

Stability analysis of spring oat genotypes in south-west Poland

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SUMMARY

Oat is a grain in high demand, due to its physiological and nutritional attributes as a functional food. Oat is rich in β -glucans, and high in tocopherol and other dietary fibre components. It is also used for forage, fodder, chaff and as a major component of infant foods. In the present study, oat yields from six experimental stations in south-western Poland, obtained in 2019–2022, were analysed using three different linear mixed models that can be associated with three different stabilities. It is shown that the genotype Perun had the highest mean yield among the tested genotypes, while the genotype Armani was the most stable. Armani and Pablo had the lowest values of the GSI index, making them the most favourable genotypes for cultivation in that region.

Key words: spring oat, south-west Poland, stability, linear mixed model, safety-first selection index

1. Introduction

Oat grains are widely used both as human food and animal feed. According to Stevens et al. (2004), oats are among the most nutritious grain cereals, with high protein and fibre content. Moreover, they claim that the protein content of rolled (flaked) oats is generally greater than that of other cereal grains. Oats suit regions with a wet climate and cool summer. They grow on a great variety of soils, in regions with temperatures between 5 and 26 degrees Celsius and precipitation over 500 mm (Assefa et al., 2003). Stevens et al. (2004) report that in warmer regions, spring type oats can be sown in autumn to avoid summer heat and drought. Moreover, they claim that

oats are better adapted to variable soil types and can perform better on acid soils than other small grain cereal crops. Duda et al. (2021) report that because autumn oat crops are sensitive to winter conditions, spring oats are preferable. Additionally, Sterna et al. (2021) claim that oats have a higher fatty acid content than other cereals from the same temperate area.

An invaluable benefit of oats is improved nutrition and health due to the consumption of dietary fibre. They have been proven to counteract heart diseases, diabetes, and some forms of cancer. Moreover, oats are among the main components of infant foods, due to their high nutritional profile, lack of allergenicity, palatable flavour, good shelf-life, stability, and low cost (Sterna et al., 2016). All of these positive properties of oats are attributed to their content of vitamins, minerals, essential fatty acids, fibre, and phytochemicals, including several phenolic compounds (Anderson and Hanna, 1999). Additionally, oats contain small amounts of free phenolic acids, including caffeic, p-coumaric, ferulic, p-hydroxybenzoic, p-hydroxyphenylacetic, protocatechuic, sinapic, syringic, and vanillic acids, and flavonoids such as apigenin, kaempferol, luteolin, quercetin, and tricetin (Chen et al., 2007).

Research on stability variances, genotype selection indices, and safety-first selection indices is essential to identify the most desirable oat genotypes in terms of average yield. Oats, like many other crops, are influenced by various environmental factors, such as temperature, precipitation, and soil conditions. These factors can lead to fluctuations in crop yield from one season to another. By studying stability variances, it is possible to assess how oat genotypes perform across different environments and identify those that consistently exhibit stable yields, regardless of changing conditions. Understanding stability variances helps ensure that the oat genotypes selected for cultivation are reliable and resilient, providing consistent yields for farmers.

Several stability measures have been described in the literature, including Shukla's stability variance (Shukla, 1972), and the regression on the environmental mean approach to assessments of stability (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966). However, with the increase in computing power and the development of statistical methods, the assessment of stability based on linear mixed models has become more popular (see e.g. Piepho, 1999; Studnicki et al., 2017). In Piepho (1999) the above-mentioned models were defined in terms of variance components.

Researching genotype selection indices and the safety-first selection index enables evaluation of the performance of different oat genotypes under

controlled experimental conditions. By analysing selection rates, researchers can identify the genotypes that exhibit the highest yields and are the most stable. These selected genotypes can then be recommended to farmers for commercial cultivation, leading to improved oat production and potentially increased agricultural profitability.

Overall, research on stability variances, genotype selection indices and safety-first selection indices is crucial for developing improved oat varieties with higher average yields and enhanced stability. This research contributes to sustainable agriculture, increased food production, and better-quality oats, benefiting farmers, consumers, and the entire agricultural industry.

2. Materials and methods

2.1. Data

The data consists of post-registration oat trials performed in south-west Poland in the years 2019–2022 ($K = 4$). The data set is part of a larger series of field trials performed by the Research Centre for Cultivar Testing (COBORU) in those years. The sites used in the present study are listed in Table 1. The location of the sites is shown in Figure 1. The total number of environments was equal to $J = 17$. The choice of south-western Poland for post-registration research on oats is justified by several factors. Firstly, the region's environmental conditions closely mimic those of other parts of Poland and neighbouring countries, making the research outcomes more broadly applicable. Secondly, south-western Poland presents a diverse range of soil types, microclimates, and altitude variations, offering a representative platform for testing oat varieties in varying conditions.

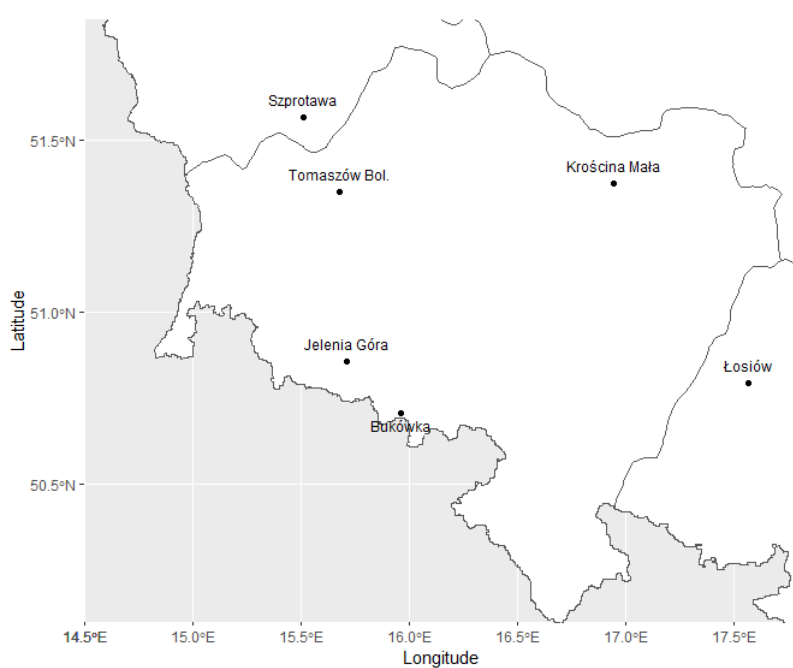
Most of the trials performed were laid out in a randomized complete block design with three replicates. In Jelenia Góra only, the trials were organized in a 1-resolvable design with three replicates and three blocks.

During the four-year study approximately 25 spring oat genotypes were tested. Since we are interested in assessing the stability of genotypes, we chose genotypes which were tested in the region of interest in at least 9 environments. For this reason, we assessed the stability of the following genotypes: Agent, Armani, Bingo, Figaro, Gepard, Harnaś, Huzar, Kozak, Lion, Monsun, Pablo, Perun, Rambo, Refleks, Scorpion, and Wulkan ($I = 16$).

In the Polish post-registration trials, one of the analysed traits is yield, which is observed on plots. In the present study, oat yield is expressed in tonnes per hectare (t/ha).

Table 1. Sites in southern Poland used in the oat trials conducted from 2019 to 2022

Site	Year			
	2019	2020	2021	2022
Tomaszów Bolesławiecki	X	X	X	X
Krościna Mała	X	X	X	X
Jelenia Góra	X	X	X	X
Bukówka	X	X	-	-
Łosiów	-	-	X	X
Szprotowa	-	-	X	-

**Figure 1.** Map of south-west Poland showing the locations of sites

2.2. Statistical analysis

The observations were modelled according to a linear mixed model. For the sake of clarity, throughout the paper, environments will mean combinations of year and site.

In the analysed data set, a 1-resolvable design was used in only four out of seventeen environments. According to Speed et al. (1985), removal of the block effect for this design still provides a valid analysis. They claim that, for all resolvable connected designs, the genotype and error mean squares have the same expectation in the absence of genotypic differences. Moreover, they prove that an unbiased estimate of the difference between the blocks stratum variance and the plots stratum variance is $(v - 1)/(s - 1)$ times the difference between the error mean square of the complete block analysis and the error mean square of the incomplete block analysis, where s is the number of blocks and v is the number of genotypes. Therefore, the effect of blocks nested within replicates and environments was omitted.

Let y_{ijk} denote the yield of the k -th ($k = 1, \dots, K$) replicate of the i -th ($i = 1, \dots, I$) genotype in the j -th ($j = 1, \dots, J$) environment. Then the linear mixed model for combined trials can be expressed as:

$$y_{ijk} = \mu + g_i + r_{jk} + u_j + w_{ij} + e_{ijk}, \quad (1)$$

where μ is a general mean, g_i is the i -th genotype main effect, u_j is the j -th environment main effect, r_{jk} is the k -th replicate effect nested within the j -th environment, and e_{ijk} is an experimental error term corresponding to y_{ijk} . It is assumed that $u_j \sim N(0, \sigma_u^2)$, $r_{jk} \sim N(0, \sigma_r^2)$ and $e_{ijk} \sim N(0, \sigma_e^2)$. The genotype $\times$ environment interaction effect is assumed to be a random effect, and is denoted in model (1) as w_{ij} . We assume that the random vector of genotype $\times$ environment effects $\mathbf{w}$ is normally distributed with mean $\mathbf{0}$ and covariance matrix $\mathbf{\Sigma} \otimes \mathbf{I}$, i.e.

$$\mathbf{w} \sim N(\mathbf{0}, \mathbf{\Sigma} \otimes \mathbf{I}).$$

Assuming that $\mathbf{\Sigma} = \text{diag}(\sigma_1^2, \sigma_2^2, \dots, \sigma_I^2)$, where I denotes the number of genotypes tested in the series of field trials, and $\mathbf{I}$ is the identity matrix of order J , we obtain Shukla's stability variance model (SH). By dropping the main effects of environments in model (1) and assuming that $\mathbf{\Sigma} = \mathbf{\Lambda}\mathbf{\Lambda}' + \mathbf{\Psi}$, where $\mathbf{\Lambda}$ is an $I \times 1$ vector of genotype loadings and $\mathbf{\Psi}$ is an $I \times I$ diagonal matrix with elements which are additive specific variances for individual genotypes ($\mathbf{\Psi} = \text{diag}(\sigma_1^2, \sigma_2^2, \dots, \sigma_I^2)$), we obtain the Eberhart and Russell regression model (ER). Furthermore, using the same list of random effects as in the ER model, and assuming that all σ_i^2 's are equal to σ^2 ($\mathbf{\Psi} = \sigma^2 \mathbf{I}$), we obtain the Finlay–Wilkinson model (FW). As in Piepho (1997), the genotype sensitivities in the FW and ER models can be calculated using

the estimated genotype loadings as:

$$b_i = \frac{\lambda_i}{\bar{\lambda}},$$

where λ_i is the loading of the i th genotype and $\bar{\lambda}$ is the mean of the genotype loadings.

For all models, the Akaike information criterion (in the smaller-is-better form) was calculated using Genstat's vaic function. For clarity, only the results for the best model are reported. Restricted Maximum Likelihood was used to estimate the variance components (Searle et al., 2006; numerical implementation Genstat 23, VSN International). The fixed effects were estimated by generalized least squares. The Wald test statistic with approximate F statistic was used to test the hypothesis

$$H_0 : \alpha_1 = \alpha_2 = \dots = \alpha_I,$$

where $\alpha_i, i = 1, 2, \dots, I$ denotes a genotype fixed effect and I is the number of genotypes. This test has an approximate F distribution with numerator degrees of freedom (d.d.f.) calculated using the Kenward–Roger approximation (Kenward and Roger, 1997).

To combine rankings based on the estimated genotype means and values of the stability measure, the genotype selection index (GSI) was calculated as:

$$GSI_i = RM_i + RW_i,$$

where RM_i is the rank of the trait mean and RW_i is the rank of Shukla's stability score for the i -th genotype.

Finally, for each genotype, we calculated the value of the safety-first selection index (Eskridge, 1990) as

$$SF_i = \mu_i - Z(1 - \alpha)(V_i)^{1/2},$$

where μ_i is a genotype mean, $Z(1 - \alpha)$ is the $1 - \alpha$ percentile from the standard normal distribution, and V_i is a model specific measure of stability. For the SH model, V_i is equal to $\hat{\sigma}_i^2 + \hat{\sigma}_u^2$. For the FW model $V_i = \hat{\lambda}_i^2 + \hat{\sigma}^2$, whereas for the ER model $V_i = \hat{\lambda}_i^2 + \hat{\sigma}_i^2$. In the present study, we took α as equal to 0.05.

All statistical analyses were conducted, and the figures were generated, using Genstat data analysis software (version 23). However, Figure 1 was generated using the statistical software R (version 4.3.0).

3. Results

Mean, standard deviation (sd), minimum (min), median (med) and maximum (max) of yield for the four studied years are reported in Table 2. A graphical summary of the data is presented in Figure 2.

Table 2. Summary statistics for yield: mean, standard deviation (sd), minimum (min), median (med), maximum (max)

Year	mean	sd	min	med	max
2019	5.421	1.750	2.073	5.421	9.152
2020	6.847	1.550	4.013	6.808	9.569
2021	6.761	1.072	3.566	6.817	8.948
2022	3.877	0.916	1.969	3.691	6.250

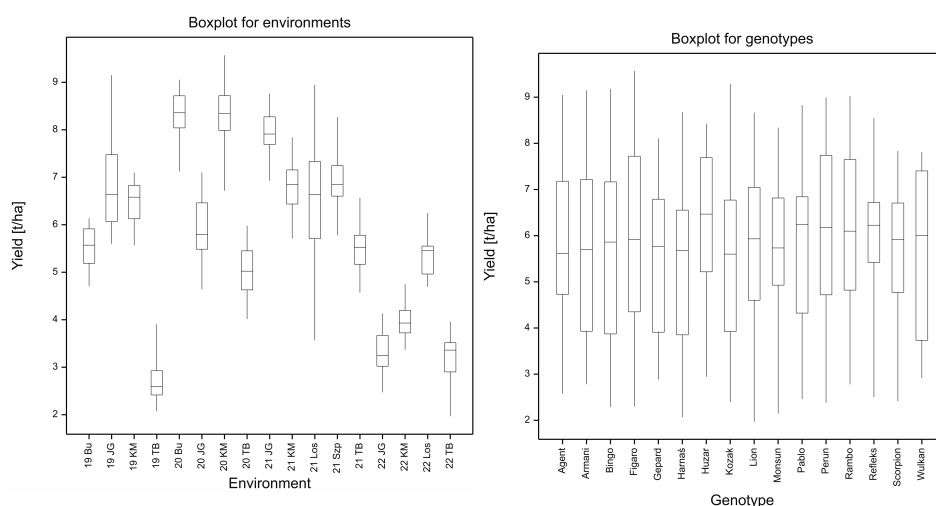


Figure 2. Boxplots for environments (left) and genotypes (right). Abbreviations for environment boxplots refer to the year (e.g. 19 means 2019) and to sites: TB – Tomaszów Bolesławiecki, KM – Krościna Mała, JG – Jelenia Góra, Bu – Bukówka, Los – Łosiów, Szp – Szprotowa.

The oat yields ranged from 1.969 t/ha to 9.569 t/ha. The lowest and the highest mean yield were observed in 2022 and 2020, respectively.

The data was analysed using the SH, FW and ER models (see Table 3), and for each model the AIC values were calculated.

It is noted that the smallest value of the AIC criterion was obtained for the SH model. This means that this model was the best among the three

Table 3. Random models, covariance matrices and values of AIC

Model	Random model	Covariance matrix for Env	Covariance matrix for Env.Gen	AIC
SH	Env + Env.Gen + Env.Rep	$\sigma_u^2 \mathbf{I}$	$\text{diag}(\sigma_1^2, \sigma_2^2, \dots, \sigma_I^2) \otimes \mathbf{I}$	1005.16
FW	Env.Gen + Env.Rep	–	$(\mathbf{\Lambda}\mathbf{\Lambda}' + \mathbf{\Psi}) \otimes \mathbf{I}$, where $\mathbf{\Lambda}$ is an $I \times 1$ vector of genotype loadings and $\mathbf{\Psi} = \sigma^2 \mathbf{I}$	1034.58
ER	Env.Gen + Env.Rep	–	$(\mathbf{\Lambda}\mathbf{\Lambda}' + \mathbf{\Psi}) \otimes \mathbf{I}$, where $\mathbf{\Lambda}$ is a $I \times 1$ vector of genotype loadings and $\mathbf{\Psi} = \text{diag}(\sigma_1^2, \sigma_2^2, \dots, \sigma_I^2)$	1019.66

fitted models. For clarity, only the results for the SH model are presented.

The analysis of the SH model provided several estimates and statistics. The variance component for environments was equal to 3.06 (s.e.=1.09), whereas the variance component for replicates nested within environments was equal to 0.06 (s.e.=0.02). Finally, the variance component for error was equal to 0.13 (s.e.=0.01).

The Wald test statistic for testing genotype effects was equal to 48.47. The approximate F statistic was equal to 2.71 (n.d.f.=15 and d.d.f.=45.5) and was highly significant ($P = 0.005$). Table 4 reports the genotype means, Shukla's stability variances and values of the GSI and SF indices. The standard errors of differences are given at the bottom.

In the third column of Table 4 the genotype means are given. It can be seen that the genotype Perun had the highest mean yield among the tested genotypes, which was equal to 6.161. The second best genotype was Figaro, with a mean yield equal to 6.033. On the other hand, the lowest mean yield was recorded for Scorpion.

The fourth and fifth columns of Table 4 contain Shukla's stability variances and their standard errors (s.e.). It is seen that the genotype Armani had the smallest Shukla's stability variance, equal to 0.199. This means that this was the most stable of the tested genotypes. The highest yielding genotype Perun was one of the least stable. The most unstable genotype was Huzar.

Table 4. Genotype means and the values of Shukla's stability variance, GSI and SF indices. The numbers in square brackets indicate the rankings of genotypes.

No.	Genotype	Mean ^a [t/ha]	Stability		GSI	SF
			Estimate	s.e.		
1	Agent	5.825 [8]	1.001 [9]	0.520	17	2.51 [9]
2	Armani	5.944 [5]	0.199 [1]	0.254	6	2.974 [1]
3	Bingo	5.854 [7]	0.476 [6]	0.349	13	2.761 [4]
4	Figaro	6.033 [2]	0.937 [7]	0.509	9	2.744 [5]
5	Gepard	5.814 [9]	0.267 [3]	0.355	12	2.813 [3]
6	Harnaś	5.519 [15]	0.417 [5]	0.329	20	2.451 [10]
7	Huzar	5.629 [13]	3.567 [16]	1.913	29	1.394 [16]
8	Kozak	5.577 [14]	3.313 [15]	1.350	29	1.424 [15]
9	Lion	5.682 [11]	1.815 [12]	0.812	23	2.050 [12]
10	Monsun	5.658 [12]	0.291 [4]	0.352	16	2.647 [6]
11	Pablo	5.946 [4]	0.237 [2]	0.261	6	2.959 [2]
12	Perun	6.161 [1]	3.18 [14]	1.303	15	2.052 [11]
13	Rambo	5.927 [6]	0.986 [8]	0.597	14	2.618 [7]
14	Refleks	5.696 [10]	1.971 [13]	1.401	23	2.006 [13]
15	Scorpion	5.25 [16]	1.619 [11]	1.107	27	1.692 [14]
16	Wulkan	6.002 [3]	1.232 [10]	0.844	13	2.594 [8]

^a Standard errors of differences: Average: 0.1868; Max: 0.3079; Min: 0.0996

In the sixth column of Table 4 the GSI indices are given. It is observed that the genotypes Armani and Pablo had the lowest GSI index values. This means that these two genotypes are the most desirable. The second best genotype in terms of the GSI index was Figaro. The highest value of the GSI index was obtained for the genotypes Huzar and Kozak.

In the last column of Table 4 the safety-first selection rule values are given. The highest value was observed for the genotype Armani, and the second highest for Pablo. The lowest value of the SF index was obtained for the genotype Huzar.

4. Conclusions

In this study we assessed the stability of 16 genotypes in south-west Poland using linear mixed models. By assuming different covariance matrices for the vector of $G \times E$ interaction effects and modifying the lists of random effects, we obtained three models, which can be associated with commonly used stability measures. Next, the models were compared in terms of the AIC.

A similar strategy was used by Piepho (1999). That author also analysed a two-way data set with the aim of identifying the most stable variety. For this purpose, he fitted several linear mixed models with different covariance matrices for the $G \times E$ interaction and modified the lists of random effects. Next, by using different goodness of fit statistics, he chose the best one. In the same paper, he also noted that within the mixed model framework the problem of choosing an appropriate stability measure is equivalent to the problem of identifying the most appropriate covariance matrix for the $G \times E$ interaction, and concluded that the choice of stability measure is data-dependent. The same approach was used in a different study (Studnicki et al., 2017). The authors of that paper were interested in finding a model with the highest predictability for means of cultivar $\times$ location and cultivar $\times$ region.

In the present study, for each genotype, the value of the safety-first selection index was calculated. This index can be treated as a different stability which combines genotypes' mean and stability variance in a meaningful way (Eskridge, 1990; Eskridge and Mumm, 1992). Eskridge (1990) and Eskridge and Mumm (1992) used the values of this index to select the highest yielding and the most stable genotypes. Macholdt et al. (2019) used a similar concept (probability of falling below certain threshold) to evaluate the yield performance and stability of winter wheat for different levels of fertilization and combinations. In a different study, Piepho (1997) proposed a simplified procedure for comparing the stability of cropping systems.

We conclude from the current study that the mean yields of 16 genotypes tested in the region of interest differed significantly. It was found that Perun was the highest yielding among the tested genotypes. The lowest mean yield was observed for the genotype Scorpion. According to the values of Shukla's stability variance, the genotype Armani was the most stable. On the other hand, the highest yielding genotype was one of the least stable. Additionally, the lowest values of the GSI index and the highest values of the SF index were obtained for genotypes Armani and Pablo. Thus, one can conclude that these two genotypes should be promoted and the genotypes Huzar and Kozak should not be recommended in the region of interest.

Finally, the same reasoning applies for the other stability models.

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