PLANT BREEDING AND SEED SCIENCE
Volume 82 2021

DOI: 10.37317/pbss-2021-0001

Dariusz R. Mańkowski [1]*, Dorota Jasińska [2], Magdalena Anioła [2], Tadeusz Śmiałowski [1],
Monika Janaszek-Mańkowska [3], Wioletta M. Dynkowska [4]

[1] Plant Breeding and Acclimatization Institute – National Research Institute, Radzików, Poland. Department of Seed Science and Seed Technology, Laboratory of Seed Production and Plant Breeding Economics.
[2] Poznańska Hodowla Roślin Sp. z o. o. Plant Breeding Station Nagrodowice, Poland.
[3] Warsaw University of Life Sciences, Warsaw, Poland. Department of Engineering
[4] Plant Breeding and Acclimatization Institute – National Research Institute, Radzików, Poland. Department of Biochemistry and Plant Physiology

*Corresponding author's e-mail: d.mankowski@ihar.edu.pl

ONE- AND MULTIVARIABLE CHARACTERISTICS OF SPRING BARLEY (*HORDEUM VULGARE* L.) GENOTYPES CROPPED IN 2017–2018 YEARS AT THE NAGRADOWICE PLANT BREEDING STATION

ABSTRACT

The aim of this study was to evaluate the yield variability of spring barley families grown at the Nagradowice Plant Breeding Station of Poznan Plant Breeding against other families studied in years 2017–2018 in Team Breeding Experiments. Research material included 250 spring barley families cultivated in 2017 and 2018 in 6 locations. Selection of spring barley families for preliminary experiments was based on synthesis of results obtained in inter-plant experiments established in 2016 and 2017 in 5 locations. Combined (due to location) analysis of variance for experimental data was performed for each year and each series of experiments separately. Best Weighted Linear Unbiased Estimators (BWLUE) for the effects of individual sources of variation were included in ANOVA model. Significant effect of location on mean yield was observed in each research year and each series of experiments. Crucial differences were also observed between tested varieties and breeding lines. Moreover, significant interaction between locations and varieties or breeding families was also observed. Self-organising map (SOM) was applied to develop multivariable characteristic of tested families and cultivars of spring barley. Analyses results, i.e. ranking of BWLUE effects as well as SOM segmentation revealed seven breading lines from Breeding Station Nagradowice, which may be considered for further breeding process.

Key words: barley, yield, cultivars scoring, BWLUE, SOM

Communicated by Grzegorz Żurek.

INTRODUCTION

Barley is one of the most important cereals in the world. The cultivation of barley has ranks fourth both in production quantity and cultivated area among grain crops (FAO, 2018). Most of the barley grain is used for animal feed (about 70%). A significant part is used for brewing and malting purposes and less than 6% is used for human nutrition (Tricase et al., 2018). In Poland spring barley is an important cereal within crop structure, too. High nutritional value of barley grain was confirmed by numerous studies on animal nutrition as well as research on characteristics of barley used for brewing purposes (Marquardt et al., 1994; Boros et al., 1996; Cyran et al., 2002; Anderson et al., 2008; Gołębiewski et al., 2014, Boros et al., 2015, Wiśniewska et al., 2020). Most cultivars of spring barley listed in Polish National List (PNL) were bred by Polish breeding companies. The PNL contains only a few foreign but very fertile cultivars (COBORU, 2019). Morever, the proportion of spring barley cultivars relative to other cereal species included in PNL is negligible. Therefore, it is important to further develop domestic barley farming and maintain high-quality barley grain. Especially since there is a growing interest in this grain as a potential raw material for the production of functional food (Boros et al., 2015; Wirkijowska et al., 2016; Grochowicz et al., 2017; Sakellariou & Mylona 2020.

Five Polish breeding companies, i.e. Malopolska Plant Breeding, Poznanska Plant Breeding, Plant Breeding Strzelce, Plant Breeding Danko and Plant Breeding Smolice conduct intensive work aimed at breeding new cultivars of spring barley. Obtaining fertile breeding lines that are resistant to changing environmental conditions can be significantly hasten by incorporating plant genetics into breeding research (Grzywa et al., 2002; Węgrzyn et al., 2002; Nadolska-Orczyk et al., 2017). However, other studies indicate that breeding progress is also conditioned by diversity of breeding materials both in terms of fertility and qualitative characteristics (Ploch et al., 2005, Gołębiewski et al., 2013; Boros et al., 2015).

The Team Breeding Experiments (TBE) carried out for many years at the stage of preliminary tests allowed for identification of spring barley lines which are the most valuable in terms of yield and qualitative traits. Selection of the best breeding lines is most often determined by scores for yields obtained during TBE. Nonetheless, there is still a lack of a consistent methodology for evaluation of breeding lines that considers all characteristics affecting the diversity of studied objects. Progress in experimental design as well as application of multivariate characteristic enabled a more precise assessment of feature diversity of tested spring barley families and cultivars (Wójcik & Laudański, 1989; Laudański, 1996; Mańkowski et al., 2014).

The aim of this study was to evaluate the yield variability of spring barley families grown at the Nagradowice Plant Breeding Station of Poznan Plant Breeding against other families studied in years 2017–2018 in TBE. Modern statistical and data-mining tools were applied to achieve this goal.

MATERIAL AND METHODS

Research material included 250 spring barley families cultivated in 2017 and 2018 in 6 locations: Bąków – BKH (Opole Voivodeship), Nagradowice – NAD (Greater Poland Voivodeship), Polanowice – POB (Lesser Poland Voivodeship), Strzelce – STH (Greater Poland Voivodeship) Modzurów – MOB (Śląskie Voivodeship), Radzików – RAH (Mazowieckie Voivodeship). This group included also reference cultivars: *Planet*, *Radek* and *Soldo* which was replaced by *Runner* in 2018 (Tab. 1). Each year, studied objects were divided as follows: 2 series of 62 objects in 2017 (2017_S1 and 2017_S2) and 2 series of 63 objects in 2018 (2018_S1 and 2018_S2). Spring barley families cultivated in Nagradowice included the F8 (27 families) and F9 (13 families) generations. Selection of spring barley families for preliminary experiments was based on synthesis of results obtained in inter-plant experiments established in 2016 and 2017 in 5 locations. These families characterised with high yielding potential and were strongly resistant to the most important barley diseases: powdery mildew, barley rust and leaf net blotch. Most of families were also highly resistant to lodging of plants before harvest. Families selected for preliminary experiments in 2017 were obtained from lines derived from crosses made in 2010. For better identification, subsequent numbers of breeding lines from Breeding Station Nagradowice were marked with NAD prefix and the remaining ones had prefix LNE.

Field experiments in each location were carried out in an incomplete balanced block design, on 10 m^2 plots in 3 blocks, using mechanical seeding, with a sowing standard of 300 grains per 1 m^2. Detailed conditions of individual field experiments are presented in Table 2. Plant condition was assessed after germination. Meteorological conditions were monitored during spring and summer period. The grain was harvested mechanically using a plot harvester. After weighing, the crop expressed in kg per plot was converted to 15% dry matter according to Śmiałowski et al. (2017) methodology.

Table 1

List of spring barley breeding lines and reference cultivars tested in Team Breeding Experiments in 2017 and 2018

Name	**Breeding Company – Breeding Station**	**2017**		**2018**		**Sum**
		Series S1	**Series S2**	**Series S1**	**Series S2**	
Breeding lines						
NAD (1–40)	Poznańska Hodowla Roślin Sp. z o. o. [PL] – Breeding Station Nagradowice	10	10	10	10	40
LNE (1–10, 50–59, 120–129, 170–179)	Małopolska Hodowla Roślin Sp. z o. o. [PL] – Breeding Station Polanowice	10	10	10	10	40
LNE (11-20, 60-69, 100-109, 150-159)	Hodowla Roślin Smolice Sp. z o. o. Grupa IHAR [PL] – Experimental Station Bąków	10	10	10	10	40
LNE (21–29, 70–78, 130–139, 180–189)	Plant Breeding and Acclimatization Institute [PL] – Experimental Station Radzików	9	9	10	10	38
LNE (30–39, 79–88, 140–149, 190–199)	Hodowla Roślin Strzelce Sp. z o. o. Grupa IHAR [PL] – Breeding Station Strzelce	10	10	10	10	40
LNE (40–49, 89–98, 110–119, 160–169)	DANKO Hodowla Roślin Sp. z o. o. [PL] – Breeding Station Modzurów	10	10	10	10	40
Reference cultivars						
Planet	Ragt Semances [FR]	1	1	1	1	4
Soldo	Saaten Union [DE]	1	1			2
Runer	Saaten Union [DE]			1	1	2
Radek	Hodowla Roślin Strzelce Sp. z o. o. Grupa IHAR [PL]	1	1	1	1	4
In total		62	62	63	63	250

Table 2

Conditions for carrying out field experiments in 2017 and 2018

Specification	**Bąków (BKH)**		**Polanowice (POB)**		**Modzurów (MOB)**		**Nagradowice (NAD)**		**Radzików (RAH)**		**Strzelce (STH)**	
	2017	**2018**	**2017**	**2018**	**2017**	**2018**	**2017**	**2018**	**2017**	**2018**	**2017**	**2018**
Soil	mugwort		less on limestone substrate		mold weakly eroded		brown on the basis of boulder clay		brown		*NA*	
Forecrop	—	oilseed rape	beet	fodder beet	beet	—	sugar beet	white mustard	beet	beet	*NA*	*NA*
Fertilization												
N	—	76	2.18	10.5	26	—	69	90	18	*NA*	*NA*	*NA*
P	—	50	80	30	20	—	46	58	46	*NA*	*NA*	*NA*
K	—	80	120	42	60	—	40	100	60	*NA*	*NA*	*NA*
Sowing date	—	m 3 d 24	m 3 d 30	m 4 d 9	m 4 d 1	—	m 3 d 30	m 4 d 6	m 3 d 31	*NA*	*NA*	*NA*
Harvesting date	—	m 8 d 10	m 8 d 7	m 7 d 24	m 7 d 6	—	m 7 d 30	m 7 d 21	m 7 d 25	*NA*	*NA*	*NA*
Chemical protection	Mustang Forte 195 SE, Bi 58 400 EC, Fastac Active		Mustang Forte 195 SE, Basfoliar 36 Extra, Bi 58 400 EC		RSM 28, Biathlon 4D + Dasch HC, Granstar Ultra SX 50 SG + Trend + Fenoxinn 110 EC, Danadim 400 EC		Mustang Forte 195 SE, Axial 50 EC, Granstar Ultra, Puma Uniwersal 069EW Danadim		Mustang Forte 195 SE, Foxtrot 069 EW, Pyrinex 480 EC		*NA*	

NA – data not available

A combined (due to location) analysis of variance for experimental data was performed for each year and each series of experiments separately, according to the following fixed model (Wójcik & Laudański, 1989; Laudański, 1996; Mańkowski et al., 2014; Śmiałowski et al., 2017):

$$y_{ijk} = \mu + \alpha_i + \chi_k(\alpha_i) + \beta_j + \gamma_{ij} + \varepsilon_{ijk} ,$$

where y_{ijk} is a value of dependent variable in the *i*th location, for the *j*th family/cultivar in the *k*th block, μ is an overall mean for dependent variable in population, α_i means the effect of the *i*th level of factor A (location), $\chi_k(\alpha_i)$ stands for the effect of the *k*th block nested in the *i*th location, is the effect of the *j*th level of factor B (family/cultivar), γ_{ij} means the interaction between the *i*th level of factor A and the *j*th level of factor B and ε_{ijk} stands for the random error.

The model mentioned above introduces a factor design for a series of experiments accounted for the genotype-location combination also called cross-hierarchical design (Wójcik & Laudański, 1989; Laudański, 1996; Mańkowski et al., 2014; Śmiałowski et al., 2017). Application of such a model allowed for a synthetic analysis of series of experiments carried out in different locations. This analysis took into account the effect of blocks nested in locations, which meant that, according to the actual state, the effect of blocks was dependent on the location where a single experiment was conducted. The matrix notation of this model is then as follows:

$$\mathbf{y} = \mathbf{X\theta} + \boldsymbol{\varepsilon} = [\mathbf{N} \quad \mathbf{A} \quad \mathbf{B} \quad \mathbf{A} \otimes \mathbf{B} \quad \mathbf{C}] \begin{bmatrix} \mu \\ \boldsymbol{\alpha} \\ \boldsymbol{\beta} \\ \boldsymbol{\gamma} \\ \boldsymbol{\chi} \end{bmatrix} + \boldsymbol{\varepsilon},$$

where $\mathbf{y}$ is the vector of dependent variable observations, $\mathbf{X}$ means the matrix consisting of $\mathbf{N}$, $\mathbf{A}$, $\mathbf{B}$, $\mathbf{A} \otimes \mathbf{B}$, and $\mathbf{C}$ submatrices, composed of linearly independent vectors representing the experimental design, $\boldsymbol{\theta}$stands for the vector of model parameters, μ is the global mean, $\boldsymbol{\alpha}$ means the vector of factor A (location) effects, $\boldsymbol{\beta}$ is the vector of factor B (family/cultivar) effects, $\boldsymbol{\gamma}$ stands for the vector of interactive effects, $\boldsymbol{\chi}$ is the vector of block effects, $\boldsymbol{\varepsilon}$ means the vector of unknown random deviations (experimental error), and $\mathbf{A} \otimes \mathbf{B}$ is the Hadamard-Kronecker product of matrices $\mathbf{A}$ and $\mathbf{B}$.

Assuming that

$$E(\mathbf{y}) = \mathbf{X\theta} = \mathbf{N}\mu + \mathbf{A}\boldsymbol{\alpha} + \mathbf{B}\boldsymbol{\beta} + (\mathbf{A} \otimes \mathbf{B})\boldsymbol{\gamma} + \mathbf{C}\boldsymbol{\chi}$$

and the vector of random deviations meets the condition (according to ANOVA assumptions)

$$\boldsymbol{\varepsilon} \sim NID(\mathbf{0}; \sigma_e^2 \mathbf{I}_n),$$

the imposed conditions of traceability are:

$$\mathbf{P_N A}\boldsymbol{\alpha} = 0 \left(\sum_i n_i \alpha_i = 0 \right), \mathbf{P_N B}\boldsymbol{\beta} = 0 \left(\sum_j n_j \beta_j = 0 \right), \mathbf{P_A C}\boldsymbol{\chi} = 0 \left(\bigwedge_i \sum_k n_{ik} \chi_{ik} = 0 \right),$$

$$\mathbf{P_{(A,B)}}(\mathbf{A} \otimes \mathbf{B})\boldsymbol{\gamma} = 0 \left(\bigwedge_j \sum_j n_{ij} \gamma_{ij} = 0 \text{ and } \bigwedge_i \sum_j n_{ij} \gamma_{ij} = 0 \right)$$

The subspace of estimated parameters may be represented as

$$R[\mathbf{N}, (\mathbf{I}_n - \mathbf{P}_{\mathbf{N}})\mathbf{A}, (\mathbf{I}_n - \mathbf{P}_{\mathbf{C}})\mathbf{B}, (\mathbf{I}_n - \mathbf{P}_{\mathbf{B,C}})(\mathbf{A} \otimes \mathbf{B}), (\mathbf{I}_n - \mathbf{P}_{\mathbf{A}\otimes\mathbf{B}})\mathbf{C}] .$$

The determination of vector $\hat{\boldsymbol{\theta}} = [\hat{\mu}, \hat{\boldsymbol{\alpha}}, \hat{\boldsymbol{\beta}}, \hat{\boldsymbol{\gamma}}, \hat{\boldsymbol{\chi}}]$leads to calculation of the following unbiased estimators:

$$\hat{\mu} = (\mathbf{N}'\mathbf{N})^{-1}\mathbf{N}'\mathbf{y}$$

$$\hat{\boldsymbol{\alpha}} = \mathbf{P}_{\mathbf{A}^*}^{\mathbf{B}}\mathbf{y}$$

$$\hat{\boldsymbol{\beta}} = (\mathbf{I}_n - \mathbf{P}_{\mathbf{C}})\mathbf{P}_{\mathbf{B}^*}^{\mathbf{C}}\mathbf{y}$$

$$\hat{\boldsymbol{\gamma}} = (\mathbf{I}_n - \mathbf{P}_{(\mathbf{B,C})})\mathbf{P}_{(\mathbf{A}\otimes\mathbf{B})^*}^{(\mathbf{B,C})}\mathbf{y}$$

$$\hat{\boldsymbol{\chi}} = (\mathbf{I}_n - \mathbf{P}_{(\mathbf{A}\otimes\mathbf{B})})\mathbf{P}_{\mathbf{C}^*}^{(\mathbf{A}\otimes\mathbf{B})}\mathbf{y} ,$$

which are called BWLUE (Mańkowski, 2013; Mańkowski et al., 2014; Śmiałowski et al., 2017) – *best weighted linear unbiased estimators* for the effects of individual sources of variation included in ANOVA model. These estimators are unbiased (they are weighted by the number of cases). This is especially important if assessing the effects of factors studied in incomplete experiments with different case rates within subclasses, since arithmetic means are incomparable in such a case. Furthermore, effect assessments obtained for tested cultivars and families might have characterised them directly, since they were not biased by any other main or interactive effects.

Families and cultivars of spring barley considered in the experiment were compared on the basis of the ranking of ratings obtained for BWLUE estimators. However, no detailed comparisons using multiple comparison procedures were made, since an interpretation of obtained results would be unreliable with such a number of examined objects (over 60 in each series). The effects' assessments obtained for families and cultivars of spring barley were then used to create multivariable characteristic of examined objects.

For the analysis purpose, locations were treated as the fixed factor, since they were selected subjectively and were not a random representation of a wider population (in this case the area of Poland). Thus, the analysis was consisted with ANOVA fixed model.

We applied a Kohonen neural network, known also as a self-organising map (SOM), to develop the multivariable characteristic of tested families and cultivars of spring barley (Kohonen, 1982). SOM rearranges multi-dimensional data by mapping them onto low-dimensional hyperplane and enabling object clusterisation on the basis of similarity between input vectors (analysed variables). The basic advantages of this solution are simplification of representation of non-linear relationships and solving problems for which one cannot accurately define the nature of relationships between objects (Lasek & Myzik, 2012), detecting relations which would be missed if using traditional approaches (Tadeusiewicz, 2001), resistance to outliers (Vensanto, 2000). SOM is also successfully applied as a pattern recognition tool since it discovers multidimensional similarities between samples and their references and map them close together building areas of the possibly highest homogeneity called Voronoi cells (Trajer & Świderski, 2009; Janaszek & Trajer, 2011).

In our studies two separate SOM models were built. These models will be further referred as SOM17 and SOM18. The former SOM was trained using data collected in 2017. And the latter was trained on data obtained in 2018. The number of nodes within both SOMs was determined as proposed by Vesanto (2000). Each feature map consisted of 121 nodes arranged in a square of dimensions of 11×11 nodes. The input data was divided into the training set and test set which consisted of 80% and 20% of all input vectors respectively. The WTA (the winner takes all) algorithm was applied for SOMs training. After training process nodes corresponding to the reference samples were discovered and Voronoi cells covering the first order neighbourhoods of these nodes were considered in further analyses. All calculations were made using the Statistica software ver. 13.3 (TIBCO Software Inc., 2017).

RESULTS AND DISCUSSION

The ANOVA results obtained for experimental data are presented in Table 3. Significant effect of location on mean yield was observed in each research year and each series of experiments. Crucial differences were also observed between tested varieties and breeding lines. Moreover, significant interaction between locations and varieties or breeding families was also observed.

The comparison of reference varieties with tested breeding families should be considered the most important result of this experiment since the ranking position of breeding lines and their relation to reference varieties is more valuable information for a breeder than joining them into homogeneous groups. Considering that, comparisons based on the BWLUE estimator turn out to be more reliable than those simply based on arithmetic means. The ranking of varieties and breeding lines, created in this analysis, is presented in Figure 1.

Table 3

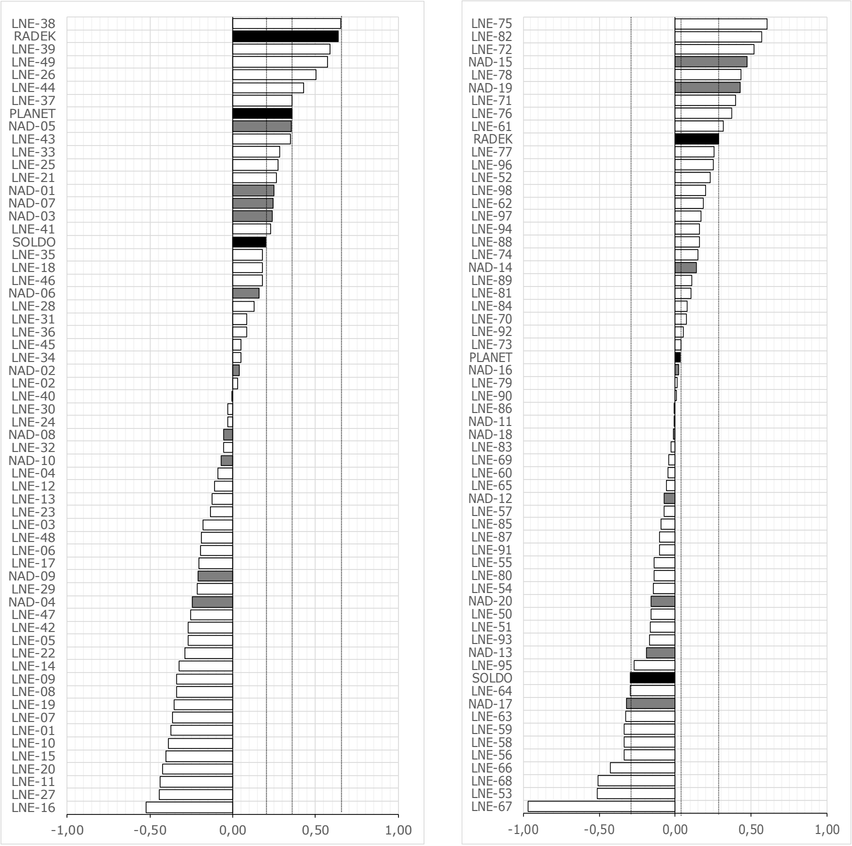
ANOVA results according to cross-hierarchical model for two years of experiment carried out in two series

Source	**Series I**					**Series II**				
	df	**SS**	**MS**	**F**	**p**	**df**	**SS**	**MS**	**F**	**p**
2017										
Location	4	1120.215	280.054	1032.976	0.0000	4	803.816	200.954	853.933	0.0000
Block (Location)	10	139.386	13.939	51.412	0.0000	10	112.342	11.234	47.738	0.0000
Cultivars and lines	61	84.605	1.387	5.116	0.0000	61	76.906	1.261	5.357	0.0000
Interaction: Location × Cultivars and lines	244	118.656	0.486	1.794	0.0000	244	128.636	0.5270	2.240	0.0000
Error	610	165.379	0.271			610	143.550	0.235		
2018										
Location	4	632.280	158.070	418.120	0.0000	4	1402.006	350.502	742.445	0.0000
Block (Location)	10	26.549	2.655	7.023	0.0000	10	151.781	15.178	32.151	0.0000
Cultivars and lines	62	90.910	1.466	3.879	0.0000	62	99.931	1.612	3.414	0.0000
Interaction: Location × Cultivars and lines	248	157.014	0.633	1.675	0.0000	248	198.881	0.802	1.699	0.0000
Error	620	234.391	0.378			620	292.696	0.472		

df – degrees of freedom, SS – sum of squares; MS – means square; F – F-statistics; p – p-vaule

Figure 1. The size of BWLUE ratings for the tested lines and cultivars in the years 2017 and 2018

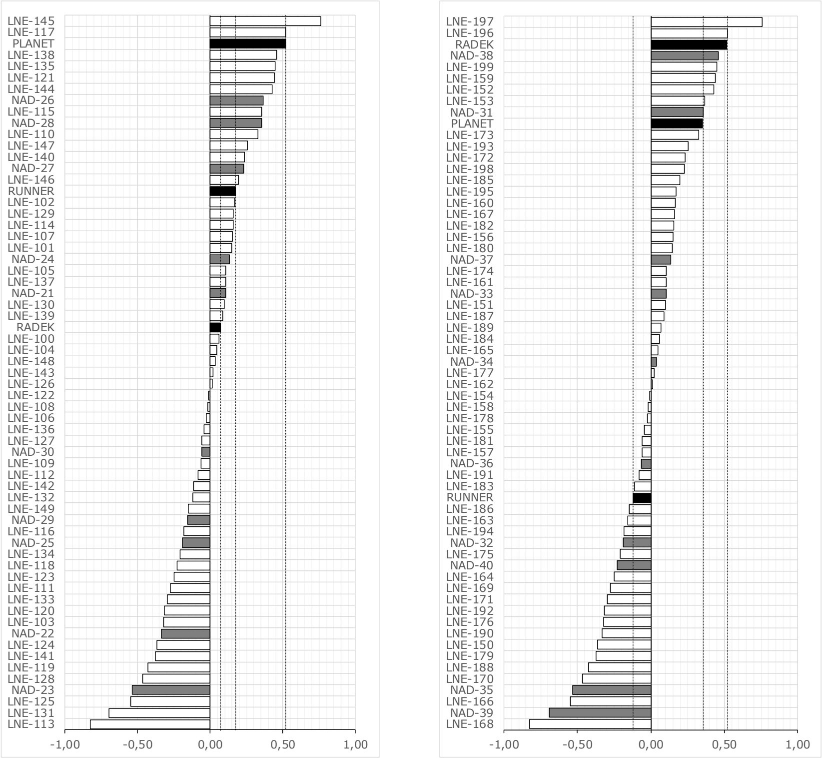
Year 2017



A) Series I

B) Series II

Figure 1 cont. The size of BWLUE ratings for the tested lines and cultivars in the years 2017 and 2018



Year 2018

Series I

Series II

Considering reference varieties in 2017_S1 group, the Radek variety had the highest BWLUE effect (Fig. 1A). Slightly lower effect was observed for Planet variety while Soldo variety characterised by the lowest value of the BWLUE estimator. The only breeding line with BWLUE effect higher than Radek was the LNE-38. Five other LNE- breeding lines had values of the BWLUE estimator on intermediate level between Radek and Planet varieties. The effect very similar to the Planet variety was observed in case of NAD-05 line, while lines NAD-01, NAD-07 and NAD-03 characterised by effects not much higher than that observed for Soldo variety. The intermediate effect between Planet and Soldo varieties was characteristic for 5 LNE- lines, while other 38 LNE- remaining lines, as well as other NAD- lines had BWLUE effect lower than Soldo variety.

Taking into account 2017_S2 group, the Radek variety characterised by the highest BWLUE effect (Fig. 1B). Higher effects were observed only in case of 9 breeding lines, including NAD-15 and NAD-19 lines. As in previous group, also in this group Planet variety had lower BWLUE effect than Radek and intermediate effects between these varieties were observed for 16 tested lines, including NAD-14. The NAD-16 breeding line had the value of the BWLUE estimator not much lower than Planet variety. The lowest value of the BWLUE estimator had Soldo variety and intermediate effects between Planet and Soldo were observed for 24 breeding lines, including NAD-11, NAD-18, NAD-12, NAD-20 and NAD-13. The other lines, with NAD-17 included, had BWLUE effect lower than Soldo variety.

In 2018_S1 group, the highest values of the BWLUE estimator were noted for LNE-145 and LNE-117 breeding lines (Fig. 1C). Regarding reference varieties, the highest BWLUE effect was observed in case of Planet variety, lower for Runner variety and the lowest for Radek variety. The BWLUE intermediate effects between Planet and Runner were noted in case of 12 lines, including NAD-26, NAD-28 and NAD-27 while intermediate effects between Runner and Radek were observed for 11 tested lines, including NAD-24 and NAD-21. Remaining 30 NLE- and 4 NAD- breeding lines had BWLUE effect lower than Radek variety.

Considering 2018_S2 group, the Radek reference variety had the highest BWLUE effect (Fig. 1D). Line LNE-197 as well as LNE-196 turned out to be better in terms of BWLUE effect. The effects lower than Radek variety but higher than the reference variety Planet were observed for 6 lines, with NAD-38 and NAD-31 included. The Runner reference variety turned out to have the lowest BWLUE effect. The intermediate effect between Planet and Runner varieties was characteristic for 32 tested lines, including NAD-37, NAD-33, NAD-34 and NAD-36, while other 16 LNE- and 4 NAD- remaining lines characterised by the effect lower than Runner variety.

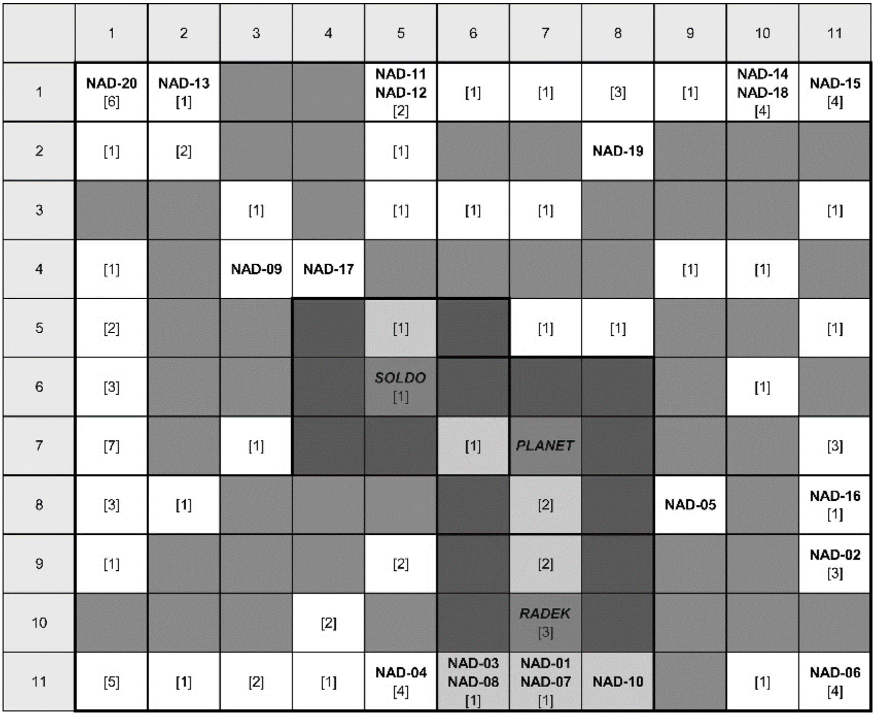
In order to identify breeding lines which were most closely related to reference varieties in terms of yield, self-organizing maps were built where results of experiments (yield) in subsequent locations were treated as input variables (Fig. 2). This approach allowed to consider the level of yield as and the existing G×E interaction at the same time. Training and testing errors of SOM17 were 0.776229 and 1.485188 respectively whereas errors for SOM18 were 0.771346 and 1.412580.

The analysis of spatial distribution of nodes which mapped lines provided by Nagradowice Breeding Station within SOM17 model revealed that five of these lines i.e. NAD-01, NAD-03, NAD-07, NAD-08 and NAD-10 had the yielding profile similar to Radek reference variety (Fig. 2A). Moreover, seven other LNE lines were related to this variety, too. In the same model, three lines included in LNE group represented a yield profile comparable to Soldo variety, and the other three to Planet variety.

Considering a spatial distribution of nodes in SOM18 we observed that there were up to twelve breading lines with yielding profile and the G×E interaction similar to Planet reference variety, including NAD-21 and NAD-24 lines (Fig. 2B). Furthermore, five breading lines characterised by a profile comparable to Radek reference variety, along with NAD-37 line, whereas four other tested lines were definitely more related to Runner reference variety.

Figure 2. Kohonen self-organizing map (SOM) for the results from 2017 and 2018. Gray color indicates inactive neurons, numbers in parentheses mean families other than NAD, dark color marked Woronoj's areas around the control cultivars.

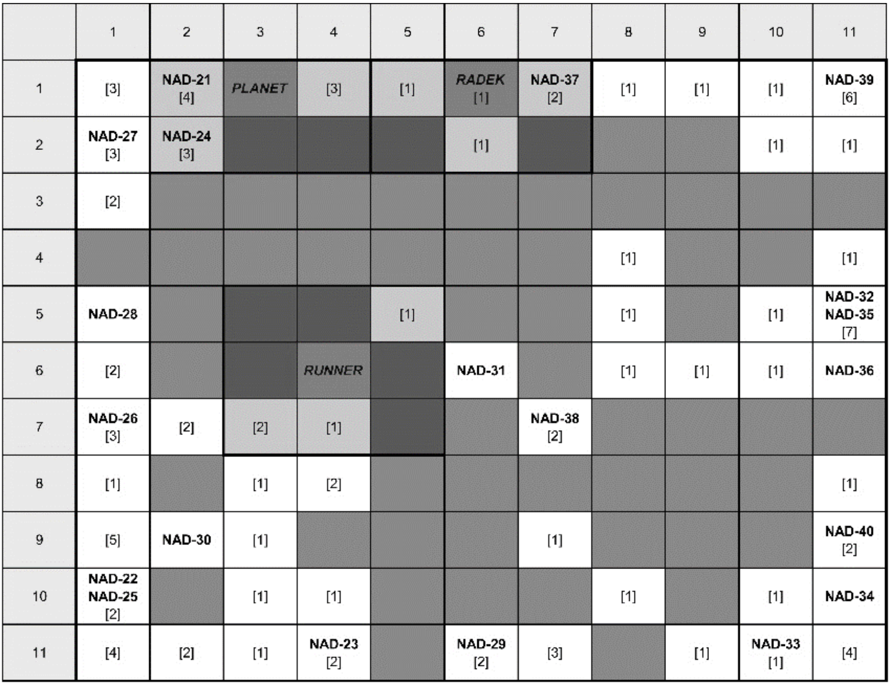
A) Year 2017



	1	2	3	4	5	6	7	8	9	10	11
1	**NAD-20** [6]	**NAD-13** [1]			**NAD-11** **NAD-12** [2]	[1]	[1]	[3]	[1]	**NAD-14** **NAD-18** [4]	**NAD-15** [4]
2	[1]	[2]			[1]			**NAD-19**			
3			[1]		[1]	[1]	[1]				[1]
4	[1]		**NAD-09**	**NAD-17**					[1]	[1]	
5	[2]				[1]		[1]	[1]			[1]
6	[3]				*SOLDO* [1]					[1]	
7	[7]		[1]			[1]	*PLANET*				[3]
8	[3]	[1]					[2]		**NAD-05**		**NAD-16** [1]
9	[1]				[2]		[2]				**NAD-02** [3]
10				[2]			*RADEK* [3]				
11	[5]	[1]	[2]	[1]	**NAD-04** [4]	**NAD-03** **NAD-08** [1]	**NAD-01** **NAD-07** [1]	**NAD-10**		[1]	**NAD-06** [4]

Figure 2 cont. Kohonen self-organizing map (SOM) for the results from 2017 and 2018. Gray color indicates inactive neurons, numbers in parentheses mean families other than NAD, dark color marked Woronoj's areas around the control cultivars.

B) Year 2018



	1	2	3	4	5	6	7	8	9	10	11
1	[3]	NAD-21 [4]	*PLANET*	[3]	[1]	*RADEK* [1]	NAD-37 [2]	[1]	[1]	[1]	NAD-39 [6]
2	NAD-27 [3]	NAD-24 [3]				[1]				[1]	[1]
3	[2]										
4								[1]			[1]
5	NAD-28				[1]			[1]		[1]	NAD-32 NAD-35 [7]
6	[2]			*RUNNER*		NAD-31		[1]	[1]	[1]	NAD-36
7	NAD-26 [3]	[2]	[2]	[1]			NAD-38 [2]				
8	[1]		[1]	[2]							[1]
9	[5]	NAD-30	[1]				[1]				NAD-40 [2]
10	NAD-22 NAD-25 [2]		[1]	[1]				[1]		[1]	NAD-34
11	[4]	[2]	[1]	NAD-23 [2]		NAD-29 [2]	[3]		[1]	NAD-33 [1]	[4]

CONCLUSIONS

Varietal ranking derived from BWLUE effects (estimators) gives a great possibility to realise breading selection on the basis of any quantitative variable, e.g. yield. Lines selected hereby may be addressed to further stages of breeding process or to registration experiments. Data-mining tools and methods enable a holistic and synthetic view of field experiments. This paper is the best example how a specific usage of self-organizing maps may be applicable to indicate varieties similar to reference ones characterised by a comparable reaction to changing environmental conditions (location of the experiment).

Analyses results, i.e. ranking of BWLUE effects as well as SOM segmentation, revealed seven breading lines (NAD-15, NAD-19, NAD-05, NAD-26, NAD-28, NAD-38 and NAD-31), from Breeding Station Nagradowice, which can be considered the best and most promising of the best chance of registration as a cultivar. These lines had high positions in BWLUE effects ranking (Fig. 1).

Regarding similarity to reference varieties, NAD-01, NAD-03, NAD-07, NAD-08, NAD-10, NAD-21, NAD-24 and NAD-37 deserve attention too. On created SOM planes these lines were located within Voronoi areas appointed around reference varieties (Fig. 2).

The methodological approach presented in this paper is a good solution in comparative breeding experiments, such as TBE realised by PBAI-NRI in cooperation with Polish breeding companies. This is confirmed by the presented research.

ACKNOWLEDGEMENTS

This research was financed within statutory topic No 2-6-00-3-01 titled "Biological progress and its components, including effects of crop cultivation in Poland, as well as selection and optimisation of statistical data analysis methods in evaluation of breeding effects."

LITERATURE

Andersson, A.A.M., Lampi, A-M., Nyström, L., Piironen, V., Li, Li., Ward, J., Gebruers, K., Courtin, C.M., Delcour, J.A., Boros, D., Fraś, A., Dynkowska, W., Rakszegi, M., Bedo, Z., Shewry, P.R., Åman, P. (2008). Phytochemical and fibre components in barley varieties in the HEALTHGRAIN diversity screen. *J. Agric. Food Chem., 56*, 9767–9776.

Boros, D., Rek-Ciepły, B., Cyran, M. (1996). A note on the composition and nutritional value of hulless barley. *J. Anim. Feed Sci., 5*, 417–424.

Boros, D., Fraś, A., Gołębiewska, K., Gołębiewski, D., Paczkowska, O., Wiśniewska, M. (2015). Nutritional value and health-promoting properties of grains of cereal and rape seed varieties recommended for cultivation in Poland. Monographs and Scientific Dissertations PBAI-NRI, 49, Radzików, Poland. *(in polish)*

COBORU (2019). Polish National List of Agricultural Plants Varieties. COBORU, Słupia Wielka, Poland.

Cyran, M., Izydorczyk, M., MacGregor, W. (2002). Structural characteristics of water-extractable nonstarch polysaccharides from barley malt. *Cereal Chem., 79*, 359–366.

FAO (2018). World Food and Agriculture – Statistical Pocketbook 2018; FAO: Rome, Italy.

Gołębiewski, D., Kamińska, B., Burek, J., Boros, D. (2014). Influence of the genotype and locality on the features determining the brewing value of grains of new spring barley lines. *Biuletyn IHAR, 274*, 3–14. *(in polish)*

Gołębiewski, D., Myszka, K., Fraś, A., Boros, D., Burek, J., Mańkowski, D. (2013). Genotypic and environmental diversity of characteristics of the brewing value of barley spring clones from pre-registration experience of 2012. *Biuletyn IHAR, 268*, 47–58. *(in polish)*

Grochowicz, J., Dominik, P., Fabisiak, A. (2017). Possibilities of using natural food as an effect of the global trend in the demand for pro-health food. *Zeszyty Naukowe UW, 54 (3)*, 223–240. *(in polish)*

Grzywa, M., Śmiałowski, T. (2002). Application of translocation to the localization of short-chain genomes in the barley Delisa mutant. *Biuletyn IHAR, 221*, 57–67. *(in polish)*

Janaszek, M.A., Trajer, J. (2011). Method of evaluating diversity of carrot roots using a self-organizing map and image data. *Computers and Electronics in Agriculture, Vol. 79, Issue 1*, 75–81.

Kohonen, T. (1982). Self-organized formation of topologically correct feature maps. *Biological Cybernetics, Vol. 48, Issue: 1*, 59–69.

Lasek, M., Myzik, A. (2012). Kohonen's neural networks in data analysis. An attempt to use data in the exploration of territorial units. *Problemy Zarządzania, 3 (38)*, vol. 10: 124–147. *(in polish)*

Laudański, Z. (1996). Application of projection operators in analysing non-orthogonal data – theory, algorithms and examples. Wydawnictwo SGGW, Warsaw, Poland. *(in polish)*

Mańkowski, D.R. (2013). Structural equations models SEM in agricultural research. Monographs and Scientific

Dissertations PBAI-NRI, 42, Radzików, Poland. *(in polish)*

Mańkowski, D.R., Śmiałowski, T., Laudański, Z., Janaszek-Mańkowska, M. (2014). Application of cultivar scoring for incomplete data (case study: field experiment with × *Triticosecale* Witt.). In: Laudański, Z., Mańkowski, D.R. (Eds.), International Conference — The 44th International Biometrical Colloquium and IV Polish-Portuguese Workshop on Biometry – Conference Papers. IHAR-PIB, Radzików, p. 39.

Marquardt, R.R., Boros, D., Guenter, W., Crow, G. (1994). The nutritive value of barley, rye, wheat and corn for young chicks as affected by use of a *Trichoderma reesei* enzyme preparation. *Anim. Feed Sci. Technol., 45*, 363–378.

Nadolska-Orczyk, A., Rajchel, I.K., Orczyk, W., Gasparis, S. (2017). Major genes determining yield-related traits in wheat and barley. *Theor Appl Genet, 130,* 1081–1098.

Ploch, M., Cyran, M., Kasztelowicz, K., Boros, D., Burek, J. (2005). Variability and interdependence of malting barley quality characteristics from the 2004 collection. *Biuletyn IHAR, 235*, 155–162. *(in polish)*

Sakellariou, M., Mylona, P. (2020). New Uses for Traditional Crops: The Case of Barley Biofortification. *Agronomy, 10 (12)*, 1964.

Śmiałowski, T., Cieplicka, A., Mańkowski, D.R. (2017). One- and multivariable characterization of spring barley (*Hordeum vulgare* L.) cultivars grown in Smolice Plant Breeding and tested in field breeding experiments in 2016. *Biuletyn IHAR, 282*, 63–78. *(in polish)*

Tadeusiewicz, R. (2001). Introduction to neural networks. StatSoft Polska, Cracow, Poland. *(in polish)*

TIBCO Software Inc., (2017). Statistica (data analysis software system), version 13, http://statistica.io

Trajer, J., Świderski, A. (2009). Using cluster analysis for examining carrot varieties diversity. *Annals of Warsaw University of Life Sciences – SGGW, Agriculture, 54,* 71—76.

Tricase, C., Amicarelli, V., Lamonaca, E., Leonardo Rana, R. (2018). Economic Analysis of the Barley Market and Related Uses. In: Grasses as Food and Feed. IntechOpen, London, UK.

Vesanto, J., (2000). Using SOM in Data Mining. Helsinki University of Technology, Espoo, Finland.

Węgrzyn, S., Grzywa, M., Śmiałowski, T. (2002). Evaluation of the combinational capacity of varieties and strains of spring barley for yield and resistance to powdery mildew. *Biuletyn IHAR, 221*, 45–55. *(in polish)*

Wirkijowska, A., Rzedzicki, Z., Sobota, A., Sykut-Domańska, E., Zarzycki, P., Bartoszek, K., Kuzawińska, E. (2016). Barley in human nutrition. *Polish Journal of Agronomy, 25*, 41–50. *(in polish)*

Wiśniewska, M., Boros, D., Zych, J. (2020). Nutritional value of selected mixtures of spring cereals with legumes. *Biuletyn IHAR, 289*, 51–62. *(in polish)*

Wójcik, A.R., Laudański, Z. (1989). Planning and statistical inference in experiments. PWN, Warsaw, Poland. *(in polish)*