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Data Article

Multiplexed SSR and agronomic data used in an investigation of obsolete diversity of rye (*Secale cereale* L.)

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ABSTRACT

Rye (*Secale cereale* L.) is one of the most important cereal crops cultivated in the world due to its ability to produce high yields even when grown under environmental stress conditions. About 27,000 *Secale* accessions have been collected and preserved in 70 gene banks worldwide. Although the germplasm represents a great source of genetic diversity, the molecular characteristics refers only to the part of them. Here, we present data obtained by the Simple Sequence Repeat markers (SSR) analysis of 100 rye accessions preserved in the gene bank of the Polish Academy of Sciences Botanical Garden – Center for Biological Diversity Conservation in Powsin. Additionally, the data presented in this article refers to evaluation of agronomoic traits and weather conditions measured for 14 years. The data was used in the research article "Investigation of obsolete diversity of rye

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(*Secale cereale* L.) using multiplexed SSR fingerprinting and evaluation of agronomic traits" [1].

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Specifications Table

Subject	Agricultural science, Agronomy and Crop science
Specific subject area	Binary genotyping data, rye phenotyping data based on 3-year field trial, data referring to field weather condition from 14 years
Type of data	Tables Excel files
How the data were acquired	Genotyping data was collected by PCR (Arktic Thermocycler, ThermoScientific) with DNA isolated from rye accessions, and then analysis in ABI 3500 Genetic Analyzer (Applied Biosystems). Phenotyping data was obtained by 3-year field observation. Meteorological data was assembled during 14 year.
Data format	Raw
Description of data collection	100 rye accessions preserved in the Polish Academy of Sciences Botanical Garden – Center for Biological Diversity Conservation in Powsin. Phentypic traits were evaluated during three-year field experiments. DNA was isolated from seedlings in the first leaf stage from 96 plants as a bulk sample. Genetic analysis was performed by 17 Simple Sequence Repeat markers in capillary sequencer. Weather data was collected continuously for 14 years at the location 52.2165, 20.6453.
Data source location	Polish Academy of Sciences Botanical Garden – Center for Biological Diversity Conservation in Powsin, Warsaw, Poland Plant Breeding and Acclimatization Institute (IHAR) - National Research Institute, Radzików, Poland
Data accessibility	Repository name: Open Science Framework Direct URL to data: (https://osf.io/wpcq9/) doi: https://doi.org/10.17605/OSF.IO/WPCQ9.
Related research article	M. Targonska-Karasek, M. Boczkowska, W. Podyma, M. Pasnik, M. Niedzielski, A. Rucinska, Z. Nowak-Zyczynska, M. Rakoczy-Trojanowska, Investigation of obsolete diversity of rye (*Secale cereale* L.) using multiplexed SSR fingerprinting and evaluation of agronomic traits. J. Appl Genetics. 61 (2020) 513–529. https://doi.org/10.1007/s13353–020–00579-z

Value of the Data

- We provide genotyping and phenotyping data of *Secale cereale* L. rare and obsolete accessions representing part of the collection preserved in the gene bank of the Polish Academy of Sciences Botanical Garden – Center for Biological Diversity Conservation in Powsin. Multi-level evaluation ensures increased use of genetic resources for breeding and scientific activities.
- Data included in this manuscript can be useful for researchers or breeders who are looking for another source of genetic diversity and are interested in including historical germplasm into breeding programs.
- Data presented in this article can be used as the training data in statistic and population structure studies.
- Data provides detailed information about weather conditions since 2005 which can be used in other studies in terms of statistics, meteorological studies, or correlations.

1. Data Description

Information about accessions deposited in the Polish Academy of Sciences Botanical Garden – Center for Biological Diversity Conservation in Powsin, which were used in the analyses with their names, gene bank accession numbers, introduction status, acquisition year, and country of origin, were in Table 1. Binary data of SSR genotyping with the use of 17 SSR markers can be found in Excel file 1. In columns, results for each marker allele can be found, where the presence of an amplified product was scored as 1 and the absence of a product as 0.

In the Excel file 2. phenotyping data from three growing periods (2015/2016, 2016/2017, and 2017/2018) can be found. The phenotypic evaluation included a total of 13 traits i.e., six qualitative and seven quantitative ones. Plant emergence, winter hardiness, snow mold resistance, powdery mildew resistance, brown rust resistance, and stem rust resistance were expressed on a 1–9 point scale.

Comprehensive and detailed information about meteorological conditions is in an Excel file 3. In the separate Excel sheets, the information about average air temperature and total rainfall between 2005 and 2019 can be found. Additionally, there is a data sheet with minimum and maximum monthly temperatures from 2006 to 2019. The last excel sheet with extended data includes next to the temperature and total rainfall data also information about factors as insolation, atmospheric pressure, dew point temperature, freezing point temperature, sunlight, net radiation, relative humidity, ground temperature. The listed measurements were taken between 2009 and 2019.

2. Experimental Design, Materials and Methods

2.1. Plant material

From the *Secale* collection preserved in the gene bank at the Polish Academy of Sciences Botanical Garden-Center for Biological Diversity Conservation in Powsin (PASBG), 100 accessions were selected for analysis (Table 1). They originated from 28 countries and were introduced to the collection between 1970 and 1990. The research material was mainly cultivars (87 accessions), to a much lesser extent landraces (10 accessions), while breeding materials were represented by only 3 accessions.

2.2. DNA isolation

From each accession, 150 seeds were prepared and treated with Funaben T (45% thiram, 20% carbendazim). For this purpose, the seeds were placed in a 100 ml glass conical flask and about 30 mg of Funaben T was added. Flask was closed with a glass stopper and shaken vigorously for about 30 s. The treated seeds were evenly placed into 20 cm diameter Petri dishes containing moist tissue paper. The procedure was carried out separately for each accession. The Petri dishes were left at room temperature on a laboratory table in a room with limited light for germination. Successively, when seedlings reached the first leaf stage, tissue was collected for DNA isolation. Fragments with a length of about 1.5 cm were taken from the central part of the leaf blade of 16 plants and placed in a 2 ml Eppendorf tube to form a pooled sample. For each accession, a total of six pooled samples were collected. Immediately after harvesting, the material was frozen in –20 °C and freeze-dried (LABCONCO) in high vacuum conditions and temperature of –50 °C for 12 h. In the next step dry plant material was ground in a bead mill MM 100 (Retch) using three 3 mm diameter glass beads for 30 s and frequency 30 Hz. DNA was isolated from pooled samples using a Clean Plant PK DNA Purification Kit (CLEANNA). This kit is designed for DNA isolation in a 96-well plate format using a magnetic separation device. The initial isolation step was adapted to the available equipment. 700 µl of CPPK lysis buffer and 20 µl Proteinase K solution from

Table 1
Rye accessions from the Polish Academy of Sciences Botanical Garden – Center for Biological Diversity Conservation in Powsin, which were used in the analyses modified from [1].

Number	Accession number	Name	Improvement status	Acquisition year	Country of origin
1	7261/76	683	Landrace	1976	AFG
2	5779/75	DEBRETT	Cultivar	1975	ARG
3	8411/78	MANFREDI SUQUIA	Cultivar	1978	ARG
4	16,286/81	TERAPICO	Cultivar	1981	ARG
5	7492/76	VARNEROG	Cultivar	1976	AUS
6	1287/71	CHRYSANTH HANSERROGGENEN	Cultivar	1971	AUT
7	2525/73	HARRACH UNIVERSAL	Cultivar	1973	AUT
8	7124/76	HOHENAUER	Cultivar	1976	AUT
9	1310/71	KARNTNER	Cultivar	1971	AUT
10	8842/79	MARCHFELDER	Cultivar	1979	AUT
11	7209/76	OTTERBACHER	Cultivar	1976	AUT
12	1276/71	SCHLAGLER	Cultivar	1971	AUT
13	1299/71	TSCHERMAKS VEREDELTER MARCHFELDER	Cultivar	1971	AUT
14	8826/79	GALMA	Cultivar	1979	BEL
15	7910/77	JOEGEWA-AUSLESE	Cultivar	1977	BGR
16	7915/77	NISKOSTEBELNAJA	Cultivar	1977	BGR
17	2369/73	PARTIZANSKAJA	Cultivar	1973	BLR
18	6984/76	CENTENO 52	Cultivar	1976	BRA
19	7049/76	GAYEROVO	Cultivar	1976	BRA
20	7465/76	SAMPLE A	Cultivar	1976	BRA
21	7044/76	FRONTIER	Cultivar	1976	CAN
22	5792/75	HORTON	Cultivar	1975	CAN
23	1198/90	SINGZHAU	Cultivar	1990	CHN
24	5780/75	DOBRENICKE KRMNE	Cultivar	1975	CSK
25	7198/76	NALZOVSKE	Cultivar	1976	CSK
26	5831/75	VALTICKE	Cultivar	1975	CSK
27	2386/73	PUDMERICKE	Cultivar	1973	CZE
28	7403/76	ZIDLOCHOWICKIE PANIS	Cultivar	1976	CZE
29	1334/71	BENDELEBENER	Cultivar	1971	DEU
30	18,702/83	DONAR	Cultivar	1983	DEU
31	4770/75	GULZOWER St. 1714	Cultivar	1975	DEU
32	4997/75	HESSDORFER JOHANNIS	Cultivar	1975	DEU
33	8830/79	HGP 20	Breeding material	1979	DEU
34	18,703/83	JANOS	Cultivar	1983	DEU
35	8840/79	LUKAS	Cultivar	1979	DEU
36	5808/75	MECKLENBURGER MARIEN	Cultivar	1975	DEU
37	14,982/80	PETKUSER MOORROGGEN	Cultivar	1980	DEU
38	18,705/83	POLLUX	Cultivar	1983	DEU
39	7039/76	FLORIDA BLACK WALLANCE SELECTION	Cultivar	1976	ESP
40	7125/76	HUESCA	Cultivar	1976	ESP
41	7281/76	SYNTHETIC V	Cultivar	1976	ESP
42	1278/71	ENSI	Cultivar	1971	FIN
43	8833/79	HJA JUSSI 20	Cultivar	1979	FIN
44	1279/71	PEKKA	Cultivar	1971	FIN
45	7380/76	VISA	Cultivar	1976	FIN
46	8823/79	DUNA TISZAKOZI	Cultivar	1979	HUN
47	7036/76	FLEISCHMANN	Cultivar	1976	HUN
48	5794/75	HUSZAJ	Cultivar	1975	HUN
49	7138/76	JAPAJEDELSKE	Cultivar	1976	HUN
50	7184/76	LOVASZPATONAI	Cultivar	1976	HUN
51	7210/76	OVARI	Cultivar	1976	HUN
52	7158/76	K 1634	Landrace	1976	IRN
53	7012/76	DOMINANT	Cultivar	1976	NLD
54	1295/71	DOMINANT	Cultivar	1971	NLD
55	7901/77	AR-3	Cultivar	1977	POL

(*continued on next page*)

Table 1 (*continued*)

Number	Accession number	Name	Improvement status	Acquisition year	Country of origin
56	18,700/83	CHODAN	Cultivar	1983	POL
57	8816/79	CH-S	Cultivar	1979	POL
58	18,701/83	DAŃKOWSKIE NOWE	Cultivar	1983	POL
59	8820/79	DAŃKOWSKIE SREBRNE	Cultivar	1979	POL
60	7047/76	GARCZYŃSKIE LUDOWE	Cultivar	1976	POL
61	18,639/83	GOLSKIE	Cultivar	1983	POL
62	4266/74	KORTOWSKIE	Cultivar	1974	POL
63	7196/76	MIKULICKIE WCZESNE	Cultivar	1976	POL
64	14,057/80	PANCERNE	Cultivar	1980	POL
65	7238/76	PULAWSKIE	Cultivar	1976	POL
66	7285/76	SZK 6B/65	Cultivar	1976	POL
67	18,657/83	TEMPO	Cultivar	1983	POL
68	7392/76	WŁOSZANOWSKIE NOWE	Cultivar	1976	POL
69	7404/76	BRIGODA DE MIRANDELA	Cultivar	1976	PRT
70	1393/71	PORTO	Cultivar	1971	PRT
71	6971/76	BRASOV 200-N	Cultivar	1976	ROM
72	8867/79	SUCEAVA 50	Cultivar	1979	ROM
73	5776/75	BURUNAJA	Cultivar	1975	RUS
74	2680/73	FALENSKAJA	Cultivar	1973	RUS
75	41/70	KAZANSKAJA	Cultivar	1970	RUS
76	14,917/80	KRUPNOZERNAJA	Cultivar	1980	RUS
77	2683/73	NOVOZYBKOVSKAJA 4	Cultivar	1973	RUS
78	45/70	SITNIKOVSKAJA	Cultivar	1970	RUS
79	14,969/80	SPASSKAJA MESTNAJA	Cultivar	1980	RUS
80	7172/76	WIR 7276	Landrace	1976	RUS
81	7449/76	87	Landrace	1976	SRB
82	8857/79	PONSI	Cultivar	1979	SWE
83	8869/79	SV. 6728	Breeding material	1979	SWE
84	7076/76	1566	Landrace	1976	TUR
85	7077/76	1794	Landrace	1976	TUR
86	7079/76	2666	Landrace	1976	TUR
87	7084/76	3525	Landrace	1976	TUR
88	7095/76	4018	Landrace	1976	TUR
89	7117/76	4317	Landrace	1976	TUR
90	2373/73	BEREGOVSKAJA	Cultivar	1973	UKR
91	14,974/80	HARKOVSKAJA	Cultivar	1980	UKR
92	6964/76	ATHENS ABRUZZI	Cultivar	1976	USA
93	14,156/80	DWARF WINTER	Cultivar	1980	USA
94	25,282/86	FREDERICK	Cultivar	1986	USA
95	7250/76	ROSEN	Cultivar	1976	USA
96	25,286/86	SCHNIDT	Cultivar	1986	USA
97	7287/76	TENNESSEE 4062	Breeding material	1976	USA
98	1306/71	WESER	Cultivar	1971	USA
99	14,059/80	BALBO	Cultivar	1980	ZAF
100	7002/76	DL67/172	Cultivar	1976	ZAF

the isolation kit was added to the ground samples remaining in the 2 ml tubes. The tubes were incubated at 56 °C in a heating block with 1000 rpm shaking for 30 min. The samples were then centrifuged at 4000 × g for 10 min. 500 ul of pure lysate was transferred to 96-well deep-well plates. The rest of the isolation followed the manufacturer's protocol using multichannel pipets. At this stage, each accession was represented by six samples in 96 well plate. After isolation, the concentration and purity of DNA were evaluated spectrophotometrically using NanoDrop 1000 (Thermo). At the end, six pooled samples for each accession were combined in one in equal proportions and diluted to a working concentration of 20 ng/µl.

2.3. SSR analysis

A total of 17 SSR markers were selected for analysis. All are available in the public domain [2,3] and are located on all rye chromosomes. The selection of markers was based on a previous study by Targońska et al [4]. The requirement for selection was an amplification of good quality polymorphic products from a single locus. Localization on genetic maps was determined for selected markers. [5–8]. Based on the length of the amplified products, primers were selected and labelled to form two multiplex reaction kits. Four fluorescent dyes: 6-FAM, VIC, NED, or PET (Thermo Fisher) were used. For detailed information on the primers, see Table 2. Multiplex PCRs were performed in a 10 µl volume containing approximately 20 ng template DNA, 1 pmol of each primer, and 5 µl AmpliTaq Gold™ 360 Master Mix (Life Technologies). Reactions were performed in an Arktik thermocycler (Life Technologies) with an initial denaturation step of 10 min at 94 °C, 10 cycles of 30 s at 94 °C, 1 min starting at 64 °C and decreasing 1 °C per cycle, 1 min at 72 °C followed by 35 cycles of 94 °C for 30 s, 55 °C for 45 s, and 72 °C for 1 min, and a final extension at 72 °C for 30 min. PCR reaction products were ten times diluted with DNAse free water. Just before electrophoresis, 1 µl of diluted PCR products were mixed with 9 µl Hi-Di™ Formamide (Thermo Fisher) and 0.25 µl of GeneScan600 LIZ Size Standard (Applied Biosystems) and formed a loading cocktail. Before loading, cocktail was denatured in the thermocycler for 3 min at 95 °C and immediately chill on a cooling block. The amplified products were analyzed by an ABI 3500 Genetic Analyzer (Applied Biosystems) using a 36 cm capillaries array filled with POP-7 polymer (Thermo Fisher). The length of fragments was assessed against the size standard GeneScan™ 500 LIZ™ Dye Size Standard (Applied Biosystems). The length of the fragments was determined using the GeneMapper (Applied Biosystems) software. The amplified fragments from each accession were transformed into a binary character matrix where 1 indicated the presence of a defined length fragment, while its absence was marked as 0.

2.4. Evaluation of agronomic traits

Phenotyping observations and measurements were performed during three consecutive growing periods: 2015/2016; 2016/2017; and 2017/2018. In experimental plots of 1.5 m^2, seeds were sown every 2–3 cm in rows of 17.5 cm spacing. Approximately 400 seeds treated with Funaben T per plot were sown in the fall. No other pathogen protection was applied during the growing season. During the growing season, morphological characters as well as basic phenological data have been evaluated according to descriptors [9,10] at the recommended time. The length of vegetation and grain filling period were calculated based on sowing, flowering, and wax maturity time. Plant emergence, winter hardiness, snow mold, powdery mildew, brown rust, and stem rust resistance were expressed on a 1–9 point scale i.e., 1 (very sensitive) – 9 (very resistance). Plant height was measured at maturity from ground to spike, including awns. At the same, time spike length excluding awns was examined. Penultimate leaf length was assessed during grain filling period. All measurements were performed for 20 plants per plot and arithmetic mean was expressed in centimetres. The number of grains per spike was the average number for 20 manually harvested and threshed ears. One thousand grains of each accession were collected at random, weighed to record the seed index, and expressed in grams.

2.5. Assembling meteorological data

Meteorological data from 2005 to 2019 concerning temperature and total rainfall data also information about factors as insolation, atmospheric pressure, dew point temperature, freezing point temperature, sunlight, net radiation, relative humidity, ground temperature were collected using meteorological station located in 52.2165, 20.6453.

Table 2
SSR markers used in the study.

Marker id	Chromosome	Forward sequence	Reverse sequence	SSR motif	Products range (bp)	Dye	Multiplex	Refs.
SCM009	1R	TGACAACCCCCTTTCCCTCGT	TCATCGACGCTAAGGAGGACCC	(GT)8	205–255	NED	A	[3]
SCM028	6R	CTGGTCCTGGTCTGGTGGGTC	CGCATCGGGTGTGTCGCATAC	(GT)26	128–130	VIC	A	[3]
SCM041	2R	TGATAGCGGGGGGAAGAG	GCTGCTTGTGCTTGAAGAGAA	(AGC)5…(AAGAG)5	131–160	FAM	A	[2]
SCM050	7R	TCGGAGGCAGCGACCACCA	TGCCAGGAACCAGGTTCTCTG	(AGG)5	98–145	PET	A	[2]
SCM063	7R	CGACTTCGAGGGCAGGAATGA	ATCCCGGGGATGAAGTGCAG	(CCG)5	224–250	NED	B	[2]
SCM101	4R	GCCAGCCGCCACCTTAATTG	AGCCCAACTCTTTCGTGCATG	(CT)18	150–200	FAM	B	[3]
SCM107	1R	CCCGAACCCTAACCCTAAAAC	AGCTCCTTCTCCTCCCTGAC	(GCC)5	232–252	FAM	A	[2]
SCM109	5R	AACCCCCTTTCGTACCTTGT	TAAAGCAAACCACCAGAGCC	(GT)9	127–145	PET	B	[3]
SCM112	3R	CCACTGCTCCTCCCAAAAG	CCCCTGCTTGTCCACATTATC	(GGC)5	375–410	NED	A	[2]
SCM118	2R	CAAGCCAGCCTCTTCTTCTTC	GAGCGTGGAGATGAACTCG	(TCT)5	145–166	VIC	A	[2]
SCM138	5R	ATAGCCGCAGATGGTTGAGGAC	GAGAAGTCTACAAATCAAGGGGGC	(AC)23	102–128	FAM	B	[3]
SCM139	4R	TACCACCGCTCTCCTCGACCT	GGTGTGCTGCTCCATGTTCAG	(ATCT)3	126–142	NED	A	[2]
SCM152	5R	CGGAGCAGCAGAGCAAGAGA	ATGTAGCCGAGGATGGTGAGC	(AG)7	320–391	VIC	B	[2]
SCM155	4R	TTCTTCTTCGCTACGCACACC	TCCGGCCACTACCACATCTT	(AAG)5	218–243	PET	A	[2]
SCM162	3R	TGGCATGGTTGGGCATTGTTC	GAGCCGGCAAAGGAGCAGAGT	(CCG)7	128–197	VIC	B	[2]
SCM171	1R	TCCCGAAACACTACAGGTTGA	AGGCCTAGGACCCGAACA	(GGC)6	216–223	PET	B	[2]
SCM180	6R	GTTTCGTCCCCGTTGCCATC	ACGTGTCGCTTTCCATTGCCC	(GT)6(GT)7	138–145	NED	B	[3]

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

CRediT Author Statement

Malgorzata Targonska-Karasek: Conceptualization, Methodology, Investigation, Writing – original draft; **Maja Boczkowska:** Conceptualization, Methodology, Investigation, Data curation, Writing – original draft; **Wieslaw Podyma:** Conceptualization, Methodology, Investigation; **Malgorzata Pasnik:** Investigation; **Maciej Niedzielski:** Conceptualization, Methodology, Investigation; **Anna Rucinska:** Conceptualization; **Zuzanna Nowak-Zyczynska:** Investigation; **Monika Rakoczy-Trojanowska:** Conceptualization, Supervision.

Supplementary Materials

Supplementary material associated with this article can be found in the online version at doi:10.1016/j.dib.2022.107910.

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