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Study of the genetic potential of autochthonous populations of perennial ryegrass (*Lolium perenne* L.) for use in breeding purposes

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Abstract: The testing and evaluation of native populations of perennial ryegrasses (*Lolium perenne* L.) collected from the Republic of Srpska, Bosnia and Herzegovina were conducted from 2020 to 2022 at experimental fields and laboratories of the Institute for Genetic Resources and the Agricultural Institute of the Republic of Srpska in Banja Luka. Six native populations (labelled G1–G6) and two cultivars, Esquire and Tivoli (labelled G7 and G8), were analysed in this study. The following traits were examined: the plant height (cm), number of generative stems per plant, inflorescence length (cm), number of spikes per inflorescence, seed mass per inflorescence (g), and seed yield per plant (g). The results showed that all the native populations exhibited higher average plant heights compared to the Esquire standard (G7). Population G2 had the highest average number of spikes per inflorescence (26.8), while population G4 achieved the greatest average inflorescence length (27.7 cm). Statistically significant differences in the inflorescence length were observed between populations G2, G3, G4, and G6, compared to the standards G7 and G8 (Esquire and Tivoli). The genotype and year had a significant impact on the seed yield per plant. The average yield ranged from 32.4 g (G7) to 53.4 g (G4). The seed yield per plant showed a strong positive correlation with the number of generative stems per plant, the inflorescence length, and the number of spikes per inflorescence. The native populations G4 and G5 achieved significantly higher seed yields per plant compared to the other populations and may serve as highly valuable material for breeding programmes.

Keywords: English ryegrass; inflorescence length; native populations; plant height; seed yield

Perennial ryegrass (*Lolium perenne* L.) thrives in various agroecological conditions, adapting to different soil types and altitudes. This species is characterised by its high resistance to trampling, rapid regeneration, and ability to grow on acidic, heavy, and waterlogged soils. Due to its characteristics,

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perennial ryegrass is considered a decorative grass, suitable for establishing specialised turfgrass, such as sports fields, parks, home gardens, erosion control, and other types of lawns (Wilkins & Humpreys 2003; Lakić et al. 2015a). Perennial ryegrass is one of the most used grass species for sowing grasslands in temperate areas, and it has received significant breeding efforts throughout the world. It is especially used in Europe where it represents as much as 50% of the marketed grass seed (Humphreys et al. 2010; Sampoux et al. 2011).

There has never been a thorough investigation of the rate of genetic gain attained by grass breeding in Bosnia and Herzegovina. The fact that the genetic gain is unique to the imposed growing circumstances and management techniques is a complex element. Different management conditions can cause varieties to re-rank. Wilkins and Humphreys (2003) documented significant geographical differences in the genetic gains from fodder grass breeding, comparing the 0–1% per decade in the USA to the 4–5% per decade in dry matter (DM) yield in North-Western Europe and New Zealand, respectively. Thanks to the diverse terrain and varying climatic conditions in Bosnia and Herzegovina, numerous native populations of perennial ryegrass have developed. The indigenous populations of this plant exhibit significant genetic variability in key traits, such as earliness, plant height, lifespan, leaf colour, and adaptability to different agroecological conditions (Lakić et al. 2015b; Zhang et al. 2020). The recent findings by Tubbs and Chastain (2022) highlight that the number of spikelets per spike is crucial for the seed yield, further emphasising the importance of genetic diversity in breeding programmes. The development of cultivars with potential for increased productivity is a key objective in forage improvement (Sartie et al. 2018). Abiotic stresses, such as drought, high salinity, and extreme temperatures, significantly affect the growth and productivity of perennial ryegrass (Harb et al. 2010; Zhang et al. 2020). The seed yield is a quantitative trait, with its expression influenced by many genes and by the environment (Casler et al. 2003).

The divergence of native populations of perennial ryegrass enables the identification of genotypes with desirable traits for selection in breeding programmes. In natural habitats, two main types of genotypes can be observed: vegetative, characterised by a large number of leaves and few stems, and stem-based, with a greater number of stems and fewer leaves (Lakić et al. 2013). The aim of this study was to analyse the yield components of selected native populations of perennial ryegrass, and based on the obtained results, select populations with desirable agronomic traits that could be used in breeding programmes for the development of varieties suitable for planting specialised-purpose turfgrass.

MATERIAL AND METHODS

The investigation of the genetic potential of native populations of perennial ryegrass (*Lolium perenne* L.) was conducted at the experimental fields and laboratories of the Institute for Genetic Resources and the Agricultural Institute of the Republic of Srpska in Banja Luka. The three-year study was carried out from 2020 to 2022. The material used consisted of progeny from native populations of perennial ryegrass, collected from the Republic of Srpska for the purpose of forming a gene bank. After multiplying seeds from the collected progeny of perennial ryegrass, the selected populations were evaluated with the aim of incorporating them into a breeding programme. For the purposes of this study, six native populations and two varieties of perennial ryegrass were selected, which represent our entire genetic material (Table 1).

Three selected native populations of perennial ryegrass originate from mountainous areas, while three come from hilly areas. Genotypes G4, G5, G6, and the varieties Esquire (G7) and Tivoli (G8) reach the full clustering stage by the end of the second decade of May and begin full flowering by June 6. In contrast, genotypes G1, G2, and G3 enter the full clustering stage in the third decade of May and start full flowering between June 6 and June 12. The experiment was carried out during the summer-autumn sowing season of 2019 on brown valley soil. Sowing was conducted in four replications, with native populations and standard varieties of perennial ryegrass sown at 30 plants per replication. Each population and standard had a total of 120 plants per clones. The plant spacing in the row was 0.5 m, while the spacing between replications was 1 m. During the experiment, standard agronomic practices were applied. The sowing was undertaken manually, with two seeds per position, and after tillering, only one plant of perennial ryegrass was retained. During the study, the following parameters measured at the same stage were analysed: the plant height (cm), number of generative stems per plant, inflorescence

Table 1. Geographical origin of the collected native populations of perennial ryegrass (G1–G7)

Genotype label	Population name	Location	Longitude and latitude	Altitude (m)	Habitat
Mountain locations					
G1	Šivolji	Kalinovik, Šivolji	43°32'N 18°30'E	1 207.9	meadow next to the house
G2	Novo Selo	Istočni Kupres, Novo Selo	44°03'N 17°03'E	1 161.2	meadow next to the house
G3	Stroice	Šipovo, Stroice	44°06'N 17°10'E	1 089	neglected meadow by the road
Hilly locations					
G4	Rajčevci	Laktaši, Rajčevci	44°48'N 17°25'E	307.8	yard of an abandoned house
G5	Bjelajce	Mrkonjić Grad, Bjelajce	44°25'N 17°08'E	383.7	meadow by the road
G6	Donje Ratkovo	Ribnik, Donje Ratkovo	44°30'N 16°52'E	654.1	meadow by the road
Standard varieties of perennial ryegrass					
G7	Esquire		turfgrass type		Institute‘s variety collection
G8	Tivoli		forage type		

length (cm), number of spikelets per inflorescence, seed mass per inflorescence (g), 1 000 seed mass (g) and seed yield per plant (g).

The 1 000 seed mass was determined from the clean seed fraction in the Seed Quality Control Laboratory. A seed counter was used to sample 100 seeds in 8 replicates (ISTA Rules 2018).

Statistical analysis. The statistical data processing and analysis were performed using the Statistica (Ver. 12, 2012). In the paper, Pearson's correlation analysis (*r*) was applied to test the association of independent samples, and a two-factor analysis (genotype × year) of analysis of variance (ANOVA) to test the difference between the groups. The levels of 0.05 and 0.01 were used for the threshold value of significance.

Agrochemical soil analysis. The analysis of the fertility of the topsoil where the experiment was conducted was performed at the Institute Soil Fertility Control Laboratory. The chemical analyses included the following soil fertility parameters: acidity (pH), humus content (%), content of readily available phosphorus (mg/100 g of soil), and content of readily available potassium (mg/100 g of soil). In the resulting filtrate, the content of easily accessible potassium (K_2O) was determined with the Egner-Riehm Al method (1958). We used the procedure to create a phosphor molybdenum complex that is reduced by a mixture of tin (II) chloride and ascorbic acid (Sarkadi et al. 1965).

The experimental field where the research was conducted, is dominated by valley-brown soil over an alluvial substrate of the Vrbas River. According to its mechanical composition, the soil belongs to the clay-loam group. The structure of the soil in the topsoil is crumbly, and the soil colour is dark brown to a depth of 40 cm.

The results of the chemical analyses of the topsoil, where the experiment was conducted, indicate that the soil is of a moderately alkaline type (Table 2). This type of soil has a moderate humus content (> 3.0%). The availability of readily available phosphorus and potassium was high. Based on the chemical analysis results of the soil sample, it can be concluded that the examined brown-valley soil is suitable for the cultivation of perennial ryegrass.

Meteorological data. Meteorological data from the Republic Hydrometeorological Institute of the Republic of Srpska for Banja Luka were used to analyse the average monthly temperatures (°C) and total monthly precipitation (mm) during the study period (2020–2022), as shown in Figure 1.

Table 2. The results of the chemical analyses of the topsoil

Depth (cm)	Humus (%)	pH		P_2O_5	K_2O
		H_2O	KCl	(mg/100 g soil)	
0–30	3.25	8.10	7.20	31.8	28.2

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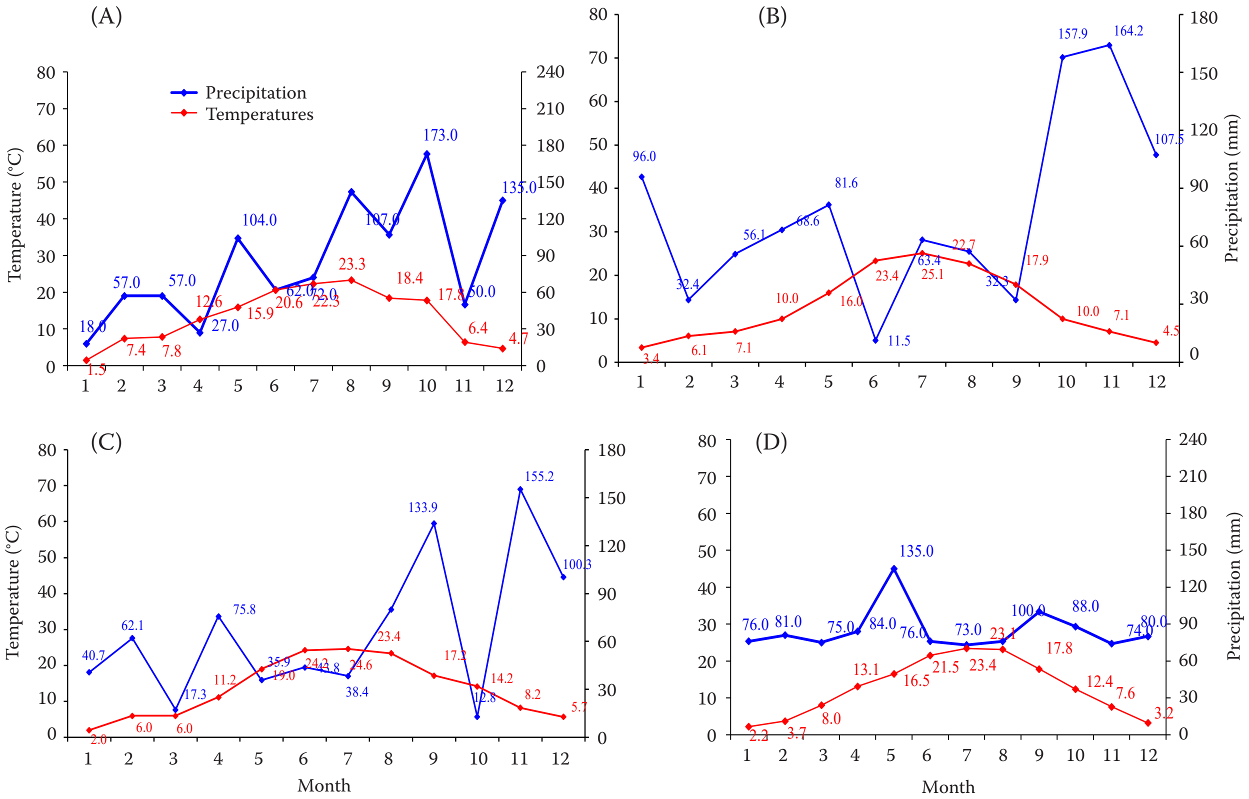

Figure 1. Precipitation and temperature in 2020 (A), in 2021 (B), in 2022 (C), and in long time period, 2011–2020 (D), Banja Luka, Bosnia and Herzegovina

In 2020, the precipitation was below the ten-year average, with only 27.0 mm in April and 62.0 mm in June. The average temperatures were slightly lower, with a cooler May and June.

In 2021, the precipitation was higher from January to May, but dropped significantly in June (11.5 mm). The rest of the growing season had adequate rainfall, though the distribution was less favourable, with a dry period starting in late May.

In 2021, the average air temperature was higher than the multi-year average (Figure 1D), with monthly temperatures ranging from 7.1 °C in March to 25.1 °C in June (Figure 1B).

From March to June 2022, the precipitation was significantly below the ten-year average, with the highest rainfall in April (Figure 1C). The air temperatures ranged from 6.0 °C in March to 24.6 °C in July, with the growing season averaging about 2.5 °C higher than the long-term average (Figure 1D).

The most favourable conditions for English ryegrass growth occurred in 2020, while 2021 had the worst conditions due to a dry period in the latter half of the growing season.

RESULTS AND DISCUSSION

Agronomic parameters of the analysed English ryegrass populations. The results of the ANOVA test for agronomic parameters of the analysed perennial ryegrass populations are presented in Table 3. The agronomic parameters of the analysed *Lolium perenne* populations revealed significant variability, reflecting the genetic potential of native populations. Our results showed that the average three-year plant height, of the tallest spike, for all the studied populations was 60.4 cm, with the G2 population recording the highest height at 67.1 cm in 2020 (Table 3, Figure 2). This is consistent with findings from international studies, such as those by Ozkose and Tamkos (2014), where the plant height varied among the tested genotypes, indicating the influence of genetic factors and environmental conditions on the growth.

The study found a highly significant effect of the genotype, year, and a significant genotype × year (G × Y) interaction on the number of generative stems per plant (Figure 3, Table 4). The average number of generative stems across all the populations over the three-year period was 184.6, ranging from 171.4 stems in 2021 to 195.3 stems in 2020, Figure 3. This is consistent with findings from Lakić et al. (2013), where the number of generative stems in examined native populations of perennial ryegrass ranged from 78.9 to 186.7. The findings from Conaghan and Casler (2011) emphasised the importance of the stem density in breeding programmes aimed at enhancing the forage yield in the *Lolium* species, but also the declining forage quality at the same time.

The genotype, agricultural practices and the environment influence spike length (Ozkose & Tamkos 2014). The spike length and the number of spikelets per spike were also significantly influenced by the genotype. The G4 population had the longest spikes on average compared to all the other tested populations. The average spike length for the studied populations from 2020 to 2022 was 24.7 cm, ranging from 24.1 cm in 2021 to 25.1 cm in 2020. Genotype G7 in 2021 (19.4 cm) had the smallest spike length (Table 3, Figure 4).

The G4 population had significantly longer spikes than all the other tested populations in 2020 and 2021, with average lengths of 29.3 and 27.4 cm, respectively, aligning with the studies by Tubbs and Chastain (2022) that highlighted the importance

Table 3. The tested agronomic parameters, depending on the genotype and year

Genotype	G1	G2	G3	G4	G5	G6	G7	G8	Average	SD
Plant height (PH, cm)										
2020	65.6	67.1	61.0	63.3	53.0	60.0	57.8	60.8	61.05	6.35
2021	66.3	56.8	65.3	61.3	57.0	58.5	53.5	63.6	60.28	5.77
2022	59.8	61.9	60.5	61.4	58.5	60.0	55.5	61.1	59.83	4.06
Average	63.8	61.9	62.3	61.9	56.2	59.5	55.6	61.8	60.4	5.4
No. of stalks per plant (NBPP)										
2020	216.0	137.0	182.0	230.0	215.0	189.0	172.0	221.0	195.3	33.1
2021	164.0	148.3	168.0	182.0	225.3	165.0	136.0	183.0	171.4	28.9
2022	180.3	158.0	193.0	201.0	201.0	208.3	148.0	207.0	187.1	25.8
Average	186.8	147.8	181.0	204.3	213.8	187.4	152.0	203.7	184.6	30.4
Spikes/ears length (SL, cm)										
2020	22.0	26.4	26.6	29.3	24.9	26.9	20.4	24.8	25.1	3.2
2021	20.4	26.0	25.4	27.4	25.9	26.1	19.4	22.3	24.1	3.3
2022	21.5	22.0	27.4	26.5	26.6	25.6	20.5	24.0	24.8	2.9
Average	21.3	26.1	26.4	27.7	25.8	26.2	20.1	23.7	24.7	3.2
No. of spikes per spikelet (No. S/S)										
2020	23.0	27.0	23.3	23.5	25.0	22.8	24.3	24.0	23.7	2.5
2021	24.5	27.5	24.3	24.0	23.0	21.8	21.5	22.3	23.6	2.8
2022	23.5	26.0	25.0	24.3	25.3	24.0	20.8	23.3	24.0	2.6
Average	23.7	26.8	24.3	23.9	24.4	22.8	21.2	23.2	23.8	2.6
Seed mass per ear (SM/PE, g)										
2020	0.25	0.38	0.29	0.26	0.30	0.27	0.22	0.23	0.27	0.06
2021	0.26	0.28	0.24	0.28	0.27	0.27	0.20	0.22	0.25	0.03
2022	0.25	0.30	0.27	0.31	0.29	0.27	0.20	0.24	0.26	0.05
Average	0.25	0.32	0.27	0.28	0.29	0.27	0.21	0.23	0.26	0.04
1 000 seed yield per plant mass (SYHSM/P, g)										
2020	1.9	2.2	2.1	2.1	2.0	2.2	2.1	2.3	2.1	0.10
2021	1.5	1.7	1.7	1.8	1.8	1.7	1.6	1.8	1.7	1.11
2022	1.7	1.9	1.8	1.9	1.9	1.9	1.8	1.9	1.8	0.08
Average	1.7	1.9	1.9	1.9	1.9	1.9	1.8	2.0	1.9	0.1

SD – standard deviation

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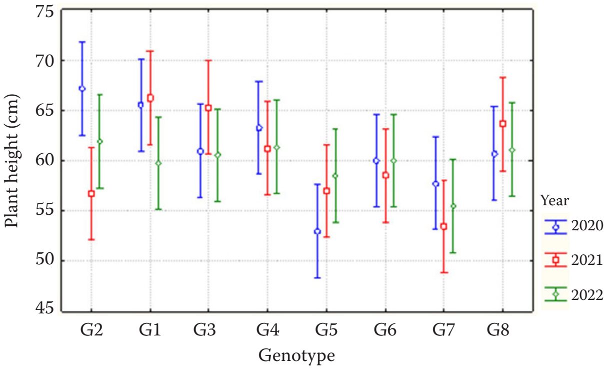

Figure 2. Interaction of the genotype (G) and year (Y) for the plant height

Bars denote the standard deviation

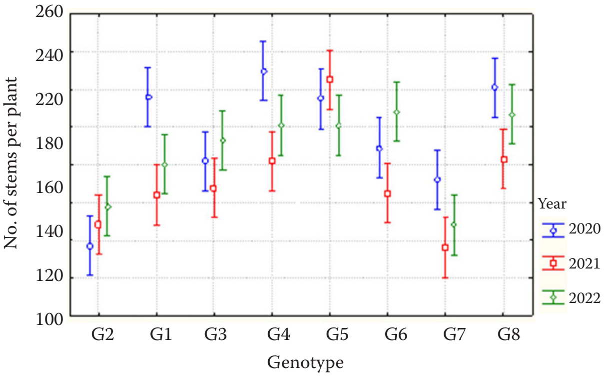

Figure 3. Interaction of the genotype (G) and year (Y) for the number of stems per plant

Bars denote the standard deviation

of the spike traits for the seed yield improvement in perennial ryegrass. In the third year of the study (2022), the G3 population had the longest spikes, measuring 27.4 cm (Table 3, Figure 4).

Differences in the spike length between the average values of populations G2, G3, G4, and G6 and the standards G7 and G8 were highly significant. According to Lakić et al. (2013), the spike length of native perennial ryegrass populations ranged from 20.9 to 24.8 cm. In a study of 568 English ryegrass genotypes, Ozkose and Tamkos (2014) reported that the number of spikelets per spike ranged from 11.6 to 23.7, with an average spike length of 17.6 cm. Additionally, Tubbs and Chastain (2024) found that in testing several perennial ryegrass genotypes, the average spike length was 19.5 cm, ranging from 13.3 to 23.3 cm, and the number of spikelets per spike ranged from 19.3 to 28.1.

The genotype had a highly significant effect on the number of spikelets per spike. The native populations G5 and G3 (27.7 and 24.2, respectively) had the highest average number of spikelets per spike compared to the other populations. The average number of spikelets per spike for the studied populations from 2020 to 2022 was 23.78, ranging from 23.59 in 2021 to 24.03 in 2022. The G2 population had significantly more spikelets per spike than all the other populations in all three years (27.0, 27.5, and 26.0) (Table 3, Figure 5), which is crucial as higher spikelet numbers have been correlated with increased seed yields (Abel et al. 2017).

The optimum breeding system is dependent on the traits required for improvement, and the available physical and human resources. The forage dry matter yield, persistency, disease resistance, nutritional value and seed yield are considered among the most important traits for improvement (Conaghan & Casler 2011). In perennial ryegrass breeding endeavours, maximising the seed yield has been a primary fo-

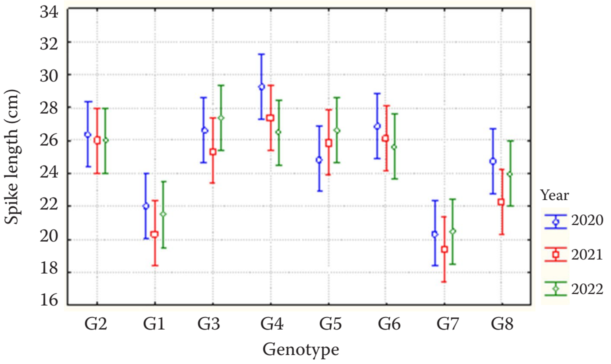

Figure 4. Interaction of the genotype (G) and year (Y) for the spikes/ears length

Bars denote the standard deviation

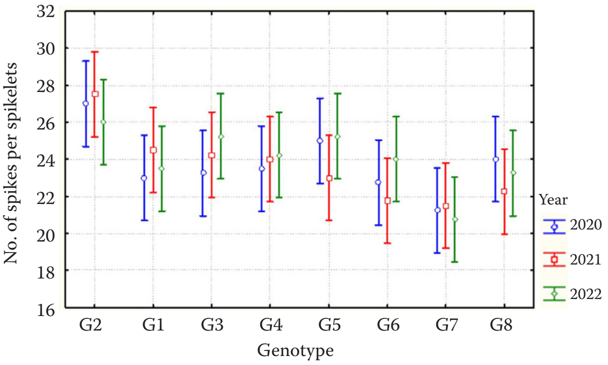

Figure 5. Interaction of the genotype (G) and year (Y) for the number of spikes per spikelet

Bars denote the standard deviation

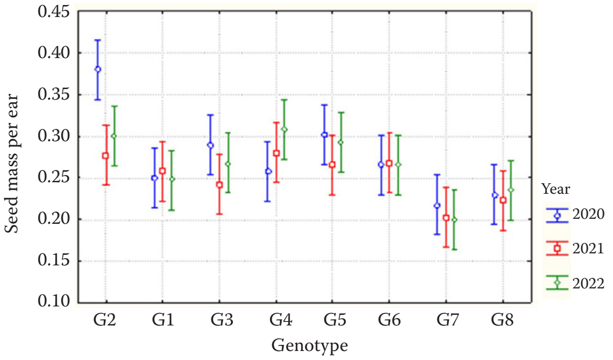

Figure 6. Interaction of the genotype (G) and year (Y) for the seed mass per ear

Bars denote the standard deviation

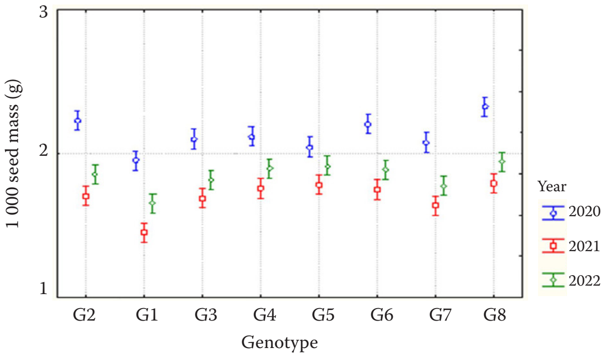

Figure 7. Interaction of genotype (G) and year (Y) for 1 000 seed mass

Bars denote the standard deviation

cus, with the number of spikelets per spike considered crucial (Tubbs & Chastain 2022). The number of spikelets per spike has a significant impact on the seed yield (Abel et al. 2017). According to Chastain et al. (2014), four tested perennial ryegrass varieties in Oregon (USA) had an average of 23 spikelets per spike, while Tubbs and Chastain (2022) indicate that the overall mean value for the 21 diverse global accessions was 23.4 spikelets per spike. Despite the high variability in spikelets per spike, the mean for this work was very close to that recorded in other published studies.

The genotype had a highly significant effect on seed mass per spike in the examined populations of perennial ryegrass. The average three-year seed mass per spike across the populations was 0.26 g/spike, ranging from 0.25 g/spike in 2021 to 0.27 g/spike in 2020 (Figure 6). The G2 population had a significantly higher seed mass per spike compared to all the other populations in 2020. In 2021, populations G2, G4, G5, and G6 had a significantly higher seed mass per spike than the other populations. In 2022, populations G2, G4, and G5 had a significantly higher seed mass per spike compared to other populations (Figure 6).

The genotype, year and G × Y interaction had a highly significant effect on the 1 000 seed mass. The average 1 000 seed mass across all the populations over the three-year period was 1.9 g, ranging from 2.1 g in 2020 to 1.7 g in 2021. The genotype G8 had a significantly higher 1 000 seed mass compared to the other populations in 2020 (Figure 7). The first year, 2020, had a higher 1 000 seed mass compared 2021 and 2022.

The genotype and year had a highly significant effect on the seed yield per plant during the study. The average seed yield per plant across all the populations over the three-year period was 46.3 g, ranging from 41.7 g in 2021 to 50.1 g in 2020. The native populations G4, G5 and the standard G8 had significantly higher seed yields per plant compared to the other populations in 2020.

In the second year (2021), the G5 population had a significantly higher seed yield per plant compared to the other populations. In 2022, the G4 and G5 populations stood out, with both having significantly higher seed yields per plant than all the other populations (Figure 8).

The different climatic conditions, temperatures, and amounts of precipitation during the examined research period, as well as the different sowing periods, had a significant impact on the increased examined parameters, showing that the investigated growing seasons differed significantly, and all this affected the high grain yield variation (Lakić 2014;

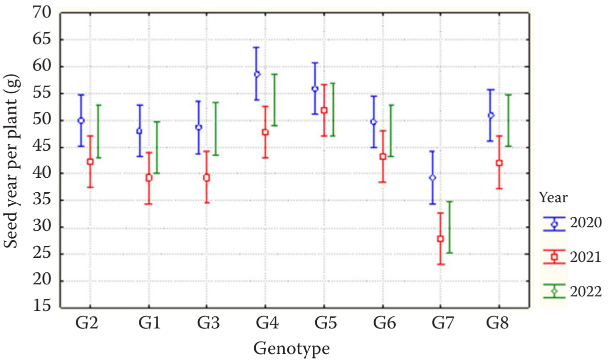

Figure 8. Interaction of genotype (G) and year (Y) for seed yields per plant

Bars denote the standard deviation

Table 4. Results of Fisher's least significant difference (LSD) test

Parameter	LSD	Genotype (G)	Year (Y)	G × Y
PH	0.05	3.2*	1.9$^{\text{ns}}$	5.5$^{\text{ns}}$
	0.01	5.1**	3.1$^{\text{ns}}$	8.7$^{\text{ns}}$
NBPP	0.05	10.8*	6.6*	18.8*
	0.01	17.3**	10.6**	30.0$^{\text{ns}}$
SL	0.05	1.4*	0.8$^{\text{ns}}$	2.4$^{\text{ns}}$
	0.01	2.2**	1.3$^{\text{ns}}$	3.7$^{\text{ns}}$
No. S/S	0.05	1.6*	1.0$^{\text{ns}}$	2.7$^{\text{ns}}$
	0.01	2.5**	1.5$^{\text{ns}}$	4.4$^{\text{ns}}$
SM/PE	0.05	0.03*	0.02$^{\text{ns}}$	0.04$^{\text{ns}}$
	0.01	0.04**	0.03$^{\text{ns}}$	0.07$^{\text{ns}}$
SY/P	0.05	3.3*	2.1*	5.7$^{\text{ns}}$
	0.01	5.3**	3.2**	9.14$^{\text{ns}}$

PH – plant height; NBPP – number of branches per plant; SL – spikelet length; No. S/S – Number of spikelets per spikelet; SM/PE – seed mass per ear; SY/P – seed yield per plant; *, ** significant at $P < 0.05$, 0.01; $^{\text{ns}}$not significant

Boelt & Studer 2010; Popović et al. 2024; Lakić et al. 2019, 2022; Bojović et al. 2024).

Correlations of the examined traits in the populations of perennial ryegrass. During these tests, correlations between the examined traits in the populations of perennial ryegrass were identified (Table 5). The calculated correlation coefficient indicates a strong positive correlation between the number of generative stems per plant and seed yield per plant (r = 0.74**) and underscores the importance of breeding for traits that enhance the overall plant productivity, as noted in global breeding initiatives. A significant positive correlation was found between the number of generative stems per plant and the spike length (r = 0.37*), as well as between the number of spikelets per spike and the number of generative stems per plant (r = 0.20*). A significant positive correlation was found between the seed yield and the 1 000 grain mass (r = 0.5**), the 1 000 seed mass and No. branches per plant (r = 0.4*), the 1 000 seed mass and the spikelet length (r = 0.3*), and the 1 000 seed mass and the seed mass per ear (r = 0.2*). The spike length showed a strong positive correlation with the seed yield per plant (r = 0.64**), which is consistent with the findings that emphasise the need for breeders to focus on the morphological traits that enhance the seed yield (Tubbs & Chastain 2022). Additionally, the spike length was significantly positively correlated with the number of generative stems per plant, the seed mass per spike, and the number of spikelets per spike. The number of spikelets per spike was strongly positively correlated with the seed yield per plant and seed mass per spike. A significant positive correlation was found between the number of spikelets per spike and the number of generative stems per plant, as well as the spike length (r = 0.34*).

The seed mass per spike showed a strong positive correlation with the seed yield per plant and the number of spikelets per spike. A significant positive correlation was also found between the seed mass per spike and spike length (r = 0.44*). The seed yield per plant had a strong positive correlation with the number of generative stems per plant, the spike length, and the number of spikelets per spike. A significant positive correlation was found between the seed yield per plant and the seed mass per spike.

The seed mass in perennial ryegrass showed a significant positive correlation with the spike length, which is consistent with the results of Abel et al. (2017), who also found a positive relationship between the seed mass and spike length. Plant breeders should focus on increasing the spikelet number. By focusing on the traits, such as the seed weight,

Table 5. Correlations of the examined traits

Parameter	Planth height	No. of branches/ plant	Spikelet length	No. of spikelets/ spike	Seed mass per ear	Seed yield/ plant	1 000 seed mass
Planth height	1.00	0.06 $^{\text{ns}}$	0.06 $^{\text{ns}}$	0.17 $^{\text{ns}}$	0.10 $^{\text{ns}}$	0.10 $^{\text{ns}}$	0.06$^{\text{ns}}$
No. of stems/plant	–	1.00	0.37*	0.20*	0.05 $^{\text{ns}}$	0.74**	0.36*
Spikelet length	–	–	1.00	0.34*	0.44*	0.64**	0.34*
No. of spikelets/spike	–	–	–	1.00	0.54**	0.53**	0.06 $^{\text{ns}}$
Seed mass/ear	–	–	–	–	1.00	0.55**	0.23*
Seed yield/plant	–	–	–	–	0.55*	1.00	0.49**

*,**significant at $P < 0.05$, 0.01; $^{\text{ns}}$not significant

spike length, and seed number per spike, breeders can anticipate improvements in the overall seed yield (Tubbs & Chastain 2022).

Given the use of a single low stress site (low disease levels, mild winters, and warm moist summers) under two fixed management regimes for more than 40 years, the current study may offer a particularly definitive measure of the rate of genetic gain in perennial ryegrass, even though all the yields are site specific and altered by the location's G × E factors. Since breeding new ryegrass types is a continuous, long-term process, a significant measure of the genetic development must be made over such a lengthy period of time. Improved perennial ryegrass breeding techniques have been made possible during this time by significant technology developments in plant breeding (Humphreys 2005) as well as advances in biology and genetics (Lee et al. 2012).

Although the rapid yield gains observed for the 1990 s in both managements were undoubtedly due to the type of selective breeding for superior genetic material described by Connolly (2001). The conclusion drawn from this 41-year analysis is that, within the context of the broader long-term trend, these times of high increase rates can also be thought of as cat.

According to Gilliland et al. (2007) and Long et al. (2011), these include shifts in farmer preferences, the introduction of a new market-leading variety, and the redirection of rival breeders' efforts from other regions in an attempt to improve the latest developments or declines in the seed markets. As a result, breeding companies merged and profitability decreased, which, in turn, decreased breeding effort in some qualities or on a periodic basis. Although recommendations for a multi-use, multi-harvest crop compromise are offered, variety testers have always aimed to increase the overall agricultural quality of grasslands (Camlin 1997). Therefore, even if this variety seems to hinder the breeding progress for simulated grazing, it may still be advised to choose a variety with outstanding conservation yields, but below the average simulated grazing yields.

CONCLUSION

The testing and evaluation of six native populations of perennial ryegrass revealed key genetic insights. The most favourable conditions for growth occurred in 2021, while 2022 was the least favourable. The genotype, year, and genotype × year (G × Y) interaction significantly affected the number of generative stems per plant. The seed mass per spike was strongly positively correlated with the seed yield per plant and the number of spikelets. The seed yield per plant also correlated positively with the generative stems, spike length, and spikelet number. Our findings align with the global research on *Lolium* species, highlighting the potential of native populations for breeding programmes. Populations G4 and G5 exhibited superior performance in the seed production traits and are recommended as valuable material for breeding new perennial ryegrass varieties. The variability observed in this study reflects the adaptability and genetic diversity present within local populations, which can be leveraged to improve resilience and productivity in changing climatic conditions.

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