

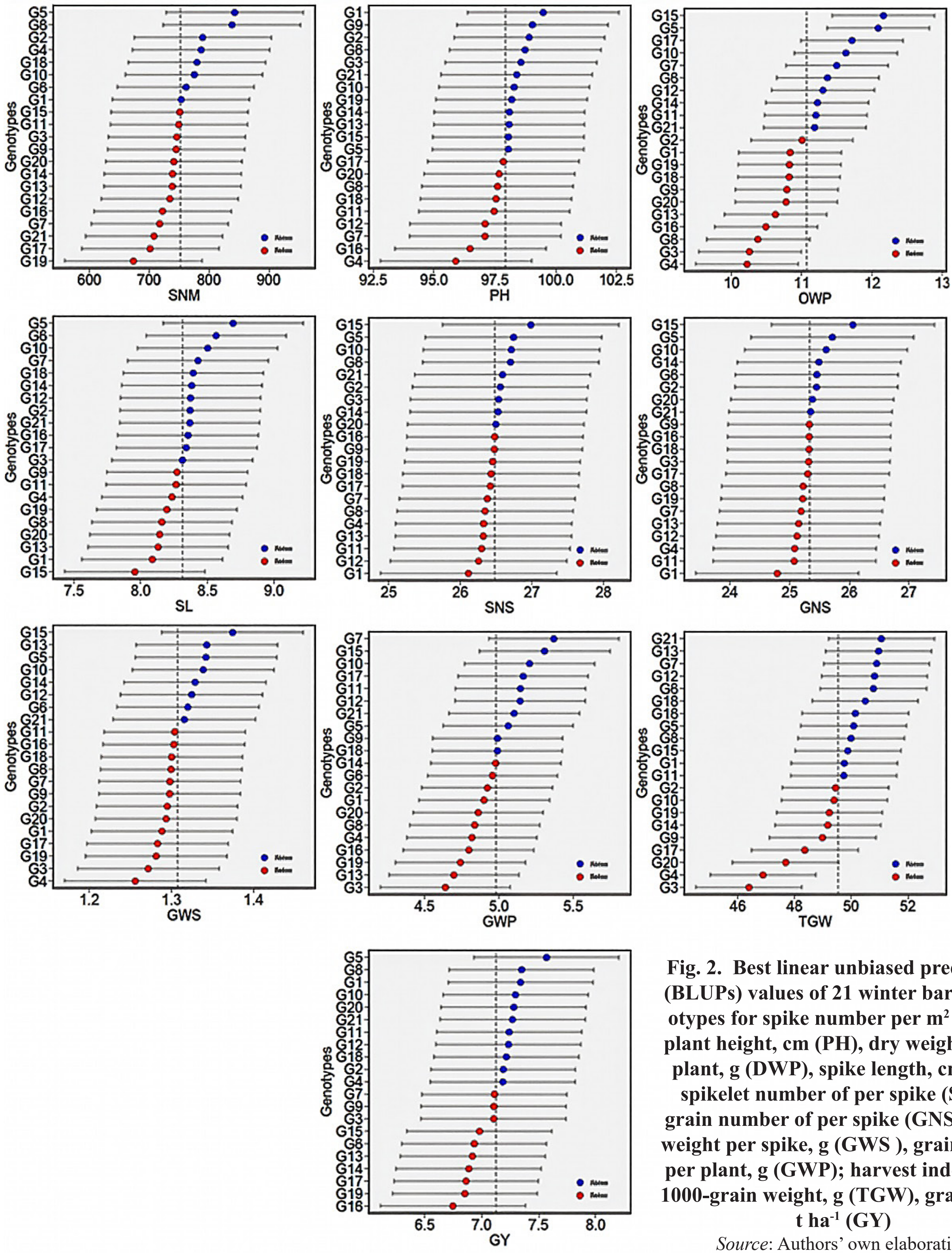

Fig. 2. Best linear unbiased predictions (BLUPs) values of 21 winter barley genotypes for spike number per m^2 (SNM), plant height, cm (PH), dry weight of per plant, g (DWP), spike length, cm (SL), spikelet number of per spike (SNS); grain number of per spike (GNS); grain weight per spike, g (GWS), grain weight per plant, g (GWP); harvest index (HI); 1000-grain weight, g (TGW), grain yield, t ha^{-1} (GY)

Source: Authors' own elaboration

with other traits in the two growing seasons. In 2021, TGW showed significant and positive correlations with SL and GWS. In 2022, TGW exhibited significant and positive correlations with GWP, GWS, and PH.

Cluster analysis

The studied genotypes can be classified into four distinct groups based on their yield-related characteristics (Figure 4). The first group comprises six genotypes: breeding lines G5, G10, G21, G6, the variety Burgaz (G14), and the standard variety Emon (G15). This group stands out for its high spike productivity, revealed by high values for SNS, GNS, and GWS.

The second group consists of four genotypes: three breeding lines (G11, G12, and G7) and the variety Hasat (G17). This group distinguished itself with shorter PH and high HI, indicating a focus on efficient resource allocation.

The third group comprises four genotypes: three breeding lines (G1, G3, G4) and the variety Sladoran (G19). Noteworthy characteristics of this group are lower values for SL, GNS, and GWS.

The fourth group comprises breeding lines G2, G8, G9, G18, G20, and varieties Bolayir (G13) and Harman (G16). These genotypes are characterized by a balanced combination of GY and SNM. However, it is interesting to note that within this group, varieties Bolayir (G13) and Harman (G16) form a separate subgroup with lower productivity. While these two varieties were clustered together, the remaining two varieties with the same origin, Burgaz (G14) and Hasat (G17), were positioned in other clusters, emphasizing distinctions in their yield components.

Selection of genotypes based on multi-trait genotype–idiotype distance index (MGIDI)

The traits in the first growing year were grouped into five factors, whereas in the second growing year, traits were grouped into four factors (Table 4). Closely related traits were grouped within the same factor. In both years, GY were grouped along with SNM, indicating the importance of this trait for GY of winter barley despite the different conditions.

In 2021, a total of 12 genotypes – 10 breeding lines (G5, G4, G7, G2, G9, G12, G11, G10, G21, G8) and two varieties (Hasat, Burgaz) – were ranked higher than the standard variety Emon (G15) (Figure 5A). This suggests that these genotypes exhibited superior performance in terms of yield-related traits compared to the standard variety. Upon applying a 15% selection intensity, the lines G18, G21, and G10 emerged as the top performers in the first cropping season.

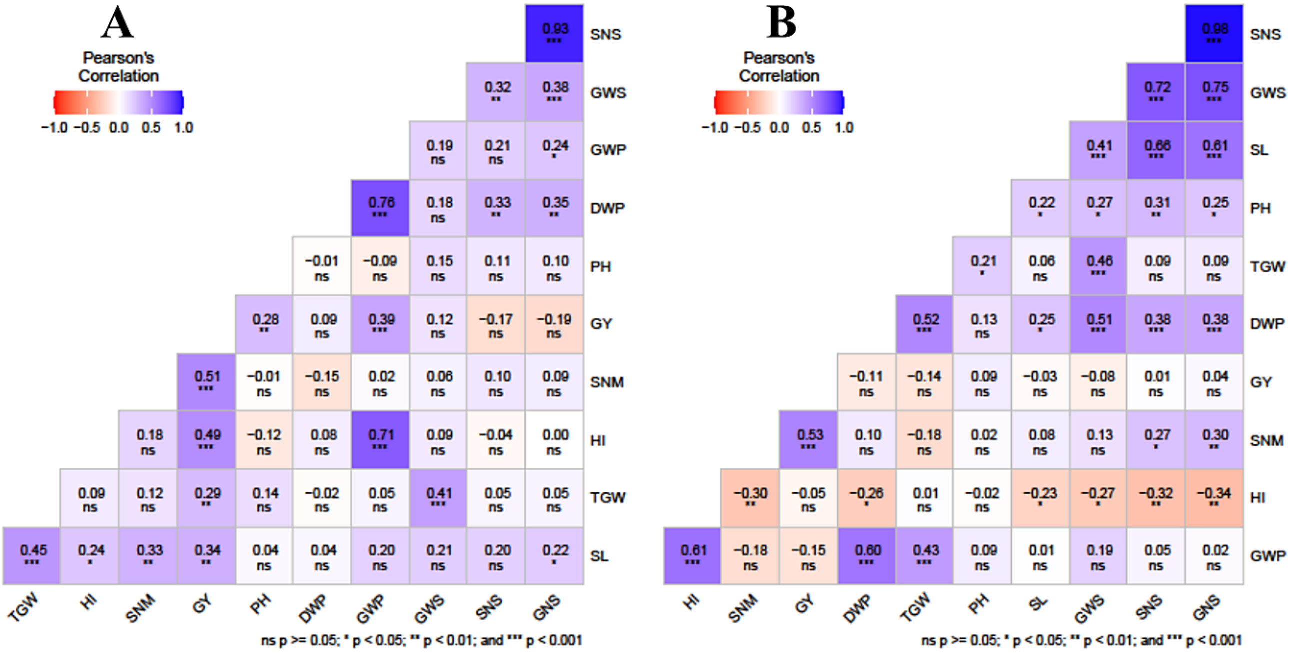

Fig. 3. Phenotypic correlation coefficients among yield-related traits for 2021 (A) and 2022 (B)
Source: Authors' own elaboration

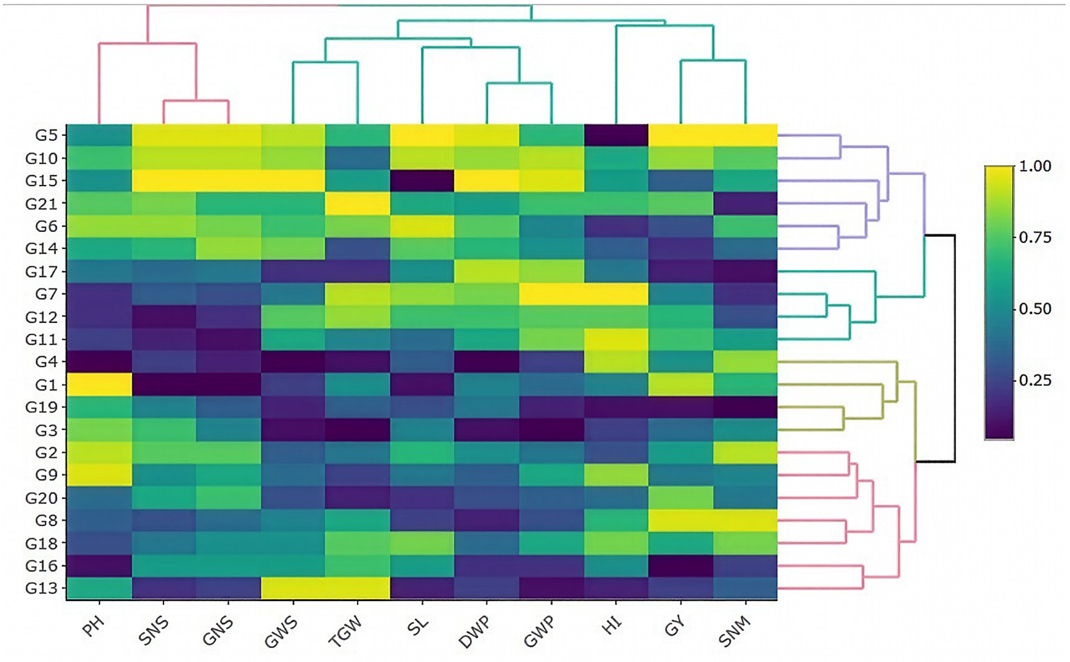

Fig. 4. Heat map and hieraclitical clustering analysis by Euclidian distance using Ward s methods

Source: Authors' own elaboration

Table 4. Groups the traits in different factors by multi-trait genotype–idiotype distance index

FA1		FA2		FA3		FA4		FA5	
2021	2022	2021	2022	2021	2022	2021	2022	2021	2022
SNS	SL	GWS	DWP	DWP	SNM	SNM	PH	PH	
GNS	SNS	TGW	GWP	GWP	GY	GY		SL	
	GNS		TGW					HI	
	GWS		HI						

SNM – spike number per m^2; PH – plant height, cm; DWP – dry weight of per plant, g; SL – spike length, cm; SNS – spikelet number of per spike; GNS – grain number of per spike, GWS – grain weight per spike, g; GWP – grain weight per plant, g; HI – harvest index; TGW – 1000- grain weight, g; GY – grain yield, t ha^{-1}

Source: Authors' own elaboration

In 2022, only two lines, G10 and G5, were positioned above the standard variety (Figure 5B). Remarkably, the lines G18 and G21, which had secured first and second places the previous year, significantly dropped in ranking, with G18 placing 10th and G21 plummeting to 18th place. Despite this variability, line G10 consistently demonstrated superior performance across both seasons, ranking among the top-selected genotypes under a 15% selection intensity. This indicates that line G10 possesses robust adaptability and consistently exhibits high performance across multiple traits, regardless of environmental conditions in different growing seasons.

In 2021, factor FA1 made the smallest contribution for genotype G21, indicating that this line exhibited spike productivity (highest GNS and GWS) among the selected ones (Figure 6A). The genotypes G21 and G10 exhibited strengths related to FA2 and FA3, suggesting that these lines should have simultaneously high values for GWS, TGW, DWP, and GWP. The three selected had strengths related to FA5 (SNM and GY). The smallest contribution of FA5 for G18 suggests that these genotypes have shorter stems, longer spikes, and higher HI compared to G10 and G21, in which FA5 had a high contribution.

In 2022, factor FA1 made the smallest contribution for genotypes G5 and G15, indicating high values of spike-related traits (SL, SNS, GNS, and GWS) (Figure 6B). G15 has strengths related to FA2, indicating that this breeding line should simultaneously have high values for DWP, GWP, TGW, and HI. The smallest contributions of FA3 for G5 indicated that this genotype had the highest GY for the cropping year. The genotype G10 has strengths related to FA4, indicating that this genotype has a short stem.

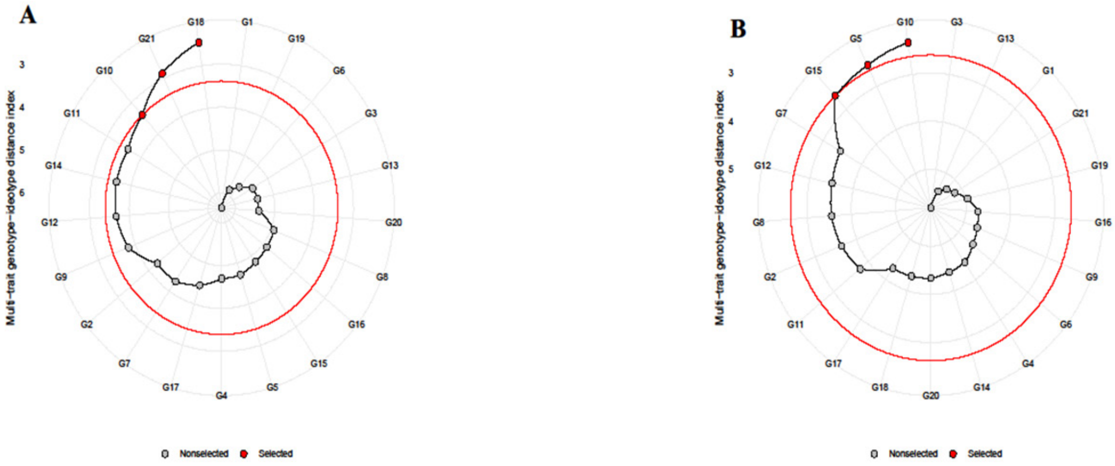

Fig. 5. Ranking of genotypes based on the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) for 2021 (A) and 2022 (B). The red line refers to the selection intensity of 15%

Source: Authors' own elaboration

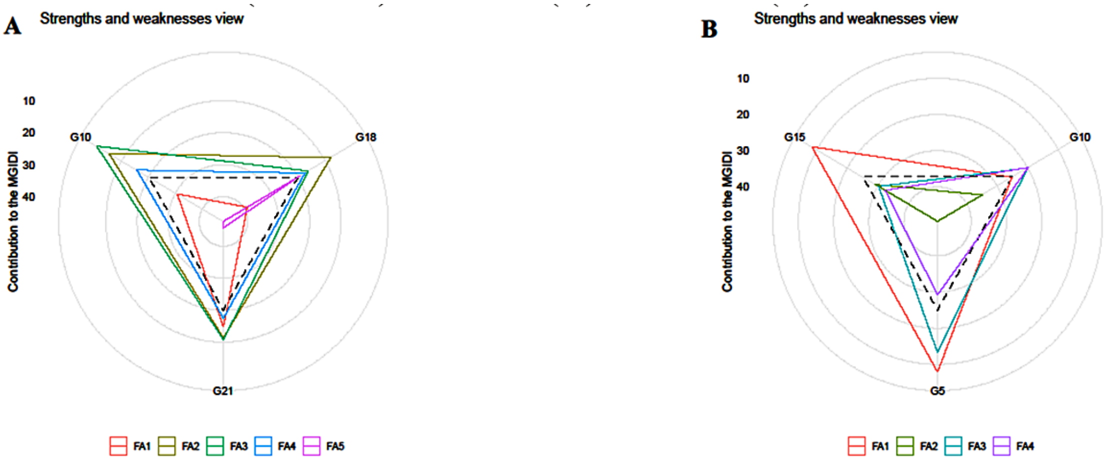

Fig. 6. Strengths and weaknesses view of the selected genotypes is shown as the proportion of each factor on the computed Multi-Trait Genotype-Ideotype Distance Index (MGIDI) for 2021 (A) and 2022 (B)

Source: Authors' own elaboration

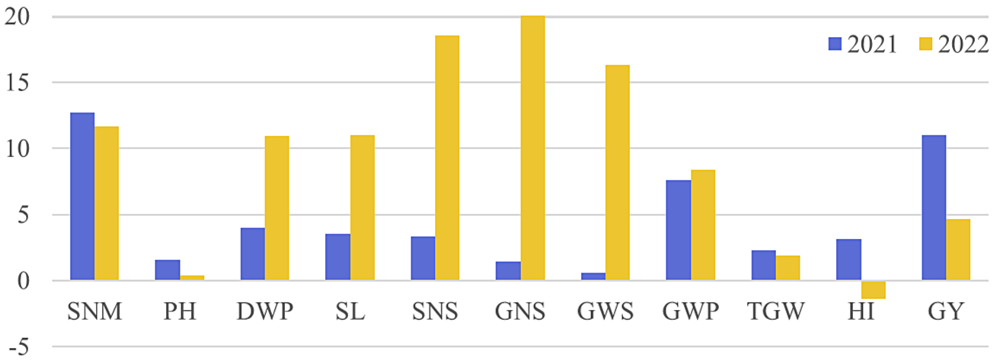

Fig. 7. Selection gain of studied traits in the selected genotypes by multi-trait genotype–ideotype distance index

Source: Authors' own elaboration

Figure 7 compares the percentage of selection gains (SG) for studied traits in 2021 and 2022. As observed, the percentage of selection gains for DWP, SL, SNS, GNS, GWS, and GWP was significantly higher in 2022 compared to 2021. However, the MGIDI index was unable to achieve negative gains for PH, the only trait that was intended to be reduced. Additionally, in 2022, the MGIDI index resulted in a negative gain for harvest index HI, indicating the selection of genotypes with lower HI. The MGIDI index demonstrated satisfactory gains and good effectiveness in selecting genotypes with high SNM (12.70% in 2021 and 11.68% in 2022, respectively), a trait with positive correlations with GY across both growing seasons. The index yielded the most substantial selection gains for GNS (20.06%), SNS (18.51%), and GWS (16.21%) during 2022. The index's efficacy in enhancing TGW was less pronounced, with gains of 2.25% in 2021 and 1.92% in 2022. The positive selection gains for GY, ranging from 11.01% in the first growing season to 4.66% in the second growing season, highlight the potential for selecting breeding lines with improved grain yield from the studied set of genotypes.

Discussion

In plant breeding, multi-trait selection is a crucial strategy for enhancing multiple desirable traits simultaneously, thereby ensuring improved crop performance across diverse environments. However, the complexity of simultaneous trait selection is amplified by the influence of meteorological conditions, which can alter the relationships between traits and their impact on yield. This dynamic interplay between environmental factors and agronomic traits poses challenges in optimizing selection strategies. In the present study, significant variations were observed in traits correlated with grain yield (GY) across both growing seasons. These differences in correlations between yield and related traits align with findings from previous studies on barley (Tawfiq et al., 2016; Akgün, 2018). Our prior investigations (Dyulgerov and Dyulgerova, 2020; Dyulgerova and Dyulgerov, 2023) have also highlighted the existence of differing correlations between yield and related traits in different growing seasons.

In recent years, Southeastern Bulgaria has experienced a rise in extreme variations in rainfall distribution. This trend is evident in the growing seasons under investigation in this study, where the uneven distribution of rainfall throughout the barley vegetation period has been observed. The differences in precipitation and temperature in the current study resulted in distinct effects on individual yield-related traits. Specifically, in 2021, traits such as SL, SNS, GNS, GWS, and TGW were higher, while in 2022, SNM, PH, DWP, and GWP exhibited higher values. Possibly, the lower values of SNS, GNS, GWS, and TGW in 2022 compared to 2021 could be attributed to insufficient rainfall in March and May. These contrasting climatic conditions in the two years underscore the dynamic influence of meteorological factors on yield-related traits in barley.

The changes in trait relationships add complexity to the identification of superior genotypes that excel across diverse environments. This differential impact necessitates a comprehensive understanding of the interaction between environmental factors and traits to effectively guide selection efforts. To address these challenges, breeders have adopted various strategies within the multi-trait selection framework. One approach is to employ multiple environments for selection, ensuring that genotypes are evaluated under a range of conditions (Malosetti et al., 2013). This approach helps identify genotypes that are relatively stable across different environments, exhibiting consistent performance regardless of meteorological fluctuations. By integrating data from various environments, breeders can enhance the reliability of genotype evaluations and promote the development of resilient and adaptable crop varieties. Another strategy involves the development of selection indices, which combine information from multiple traits into a single numerical value. These indices enable breeders to prioritize genotypes that excel in multiple traits, taking into account the varying importance of each trait in contributing to overall yield.

While heritability can guide trait improvement through breeding, complex traits such as grain yield are influenced by unpredictable interactions between genes and the environment, making precise outcomes challenging (Cooper et al., 2009). Low heritability for GY and most of the grain-related traits was found in the present study. Previous studies also found low heritability of barley GY, showing that the seasonal effects may seriously obstruct the selection of barley genotypes with improved grain yield (Addisu and Shumet, 2015; Ahmadi et al., 2016; Hailu et al., 2016). The discovery of low heritability for yield in our study underscores the notion that relying solely on yield as a criterion for genotype selection may not be an effective strategy in this specific environment.

Moderate heritability values were observed for DWP, GWP, TGW, and HI in the current study. Previous research consistently identifies thousand-grain weight (TGW) as a barley yield-related trait with higher heritability (Kumar et al., 2013; Devı et al., 2020).

The traits SL, SNS, and GNS exhibited remarkably high values for the coefficient of determination of the interaction effects (GEIr2) in our study. Coupled with low heritability, these findings strongly suggest that these traits are susceptible to environmental variation.

The use of the multi-trait genotype-idiotype distance index (MGIDI) has gained prominence in recent years as an effective tool for selecting genotypes exhibiting superior performance. Extensive research has demonstrated its efficacy in identifying genotypes with desirable characteristics such as high yield, disease resistance, and environmental adaptation (Olivoto et al., 2021; Uddin et al., 2021; Jalalifar et al., 2023). A notable advantage of MGIDI lies in its consideration of the relative importance of different traits, a departure from traditional single-trait selection methods.

The MGIDI index provides a comprehensive assessment of a genotype's performance, allowing breeders to make informed decisions regarding further breeding efforts. Grounded in the concept of an ideotype, representing the optimal combination of traits for a specific crop, MGIDI's effectiveness hinges on the accuracy of this ideotype. However, its predictive power may be diminished in environments significantly divergent from those in which the genotypes were initially selected.

In our study, while several genotypes exhibited superior performance compared to the standard variety Emon in 2021, only a subset maintained this advantage in 2022. This observation underscores the dynamic nature of genotype-environment interactions and highlights the importance of comprehensive assessments.

Usually, breeders initiate selection under a single environment with a single specific stress or stress-free conditions. However, a narrow focus during the early stages of breeding may inadvertently lead to the loss of crucial alleles or genetic variability necessary for addressing additional stresses. Hence, the adoption of the MGIDI index becomes crucial, allowing for the thorough evaluation of multiple traits under diverse stress environments. By considering not only grain yield but also various secondary traits, the MGIDI approach captures complex genetic-environment interactions, enhancing the selection of genotypes that perform well across a range of conditions.

Our study aligns with the broader perspective that employing the MGIDI index enables breeders to understand better and navigate the complexities of genotype-environment interactions. This integrated approach enhances the likelihood of developing resilient and high-performing plant varieties that can withstand diverse stressors, ultimately contributing to the success and sustainability of breeding programs. Despite its merits, it is essential to acknowledge the limitations of the MGIDI index and to complement its use with other robust selection methods.

Conclusions

The combined analysis of variance indicated highly significant variations among genotypes, years, and their interaction for all the studied traits, including SNM, PH, DWP, SL, SNS, GNS, GWS, GWP, TGW, and GY. However, no significant variation was observed for HI between growing seasons.

Grain yield (GY) demonstrated diverse associations with different traits in each season, underscoring the impact of specific environmental conditions. Throughout both growing years, GY exhibited a significant correlation with SNM, highlighting the crucial role of this trait in selecting high-yielding genotypes of winter barley.

In 2021, MGIDI identified a total of 12 genotypes (10 breeding lines: G5, G4, G7, G2, G9, G12, G11, G10, G21, G8, and two varieties, Hasat and Burgaz) that outperformed the standard variety. However, only two lines (G10 and G5) maintained their excellence in 2022, highlighting the importance of genotype adaptability. Among the selected genotypes, the breeding line 671D-3/10 (G10) consistently demonstrated superior performance in both growing seasons, showcasing its adaptability and breeding value.

Acknowledgements

The authors thank the Bulgarian Ministry of Education and Science for its support of the National Research Programme "Smart crop production", approved by Decision of the Ministry Council No. 866/26.11.2020.

References

Addisu, A. & Shumet, T. (2015). Variability, heritability and genetic advance for some yield and yield related traits in barley (*Hordeum vulgare* L.) landraces in Ethiopia. International *Journal of Plant Breeding and Genetics, 9*(2), 68 – 76. http://dx.doi.org/10.3923/ijpbg.2015.68.76.

Ahmadi, J., Vaezi, B. & Pour Aboughadareh, A. (2016). Analysis of variability, heritability, and interrelationships among grain yield and related characters in barley advanced lines. *Genetika, 48*(1), 73 – 85. http://dx.doi.org/10.2298/GENSR1601073A.

Akgün, N. (2017). Genetic variability and correlation studies in yield and yield related characters of barley (*Hordeum vulgare* L.) genotypes. *Selcuk Journal of Agriculture and Food Sciences, 30*(2), 88 – 95.

Bizari, E. H., Uneda-Trevisoli, S. H., Val, B. H. P., Pereira, E. d. M. & Mauro, A. O. D. (2017) Selection indices for agronomic traits in segregating populations of soybean. *Rev. Cienc. Agron, 48*, 110 – 117. http://dx.doi.org/10.5935/1806-6690.20170012.

Cooper, M., van Eeuwijk, F. A., Hammer, G. L., Podlich, D. W. & Messina, C. (2009). Modeling QTL for complex traits: detection and context for plant breeding. *Current opinion in plant biology, 12*(2), 231 – 240. http://dx.doi.org/10.1016/j.pbi.2009.01.006.

Debsharma, S. K., Syed, M. A., Ali, M. H., Maniruzzaman, S.,

Roy, P. R., Brestic, M., Gaber, A. & Hossain, A. (2022). Harnessing on Genetic Variability and Diversity of Rice (*Oryza sativa* L.) Genotypes Based on Quantitative and Qualitative Traits for Desirable Crossing Materials. *Genes, 14*(1), 10. https://doi.org/10.3390/genes14010010.

Devı, S., Kumar, Y., Bhuker, A. & **Niwas, R.** (2020). Assessment of genetic variability for metric traits in barley under different sowing conditions. *Forage Res., 45*, 277 – 280.

Dyulgerov, N. & Dyulgerova, B. (2020). Variability, heritability, and correlations among grain yield and related traits in hulless barley accessions. *Trakia Journal of Sciences, 18*(4), 285 – 293. http://dx.doi.org/10.15547/tjs.2020.04.002.

Dyulgerova, B. & Dyulgerov, N. (2023). Evaluation of genetic parameters of winter barley varieties under water deficit conditions. *Journal of Central European Agriculture, 24*(4), 862 – 872. http://dx.doi.org/10.5513/JCEA01/24.4.3884.

Elsen, J. M. (2016). Prediction of genetic gain in finite populations with heterogeneous predicted breeding values accuracies. *Journal of Animal Breeding and Genetics, 133*(6), 493 – 502. http://dx.doi.org/10.1111/jbg.12222.

H**ailu, A., Alamerew, S., Nigussie, M. & Assefa, E.** (2016). Genetic variability, heritability and genetic advance for yield and yield related traits in barley (Hordeum vulgare L.) germplasm. *World Journal of Agricultural Sciences, 12*(1), 36 – 44.

Jahufer, M. Z. Z. & Casler, M. D. (2015). Application of the Smith-Hazel selection index for improving biomass yield and quality of switchgrass. *Crop Science, 55*(3), 1212 – 1222. http://dx.doi.org/10.2135/cropsci2014.08.0575.

Jalalifar, R., Sabouri, A., Mousanejad, S. & Dadras, A. R. (2023). Estimation of Genetic Parameters and Identification of Leaf Blast-Resistant Rice RILs Using Cluster Analysis and MGIDI. *Agronomy, 13*(11), 2730. http://dx.doi.org/10.3390/agronomy13112730.

Klein, L. A., Marchioro, V. S., Toebe, M., Olivoto, T., Meira, D., Meier, C., Benin, G., Busatto, A. C., Garafini, D. C., Alberti, J. V. & Finatto, J. L. B. (2023). Selection of superior black oat lines using the MGIDI index. *Crop Breeding and Applied Biotechnology, 23,* e45112332. http://dx.doi.org/10.1590/1984-70332023v23n3a25.

Kolde, R. & Kolde, M. R. (2015). Package 'pheatmap'. R package, 2022. https://cran-r.c3sl.ufpr.br/web/packages/pheatmap/pheatmap.pdf.

Kumar, M., Vishwakarma, S. R., Bhushan, B. & Kumar, A. (2013). Estimation of genetic parameters and character association in barley (*Hordeum vulgare* L.). *Journal of Cereal Research, 5*(2), 76 – 78.

Malosetti, M., Ribaut, J. M. & van Eeuwijk, F. A. (2013). The statistical analysis of multi-environment data: modeling genotype-by-environment interaction and its genetic basis. *Frontiers in physiology, 4,* 44. https://doi.org/10.3389/fphys.2013.00044.

Olivoto, T. & Lúcio, A. **D. C.** (2020). Metan: An R package for multi environment trial analysis. *Methods in Ecology and Evolution*, *11*, 783 – 789. http://dx.doi.org/10.1111/2041-210X.13384.

Olivoto, T. & Nardino, M. (2021). MGIDI: Toward an effective multivariate selection in biological experiments. *Bioinformatics, 37*(10), 1383 – 1389. http://dx.doi.org/10.1093/bioinformatics/btaa981.

Olivoto, T., Nardino, M., Meira, D., Meier, C., Follmann, D. N., de Souza, V. Q., Konflanz, D. B. & Baretta, D. (2021). Multi-trait selection for mean performance and stability in maize. *Agronomy Journal, 113*(5), 3968 – 3974. http://dx.doi.org/10.1002/agj2.20741.

Piepho, H. P., Möhring, J., Melchinger, A. E. & Büchse, A. (2008). BLUP for phenotypic selection in plant breeding and variety testing. *Euphytica, 161*(1-2), 209 – 228. http://dx.doi.org/10.1007/s10681-007-9449-8.

Pour-Aboughadareh, A. & Poczai, P. (2021). Dataset on the use of MGIDI index in screening drought-tolerant wild wheat accessions at the early growth stage. *Data in Brief, 36,* 107096. http://dx.doi.org/10.1016/j.dib.2021.107096.

Ramalho, M. A. P. & Araújo, L. C. A. D. (2011) Breeding self-pollinated plants. *Crop Breeding and Applied Biotechnology, 11*(1), 1 – 7. http://dx.doi.org/10.1007/s10681-007-9449-8.

Resende, M. D. V. & Duarte, J. B. (2007) Precisão e controle de qualidade em experimentos de avaliação de cultivares. *Pesquisa Agropecuária Tropical, 37,* 182 – 194 (in Portuguese).

Rocha, J. R. D. A. S. D. C., Machado, J. C. & Carneiro, P. C. S. (2018). Multitrait index based on factor analysis and ideotype-design: Proposal and application on elephant grass breeding for bioenergy. *GCB Bioenergy, 10*(1), 52 – 60. http://dx.doi.org/10.1111/gcbb.12443.

Sanhueza, R. P., White, T. L., Huber, D. A. & Griffin, A. R. (2002) Genetic parameter estimates, selection indices and predicted genetic gains from selection of Eucalyptus globulus in Chile. *For. Genet., 9*, 19 – 29.

Singamsetti, A., Zaidi, P. H., Seetharam, K., Vinayan, M. T., Olivoto, T., Mahato, A., Madankar, K., Kumar M. & Shikha, K. (2023). Genetic gains in tropical maize hybrids across moisture regimes with multi-trait-based index selection. *Frontiers in Plant Science, 14,* 1147424. http://dx.doi.org/10.3389/fpls.2023.1147424.

Singh, B. D. (1990) Plant Breeding: Principles and Methods (4th Edn.). Kalyani Publishers, New Delhi, 654.

Tawfiq, S. I., Abdulkhaleq, D. A., Hama, S. J. & Abdulqader, S. H. (2016). Correlation and path analysis in barley under rainfall conditions. *Journal of Zankoy Sulaimani, 18*(3-A), 1 – 7. http://dx.doi.org/10.17656/jzs.10538.

Uddin, M. S., Billah, M., Afroz, R., Rahman, S., Jahan, N., Hossain, M. G., Bagum S. A., Uddin M. S., Khaldun A. B. M., Azam M. G., Hossain N., Akanda M. A. L., Alhomrani M., Gaber A. & Hossain, A. (2021). Evaluation of 130 Eggplant (*Solanum melongena* L.) genotypes for future breeding program based on qualitative and quantitative traits, and various genetic parameters. *Horticulturae, 7*(10). 376. http://dx.doi.org/10.3390/horticulturae7100376.

Vieira, R. A., Rocha, R., Scapim, C. A., Amaral, A. T., Jr. & Vivas, M. (2016). Selection index based on the relative importance of traits and possibilities in breeding popcorn. *Genet. Mol. Res., 15*, 1 – 10. http://dx.doi.org/10.4238/gmr.1502771.

Received: **May 07, 2024**; *Approved*: **June, 15, 2024**; *Published*: **December, 2025**