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Original Study Article

Genetic diversity of naked barley accessions from the VIR collection for resistance to powdery mildew in the North-West Region of the Russian Federation

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ABSTRACT

BACKGROUND: Barley is an important grain crop characterized by adaptability to various growing conditions. In recent years close attention has been paid to groups of naked barley which compared to covered barley is more susceptible to the influence of pathogens, that decreases the yield and quality of grain. Powdery mildew is the most harmful diseases of barley (caused by the biotrophic fungus *Blumeria graminis* (DC.) Golovin ex Speer f. sp. *hordei* Marchal). The search for new promising sources of resistance to powdery mildew is necessary for barley breeding.

AIM: The aim is studying the powdery mildew resistance of naked spring barley accessions from the world collection of VIR and identifying promising sources for economically valuable traits.

MATERIALS AND METHODS: In field and laboratory conditions 271 of naked barley accessions of different ecological and geographical origin were studied for powdery mildew resistance and other economically valuable traits (lodging resistance, duration of the vegetative period, yield). The pathogen inoculum for laboratory work was represented by the north-western population of the pathogen. The resistance of barley samples was assessed in the field using the VIR point scale, in the laboratory using the E.B. Mains, S.M. Dietz point scale. The highly effective to powdery mildew resistance allele *mlo11* was identified using PCR.

RESULTS: The diversity of barley of different origins in resistance to powdery mildew is shown. 16 samples mainly from Europe, local forms from Ethiopia, Japan and India, were found to be resistant in field condition. According to the results of the assessment at the juvenile stage, 1 highly resistant sample k-31058 and 5 moderately resistant (k-20923, k-25801, k-27165, k-29911, k-30231) were identified. The naked forms k-20923 from Germany and k-29911 from Poland were resistant at all stages of plant development. The *mlo11* allele was detected in the Arabische variety (k-20923) and heterogeneous pathogen resistance accessions k-20921, k-25793, k-27080, k-29440, k-29820.

CONCLUSIONS: As a result of the work the sources of resistance to powdery mildew with a complex of economically valuable traits were identified, which can be involve in the breeding.

Keywords: naked barley; resistance to powdery mildew; *mlo11* allele; economically valuable traits.

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Оригинальное исследование

Разнообразие голозерных образцов ячменя из коллекции ВИР по устойчивости к мучнистой росе в условиях Северо-Западного региона Российской Федерации

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АННОТАЦИЯ

Актуальность. Ячмень — важная зерновая культура, отличающаяся высокой адаптивностью к различным условиям выращивания. В последние годы пристальное внимание уделяется голозерному ячменю, который по сравнению с пленчатым требует меньших затрат на механизированную переработку и обладает рядом биохимических преимуществ. В то же время он сильнее подвержен влиянию патогенов, что приводит к снижению урожайности и качества зерна. К наиболее вредоносным болезням ячменя относится мучнистая роса, возбудитель — *Blumeria graminis* (DC.) Golovin ex Speer f. sp. *hordei* Marchal. Поиск новых перспективных источников устойчивости к мучнистой росе необходим для селекции ячменя.

Цель — изучение устойчивости к мучнистой росе голозерных образцов ярового ячменя из мировой коллекции ВИР и выявление перспективных источников по хозяйственно ценным признакам.

Материалы и методы. В полевых и лабораторных условиях исследовали 271 образец голозерного ячменя по устойчивости к мучнистой росе, полеганию, продолжительности вегетационного периода и урожайности. Изучение образцов ячменя в поле проводили с использованием «Методических указаний по изучению и сохранению мировой коллекции ячменя и овса». Инокулюм для лабораторной работы был представлен северо-западной популяцией *B. graminis*. Тип реакции на заражение в лаборатории оценивали с помощью шкалы E.B. Mains, S.M. Dietz, где 0 — иммунный, 4 — высоко восприимчивый. Высокоэффективный аллель *mlo11* идентифицировали с помощью ПЦР.

Результаты. Показано разнообразие ячменя по устойчивости к *B. graminis*. Устойчивыми на естественном фоне оказались 16 образцов, преимущественно из Европы, а также местные формы из Эфиопии, Японии и Индии. По результатам оценки на ювенильной стадии выявлены один высокоустойчивый образец к-31058 и пять умеренно устойчивых к-20923, к-25801, к-27165, к-29911, к-30231. Среди голозерных форм на всех стадиях развития растений устойчивостью отличались к-20923 из Германии и к-29911 из Польши. Аллель *mlo11* был обнаружен у сорта Arabische к-20923 и гетерогенных по устойчивости к патогену образцов к-20921, к-25793, к-27080, к-29440, к-29820.

Выводы. В результате выполненной работы выделены источники устойчивости к мучнистой росе с комплексом хозяйственно ценных признаков, которые могут быть успешно использованы для создания новых сортов голозерного ячменя.

Ключевые слова: голозерный ячмень; устойчивость к мучнистой росе; аллель *mlo11*; хозяйственно ценные признаки.

Как цитировать

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BACKGROUND

Barley (*Hordeum vulgare* L.) is an important forage, food, and brewing crop that is well adapted to various growing conditions. Owing to its wide distribution and long history of cultivation, barley exhibits a high intraspecific diversity [1]. Currently, close attention is on groups of naked barley, which has various forms with more biochemical advantages than hulled ones and require lower costs for mechanized processing. However, naked barley is characterized by low resistance to several diseases, which decreases the grain quality [2]. Naked barley varieties are found in all cultivation zones, mainly in southeast, central, south Asia, and northeast Africa [1]. In Russia, naked barley crops are insignificant; the state register contains only eight varieties created by using local material [3].

There are many pathogens that can have a negative impact on barley plants and reduce their yield. Naked barley groups are characterized by a few number of resistance sources to harmful microorganisms. Powdery mildew [caused by the obligate pathogen *Blumeria graminis* (DC.) Golovin ex Speer f. sp. *hordei* Marchal] is one of the most harmful barley diseases, which occurs in all regions where it is cultivated [4]. Powdery mildew affects all green parts of the plant, causing premature aging of tissues, which decreases the yield by an average of 5%–10%, and in epiphytotics years yield losses can reach 50% [5, 6].

More than 100 alleles controlling resistance to *B. graminis* have been identified in barley, many of which are represented by *Mla, Mlo*, and *Ml* genes [4, 7–9]. Most alleles have lost their effectiveness against the causative agent of the disease due to changes in the structure of the fungal population and the emergence of new races. In northwestern Russia, the alleles *mlo1*, *mlo3–mlo5*, *mlo8–mlo11*, *Mla16*, *Mla18*, *Mla19*, and *Mlai* are currently effective [10]. The long-term and effective barley resistance to many powdery mildew populations is provided by *mlo11* and *mlo9* [11]. Currently, these alleles are most often used in European countries when creating spring barley varieties [12]. The mechanism of *mlo* genes action involves preventing the fungus from penetrating the host's epidermal cells and, thus, preventing the formation and infection of haustoria [13].

Powdery mildew in barley is one of the most studied systems of interaction between the host and the pathogen. Geneticists, phytopathologists, and breeders working with barley are constantly looking for new sources of genetic material from which the genes for resistance to *B. graminis* can be transferred to new varieties. Breeding for immunity is the most profitable and environmentally friendly way to combat powdery mildew and other diseases. The world collection at the N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR) is a rich source of initial material for hybridization. Correctly selected and well-studied plant materials ensure success in creating resistant varieties. Local forms and ancient varieties of naked barley are the most promising sources of new material during creation productive varieties of the crop.

This study aimed to analyze the resistance of naked spring barley accessions from the world collection of VIR to powdery mildew and to identify promising sources of economically valuable traits.

MATERIALS AND METHODS

The resistance of barley accessions set was examined in the fields at the Pushkin and Pavlovsk Laboratories of N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR) from 2021 to 2023. A total of 271 samples of naked barley of various ecological and geographical origins were analyzed. The set includes local forms, ancient and modern varieties, and breeding lines. 30 modern hulled barley varieties were selected for a comparative study. The meteo conditions during these three years of study were varied. The weather conditions in 2021 were characterized by severe drought, and the shortened vegetation period of barley enabled “avoidance” of the disease (Table 1). The weather conditions in 2022 and 2023 differed slightly from the average long-term annual data and were more favorable for plant growth and development.

Observations and evaluation of accessions for economically valuable traits (resistance to powdery mildew, resistance to lodging, duration of the growing season, and yield) were performed using the “Methodological guidelines for the study and preservation of the world collection of barley and oats” [14]. Resistance of barley accessions to powdery mildew was assessed against a natural background during the heading period and in the milky ripeness phase (Fig. 1). A 9-point VIR scale was used, in which 1 indicates very low resistance (pads abundantly cover all leaves and internodes, including the upper ones, the infection can also affect the ear); 3 means low resistance (pads develop en masse mainly on the lower leaves and internodes, with individual scattered spots on the upper tier of leaves); and 5 means average resistance (moderate number of pads on leaves and internodes of the lower tier); 7 indicates high resistance (single small pads on leaves and internodes of the lower tier, pads can be more numerous, but small, in the form of a mild coating), and 9 indicates very high resistance (no damage). In this study, resistance to powdery mildew was assessed by the maximum damage to plants by the pathogen over a three-year study period.

Samples characterized by high or medium resistance in the field at the milky ripeness stage were identified at

Table 1. Meteo conditions during the vegetative season for 2021–2023 (St. Petersburg, Pushkin)
Таблица 1. Погодные условия в период вегетации за 2021–2023 гг. (Санкт-Петербург, Пушкин)

Year of study	Month			
	May	June	July	August
Average air temperature, °C				
2021	12.1	21.4	23.1	16.9
2022	10.0	17.6	19.9	20.6
2023	11.9	17.3	18.5	19.9
Average long-term temperature, °C	11.5	16.1	19.1	17.4
Precipitation amount, mm				
2021	139.4	22.1	50.3	135.1
2022	25.6	47	75.5	112.6
2023	16.7	47.9	95.0	48.5
Average long-term precipitation amount (mm)	47.0	69.0	84.0	87.0

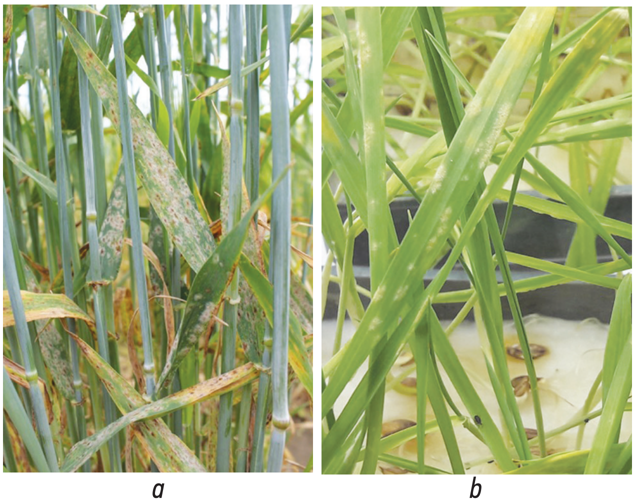
a *b*

Fig. 1. Powdery mildew symptoms on naked barley in the field at the milky stage of grain ripeness (*a*) and at the seedling stage in the laboratory (*b*)
Рис. 1. Симптомы мучнистой росы на голозерном ячмене в полевых условиях в фазе молочной спелости зерна (*a*) и в фазе проростков в лаборатории (*b*)

the seedling stage during inoculation in the laboratory (Fig. 1). A total of 15 grains of each sample were sown in plastic cuvettes on cotton wool moistened with water and placed in a Barnstead 845-2 climate chamber with a 16-h photoperiod and a temperature of 16 °C. After 7 days, the seedlings were infected with powdery mildew by shaking off fungal conidia onto the them. The northwestern population of the pathogen, which was maintained on the susceptible Belogorsky variety, was used as the inoculum. The plants were sprayed daily with streaming water from a water diffuser to create high humidity. The variety Solist, which is characterized by the presence of the recessive allele *mlo11*, was used as a resistance control [15]. The type of response to infection under laboratory conditions was assessed using the scale of Mains and Dietz (1930), where 0 indicated the immune type (no visible mycelium); 1 indicated the highly resistant type (weak mycelium development); 2 indicated the moderately resistant type (moderate mycelium development); 3 indicated the moderately susceptible type (moderate mycelium development and moderate sporulation), and 4 indicated the highly susceptible type (abundant mycelium development, abundant sporulation) [16].

The gene *mlo11*, which provides long-term resistance to the pathogen, was detected in the resistant genotypes and heterogeneous samples with various levels of resistance of individual plants to the northwestern powdery mildew population, which were isolated under laboratory conditions. Total DNA was isolated from 3 to 5 seedlings of each sample using the SDS method [17]. The concentration of the isolated DNA was measured using an Implen N60 nanophotometer (Germany). To detect the allele *mlo11*, ADUP7-Mlo6 and Mlo6-Mlo10 markers were used [18], and their characteristics are presented in Table 2. PCR was performed in a 25 µl reaction mixture containing 50 ng of template DNA, ×1 reaction buffer (Dialat, Russia), 2 mM $MgCl_2$, 0.2 mM of each dNTP's, 0.25 µM of forward and reverse primers (Eurogen, Russia), and 1 unit of Taq polymerase (Dialat, Russia). Amplification was performed on a MiniAmp Plus device (Thermo FS, USA). PCR products were separated by electrophoresis on a 1.5% agarose gel at 5 V/cm for 1.5 h. DNA was stained with ethidium bromide and visualized under UV light. The Fast Ruler Middle Range DNA Ladder DNA marker (Fermentas) was used to estimate fragment sizes.

Table 2. Primers for *mlo11* allele identification in barley

Таблица 2. Праймеры для идентификации аллеля *mlo11* у ячменя, использованные в исследовании

Primer name	Nucleotide sequence 5'→3'	Program	Fragment — target allele
ADUP7	CTCAAGCTTGCCACCATGTCGGACAAAAAAGGG	94 °C — 3 min 30 s; 37 cycles (94 °C — 45 s, 47 °C — 45 s, 72 °C — 1 min); 72 °C — 7 min	1200 bp — *mlo11*
Mlo6	CATCTACTACTAGCATGTACC		
Mlo10	GTCCTGCCACCTAAGTAGCAG	94 °C — 3 min 30 s; 37 cycles (94 °C — 45 s, 54 °C — 45 s, 72 °C — 1 min); 72 °C — 7 min	440 bp — *mlo11* 380 bp — *Mlo11*
Mlo6	CATCTACTACTAGCATGTACC		

RESULTS

The most pronounced development of *B. graminis* on barley was recorded in the milky ripeness phase of grain in 2022 and 2023. Evaluation of the 271 naked accessions showed a wide diversity of barley in terms of resistance to powdery mildew at the adult stage of the plant. Sixteen accessions, mainly from Europe, as well as local forms from Ethiopia, Japan and India, were resistant at natural condition. A total of 55 samples showed moderate resistance to the pathogen; their damage was characterized by the development of fungal mycelium on the lower, more shaded tiers of plants. All other samples of naked barley, including the naked Russian economically important varieties, were highly susceptible to the disease. Among the hulled barley, three samples were resistant, 11 samples were moderately resistant, and the rest were susceptible.

Resistant and moderately resistant naked (71 samples) and hulled (14) samples isolated in the field were studied under laboratory conditions with artificial infection of plants with the northwestern strain of the fungus *B. graminis*. Results of the assessment at the juvenile stage showed that four were highly resistant (0, 1 points) samples, comprising naked k-31058 (USA) and hulled varieties of modern selection, namely, k-31380, k-31488, and k-31494 (Germany). Moderate resistance (2 points) was exhibited by five accessions of the naked barley, namely, k-20923, k-25801 (Germany), k-27165 (Bolivia), k-29911 (Poland), k-30231 (USA), and one hulled barley genotype k-27295 (Germany). Some samples showed resistance to powdery mildew in the field under natural conditions but were strong affected by the fungus under artificial infection. Only two naked barley accessions k-20923 and k-29911 were highly resistant during the heading period and moderately resistant at the juvenile stage of plant development. Differences in the degree of damage among genotypes at various stages of plant development can be attributed to a genetic system that is effective only at the stage of adult plants (APR, adult plant resistance). Fourteen forms of the naked barley were heterogeneous (Table 3).

Using molecular screening of resistant and heterogeneous samples under laboratory conditions, the recessive allele *mlo11* was detected in five hulled varieties from Germany, including the control variety Solist. Among the naked barley samples, six samples with *mlo11* were identified, originating mainly from Ethiopia or obtained using samples from this center of crop diversity (Table 2, Fig. 2). All samples carrying the allele *mlo11*, as well as heterogeneous forms, exhibited high and medium resistance under an artificial infectious background. The rest of the samples resistant to powdery mildew carried other effective alleles or genes. Resistance to *B. graminis* of modern hulled varieties of the European

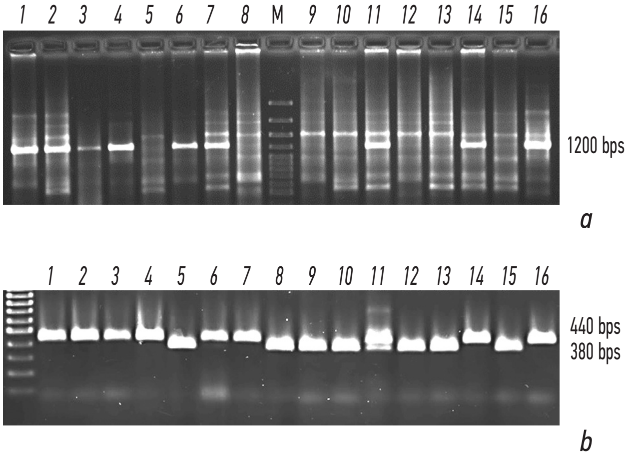

Fig. 2. Identification of the allelic composition of the mlo11 allele using the markers ADUP7 and Mlo6 (*a*) and Mlo6 and Mlo10 (*b*). The barley accessions are marked: *1* — k-31494; *2* — k-20923; *3* — k-31332 control; *4* — k-31488; *5* — k-31540; *6* — k-31380; *7* — k-20921; *8* — k-29440; *9* — k-25873; *10* — k-29719; *11* — k-25793; *12* — k-25872; *13* — k-19483; *14* — k-29820; *15* — k-31367; *16* — k-29820. M is a molecular weight marker of 3000 (*a*) and 1000 (*b*) b.p.

Рис. 2. Идентификация аллельного состава аллеля *mlo11* с использованием маркеров ADUP7 и Mlo6 (*a*), Mlo6 и Mlo10 (*b*). Цифрами обозначены образцы ячменя: *1* — к-31494; *2* — к-20923; *3* — к-31332 контроль; *4* — к-31488; *5* — к-31540; *6* — к-31380; *7* — к-20921; *8* — к-29440; *9* — к-25873; *10* — к-29719; *11* — к-25793; *12* — к-25872; *13* — к-19483; *14* — к-29820; *15* — к-31367; *16* — к-29820. *M* — маркер молекулярного веса 3000 (*a*) и 1000 (*b*) п. о.

Table 3. Resistant to powdery mildew barley accessions at different stages of plant development

Таблица 3. Образцы ячменя, устойчивые к мучнистой росе на разных стадиях развития растений

Number by VIR catalog	Sample	Origin	Variety	Resistance to powdery mildew, points		Presence of the allele *mlo11*
				field conditions (natural background), milky ripeness phase of the grain	Laboratory conditions, artificial infection (seedling phase)	
			Naked barley			
19483	Nudo Bianco	Italy	*coeleste*	3	1, 3*	–
20921	Abyssinian 1102=L94	Ethiopia	*nigrinudum*	5	2, 3	+
20923	Arabische	Germany	*duplinigrum*	7	2	+
23380	Mestnyi	Bolivia	*trifurcatum*	3	2, 3	–
25793	L94	Ethiopia	*nigrinudum*	7	1, 4	+
25801	Lascнкеs Korona	Germany	*coeleste*	3	2	–
25872	EB1626	India	*nigrinudum*	7	1, 3	–
25873	EB145	India	*nigrinudum*	7	1, 3	–
27080	Belorusskiy 76	Belarus	*nudum*	5	1, 3	+
27156	San Benito-80	Bolivia	*coeleste*	3	1, 2	–
27165	Staromestnyi	Bolivia	*trifurcatum*	3	2	–
27176	CM67-V-Sask 1800C	Bolivia	*himalayense*	3	2, 3	-
28684	EP 79=L 92	Germany	*duplialbum*	7	1, 3	+
29440	N16	Belarus	*neogenes*	5	1, 3	–
29719	Ethionia EP 76	Ethiopia	*neogenes*	3	1, 3	–
29820	Abyssinian 1105	Belgium	*nigrinudum*	5	1, 3	+
29911	Nagiz Podhala 33	Poland	*coeleste*	7	2	–
30231	OUM5 lzd,=uz	USA	*coeleste*	5	2	–
31058	Thual	USA	*coeleste*	5	1	–
31367	Kornelja	Latvia	*nudum*	3	2, 4	–
31540	Lotos	Germany	*nudum*	7	1, 3	–
			Hulled barley			
27295	90391/71	Germany	*nigricans*	5	2	+
31380	KWS Harris	Germany	*nutans*	7	1	+
31488	Su Zaza	Germany	*nutans*	5	1	+
31494	Salome	Germany	*nutans*	7	0	+
Solist (k-31332, resistant control)		Germany	*nutans*	7	0	+
Belogorskiy (k-22089, susceptible control)		Russia	*pallidum*	1	4	–

*Heterogeneous accession (splitting by resistance within the accession).

*Гетерогенный образец (расщепление по устойчивости внутри образца).

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selection is mainly due to the presence of the allele *mlo11*. This is one of the advantages of these varieties over varieties of the Russian selection, which are heavily affected under field conditions. Results of laboratory and field studies, showed that some plants resistant to the fungus were among the heterogeneous forms.

For the using in breeding resistance material have to include several economically valuable traits. All samples were studied for three years in the field to identify economically valuable traits (Table 4). The length of the growing season is an important biological trait of barley, mainly determining its productivity. In terms of maturity time, most of the samples were early- and middle- maturity. The most suitable for northwest region of Russia are the early-maturity accessions, as a short growing period helps to avoid the intense development of diseases and unfavorable weather conditions during the harvesting period. Among the forms resistant to powdery mildew, the early-ripening samples k-20923, k-25793, and k-28684 were outstanding as the length of their growing period remained virtually unchanged during the three-year study.

Table 4. Characteristics of resistance to powdery mildew sources based on economically valuable traits

Таблица 4. Характеристика источников устойчивости к мучнистой росе по хозяйственно ценным признакам

Number by VIR catalog	Sample	Origin	Variety	Resistance to lodging, points	Duration of vegetation period, days	Yield, g/m^2
			Naked barley			
19483	Nudo Bianco	Italy	*coeleste*	3	71.3 ± 3.4	187 (63–252)*
20921	Abyssinian 1102=L94	Ethiopia	*nigrinudum*	3	67.7 ± 3.8	147 (59–226)
20923	Arabische	Germany	*duplinigrum*	7	64.0 ± 0.6	257 (219–292)
23380	Mestnyi	Bolivia	*trifurcatum*	3	75.0 ± 3.1	193 (54–294)
25793	L94	Ethiopia	*nigrinudum*	3	63.7 ± 1.2	224 (117–372)
25801	Lascнкes Korona	Germany	*coeleste*	3	68.3 ± 1.2	287 (75–411)
25872	EB1626	India	*nigrinudum*	3	77.7 ± 1.8	237 (113–372)
25873	EB145	India	*nigrinudum*	5	79.3 ± 2.2	177 (57–344)
27080	Belorusskiy 76	Belarus	*nudum*	5	78.2 ± 0.7	184 (42–264)
27156	San Benito-80	Bolivia	*coeleste*	5	69.7 ± 3.2	126 (64–208)
27165	Staromestnyi	Bolivia	*trifurcatum*	5	71.0 ± 1.5	163 (86–219)
27176	CM67-V-Sask 1800C	Bolivia	*himalayense*	5	67.3 ± 1.2	179 (152–223)
28684	EP 79=L 92	Germany	*duplialbum*	5	62.7 ± 1.5	270 (220–334)
29440	N16	Belarus	*neogenes*	5	77.7 ± 4.9	196 (121–283)
29719	Ethionia EP 76	Ethiopia	*neogenes*	5	69.0 ± 3.6	113 (89–134)
29820	Abyssinian 1105	Belgium	*nigrinudum*	5	76.0 ± 3.5	187 (84–246)
29911	Nagiz Podhala 33	Poland	*coeleste*	3	69.3 ± 5.0	257 (235–272)
30231	OUM5 lzd,=uz	USA	*coeleste*	3	69.0 ± 3.2	262 (25–441)
31058	Thual	USA	*coeleste*	3	67.3 ± 2.7	318 (245–434)
31540	Lotos	Germany	*nudum*	9	72.0 ± 1.0	251 (165–337)
31367	Kornelja	Latvia	*nudum*	5	67.3 ± 1.7	133 (106–155)
			Hulled barley			
St. 31332	Solist	Germany	*nutans*	7	76.7 ± 2.7	323 (196–432)
27295	90391/71	Germany	*nigricans*	5	79.3 ± 2.7	256 (64–422)
31380	KWS Harris	Germany	*nutans*	5	74.3 ± 4.3	468 (350–565)
31488	Su Zaza	Germany	*nutans*	7	70.7 ± 2.7	312 (253–359)
31494	Salome	Germany	*nutans*	7	76.3 ± 1.9	273 (210–321)

*The range of variability by year is given in parentheses.

*В скобках приведен размах изменчивости по годам.

The drought-afflicted weather of 2021 was unfavorable for assessing lodging resistance, as there were no factors causing it (heavy rains and strong winds). Heavy rains during the vegetation period of 2022 and 2023 caused severe lodging of most of the crops, which enabled identifying forms resistant to this trait. Thus, the modern hulled varieties k-31488, and k-31494 from Germany, as well as the two naked samples k-20923 and k-31540, were lodging resistant. Variety k-27080 (Belorusskiy 76) from Belarus, which is resistant to powdery mildew and characterized by the presence of the allele *mlo11*, is also a carrier of the *sdw1.d* semi-dwarf allele of the *sdw1* gene and is characterized as moderately lodging resistant [19].

Grain productivity is the most important property of a variety, and the goal of all agricultural production is to maximize it. The most productive accessions were the six-row naked samples mainly from the USA and Europe. The yield of some *B. graminis*-resistant samples (k-31540, k-31058, and k-28684) was similar to those of hulled samples, indicating their potential to become sources of productivity in the northwest region. Accessions k-20923, k-28684, and k-29911 are characterized as drought-resistant because in the dry and atypical 2021, they produced yields similar to those in 2022 and 2023.

Although a comparative assessment of naked barley and hulled barley showed low diversity in terms of resistance to *B. graminis*. Unique identifited samples can serve as a source material for creating highly resistant varieties. Under the conditions of the northwestern region of Russia, samples of naked barley resistant to powdery mildew and with other valuable characteristics were identified and can be recommended for further use in breeding. This comprehensive study of the naked barley accessions from the VIR collection is important conduct for the first time.

DISCUSSION

According to Dreiseitl [12], the allele *mlo11* is widely used in European breeding and is present in most varieties registered in the Czech Republic from 2011 to 2015. Outside Europe, the allele *mlo11* is rare in modern barley varieties [20]. These findings of previous studies are consistent with our results, as most modern international hulled varieties resistant to powdery mildew, imported from Europe and stored in the VIR collection, have the allele *mlo11*. This allele has been used since the mid-1970s as a reliable and effective source of resistance to *B. graminis*. However, many breeders are concerned about the excessive dependence of barley breeding on only one resistance gene, which exerts strong selection pressure on the pathogen and promotes the emergence of new virulence. Various levels of resistance to powdery mildew in samples carrying the resistance allele *mlo11* in northwestern region of Russia has been reported in an earlier study [15] and is confirmed in this study. The degree of damage to the accessions might depend on their genetics; for example, the influence of the genes *Ror1* and *Ror2* confers complete plant resistance to *B. graminis* [4, 21, 22].

Although *mlo*-based resistance is usually very stable in the field, several studies have reported the influence of weather conditions on *mlo*-protected plants. Severe drought followed by sudden irrigation resulted in moderate susceptibility of such barley varieties [13, 23, 24]. In this study, this phenomenon was not observed for some moderately resistant forms, as the difference in the degree of damage was noted not only in the field but also in the climate chamber.

Barley from the Abyssinian (Ethiopian) Diversity Center is interesting and importance in botanical-geographical and agronomic terms and is also a source of many valuable traits. Orlov [25] indicated that barley from Abyssinia and Eritrea is characterized by many valuable features. In particular, they are resistant to powdery mildew under field conditions and are relatively resistant to other fungal diseases, namely, various types of rust, leaf spots, and smut [25]. Additionally, from local Ethiopian samples the powdery mildew-resistant hulled barley varieties, Atem in 1979, Salome in 1981, and Apex in 1982, were developed [20, 26]. These varieties are included in many pedigrees of modern hulled varieties with *mlo11*. In the set we studied, only one naked barley variety, Belorusskiy 76, carries the allele *mlo11*, the rest accessions are local forms or selection lines. The pedigree of all samples with *mlo11* includes genetic material from Ethiopia barley.

CONCLUSION

A study of 271 samples of naked and 30 samples of hulled barley under conditions of the North-West region of Russia showed diversity in the level of resistance to powdery mildew. Based on the results of a comprehensive study in the field at natural condition and in the laboratory at artificial infectious condition, resistant and moderately resistant samples were identified. They can be recommended as sources of resistance to powdery mildew. Among the naked forms, resistance at all stages of plant development, was recorded in k-20923 from Germany and k-29911 from Poland. More than 97% of the naked barley accessions were sensitive to powdery mildew. Among the hulled varieties, samples k-31380 and k-31494 from Germany exhibited high resistance during the earing period and at the juvenile stage of plant development. All resistant hulled samples belong to modern varieties of the European selection. Additionally, among the 14 heterogeneous forms, plants resistant to powdery mildew were selected.

Using molecular screening, the *mlo11* allele was identified in all inoculation-resistant hulled barley varieties. Among naked barley, this allele is carried by 5 heterogeneous accessions (k-20921, k-25793, k-27080, k-29440, k-29820) and one moderately resistant (k-20923) accession.

The data obtained from the study of collection accessions represent an important step for the practical use of barley genetic resources in breeding programs. Described in this study the sources of spring barley resistance to powdery mildew can be successfully used to create new varieties.

ADDITIONAL INFO

Authors' contribution. All authors made a substantial contribution to the conception of the study, acquisition, analysis, interpretation of data for the work, drafting and revising the article, final approval of the version to be published and agree to be accountable for all aspects of the study. Personal contribution of each author: K.A. Lukina — collecting and preparation of samples, field and laboratory research, data analysis, writing the main part of the text; R.A. Abdullaev — experimental design, collecting and preparation of samples, laboratory research, data analysis, writing the main part of the text; N.V. Alpatieva — collecting and preparation of samples, laboratory research, data analysis; I.G. Loskutov — experimental design, data analysis, funding acquisition, funding acquisition, making final edits; O.N. Kovaleva — experimental design, collecting and preparation of samples, data analysis, literature review, making final edits.

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