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PARAMETRIC AND NON-PARAMETRIC METHODS FOR THE EVALUATION OF WINTER RYE GENOTYPES BY GRAIN YIELD STABILITY

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Abstract: The analysis of yield stability has become increasingly relevant in recent years due to changing climatic conditions that negatively affect crop yields. It is of utmost importance for farmers to cultivate widely adaptable and yield-stable varieties with high yield potential, as this determines economic predictability and mitigates their risk. Stability is also crucial for plant breeders to create genotypes adapted to a wide range of diverse environments. The aim of this study was to identify high-yielding, stable and adaptive rye landraces and cultivars for commercial and breeding purposes. The trial was carried out from 2014 to 2022 and included 16 cultivars and 7 Bulgarian landraces. The experiment was conducted in a block design with the randomized design of the variants in four replications. Sixteen parametric and non-parametric parameters of grain yield stability were determined. The average of the sum ranks (ASR), the AMMI stability value (ASV), the yield stability index (YSI) and the genotype selection index (GSI) were also calculated. Year had the highest statistically significant effect on the grain yield per hectare. Parametric and non-parametric stability parameters estimated G13, G12, G20 and G21 genotypes as the most stable. ASV identified G13, G18, G12 and G9 as the most stable genotypes, while YSI identified G13, G19, G12 and G18, respectively. GSI classified G13, G12, G18, and G19 as genotypes with the broadest adaptability to adverse climatic conditions. They could serve as source material for rye breeding programs.

Key words: rye, yield, stability analysis, adaptability.

Introduction

The analysis of yield stability has become increasingly relevant in recent years due to changing climatic conditions that negatively affect crop yields. It is of utmost importance for farmers to cultivate widely adaptable and yield-stable varieties with high yield potential, as this determines economic predictability and mitigates their risk. Stability is also crucial for plant breeders to create genotypes

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adapted to a wide range of diverse environments. Human food security also depends on crop yield stability (Ahrends et al., 2021; Reckling et al., 2021).

Yield stability is a complex indicator of a genotype's ability to fully utilize the available environmental factors and achieve its maximum potential, and is closely linked to its adaptability (Hassani et al., 2023). A number of statistical methods have been devised to quantify the stability of genotypes. Stability analyses (parametric and non-parametric) simultaneously estimate the relative ranking of genotypes tested in a series of environments. The most commonly used parametric estimates of stability are: regression coefficient, deviation from regression, coefficient of determination, coefficient of variance, Wricke's ecovariance, Shukla's stability variance, mean variance component, GE variance component, Kang's rank-sum, yield stability index, AMMI stability value (Sabaghnia, 2010; Karimizadeh et al., 2012; Fasahat et al., 2015; Pour-Aboughadareh et al., 2022). Non-parametric measures of phenotypic stability are based on ranking the genotypes in each environment. Genotypes with close rank values in different environments are referred to as stable (Sabaghnia, 2015).

Rye is a crop mainly used for the production of dietary bread and as animal feed. It is grown on infertile and sandy soils (Klimek-Kopyra et al., 2023). The crop possesses a great number of advantages such as a unique nutritional value, winter hardiness and tolerance to environmental stresses such as low temperatures, drought and poor soil conditions (Laidig et al., 2017; Desheva and Valchinova, 2023). Interest in culture has grown in recent years due to changes in consumption needs (Podolska and Aleksandrowicz, 2019). The development of new rye varieties with improved performance and persistence is fundamental to the resurgence of the crop as a uniform and cultivated commodity in Europe (Haffke et al., 2015; Hackauf et al., 2022). Therefore, it is crucial to have information on the yield stability and variability of winter rye cultivars before releasing them for commercial cultivation and to enhance the effectiveness of cultivar improvement programs.

The aim of this study was to identify high-yielding, stable and adaptive rye landraces and cultivars for commercial and breeding purposes.

Material and Methods

The studies were carried out from 2015 to 2022 in the experimental area of the IPGR "K. Malkov" in Sadovo, Bulgaria, on clay soil. It involved 23 accessions from the National Seed Gene Bank, including 16 cultivars and 7 Bulgarian landraces (Table 1). Sowing was conducted between 20 and 30 October, after the predecessor pea, at the favorable timing for the region. The experiment was arranged in a block scheme with the randomized design of the variants in four replications. The size of the experimental plot was 10 m^2. The necessary agronomic practices were employed during the whole vegetation period to assure equal plant development.

The grain yield data (t/ha) from seven-year genotype testing were statistically analyzed using one-way and two-way ANOVA. To measure specific differences between pairs of means, the Duncan's multiple range test was employed. Statistical processing of the data was carried out using the IBM SPSS Statistics 22 for Windows program.

Table 1. A list of the rye accessions involved in the trial.

Genotype code	Species	Name of accessions	Biological status	Origin
G1	Secale cereale L.	Milenium	cultivar	BGR
G2	Secale cereale L.	Danae	cultivar	DEU
G3	Secale cereale L.	A9E0050	landrace	BGR
G4	Secale cereale L.	A9E0053	landrace	BGR
G5	Secale cereale L.	A9E1386	landrace	BGR
G6	Secale cereale L.	A9E1390	landrace	BGR
G7	Secale cereale L.	A9E1387	landrace	BGR
G8	Secale cereale L.	A9E1388	landrace	BGR
G9	Secale cereale L.	A9E1389	landrace	BGR
G10	Secale cereale L.	Igusinskaja	cultivar	BLR
G11	Secale cereale L.	Sjabrouka	cultivar	BLR
G12	Secale cereale L.	Albedo	cultivar	CZE
G13	Secale cereale L.	Aventino	cultivar	CZE
G14	Secale cereale L.	Matador	cultivar	CZE
G15	Secale cereale L.	Selgo	cultivar	CZE
G16	Secale cereale L.	Visello	cultivar	CZE
G17	Secale cereale L.	Veronika	cultivar	UKR
G18	Secale cereale L.	Harkovskaya 88	cultivar	UKR
G19	Secale cereale L.	Harkovskaya 95	cultivar	UKR
G20	Secale cereale L.	Harkovskaya 98	cultivar	UKR
G21	Secale cereale L.	Prima	cultivar	CAN
G22	Secale cereale L.	AC Rifle	cultivar	CAN
G23	Secale cereale L.	AC Remington	cultivar	CAN

The *Stabilitysoft* statistical program was used to calculate sixteen stability parameters for grain yield. These parameters included: mean variance component (θ_i) (Plaisted and Peterson, 1959), GE variance component ($\theta_{(i)}$) (Plaisted, 1960), Wricke's ecovariance (W_i^2) (Wricke, 1962), regression coefficient (b_i) (Finlay and Wilkinson, 1963), deviation from regression (S^2d_i) (Eberhart and Russel, 1966), Shukla's stability variance (σ^2_i) (Shukla, 1972), coefficient of variance (CV_i) (Francis and Kannenberg, 1978), parameters of Nassar and Huehn (1987) ($S^{(1)}$ – the mean of the absolute rank differences of the genotype across all environments tested, $S^{(2)}$ – the variance between ranks across all environments tested, $S^{(3)}$ – the sum of the absolute deviations for each genotype relative to the mean of the ranks, $S^{(6)}$ – the sum of the squares of the ranks for each genotype relative to the mean of the ranks), Thennarasu parameters (1995) ($NP^{(1)}$, $NP^{(2)}$, $NP^{(3)}$, and $NP^{(4)}$), and Kang's rank-sum (KR) (Kang, 1988).

The additive main effect and multiplicative interaction (AMMI) analysis and genotype plus genotype by environment interaction (GGE) biplot analysis were performed using the PBTools software. The AMMI stability value (ASV) was calculated based on the interaction principal component axis of the AMMI model (IPCA1 and IPCA2 values) for each genotype and each environment, as suggested by Purchase (1997), using the PBTools Software and Microsoft Excel 2010.

The study utilized the yield stability index (YSI) to assess genotype stability based on the mean yield rank across environments and the ASV rank (Farshadfar et al., 2011).

Additionally, the genotype selection index (GSI) was calculated as the sum of the ASV and YSI ranking positions (Köse, 2022).

Results and Discussion

Over the seven-year study period, the rye genotypes had an average grain yield ranging from 3.61 t ha^{-1} to 5.22 t ha^{-1}, with an overall average of 4.51 t ha^{-1}. The highest yield was reported for G13 and the lowest for G4. The Duncan's multiple range test revealed significant differences between the means, indicating considerable variation between genotypes for the trait studied (Figure 1).

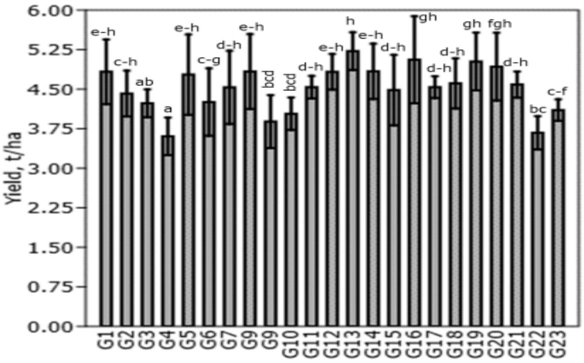

Figure 1. Mean yield (t ha^{-1}) for 23 winter rye genotypes for the period of 7 years (data are presented as mean ± standard error, different letters indicate the statistically significant differences between the means at $p \leq 0.05$).

Genotype, environment, and genotype x environment interaction (GEI) all contribute to grain yield (Đekić et al., 2018; Kartina et al., 2019; Egea-Gilabert et al., 2021). GEI studies help in selecting genotypes for breeding, based on their suitability for general or specific purposes, and provide information on how the environment affects crop performance (Amelework et al., 2023; de Filho et al., 2023).

In this study, the analysis of variance showed that there were highly significant differences in grain yield in regard to the genotype and the years investigated. This indicates the presence of both environmental and genetic variability. Year had the highest statistically significant effect on the trait (η^2=58.50%), followed by year x genotype interaction (η^2= 30.25%) (Table 2). Siekmann et al. (2021) also found that the GxE interaction variances of grain yield were larger than the variances of the genotype.

Table 2. Two-way ANOVA and the degree of influence of the sources of variation (η^2, %) on yield in 23 rye genotypes.

SV	df	MS	η^2, %
G	22.00	53546.08***	10.45
Y	6.00	1099084.01***	58.50
GYI	132.00	25835.39***	30.25
Error	483.00	186.93	0.80
Total	643.00		

SV – sources of variation; G – genotype; Y – year; GYI – genotype x year interaction; df – degree of freedom; MS – mean squared; η^2 – strength of influence of sources of variation – genotype, year and genotype x year interaction; *** – statistically significant values at $p \leq 0.001$.

Several studies emphasize the significance of stability parameters in identifying genotypes that are widely adapted (Hadasch et al., 2020; de Souza et al., 2020; Dias et al., 2022; Matova et al., 2022; Amelework et al., 2023; de Filho et al., 2023; Matongera et al., 2023; Mengistu and Abu, 2023).

To ensure a dependable evaluation of the genotype in terms of grain yield stability and adaptability, a proven effect of the genotype x environment interaction on the expression of the trait under study is essential. The impact of G×E interaction is demonstrated by the varying response of genotypes in different environments. To identify yield-stable genotypes in our study, we used both parametric and non-parametric stability parameters. Based on the ecovalence method of Wricke and Shukla's stability variance (σ^2_i), genotypes G13, G12, and G18 were identified as the most stable. With the exception of G13, which was ranked as the highest yielding, it should be noted that the other two were not the top performers in terms of mean yield, but ranked 8th and 10th, although their yield was above the mean. Conversely, the most unstable genotypes were G16, G22, and G10, which ranked 2nd, 22nd, and 20th respectively for mean yield (Table 3).

The most desirable genotypes are those with above-average productivity and low CV_i (Pour-Aboughadareh et al., 2022), as demonstrated by G17 and G11 in this study. Conversely, G16, G5, and G7 had the highest CV_i values, indicating lower stability and variability in their yield over the years of the study (Table 3).

Based on the lower mean variance component (θ_i) of Plaisted and Peterson (1959) and the higher GE variance component $\theta_{(i)}$ of Plaisted (1960), G13, G12 and G18 were found to be more stable (Table 3).

The results of the stability analysis, presented as linear regression for each cultivar using the Finley-Wilkinson (1963) model, indicate that 11 genotypes (G1, G5, G6, G7, G8, G14, G15, G16, G18, G19, G20) had a b_i value greater than 1 (Table 3). This suggests that these genotypes are more sensitive to changing environmental conditions and have a greater specific adaptability to high-diversity environments. G9 was found to be the most adaptive to all environments with a b_i value of 1. Genotypes G2, G3, G4, G10, G11, G12, G13, G17, G21, G22, and G23 were found to have a b_i value less than 1 (Table 3). This indicates that these genotypes are more resistant to environmental changes, making them more adaptable to low-yielding environments (Shojaei et al., 2022; Pour-Aboughadareh et al., 2022; Kebede et al., 2023). The b_i-value variation confirms that the genotypes studied respond differently to environmental changes (Akbar et al., 2021).

Table 3. Yield parametric stability parameters for 23 rye genotypes and their ranking.

G	Y	R	W_i^2	R	σ^2_i	R	CV_i	R	$\theta_{(i)}$	R	θ_i	R	b_i	s^2d_i	R
G1	4.83	7	2.22	6	0.37	6	33.57	15	0.66	6	0.53	18	1.45	0.11	8
G2	4.42	16	3.71	15	0.65	15	25.94	10	0.65	15	0.66	9	0.79	0.48	20
G3	4.23	18	2.22	5	0.37	5	16.41	5	0.66	5	0.53	19	0.55	0.11	7
G4	3.61	23	3.30	10	0.57	10	26.12	11	0.65	10	0.63	14	0.64	0.34	16
G5	4.78	9	5.30	20	0.94	20	42.25	22	0.63	20	0.80	4	1.83	0.04	2
G6	4.25	17	3.81	16	0.67	16	39.80	20	0.65	16	0.67	8	1.43	0.35	17
G7	4.53	14	3.96	17	0.69	17	40.57	21	0.64	17	0.68	7	1.64	0.15	10
G8	4.83	6	4.83	18	0.85	18	38.78	18	0.64	18	0.76	6	1.63	0.28	14
G9	3.88	21	3.42	11	0.59	11	34.18	16	0.65	11	0.64	13	1.00	0.49	21
G10	4.03	20	6.33	21	1.12	21	20.12	8	0.62	21	0.89	3	0.33	0.45	19
G11	4.54	12	3.57	13	0.62	13	12.44	2	0.65	13	0.65	11	0.38	0.12	9
G12	4.83	8	1.11	2	0.17	2	18.44	7	0.67	2	0.43	22	0.75	0.10	5
G13	5.22	1	0.33	1	0.03	1	18.11	6	0.67	1	0.37	23	0.85	0.02	1
G14	4.84	5	2.65	9	0.45	9	28.66	13	0.65	9	0.57	15	1.12	0.36	18
G15	4.48	15	3.61	14	0.63	14	39.51	19	0.65	14	0.65	10	1.56	0.19	13
G16	5.06	2	9.20	23	1.65	23	43.20	23	0.60	23	1.14	1	1.86	0.56	22
G17	4.54	13	3.49	12	0.61	12	12.04	1	0.65	12	0.64	12	0.38	0.11	6
G18	4.61	10	1.16	3	0.18	3	27.29	12	0.67	3	0.44	21	1.08	0.16	11
G19	5.02	3	2.57	8	0.44	8	28.85	14	0.66	8	0.56	16	1.20	0.33	15
G20	4.93	4	2.54	7	0.43	7	34.46	17	0.66	7	0.56	17	1.53	0.08	3
G21	4.59	11	2.11	4	0.35	4	14.34	4	0.66	4	0.52	20	0.53	0.08	4
G22	3.67	22	8.91	22	1.59	22	22.74	9	0.60	22	1.11	2	0.17	0.57	23
G23	4.10	19	4.91	19	0.87	19	13.04	3	0.64	19	0.77	5	0.28	0.17	12
Mean	4.51		3.71		0.65		27.43		0.65		0.66		1.00	0.25	

G – genotype code; R – rank; W_i^2 – Wricke's ecovariance; σ^2_i – Shukla's stability variance; CV_i – coefficient of variation; $\theta_{(i)}$ – GE variance component; θ_i – mean variance component; b_i – regression coefficient; S^2d_i – regression variance.

Based on the yield stability metrics of Becker and Leon (1988), Finlay and Wilkinson (1963), and Eberhart and Russell (1966), the perfect genotype should have a higher mean yield, a b_i value equal to or closer to one, and an S^2d_i value close to or equal to zero. Among the variants tested, G13 proved to be the ideal genotype. G23, G16 and G9 had the highest S^2d_i value, indicating the lower stability across all environments (Table 3) (Pour-Aboughadareh et al., 2023).

Table 4. Non-parametric yield stability parameters of Nassar and Hühn (1987) for 23 rye genotypes.

Genotype code	$S^{(1)}$	R	$S^{(2)}$	R	$S^{(3)}$	R	$S^{(6)}$	R
G1	5.62	7	22.29	5	9.18	5	1.69	4
G2	8.38	21	59.81	21	30.27	19	3.76	16
G3	5.71	8	28.00	8	21.00	14	3.00	15
G4	5.52	6	27.33	7	32.80	20	6.00	22
G5	8.29	19	48.67	19	19.47	12	2.80	12
G6	6.57	10	31.62	10	22.13	15	4.03	18
G7	5.90	9	29.14	9	14.75	8	2.31	9
G8	6.67	11	42.14	16	15.95	9	1.86	5
G9	6.76	12	38.81	13	28.60	18	4.35	20
G10	9.90	22	75.95	22	48.33	22	5.88	21
G11	7.05	13	37.67	11	18.83	11	2.83	13
G12	4.67	3	15.81	3	6.26	2	1.38	2
G13	3.33	1	7.90	1	2.53	1	0.87	1
G14	7.33	15	39.57	15	17.31	10	2.35	10
G15	7.62	18	44.48	18	23.95	16	2.77	11
G16	10.19	23	77.48	23	33.55	21	3.96	17
G17	7.14	14	39.48	14	19.98	13	2.92	14
G18	4.29	2	15.57	2	9.08	4	2.11	7
G19	7.33	15	38.48	12	14.56	7	2.22	8
G20	5.24	4	20.48	4	7.29	3	1.47	3
G21	5.33	5	25.48	6	13.72	6	1.92	6
G22	8.29	19	56.90	20	50.85	23	6.43	23
G23	7.52	17	42.48	17	27.88	17	4.28	19
Mean	6.72		37.63		21.23		3.10	

G – genotype code; R – rank; $S^{(1)}$ – the mean of absolute rank differences of the genotype across all environments tested; $S^{(2)}$ – the variance between ranks across all environments tested; $S^{(3)}$ – sum of the absolute deviations for each genotype relative to the mean of the ranks; and $S^{(6)}$ – sum of the squares of the ranks for each genotype relative to the mean of the ranks.

Tables 4 and 5 show the non-parametric yield stability parameters. In this study, the seven non-parametric estimates of phenotypic stability, $S^{(1)}$, $S^{(2)}$, $S^{(3)}$ and $S^{(6)}$ of Nassar and Hühn (1987), and $NP^{(1)}$, $NP^{(3)}$ and $NP^{(4)}$ parameters of Thennarasu (1995) identified G13 as the most stable, while $NP^{(2)}$ ranked G20 as the most stable. According to KR (Kang's rank-sum) (Kang, 1988), which uses both yield and σ^2_i as selection criteria, G13 was also ranked as the most stable genotype followed by G12, G19 and G20, which were characterized by higher yields than the average in the set of genotypes studied. The undesirable genotypes with the highest rank sums were G22, G23 and G10. $S^{(1)}$, $S^{(2)}$ and $NP^{(1)}$ classified G16 as the most unstable, while $S^{(3)}$, $S^{(6)}$, $NP^{(3)}$ and $NP^{(4)}$ ranked G22 as the most unstable. According to $NP^{(2)}$, G4 was considered as the most unstable.

Table 5. Non-parametric yield stability parameters of Thennarasu (1995) for 23 rye genotypes.

Genotype code	$NP^{(1)}$	R	$NP^{(2)}$	R	$NP^{(3)}$	R	$NP^{(4)}$	R	KR	R
G1	4.71	9	0.22	5	0.35	4	0.39	4	13	5
G2	6.86	16	0.77	19	0.61	16	0.71	15	31	16
G3	3.29	4	0.75	18	0.52	13	0.71	16	23	9
G4	6.43	12	3.67	23	1.24	22	1.10	22	33	19
G5	6.86	16	0.28	10	0.51	10	0.55	11	29	14
G6	7.29	20	0.82	20	0.81	19	0.77	18	33	19
G7	4.00	5	0.25	7	0.47	7	0.50	9	31	16
G8	4.43	7	0.20	2	0.38	6	0.42	6	24	10
G9	6.57	13	1.69	21	0.77	18	0.83	20	32	18
G10	9.57	22	0.59	16	0.91	21	1.05	21	41	22
G11	6.14	11	0.55	15	0.52	14	0.59	12	25	11
G12	3.00	3	0.20	3	0.24	2	0.31	2	10	2
G13	1.71	1	0.24	6	0.09	1	0.18	1	2	1
G14	6.71	14	0.28	9	0.52	12	0.53	10	14	7
G15	4.43	7	0.39	12	0.54	15	0.68	14	29	14
G16	11.71	23	0.40	13	0.73	17	0.74	17	25	11
G17	5.57	10	0.49	14	0.52	11	0.60	13	25	11
G18	4.00	5	0.21	4	0.49	9	0.42	5	13	5
G19	6.86	16	0.29	11	0.48	8	0.46	7	11	3
G20	6.71	14	0.18	1	0.36	5	0.31	3	11	3
G21	2.57	2	0.26	8	0.35	3	0.48	8	15	8
G22	8.71	21	2.26	22	1.43	23	1.23	23	44	23
G23	6.86	16	0.67	17	0.85	20	0.82	19	38	21
Mean	5.87		0.68		0.60		0.63		24	

R – rank; $NP^{(1)}$; $NP^{(2)}$, $NP^{(3)}$, and $NP^{(4)}$ – Thennarasu’s non-parametric estimates; KR – Kang’s rank sum.

To select potentially better stable genotypes, the average of the sum ranks (ASR) was calculated for all statistics. The genotype with a low ASR value is considered the most superior stable genotype, as explained by Pour-Aboughadareh et al. (2019). The results indicated that G13 (ASR = 3) was the most stable genotype among the studied genotypes, followed by G12 (ASR = 4.38), G20 (ASR = 6.38), G21 (ASR = 6.44), G18 (ASR = 6.63), G1 (ASR = 9.94) and G19 (Table 6).

Table 6. Sum of ranks (SR), mean sum of ranks (ASR) and standard deviation (SD) calculated on the base of parametric and non-parametric stability estimates.

Genotype code	SR	ASR	SD
G1	114	7.13	3.96
G2	259	16.19	3.39
G3	169	10.56	5.44
G4	247	15.44	6.11
G5	220	13.75	6.02
G6	259	16.19	3.76
G7	182	11.38	4.83
G8	170	10.63	5.57
G9	257	16.06	3.97
G10	302	18.88	5.51
G11	184	11.50	2.92
G12	70	4.38	5.06
G13	48	3.00	5.60
G14	180	11.25	3.47
G15	224	14.00	3.08
G16	282	17.63	7.39
G17	182	11.38	3.42
G18	106	6.63	5.00
G19	159	9.94	4.31
G20	102	6.38	5.10
G21	103	6.44	4.29
G22	319	19.94	5.89
G23	259	16.19	5.19

The AMMI stability value (ASV) is a suitable statistic in situations where the first two principal component interactions explain a significant G x E interaction (Ghazvini et al., 2018). It has been used to measure and classify stable genotypes from the smallest value range (Karuniawan et al., 2021). Using the ASV parameter, all genotypes were ranked by stability. Four genotypes, namely Aventino (G13), Harkovskaya 88 (G18), Albedo (G12), and A9E1389 (G9), were identified as stable with values below 1 (Table 7).

Poudel et al. (2020) noted that stability should not be the only parameter considered when selecting genotypes. This is because the most stable genotypes may not necessarily provide the best yield performance. Therefore, it is important to use approaches that take into account both mean yield and stability in a single index. The YSI provides a more effective means of evaluating the potential of a genotype in various environments. The genotype with the lowest YSI is considered the most stable (Thiam et al., 2023). In our study, according to this index, the most stable genotype was G13, followed by G19, G12 and G18. The genotype selection index (GSI) allows for the ranking and clear classification of the breeding value of genotypes. It is important to note that genotypes with the lowest GSI coefficient exhibit broad adaptation (Wodebo et al., 2023). In our study, these were genotypes G13 (GSI=2), G12 (GSI=6), G18 (GSI=6) and G19 (GSI=9) (Table 7).

Table 7. Mean performance of rye genotypes based on AMMI stability value (ASV), yield stability index (YSI) and genotype selection index (GSI).

G	Y, t ha^{-1}	R	ASV	R	YSI	R	GSI	R
G1	4.83	7	1.617	11	18	7	18	8
G2	4.42	16	1.162	5	21	9	14	5
G3	4.23	18	1.407	10	28	13	23	10
G4	3.60	23	1.917	12	35	17	29	14
G5	4.78	9	2.659	20	29	14	34	16
G6	4.25	17	2.236	16	33	16	32	15
G7	4.53	14	2.258	17	31	15	32	15
G8	4.83	6	2.345	18	24	10	28	13
G9	3.88	21	0.933	4	25	11	15	6
G10	4.03	20	2.926	21	41	19	40	18
G11	4.54	12	2.205	15	27	12	27	12
G12	4.83	8	0.810	3	11	3	6	2
G13	5.22	1	0.489	1	2	1	2	1
G14	4.84	5	1.362	8	13	5	13	4
G15	4.48	15	1.177	6	21	9	15	6
G16	5.06	2	3.572	22	24	10	32	15
G17	4.54	13	2.019	14	27	12	26	11
G18	4.61	10	0.652	2	12	4	6	2
G19	5.02	3	1.180	7	10	2	9	3
G20	4.93	4	1.985	13	17	6	19	9
G21	4.59	11	1.378	9	20	8	17	7
G22	3.67	22	3.644	23	45	20	43	19
G23	4.10	19	2.588	19	38	18	37	17

G – genotype code, Y – yield (t ha^{-1}); ASV – AMMI stability value; YSI – yield stability index; GSI – genotype selection index; R – rank of genotype.

The AMMI1 biplot was instrumental in facilitating the interpretation of the interaction effects among genotypes and environments, as well as in assessing the adaptability of genotypes. Al-Naggar et al. (2020) have noted that the genotypes on the right side of the axis have higher yields than those on the left side. A high average yield and a high interaction score, both pointing, characterize the optimally adapted genotype in environments in the same direction (Sitaresmi et al., 2019; Bishwas et al., 2021). Genotypes G18, G12, G13 and G19 exhibited mean values that exceeded the overall mean and showed PC1 scores close to zero. Consequently, they were regarded as exhibiting broad adaptability across diverse environmental contexts. On the other hand, G16, which had high mean values and a high score for PC1 but far from the origin showed specific adaptability to the environment (Figure 2 left) (Khan et al., 2021; Gerema et al., 2024). In accordance with the findings of the AMMI2-based analysis, genotypes and environments exhibiting lower PC1 and PC2 values that are closer to the origin are deemed to be the most stable (Bishwas et al., 2021). In the present study, genotypes G13 and G12 were identified as the most stable (Figure 2 right).

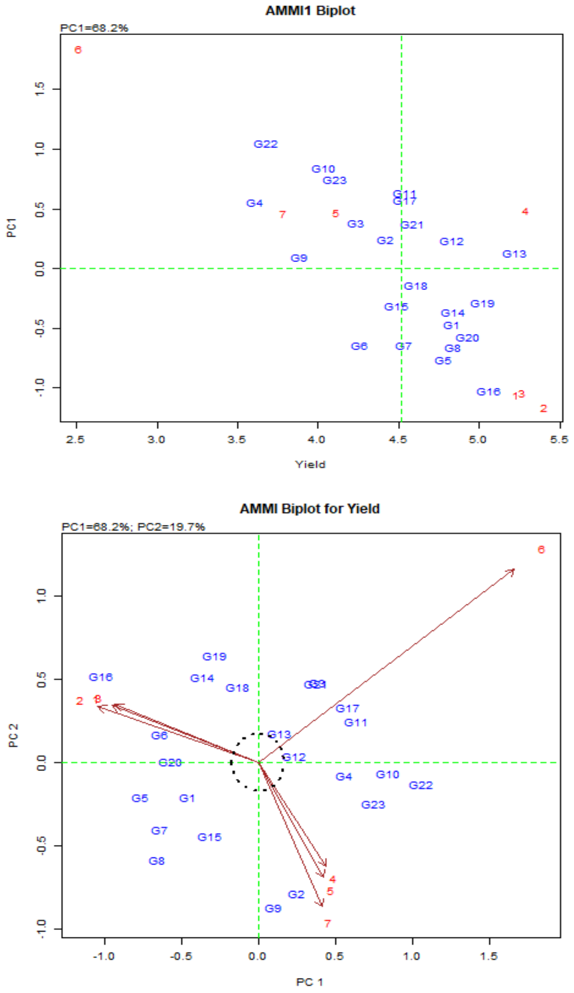

Figure 2. The AMMI1 biplot of PC1 for yield (left) and the AMMI2 biplot of PC1 and PC2 for grain yield (right).

The identification of mega-environments has the potential to facilitate the management of genotype-by-environment interactions, with the subsequent possibility of generalizing results to analogous agroclimatic locations (Fekadu et al., 2023). The best way to sum up the genotype and genotype-environment interaction of the dataset is the polygon-view of the GGE biplot, which visualizes the "which-won-where" pattern of a multi-environment dataset. German et al. (2024) observed that the GGE biplot possessed a more comprehensive and versatile nature, offering a more profound comprehension of the GGE interaction compared to alternative methods. In this study, the GGE biplot analysis revealed that the total GGE variation for grain yield of the genotypes evaluated at seven growing seasons was 83.9%, of which 64.2% was explained by PC1 and 19.7% by PC2. The "which-won-where" model of the GGE biplot polygonal view showed the main effect of genotype plus the G × E interaction effect of the 23 genotypes studied in seven seasons for grain yield. According to the polygon view, the investigated 23 genotypes fell under 4 sectors, while 7 environments fell under 3 sectors in the polygon. Genotype G22, G11, G17 and G21 were recorded as high-yielding and stable for environment E6 (growing season 2020–2021), while genotypes G7 and G8, respectively for environments E4 (growing season 2018–2019) and E7 (growing season 2021–2022). G13, G19, G16 and G5 were recorded as the most stable and high-yielding for environments E1 (2015–2016), E2 (2016–2017), E3 (2017–2018), E5 (2019–2020). Genotype G9, which was located at the top of the polygon in a section of the biplot where no environmental indicator was present, exhibited the poorest performance in all environments tested (Figure 3).

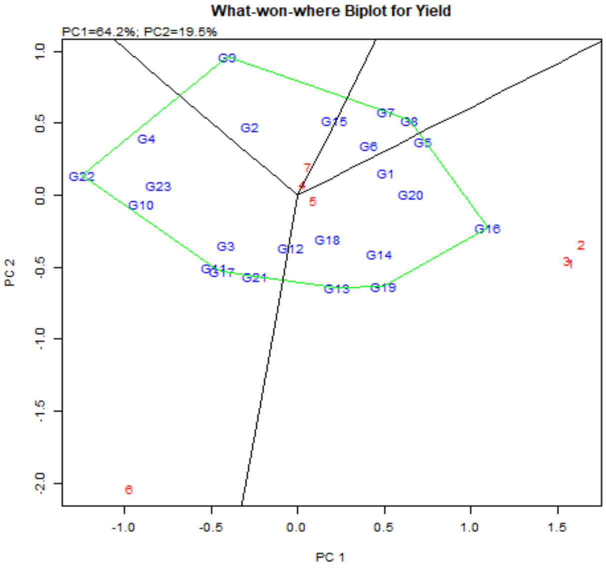

Figure 3. GGE biplot of the polygon view displaying 23 genotypes and 7 environments for grain yield.

The identification of an ideal genotype is of paramount importance in the selection of genotypes that perform well in a range of environments. This in turn can result in enhanced crop yields and more stable agricultural production. The utilization of the ideal genotype concept as a reference within breeding programs has been observed in numerous studies (Omrani et al., 2022; Ahakpaz et al., 2023; Mullualem et al., 2024; Pramanik et al., 2024). Wardofa et al. (2019) noted that genotypes deviating from the ideal genotype can be eliminated in early selection cycles, while those that are closer to the ideal genotype can be subjected to further testing. Mullualem et al. (2024) observed that genotypes located in the inner circle are considered to be more desirable than those in the outer circle. In this study, G16 was identified as a superior genotype. It was located in the center of the first concentric circle in the biplot, therefore close to the ideal genotype, followed by the genotypes in the following order G19, G14, G13, G20, G18, while G22, G4 and G9 were the most unstable and unfavorable genotypes, because they were located far from the ideal genotypes (Figure 4). The GGE biplot for genotypes also shows the stability of genotypes as a function of environments. The stable genotypes are those located closest to the AEA axis. Genotypes G19, G14, G18, G13, G12 were the most stable genotypes, because they showed the shortest distance from the average environment abscissa. However, taking into account the stability of the yield with the average yield and the location of the genotypes relative to the ideal genotype, genotypes G19, G12, G13 and G18 could be considered as the most favorable and adaptable to a wide range of environments (Figure 5).

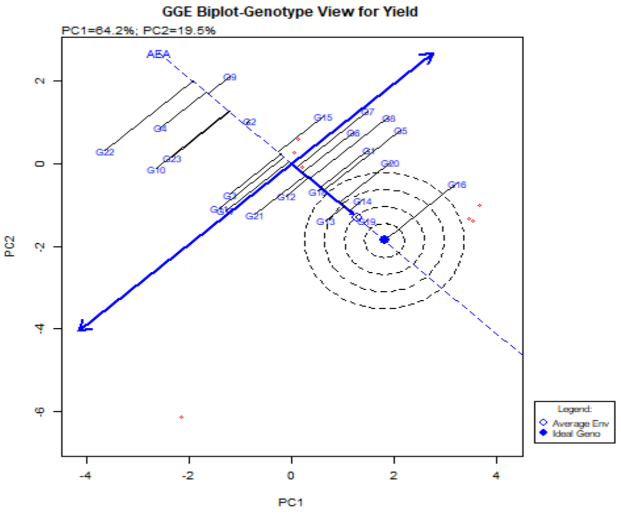

Figure 4. GGE-biplot based on genotype-focused scaling for comparing the genotypes with the ideal genotype.

The findings of the study indicate the presence of substantial disparities between genotypes, environments, and the interplay between environment and genotype. Consequently, stability analyses have been conducted to determine which genotypes possess the capacity to adapt to diverse environments. These analyses reveal that certain genotypes are stable and have the ability to adapt to various environments, while others are unstable and can only adapt to specific environments. The most stable genotypes identified by the univariate (parametric and non-parametric) models, which had the lowest ASR values were G13, G12, G20, G21, G18 and G19. The AMMI stability value (ASV) identified G13, G18, G12 and G9 as stable, while the most stable genotypes with high yield mean according to YSI were G13, G19, G12 and G18. The last genotypes were also classified as genotypes with broad adaptation to adverse climatic conditions according to GSI, AMMI biplot and GGE biplot analyses. The "which-won-where" model of the GGE biplot polygonal view, which shows the main effect of genotype plus the G × E interaction effect, which shows the main effect of genotype plus the effect of a G × E interaction, identified genotypes G16, G8, G9, G22, G17, and G19 as corner genotypes suitable for certain environments.

Conclusion

The study revealed that rye productivity (t/ha) fluctuated significantly depending on year, genotype and the interaction between year and genotype. Year exerted the largest effect on trait performance, followed by the interaction between genotype and year. Genotypes G13, G12, G19 and G18 were identified as high-yielding and stable, with the broadest adaptability to unfavorable environmental conditions. These genotypes are suitable for growth under various climatic conditions and can be a suitable source material in rye breeding programs. Further research on genotypes at diverse locations is required to enhance the validity of these results.

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References

Ahakpaz, F., Majidi, H.E., Roostaei, M., Bihamta, M.R., & Mohammadi, S. (2023). Comprehensive stability analysis of wheat genotypes through multi-environmental trials. *Journal of Agricultural Sciences (Tarim Bilimleri Dergisi)*, 29 (1), 317-334.

Ahrends, H.E., Siebert, S., Rezaei, E.E., Seidel, S.J., Hüging, H., Ewert, F., Döring, T., Rueda-Ayala, V., Eugster, W., & Gaiser, T. (2021). Nutrient supply affects the yield stability of major European crops—a 50 year study. *Environment Research Letter*, *16,* 014003.

Akbar, M.R., Purwoko, B.S., Dewi, I.S., Suwarno, W.B., & Sugiyanta (2021). Genotype × environment interaction and stability analysis for high yielding doubled haploid lines of lowland rice. *Turkish Journal of Field Crops, 26* (2), 218-225.

Al-Naggar, A. M.M., Shafik, M.M., & Musa, R.Y.M. (2020). AMMI and GGE Biplot analyses for yield stability of nineteen maize genotypes under different nitrogen and irrigation levels. *Plant Archives*, *20* (2), 4431-4443.

Amelework, A.B., Bairu, M.W., Marx, R., Laing, M., & Venter, S.L. (2023). Genotype × Environment Interaction and stability analysis of selected cassava cultivars in South Africa. *Plants (Basel)*, *12* (13), 2490.

Bishwas, K.C., Poudel, M.R., & Regmi, D. (2021). AMMI and GGE biplot analysis of yield of different elite wheat line under terminal heat stress and irrigated environments. *Heliyon*, *7*, e07206.

Becker, H.C., & Leon, J. (1988). Stability analysis in plant breeding. *Plant Breeding*, *101,* 1-23.

de Filho, J.S.S., Olivoto, T., de Souza, C.M., & de Oliveira, E.J. (2023). Multi-trait selection in multi-environments for performance and stability in cassava genotypes. *Frontiers in Plant Science*, *14*, 1282221.

de Souza, M.H., Júnior, J.D.P., De Marco, Steckling, S., Mencalha, J., Dias, F.S., de Carvalho, Rocha, J.R.A.S., Carneiro, P.C.S., & de Souza, Carneiro, J.E. (2020). Adaptability and stability analyses of plants using random regression models. *PLoS ONE*, *15* (12), e0233200.

Đekić, V., Milivojević, J., & Branković, S. (2018). The interaction of genotype and environment on yield and quality components in triticale. *Biologica Nyssana*, *9* (1), 45-53.

Desheva, G., & Valchinova, E. (2023). Morpho-agronomic assessment of genetic diversity among rye accessions using multivariate analyses. *Bulgarian Journal of Agricultural Science*, *29* (2), 338-350.

Dias, C., Santos, C., & Mexia, J.T. (2022). Adaptability and stability analysis of common wheat production. *AIP Conference Proceedings*, *2611*, 090007.

Eberhart, S.A.T., & Russell, W.A. (1966). Stability parameters for comparing varieties. *Crop Science*, *6*, 36-40.

Egea-Gilabert, C., Pagnotta, M.A., & Tripodi, P. (2021). Genotype × Environment Interactions in crop breeding. *Agronomy*, *11*, 1644.

Fasahat, P., Rajabi, A., Mahmoudi, S. B., Noghabi, M.A., & Rad, J.M. (2015). An overview on the use of stability parameters in plant breeding. *Biometrics & Biostatistics International Journal*, *2* (5), 149-159.

Farshadfar, E., Mahmodi, N., & Yaghotipoor, A. (2011). AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum* L.). *Australian Journal of Crop Science*, *5* (13), 1837-1844.

Fekadu, W., Mekbib, F., Lakew, B., & Haussmann, B.I. (2023). Genotype × environment interaction and yield stability in barley (*Hordeum vulgare* L.) genotypes in the central highland of Ethiopia. *Journal of Crop Science and Biotechnology, 26* (2), 119-133.

Finlay, K.W., & Wilkinson, G.N. (1963). The Analysis of Adaptation in a Plant-Breeding Programme. *Australian Journal of Agricultural Research*, *14*, 742-754.

Francis, T.R., & Kannenberg, L.W. (1978). Yield stability studies in short-season maize. 1. A Descriptive method for grouping genotypes. *Canadian Journal of Plant Science*, *58*, 1029-1034.

Gerema, G., Mengistu, G., Bayisa, T., & Balcha, U. (2024). Application of univariate, multivariate, and mixed models to the stability analysis of Ethiopian tetraploid wheat cultivars under irrigation condition. *Agrosystematic, Geosciences & Environment*, *7*, e20574.

Ghazvini, H., Pour-Aboughadareh, A., Sharifalhosseini, M., Razavi, S.A., Mohammadi, S., Kalkhoran, M.G., Hafshejani, A.F., & Khakizadeh, Gh. (2018). Phenotypic stability analysis of barley promising lines in the cold regions of Iran. *Crop Breeding Journal*, *8* (1-2), 17-29.

Hackauf, B., Siekmann, D., & Fromme, F.J. (2022). Improving yield and yield stability in winter rye by hybrid breeding. *Plants*, *11* (19), 2666.

Hadasch, S., Laidig, F., Macholdt, J., Bönecke, E., & Piepho, H.P. (2020). Trends in mean performance and stability of winter wheat and winter rye yields in a long-term series of variety trials. *Field Crops Research*, *252*, 107792.

Haffke, S., Wilde, P., Schmiedchen, B., Hackauf, B., Roux, S., Gottwald, M., & Miedaner, T. (2015). Toward a selection of broadly adapted germplasm for yield stability of hybrid rye under normal and managed drought stress conditions. *Crop Science*, *55* (3), 1026-1034.

Hassani, M., Mahmoud, S.B., Saremirad, A., & Taleghani, D. (2023). Genotype by environment and genotype by yield*trait interactions in sugar beet: analyzing yield stability and determining key traits association. *Scientific Report*, *13*, 23111.

Karimizadeh, R., Mohammadi, M., & Shefazadeh, M.K. (2012). A review on parametric stability analysis methods: set up by Matlab program. *International Journal of Agriculture: Research and Review*, *2* (4), 433-442.

Kang, M.S. (1988). A rank-sum method for selecting high-yielding, stable corn genotypes. *Cereal Research Communication*, *16*, 113-115.

Khan, M. M. H., Rafii, M. Y., Ramlee, S. I., Jusoh, M., & Al Mamun, M. (2021). AMMI and GGE biplot analysis for yield performance and stability assessment of selected Bambara groundnut (*Vigna subterranea* L. Verdc.) genotypes under the multi-environmental trials (METs). *Scientific Reports, 11* (1), 22791.

Kartina, N., Purwoko, B.S., Dewi, I.S., Wirnas, D., & Sugiyanta, A. (2019). Genotype by environment interaction and yield stability analysis of doubled haploid lines of upland rice. *SABRAO Journal of Breeding and Genetics*, *51* (2), 191-204.

Karuniawan, A., Maulana, H., Ustari, D., Dewayani, S., Solihin, E., Solihin, M.A., Amien, S., & Arifin, M. (2021). Yield stability analysis of orange - Fleshed sweet potato in Indonesia using AMMI and GGE biplot. *Heliyon*, *7* (4), e06881.

Kebede, G., Worku, W., Jifar, H., & Feyissa, F. (2023). Stability analysis for fodder yield of oat (Avena sativa L.) genotypes using univariate statistical models under diverse environmental conditions in Ethiopia. *Ecological Genetics and Genomics*, *29*, 100202.

Klimek-Kopyra, A., Bacior, M., & Neugschwandtner, R. (2023). Hybrid rye (*Secale cereale* L.) as a good crop component to enhance yield stability in a winter cereal mixture. *Acta Agrobotanica, 76*, 172670.

Köse, O.D.E. (2022). Multi-Environment Analysis of grain yield and quality traits in oat (*Avena sativa* L.). *Journal of Agricultural Sciences (Tarim Bilimleri Dergisi)*, *28* (2), 278-286.

Laidig, F., Hans-Peter, P., Rentel, D., Drobek, T., Meyer, U., & Huesken, A. (2017). Breeding progress, variation, and correlation of grain and quality traits in winter rye hybrid and population varieties and national on-farm progress in Germany over 26 years. *Theoretical and Applied Genetic*, *130*, 981-998.

Matongera, N., Ndhlela, T., van Biljon, A., & Labuschagneet, M. (2023). Genotype x environment interaction and yield stability of normal and biofortified maize inbred lines in stress and non-stress environments. *Cogent Food and Agriculture*, *9* (1), 2163868.

Matova, P.M., Kamutando, C.N., Mutari, B., Magorokosho, C., & Labuschagne, M. (2022). Adaptability and stability analysis of commercial cultivars, experimental hybrids and lines under natural fall armyworm infestation in Zimbabwe using different stability models. *Agronomy*, *12*, 1724.

Mengistu, B., & Abu, M. (2023). Evaluation of stability parameters for the selection of stable and superior sunflower genotypes. *Cogent Food and Agriculture*, *9* (2), 2275406.

Mullualem, D., Tsega, A., Mengie, T., Fentie, D., Kassa, Z., Fassil, A., Wondaferew, D., Gelaw, T.A., & Astatkie, T. (2024). Genotype-by-environment interaction and stability analysis of grain yield of bread wheat (*Triticum aestivum* L.) genotypes using AMMI and GGE biplot analyses. *Heliyon*, *10* (12), e32918.

Nassar, R., & Hühn, M. (1987). Studies on estimation of phenotypic stability: tests of significance for nonparametric measures of phenotypic stability. *Biometrics*, *43*, 45-53.

Omrani, A., Omrani, S., Khodarahmi, M., Shojaei, S.H., Illés, Á. Bojtor, C., Mousavi, S.M.N., & Nagy, J. (2022). Evaluation of Grain Yield Stability in Some Selected Wheat Genotypes Using AMMI and GGE Biplot Methods. *Agronomy, 12*, 1130.

Pramanik, K., Sahu, G.S., Chandra Acharya, G., Tripathy, P., Dash, M., Koundinya, A.V.V., Jena, C., Kumar, D.S., Mohapatra, P.P., Pradhan, J., & Karubakee, S. (2024). Estimating phenotypic stability for relevant yield and quality traits in French bean (*Phaseolus vulgaris* L.) using AMMI analysis. *Heliyon*, *10* (5), e26918.

Plaisted, R.I., & Peterson, L.C. (1959). A technique for evaluating the ability of selection to yield consistently in different locations or seasons. *American Potato Journal, 36*, 381-385.

Plaisted, R.L. (1960). A shorter method for evaluating the ability of selections to yield consistently over locations. *American Potato Journal*, *37*, 166-172.

Podolska, G., & Aleksandrowicz, E. (2019). Progress in cereal varieties for bread purposes. *ZESZYT*, *60* (14), 25-35.

Poudel, M.R., Ghimire, S., Pandey, M.P., Dhakal, K., Thapa, D.B., & Poudel, H.K. (2020). Yield stability analysis of wheat genotypes at irrigated, heat stress and drought condition. *Journal of Biology and Today's World*, *9* (5), 220.

Pour-Aboughadareh, A., Yousefian, M., Moradkhani, H., Poczai, P., & Siddique, K.H.M. (2019). Stabilitysoft: A new online program to calculate parametric and non-parametric stability statistics for crop traits. *Applications in Plant Sciences*, *7* (1), e1211.

Pour-Aboughadareh, A., Khalili, M., Poczai, P., & Olivoto, T. (2022). Stability indices to deciphering the Genotype-by-Environment Interaction (GEI) effect: An applicable review for use in plant breeding programs. *Plants*, *11*, 414.

Pour-Aboughadareh, A., Barati, A., Gholipoor, A., Zali, H., Marzooghian, A., Koohkan, S.A., Shahbazi-Homonloo, K., & Houseinpour, A. (2023). Deciphering genotype-by-environment interaction in barley genotypes using different adaptability and stability methods. *Journal of Crop Science and Biotechnology*, *26*, 547-562.

Purchase, R.L. (1997). Parametric analysis to describe genotype by environment interaction and yield stability in winter wheat. Ph.D. Thesis, Department of Agronomy, Faculty of Agriculture of the University of the Free State, Bloemfontein, South Africa.

Reckling, M., Ahrends, H., Tsu-Wei, C., Eugster, W., Hadasch, S., Knapp, S., Laidig, F., Linstädter, A., Macholdt, J., Hans-Peter, P., Schiffers, K., & Döring, T.F. (2021). Methods of yield stability analysis in long-term field experiments. A review. *Agronomy for Sustainable Development, 41*, 27.

Sabaghnia, N. (2010). Multivariate statistical analysis of genotype × environment interaction in multi-environment trials of breeding programs. *Poljoprivreda i Sumarstvo*, 56 (1-4), 19-38.

Sabaghnia, N. (2015). Identification of the most stable genotypes in multi-environment trials by using nonparametric methods. *Acta Agriculturae Slovenica*, *105* (1), 103-110.

Shojaei, S.H., Mostafavi, K., Lak, A., Omrani, A., Omrani, S., Mousavi, S.M.N., Illés, Á. Bojtor, C., & Nagy, J. (2022). Evaluation of stability in maize hybrids using univariate parametric methods. *Journal of Crop Science and Biotechnology*, *25*, 269-276.

Siekmann, D., Jansen, G., Zaar, A., Kilian, A., Fromme, F.J., & Hackauf, B.A. (2021). Genome-wide association study pinpoints quantitative trait genes for plant height, heading date, grain quality, and yield in rye (Secale cereale L.). *Frontiers in Plant Science*, *12*, 718081.

Shukla, G. (1972). Some statistical aspects of partitioning genotype-environmental components of variability. *Heredity*, *29*, 237-245.

Sitaresmi, T., Suwarno, W.B., Gunarsih, C., Nafisah, Nugraha, Y., Sasmita, P., & Daradjat, A.A. (2019). Comprehensive stability analysis of rice genotypes through multi-location yield trials using PBSTAT-GE. *SABRAO Journal of Breeding and Genetics*, *51* (4) 355-372.

Thennarasu, K. (1995). On certain non-parametric procedures for studying genotype-environment interactions and yield stability. PhD thesis, PJ School, IARI, New Delhi, India.

Thiam, E.H., Jellen, E.N., Jackson, E.W., Nelson, M., Rogers, W., El Mouttaqi, A., & Benlhabib, O. (2023). Productivity and stability evaluation of 12 selected *Avena magna* ssp. domestica lines based on multi-location experiments during three cropping seasons in Morocco. *Agriculture*, *13*, 1486.

Wardofa, G. A., Asnake, D., & Mohammed, H. (2019). GGE biplot analysis of genotype by environment interaction and grain yield stability of bread wheat genotypes in Central Ethiopia. *Journal of Plant Breeding and Genetics*, *07(02)*, 75–85.

Wodebo, K.Y., Tolemariam, T., Demeke, S., Garedew, W., Tesfaye, T., Zeleke, M., Gemiyu, D., Bedeke, W., Wamatu, J., & Sharma, M. (2023). AMMI and GGE Biplot analyses for mega-environment identification and selection of some high-yielding oat (*Avena sativa* L.) genotypes for multiple environments. *Plants, 12*, 3064.

Wricke, G. (1962). Übereine Methode zur Erfassung der ökologischen Streubreite in Feldversuchen. *Zeitschrift für Pflanzenzüchtung*, *47*, 92-96.

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PARAMETARSKE I NEPARAMETARSKE METODE ZA EVALUACIJU GENOTIPOVA OZIME RAŽI PREMA STABILNOSTI PRINOSA ZRNA

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Rezime

Analiza stabilnosti prinosa postala je sve relevantnija poslednjih godina zbog promenljivih klimatskih uslova koji negativno utiču na prinose useva. Od suštinskog je značaja da poljoprivrednici uzgajaju vrlo prilagodljive i stabilne sorte sa visokim potencijalom prinosa, jer to određuje ekonomsku predvidljivost i smanjuje njihov rizik. Stabilnost je takođe od ključnog značaja za oplemenjivače biljaka, kako bi stvorili genotipove prilagođene širokom spektru različitih okruženja. Cilj ovog istraživanja bio je da se identifikuju visokoprinosne, stabilne i prilagodljive lokalne populacije i sorte raži za komercijalne i oplemenjivačke svrhe. Ogled je sproveden u periodu od 2014. do 2022. godine i obuhvatio je 16 sorti i 7 lokalnih populacija poreklom iz Bugarske. Ogled je sproveden u slučajnom blok rasporedu u četiri ponavljanja. Određeno je šesnaest parametarskih i neparametarskih pokazatelja stabilnosti prinosa zrna. Takođe su izračunati: prosek zbira rangova (engl. *average of the sum ranks* – ASR), vrednost stabilnosti AMMI (engl. *AMMI stability value* – ASV), indeks stabilnosti prinosa (engl. *yield stability index* – YSI) i indeks selekcije genotipova (engl. *genotype selection index* – GSI). Godina je imala najznačajniji statistički uticaj na prinos zrna po hektaru. Parametarskim i neparametarskim pokazateljima stabilnosti ocenjeno je da su genotipovi G13, G12, G20 i G21 najstabilniji. ASV je pokazao da su genotipovi G13, G18, G12 i G9 najstabilniji, dok je YSI izdvojio G13, G19, G12 odnosno G18. GSI je kao najprilagodljivije genotipove na nepovoljne klimatske uslove identifikovao G13, G12, G18 i G19. Oni mogu poslužiti kao izvorni materijal za programe oplemenjivanja raži.

Ključne reči: raž, prinos, analiza stabilnosti, prilagodljivost.

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