



Multi-environmental evaluation of winter oilseed rape genotypic performance using mixed models

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Abstract The production of winter oilseed rape (WOSR) (*Brassica napus*) together with increasing seed yields per hectare is one of the strategies for breeding the genetic base of oilseed rape genotypes adapted to different environments. The main objective of this study was to evaluate the genotypic performance of 25 winter oilseed rape genotypes using mixed models. The plant material was examined in five locations in Poland. Field trials were carried out in a randomized complete block design with four replicates. The REML/BLUP was used to estimate genetic parameters. Selection of genotypes was made on the basis of genetic values by the harmonic mean of relative performance these parameters. The mean heritability for genotype had an average value at a high accuracy of selection, while additionally it facilitated selection of agronomically superior individuals. Three restorer lines PN18, PN17 and PN21, CMS *ogura* line PN64 as well as hybrids PN66 × PN21 and PN64 × PN21 characterized good adaptability and stability of seed yield. There were similarities among the statistics

($\hat{\mu} + \hat{g}$), adaptability and stability of genetic values in the discrimination of the most productive genotypes by best linear unbiased predictor analysis. Mixed models can be recommended as a potential selection method for the inclusion of new plant material in different oilseed rape breeding programs aimed at developing new WOSR cultivars.

Keywords *Brassica napus* L. · Adaptability · Productivity · Restricted maximum likelihood/best linear unbiased predictor · Stability

Abbreviations

BLUP	Best linear unbiased predictor
MHPRVG	Stability and adaptability of genetic values
MHVG	Stability of genetic values
PRVG	Adaptability of genetic values
REML	REstricted Maximum Likelihood

Introduction

Winter oilseed rape (WOSR, rapeseed, canola) (*Brassica napus* L.) is the most important oil and protein crop in Europe. In Poland in 2017 the cultivated area was 914 thousand ha with an average seed yield of 2950 t ha⁻¹ (www.fao.org.2019). Double-low quality cultivars with zero erucic acid and low glucosinolate

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contents are a source of the healthiest vegetable oils with a balanced fatty acid composition (Szydłowska-Czerniak et al. 2011). Its oil is also used as a green biofuel, an animal feed component and a valuable material for many products in chemical and pharmaceutical industries (lubricants, hydraulic oils, soap and biodegradable plastics) (Friedt and Snowdon 2009; Huang et al. 2016). The residual meal from oilseed rape seeds after oil extraction provides a protein-rich (38–44%) animal feed. Thanks to its nutritional value oilseed rape may be considered as an alternative source of protein to replace soya in countries with moderate climate, such as Poland. This meal represents a favorable composition of amino acids, including comparatively high contents of the essential sulfuric amino acids: methionine and cysteine (Downey and Bell 1991). In addition, the meal is rich in minerals, particularly Ca, Mg and P, and contains vitamins B4 and E (Thies 1994).

The constantly growing demand for high-quality human food and animal feed is a challenge for researchers, farmers and food producers. The main objective in many WOSR breeding programs is to develop high yielding cultivars, with satisfactory resistance to biotic and abiotic stresses and good seed quality traits (oil and protein contents, fatty acid composition as well as low glucosinolate and fiber levels) (Körber et al. 2016). Many traits of agronomic importance are controlled by multiple genes of small effect, while their phenotypic expressions is strongly affected by non-genetic factors as well as genotype by environment interactions (Piepho 1994; Nowosad et al. 2016; Werner et al. 2018; Bocianowski et al. 2019a, 2020; Liersch et al. 2020).

In many plant species the multi-environmental analysis of breeding materials is extensively used for the characterization of germplasm collections from an agronomic point of view. Apart from the genotypes, the environment and the environment \times genotype interactions also show information concerning the particular genotype variation in particular environment, as well as its adaptability and stability (Nowosad et al. 2017; Bocianowski et al. 2019b, c). Reliable performance prediction of combinations of parental lines (CMS *ogura*, restorer lines) is a key factor for success in F₁ CMS *ogura* hybrid breeding programs (Werner et al. 2018). Testing of the response of parental lines and hybrids to diverse environmental conditions during growing seasons determines their

essential traits (e.g. vigor, yield, yield-related traits or seed quality traits). Complex traits, such as e.g. seed yield, yield components and oil content in seeds are controlled by multiple genetic factors, which expression is the result of the interaction between the genotype and the environment. Studies on GEIs for agronomic traits in oilseed rape are frequent (Seyis et al. 2006; Nowosad et al. 2016; Bocianowski et al. 2019d). The aim of a breeding strategy in oilseed rape (parental forms of CMS *ogura* hybrids, semi-resynthesized lines and genotypes with other quality traits) is to generate stable genotypes with the capacity to adapt to different soil and climatic conditions. Szała et al. (2019) and Spasibionek et al. (2020) reported that seed yields of CMS *ogura* F₁ hybrids as well as WOSR breeding lines with a modified fatty acid composition of seed oil were the result of the effect of genotypes, the environment and their interactions. Additionally, Fletcher et al. (2015) indicated that *Brassica napus* lines should be grown under diverse growing conditions and different geographies to understand the role of the environment in agronomically important traits and their interaction with the underlying genetic factors.

Restricted maximum likelihood/best linear unbiased predictor (REML/BLUP) analysis makes it possible to consider correlated errors within locations as well as the stability and adaptability in superior genotype selection. Thus, genetic values may be obtained, instability may be calculated and the values may be applied to any number of environments. In addition, this method generates results in the unit of a given observed trait that can be directly interpreted as genetic values. Selection for seed yield and yield stability was based on the harmonic mean of the relative performance of genotypic predicted values. This refers to the relative performance of the genotypic values in the studied environment. In this case, the predicted genotypic values are expressed as a proportion of the overall average for each location and, subsequently, an average value of this ratio for all locations is obtained. Simultaneous selection for adaptability, seed yield and phenotypic stability in the context of mixed models can be performed using the MHPRVG method (Mohammadi and Amri 2008; Mendes et al. 2012).

This method has been used to interpret adaptability and genotypic stability of such crops as the common bean (Lin and Binns 1988), sugarcane (Bajpai and

Kumar 2005), wheat (Mohammadi and Amri 2008) and popcorn cultivars (Scapim et al. 2010). However, its application in winter oilseed rape has been limited.

Genotypic effects in the MHPRVG model are random. Therefore, this model shows genotypic, rather than phenotypic, adaptability and stability. The model analyzes adaptability and stability in the selection of individuals within progenies and provides genetic values after instability is excluded, while additionally it may be potentially used to different environments. So, the main objective of this study was to estimations the genotypic parameters of winter oilseed rape parental lines and experimental hybrids CMS *ogura* (*Brassica napus* L.) through mixed models proposed by de Souza et al. (2018).

Material and methods

The plant material used in this study comprised open pollinated cultivar Californium and Hercules F₁—hybrid cultivar, 15 Polish Ogura F₁ hybrids under development [PN64 × PN17, PN64 × PN18, PN64 × PN21, PN64 × PN05, PN64 × PN07, PN66 × PN17, PN66 × PN18, PN66 × PN21, PN66 × PN05, PN66 × PN07, PN68 × PN17, PN68 × PN18, PN68 × PN21, PN68 × PN05, PN68 × PN07] and their eight parental lines, i.e. three Ogura CMS lines—PN64, PN66, PN68 and five restorer lines—PN05, PN07, PN17, PN18, PN21].

The plant material was tested in five locations: an experimental station in Bąków (E1), the Opolskie Province, and four experimental stations in the Wielkopolska Province—Borowo (E2), Łagiewniki (E3), Małyszyn (E4) and Zielęcin (E5). Our study was arranged in a randomized complete block design with four replicates. Plot size was four rows × 0.30 m row spacing and sowing density of 80 seeds m⁻². Full chemical plant protection of the crop was applied. Other agronomical practices were optimal for local agroecological conditions in all the investigated seasons. Soil types, previous crops and soil pH were the same as in Nowosad et al. (2016). Weather conditions in Poland varied moderately during the investigated growing seasons of 2006/2007, 2007/2008 and 2008/2009. Precipitation at the experimental sites from August to July was 731 mm in Bąków, 681 mm in Borowo, 559 mm in Łagiewniki, 588 mm in Małyszyn and 514 mm in Zielęcin,

respectively. Mean annual temperature during the growing seasons (from August to July) were, respectively, 7.2 °C in Bąków, 11.8 °C in Borowo, 9.6 °C in Łagiewniki, 9.2 °C in Małyszyn and 10.5 °C in Zielęcin (Table 1).

Seeds were harvested at the seed maturity stage using a plot harvester. Seed yields per plot of 10.0 m² (Borowo and Bąków), 12.0 m² (Zielęcin), 9.6 m² (Łagiewniki) and 11.2 m² (Małyszyn) were measured and converted to t ha⁻¹ for our statistical analyses.

The genetic parameters and the genotype-by-environment interaction (GEI) of seed yield were estimated on the basis of mixed modeling in the GenStat software by the model (de Souza et al. 2018):

$$y = Xb + Zg + Wc + e,$$

where y is the vector of seed yield values; b is the vector of the fixed block effects within particular environments; g is the vector of genotype random effects; c is the vector of random GEI effects; e is the vector of random errors, X , Z and W are the incidence matrices of blocks, genotypes and GEI, respectively. We assumed distributions and structures of means (E) and variances (Var) as:

$$E \begin{bmatrix} y \\ g \\ c \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \end{bmatrix}; \quad Var \begin{bmatrix} g \\ c \\ e \end{bmatrix} = \begin{bmatrix} I\sigma_g^2 & 0 & 0 \\ 0 & I\sigma_c^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}.$$

Model adjustment was made on the basis of mixed model equations (de Souza et al. 2018):

$$\begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + I\lambda_1 & Z'W \\ W'X & W'Z & W'W + I\lambda_2 \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{g} \\ \hat{c} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix},$$

where $\lambda_1 = \frac{\sigma_g^2}{\sigma_g^2} = \frac{(1-h_g^2-c^2)}{h_g^2}$, $\lambda_2 = \frac{\sigma_c^2}{\sigma_c^2} = \frac{(1-h_g^2-c^2)}{c_g^2}$, h_g^2 —the individual heritability in the broad sense, $c^2 = \frac{\sigma_c^2}{(\sigma_g^2 + \sigma_c^2 + \sigma_e^2)}$ is the coefficient of determination of the GEI effects; σ_g^2 —the genotypic variance, σ_c^2 —the GEI variance, σ_e^2 —the residual variance between plots, c_g^2 —the coefficient of determination of the genotypic effects, $\hat{r}_{gloc} = \frac{\sigma_c^2}{(\sigma_g^2 + \sigma_c^2)} = \frac{h_g^2}{(h_g^2 + c^2)}$ —the genotypic correlation for genotypes, by environments,

Table 1 Weather conditions in Bąków, Borowo, Łagiewniki, Małyszyn and Zieleńcin during the vegetation seasons of winter oilseed rape in 2006/2007–2008/2009 and over an extended period (Nowosad et al. 2016)

Basic weather parameters	Bąków		Borowo		Łagiewniki		Małyszyn		Zieleńcin	
	2008/2009	1957–2009	2006/2007	1957–2009	2007/2008	1957–2009	2008/2009	1957–2009	2007/2008	1957–2009
<i>Mean temperature [°C]</i>										
Annual	7.2	6.8	11.8	8.8	9.6	8.5	9.2	8.5	10.5	8.9
Critical season of autumn ^a	7.3	6.4	11.9	8	8.2	9.6	9	9.4	8.8	9.7
Of the coldest month of winter	– 4.5/ I	– 2.8/I	2.1/II	– 1.7/I	1.0/ XII	– 1.5/I	– 2.0/ I	– 1.1/I	1.7/ XII	– 1.1/I
Critical season of spring ^c	13.4	13.1	17.2	14.9	15.1	14.3	15.5	13.8	16.2	14.6
<i>Sum of precipitation [mm]</i>										
In whole year	731	661	681	538	419	559	588	586	514	594
In critical season of autumn ^a	92	128	90	103	62	101	155	101	93	105
In critical season of winter ^b	207	186	174	141	147	157	112	150	231	173
In critical season of spring ^c	265	212	167	177	97	191	109	218	143	204
<i>Precipitation in % of a many years background</i>										
In whole year	111	100	126	100	75	100	100	100	87	100
In critical season of autumn ^a	72	100	87	100	61	100	153	100	89	100
In critical season of winter ^b	111	100	123	100	94	100	75	100	134	100
In critical season of spring ^c	125	100	94	100	50	100	50	100	70	100

^aMonths: September, October, first and second decades of November

^bMonths: third decade of November, December, January, February and March

^cMonths: April, May, June and first decade of July

$h_{mg}^2 = \frac{\sigma_g^2}{(\sigma_g^2 + \sigma_e^2/J)}$ —the mean heritability for genotype,

$r_{gg}^2 = \sqrt{h_{mg}^2}$ —the genotype selection accuracy.

The empirical REML/BLUP predictors of the interaction values is given by $\hat{\mu} + \hat{g}_i$, where μ —the general mean value, \hat{g}_i —the genotypic effect with lack of the GEI were obtained on the basis of proposed model. For each environment, genotypic values (V_g) are predicted by $\hat{\mu}_j + \hat{g}_i + (\hat{g}a)_{ij}$, where $\hat{\mu}_j$ —the mean of the j -th environment, \hat{g}_i —the genotypic effect from the i -th genotype, $(\hat{g}a)_{ij}$ —the effect from the GEI on the i -th genotype in the j -th environment.

Prediction of genotypic values is given by the formula:

$$\hat{\mu}_j + \frac{(\sigma_g^2 + \sigma_e^2)}{\sigma_g^2} \hat{g}_i,$$

where $\hat{\mu}$ —the general mean, n —the number of environments, and \hat{g}_i —the genotypic effect of the i -th genotype.

Stability of genetic values, MHVG, was calculated by the formula:

$$MHVG_i = n \left/ \sum_{j=1}^n (1/Vg_{ij}), \right.$$

where n —the number of environments ($n = 5$), Vg_{ij} —the genotypic value of the i -th genotype in the j -th

environment. Adaptability of genetic values, PRVG, was calculated by the formula:

$$PRVG_i = \frac{1}{n} \sum_{j=1}^n \frac{Vg_{ij}}{M_j},$$

where M_j —the mean of seed yield in the j -th environment.

Selection of genotypes (MHPRVG) was made on the basis of productivity, adaptability and stability and calculated by the formula (de Souza et al. 2018):

$$MHPRVG_i = \frac{Vg_{ij}}{n}.$$

Selection of the best genotypes was made on the basis of the MHPRVG values and on three criteria: (1) genetic values predicted across the locations with lack of interaction effects, (2) genetic value predicted with the GEI, and (3) selection on the basis of adaptability, production and stability.

Results and discussion

A prerequisite for the achievement of genetic progress in plant breeding is to use biometric methods and advanced biotechnology techniques (in vitro cultures, molecular biology). The process of breeding hybrid varieties requires a large number of cross-pollination combinations of parental lines and their evaluation in field trials in terms of general and specific combining ability, with simultaneously very careful selection of the components based on a number of qualitative characteristics and good adaptability for different environments.

Genetically, OSR is an allopolyploid (genome AACC, $2n = 38$) and contains full genomes of turnip rape and cabbage. The most important rapeseed breeding efforts include improvement of yielding ability via an introduction of hybrid varieties into cultivation, and an improvement of seed quality. Table 2 presents the WOSR genetic structure, which is divided by predictors of mean component and estimates of variance components. Intensive phenotyping in multi-environmental trials may provide the most desirable information to broaden our understanding of important complex traits such as seed development characters, biotic and abiotic stress tolerance and the manifestation of yield characters in oilseed rape

(Friedt and Snowdon 2009). This set of information should be a definite priority in order to facilitate selection of economically important traits, providing both researchers and breeders with an additional tool increasing the efficiency of the breeding process.

Seed yield, as well as seed quality parameters such as oil, protein and glucosinolate contents are strongly influenced by the environment (Quarrie et al. 2006; Nowosad et al. 2016; Bocianowski et al. 2019b) and the CV_e result (45.17) (Pereira et al. 2018) (Table 2). High CV_g values are desirable, since CV_g defines the size of the genetic variation in selection process (Fogaça et al. 2012). The genetic variation coefficient is equal to 41.01% and showed that the median portion of genetic variances was extracted from the total phenotypic variance. Similar results were obtained by de Souza et al. (2018), who used the same method and mixed models for 14 genotypes of carioca bean in four locations. Torres et al. (2016) and Rocha et al. (2017) obtained similar results for seed yield in oilseed rape genotypes in multi-environments experiments (Szała et al. 2019).

Joint assessment of CV_e and CV_g is relevant to breeding programs based on selection by the effect of selective accuracy (\hat{r}_{gg}). In the current study accuracy reached 91.0%, which is a high value. Obtained results showed compatibility of the genotypic values with real genotype values, thus ensuring better selection of winter oilseed rape (*Brassica napus* L.) genotypes to seed yield.

Heritability is one of the most important genetic parameters, since it measures the fraction of phenotypic variation of inheritable nature and can be explored in selection processes (Würschum et al. 2012). The mean heritability for genotype (\hat{h}_{mg}^2) is estimated when means are used as selection criteria. The heritability value (0.80) obtained in this study provided grounds for showing that selection of the best genotypes can be based on predicted genotypic values.

The heritability in the broad sense (\hat{h}_g^2) was estimated as 0.11 ± 0.04 . The size of the obtained deviation (0.04) didn't have the estimate to the zero value, which was expected and favorable for the seed yield. Torres et al. (2016) obtained \hat{h}_{mg}^2 and \hat{h}_g^2 values, similar to our results.

The individual phenotypic variance ($\hat{\sigma}_f^2$) is a summ of the genotypic variance, the residual variance

Table 2 Estimates of variance component (REML individual) of seed yield (dt ha^{-1}) in 25 winter oilseed rape (*Brassica napus* L.) genotypes cultivated in five environments

Variance components (REML) individuals	Estimators
Genotypic variance, $\hat{\sigma}_g^2$	1.0557
Variance of GEI, $\hat{\sigma}_c^2$	0.2293
Residual variance between plots, $\hat{\sigma}_e^2$	1.2890
Individual phenotypic variance, $\hat{\sigma}_f^2$	2.574
Heritability in the broad sense, h_g^2	0.11 \pm 0.04
Heritability of the mean genotype, h_{mg}^2	0.80
Accuracy of genotype selection, \hat{r}_{gg}	0.91
Determination coefficient of the GEI effects, c^2	0.09
Genotypic correlation coefficient across environments, \hat{r}_{gloc}	0.18
Coefficient of genetic variation, $CV_g(\%)$	39.77
Coefficient of experimental variation, $CV_e(\%)$	45.17
Mean, μ	3.969

Table 3 Estimates of genotypic value of seed yield (t ha^{-1}) in 25 winter oilseed rape genotypes cultivated in five different locations

Genotypes	Bąków	Borowo	Łagiewniki	Małyszyn	Zielęcín	Location means
Californium	2.269	3.370	4.986	6.371	5.000	4.399
Hercules F1	3.117	3.032	5.936	8.099	6.916	5.420
PN17	2.597	2.000	3.446	4.112	3.146	3.060
PN18	2.251	2.085	3.832	4.252	2.666	3.017
PN21	2.581	2.035	3.727	4.567	3.656	3.313
PN5	2.494	1.715	3.368	5.245	3.979	3.360
PN64	3.061	1.590	3.036	4.563	3.614	3.173
PN7	2.406	1.645	3.216	4.990	3.271	3.106
PN64 \times PN17	2.845	2.943	4.553	6.546	5.229	4.423
PN64 \times PN18	2.916	3.052	4.082	5.927	5.239	4.243
PN64 \times PN21	2.577	2.440	4.409	6.381	5.323	4.226
PN64 \times PN5	2.281	2.525	4.208	6.112	4.739	3.973
PN64 \times PN7	2.099	2.293	4.142	7.348	5.270	4.230
PN66	2.735	2.305	3.160	5.216	3.365	3.356
PN66 \times PN17	2.987	3.295	4.408	6.189	5.145	4.405
PN66 \times PN18	2.488	3.270	4.319	6.314	4.781	4.234
PN66 \times PN21	2.288	3.045	4.617	6.317	5.072	4.268
PN66 \times PN5	2.665	2.388	4.106	7.027	5.510	4.339
PN66 \times PN7	2.292	2.585	4.145	6.768	5.031	4.164
PN68	2.717	1.632	2.898	5.632	3.250	3.226
PN68 \times PN17	2.485	2.555	4.732	7.188	4.677	4.327
PN68 \times PN18	2.672	2.675	4.500	6.697	4.521	4.213
PN68 \times PN21	3.096	2.895	4.682	6.737	4.021	4.286
PN68 \times PN5	2.580	2.477	4.715	6.520	4.822	4.223
PN68 \times PN7	2.477	3.020	4.464	6.196	5.041	4.240
Mean	2.599	2.515	4.147	6.053	4.531	3.969

between plots and the variance in the GEI. The residual effect variance ($\hat{\sigma}_e^2$) represented 50.01% of the $\hat{\sigma}_f^2$ (Table 3). Obtained results had been expected, because seed yield is a quantitative trait determined by many QTLs (Bocianowski et al. 2011) and, consequently, highly influenced by the environment. Seyis et al. (2006) and Wójtowicz (2013) obtained similar results.

The GEI ($\hat{\sigma}_c^2$) variance determine the phenotypic expression of a quantitative trait depending on the individuals' degree of genetic adaptability and/or stability. The $\hat{\sigma}_c^2 = 0.2293$ obtained for seed yield corresponded to 8.91% of the total phenotypic variability, thus allowing to find a genotypic correlation across environments ($\hat{r}_{gloc} = 0.18$). Hence, it reinforces the importance of assessing the adaptability and stability of winter oilseed rape genotypes in order to provide accurate recommendations to farmers and breeders in different regions (Kaczmarek et al. 2003).

Three different strategies were used to selection of the best genotypes (Tables 3, 4). Based on the mean genotype in all environments, it may be seen here that cv. Hercules F1 and hybrids PN64 × PN17 and PN66 × PN17 were exceptional, because they presented the highest ($\hat{\mu} + \hat{g}$) values: 5.42, 4.42 and 4.41 t ha⁻¹, respectively (Table 3). The genetic gains from the selection of these genotypes were 11.16%, 7.73% and 6.17%, respectively.

The ($\hat{\mu} + \hat{g}$) values showed similar to results obtained by methods, wherein PRVG, and MHPRVG were simultaneously used (Table 4). Three restorer lines PN18, PN17 and PN21, CMS *ogura* line PN64 as well as hybrids PN66 × PN21 and PN64 × PN21, selected previously, stood out on the basis of this criterion. Such interaction capitalization is intrinsic to the selection of genotypes presenting greater adaptability and stability in the studied locations.

Table 4 Stability of genetic values (MHVG), adaptability of genetic values (PRVG and PRVG_m), and stability and adaptability of genetic values (MHPRVG and MHPRVG_μ) of 25 winter oilseed rape (*Brassica napus* L.) genotypes as predicted by BLUP analysis

Genotypes	MHVG	PRVG	MHPRVG	PRVG _μ	MHPRVG _μ
Californium	10.91	0.37	12.30	0.79	12.01
Hercules F1	10.73	0.32	12.87	0.74	13.14
PN17	13.39	0.53	15.02	0.91	14.24
PN18	13.75	0.65	18.54	1.15	19.88
PN21	14.71	0.53	15.53	0.93	13.58
PN5	7.55	0.41	10.11	1.13	11.29
PN64	10.84	0.63	15.73	1.11	14.01
PN7	13.52	0.56	14.72	1.26	18.21
PN64 × PN17	10.46	0.30	11.37	0.77	12.00
PN64 × PN18	8.87	0.25	10.15	0.72	12.99
PN64 × PN21	5.73	0.51	15.47	0.94	13.11
PN64 × PN5	7.51	0.31	9.62	0.95	11.24
PN64 × PN7	5.59	0.29	8.83	1.13	14.00
PN66	6.28	0.38	10.48	0.96	10.25
PN66 × PN17	16.74	0.47	18.43	0.73	15.45
PN66 × PN18	7.45	0.23	8.69	0.78	10.73
PN66 × PN21	7.40	0.64	18.77	0.89	11.98
PN66 × PN5	5.75	0.30	8.66	0.96	10.73
PN66 × PN7	10.64	0.34	11.71	1.01	15.01
PN68	11.13	0.49	14.30	1.39	19.64
PN68 × PN17	9.55	0.36	12.37	0.98	14.51
PN68 × PN18	9.87	0.28	10.93	0.90	14.55
PN68 × PN21	12.67	0.38	13.91	0.82	14.01
PN68 × PN5	9.15	0.48	14.38	0.92	12.14
PN68 × PN7	9.01	0.27	9.85	0.80	11.10

Adaptability of genetic values (PRVG) of line PN18 and hybrid PN66 × PN21 was equal to 0.65 and 0.64 times, respectively. The selection of two the best genotypes by the stability and adaptability of genetic values using the predicted genetic value resulted in a new mean seed yield equal to 1.67 t ha⁻¹ (Table 4). This is lower than value estimated in the selection for mean seed yield of 5.42 t ha⁻¹ in all environments (Table 3).

Conclusion

The mean heritability of genotype showed average size and high accuracy of selection, while allowing the selection of agronomically the best individuals. Parental lines with the restorer gene (*Rfo*), i.e. PN18, PN17 and PN21, maternal line PN64 as well as hybrids PN66 × PN21 and PN64 × PN21 exhibited high seed yield adaptability and stability. There was an agreement between statistics of MHVG, PRVG and MHPRVG in the discrimination of the most productive genotypes, which presented high adaptability and stability. Such results indicated that these genotypes can be part of the selection criteria regularly used in winter oilseed rape breeding programs.

The implementation of the MHPRVG method provides preselection of superior parental lines and hybrid combinations, facilitates the selection process and shortens the breeding cycle. A promising MHPRVG method focusses selection on breeding materials and aims to predict parental lines with the highest potential to produce high oleic (HO), high yield (HY) and high protein (HP) winter oilseed rape hybrid cultivars well adapted to the changing climate.

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Declarations

Conflict of interest Authors declare that they have no conflict of interest.

Ethical approval This article does not contain any studies with human participants or animals performed by any of the authors.

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