



Effectiveness of new sources of resistance against oat powdery mildew identified in *A. sterilis*

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Abstract

The assessment of the effectiveness of resistance sources to fungal diseases is a very important issue allowing to determine the possibilities of effective use of new resistance genes in breeding programs. In the present work, the effectiveness of new resistance sources to oat powdery mildew identified in wild *A. sterilis* species was determined. The level of effectiveness was assessed based on host–pathogen tests. A set of 50 *Blumeria graminis* f. sp. *avenae* isolates was selected for these tests, which allowed to analyze the effectiveness in different geographical conditions. The isolates were collected in 2010–2017, which allowed to observe changes in the effectiveness of new resistance sources in recent years. Furthermore, based on the results, we postulated the presence of new resistance genes in *A. sterilis* genotypes identified as resistant. Two of the seven tested genotypes were characterized by a high level of resistance against the used isolates. Moreover, the patterns of infection indicated that the resistance identified in these genotypes was conditioned by a new powdery mildew resistance.

Keywords *Blumeria graminis* f. sp. *avenae* · Fungal disease · Oat · Resistance genes

Introduction

Powdery mildew caused by an obligate biotroph, *Blumeria graminis* f. sp. *avenae*, is a common disease of oat in temperate regions of Europe and North America, north-western Himalayan region and China (Aung et al. 1977; Schwarzbach and Smith 1988; Banyal et al. 2016; Okoń and Ociepa 2017; Xue et al. 2017). Crop losses caused by powdery mildew are significant, with estimates up to 39% (Lawes and Hayes 1965; Jones 1977; Clifford 1995).

There are a few main ways of controlling the disease in oat. First, the occurrence of powdery mildew can be reduced by the application of fungicides (Martinelli 2004). However, excessive use of fungicides may lead to rapid adaptation of pathogens and insensitivity to the chemicals applied. Furthermore, this method is ecologically undesirable. Nowadays, plant protection methods must be compliant with the assumptions of sustainable agriculture that

promote economically profitable, environmentally friendly and accepted in community methods of plant protection. In practice, this means using alternative methods of chemical protection. In accordance with the principles of integrated plant protection, the occurrence of powdery mildew can be reduced by proper agricultural science, crop rotation or sowing of intercultural or interspecific mixtures (Strzembicka et al. 1998; Gacek 2000; Tratwal and Rosiak 2010). The use of genetically mildew resistant cultivars is the most effective and environmentally safety method to reduce the occurrence of powdery mildew.

The possibility of using resistance genes in breeding programs depends on their effectiveness against the existing pathogen races. To date, 8 powdery mildew resistant genes have been described in oat, but only 4 of them provide the resistance to the current *B. graminis* f. sp. *avenae* pathotypes (Okoń 2015; Okoń and Ociepa 2017). Okoń and Ociepa (2017) have demonstrated that *B. graminis* f. sp. *avenae* population occurring in Poland is constantly changing and new virulent pathotypes can appear. Moreover, the continuous use of the same set of resistant genes often results in the selection of pathotypes

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with the matching virulence genes, resulting in resistance breakdown (Czembor and Czembor 2001).

Therefore, it is necessary to search for new sources of resistance and introduce them to breeding programs. From the breeding point of view, new sources of resistance should be characterized by a high level of effectiveness to pathogen pathotypes occurring in a given area and over a long period of time.

Hence, the aim of present study was the assessment of the effectiveness of new potential sources of resistance to powdery mildew identified previously in *A. sterilis* genotypes (Okoń et al. 2016).

Materials and methods

A set of 50 single spore isolates of powdery mildew were used to check effectiveness of 7 different sources of resistance against oat powdery mildew identified in *A. sterilis* accessions. As a control, set of cultivars and lines with known resistance genes were used: Jumbo—Pm1, Mostyn—Pm3, AV1860—Pm4, Am25—Pm5, Bruno—Pm6, APR122—Pm7 and Fuchs susceptible to powdery mildew. Control plant materials were kindly supplied by Sai L. K. Hsam from the Technical University of Munich, Germany. Populations of *Blumeria graminis* f. sp. *avenae* were collected from different regions of Poland in the years 2010–2017 (Fig. 1). Single spore isolates were obtained in laboratory condition from *Blumeria graminis* f. sp. *avenae* samples.

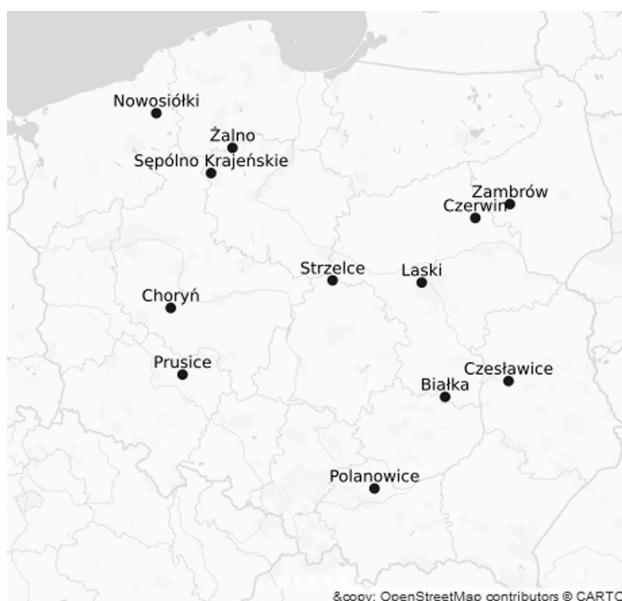


Fig. 1 The geographical distribution of *Blumeria graminis* f.sp. *avenae* isolates used in the host–pathogen tests

Host–pathogen tests were carried out according to the method described by Okoń and Kowalczyk (2012). Fragments of leaves were put on agar medium in Petri dishes supplemented with benzimidazole (6 g agar per 1L of water and 35 mg/L of benzimidazole) and inoculated with powdery mildew isolates. Disease on the leaves was rated 10 days after inoculation. Reactions to the isolates were grouped into three classes: *R* (resistant)—from 0 to 20% leaf area affected relative to Fuchs, *I* (intermediate) from 20 to 50% affected and *S* (susceptible)—greater than 50% affected.

Results

Host–pathogen tests were based on isolates collected in the years 2010–2017 in order to evaluate changes in the effectiveness in recent years. Fifty isolates, selected for the effectiveness analysis, were characterized by a diversified infection pattern of control lines and cultivars (Table 1). Comparison of infection patterns of *A. sterilis* genotypes and control lines allowed to exclude the presence of known and described resistant genes in the tested accessions.

Seven *A. sterilis* genotypes identified in our previous study (Okoń et al. 2016) as promising sources of resistance to oat powdery mildew were tested to determine their effectiveness. The analyzed genotypes showed varied efficiency levels to 50 *B. graminis* f. sp. *avenae* isolates used in host–pathogen tests.

Genotypes PI287211, CN113554 and CN67349 showed the lowest level of resistance to the isolates used in host–pathogen tests. These genotypes were resistant to 23, 22 and 22 isolates, respectively, while they showed a susceptible response to 10, 15 and 16 isolates, respectively. For the remaining isolates these genotypes showed an intermediate response (Table 1, Fig. 2). An increasing number of isolates overcame the resistance identified in these genotypes in the years 2015–2017.

Genotypes CN22667 and CN22668 were resistant to 40 and 36 of 50 *B. graminis* isolates used in host–pathogen tests. A susceptible response was obtained for 6 and 9 isolates, and an intermediate response for 4 and 5 (Table 1, Fig. 2). These *A. sterilis* genotypes were resistant to all isolates collected in 2010–2013. In 2014–2017, some of *B. graminis* isolates overcame the resistance identified in these genotypes. A changing virulence spectrum in the following years may lower the efficiency of resistances identified in genotypes CN22667 and CN22668.

The highest level of resistance was observed for genotypes CN67383 and CN113536. These genotypes were resistant to 48 and 43 isolates, respectively, while they showed an intermediate response for 2 and 7 isolates, respectively (Table 1, Fig. 2). They exhibited a high level

Table 1 Infection patterns of tested *A. sterilis* genotypes and control lines and cultivars

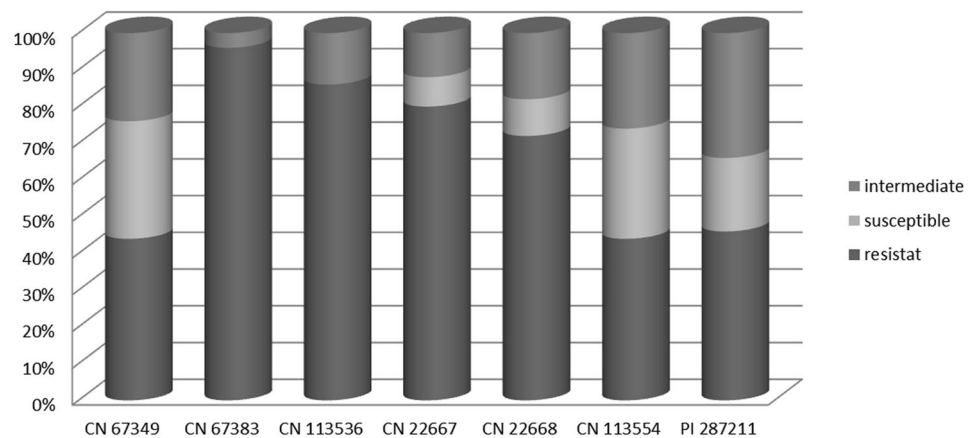
	<i>A. sterilis</i> accession numbers										Control line and cultivars					
	CN 67349	CN 67383	CN 113536	CN 22667	CN 22668	CN 113554	PI 287211	Bruno (Pm6)	Jumbo (Pm1)	Mostyn (Pm3)	Av1860 (Pm4)	APR 122 (Pm7)	Am25 (Pm5)	Fuchs		
Białka 2014	R	R	R	R	R	R	R	S	R	S	R	R	R	S		
Choryń 2010 (2)	R	R	R	I	R	S	I	I	S	S	R	R	R	S		
Choryń 2014 (4)	R	R	R	R	S	R	R	S	S	S	R	R	R	S		
Choryń 2014 (4) PK	S	I	R	R	R	S	I	S	S	S	R	R	R	S		
Choryń 2015 (1)	R	R	R	R	R	R	R	S	S	S	R	R	R	I		
Choryń 2015 (2)	R	R	I	S	R	S	I	S	S	S	R	R	R	S		
Choryń 2016	S	R	R	I	I	S	I	S	S	S	R	R	R	S		
Choryń 2016 3/1	S	R	R	R	R	R	R	S	S	S	R	R	R	S		
Choryń 2017 1/1	R	R	I	S	I	I	S	I	R	R	R	R	R	S		
Choryń 2017 1/2	I	R	R	I	R	I	S	S	S	R	S	I	I	S		
Choryń 2017 4/1	R	R	R	S	I	I	S	S	S	R	I	R	R	S		
Choryń 2017 4/2	I	R	R	R	R	R	R	S	S	R	S	S	S	S		
Czerwin 2015	R	R	R	S	R	S	S	S	R	S	R	R	R	S		
Czesławice 2013 (4)	I	R	R	R	R	R	R	S	S	S	R	R	R	S		
Czesławice 2013 (5)	S	R	R	R	R	S	R	I	R	R	R	R	R	S		
Czesławice 2015 (4) PK	I	R	I	I	R	I	I	S	S	S	R	R	R	S		
Czesławice 2016 1/1	I	R	R	R	R	R	I	S	S	S	R	R	R	S		
Czesławice 2016 4/1	R	R	R	R	R	R	S	I	S	I	R	R	R	I		
Czesławice 2017 (4)	S	R	R	R	R	I	R	S	S	R	S	I	I	S		
Czesławice 2017 2/2	R	R	R	R	R	R	S	S	S	R	S	R	R	S		
Czesławice 2017 4/1	S	I	R	R	S	S	S	S	S	R	S	R	R	S		
Czesławice 2017 4/2	S	R	R	R	S	S	I	S	S	R	S	S	S	S		
Laski 2014	S	R	R	R	R	R	R	S	S	S	R	R	R	S		
Nagi Sad PK1	I	R	R	I	I	I	S	S	S	R	S	S	S	S		
Nagi Sad PK2	R	R	I	R	R	I	I	S	S	R	S	R	R	S		
Nowosiółki 2015	R	R	R	R	R	S	I	R	S	I	R	R	R	S		
Polanowice 2013 (3)	R	R	R	R	R	R	I	S	S	S	R	R	R	S		
Polanowice 2013 (4)	I	R	R	R	S	I	R	I	I	I	R	R	R	I		
Polanowice 2014	S	R	R	R	I	I	R	S	S	S	R	R	R	S		
Polanowice 2015 (1)	I	R	R	I	R	R	R	I	I	I	R	R	R	I		
Polanowice 2016 2/1	I	R	R	R	R	R	R	S	S	S	R	R	R	S		
Polanowice 2016 3/2	R	R	R	R	R	R	R	S	S	S	R	R	R	S		
Polanowice 2017 (1)	R	R	R	R	R	R	R	S	S	R	S	I	I	S		
Polanowice 2017 (2)	R	R	I	R	R	S	I	S	R	R	S	R	R	S		

Table 1 (continued)

<i>Blumeria graminis</i> f. sp. <i>avenae</i> isolates	<i>A. sterilis</i> accession numbers										Control line and cultivars							
	CN	CN	CN	CN	CN	CN	CN	CN	CN	CN	PI	Bruno (Pm6)	Jumbo (Pm1)	Mostyn (Pm3)	Av1860 (Pm4)	APR 122 (Pm7)	Am25 (Pm5)	Fuchs
67349	67383	113536	22667	22668	113554	287211												
S	R	R	R	R	R	R	R	R	R	R	R	S	S	R	R	S	I	S
Polanowice 2017 1/1																		
S	R	I	R	I	I	I	R	I	I	S	S	S	R	R	S	I	S	S
Polanowice 2017 2/2																		
S	R	R	R	R	R	I	R	R	R	I	S	S	S	R	R	R	R	S
Prusice 2015																		
S	R	I	R	R	S	I	R	R	R	I	S	S	S	R	R	R	R	S
Sepólno Krajeńskie 2014																		
R	R	R	R	R	I	R	R	R	R	R	S	S	S	R	R	R	R	S
Strzelce 2013 (2)																		
R	R	R	R	R	R	R	R	R	R	R	S	S	S	R	R	R	R	S
Strzelce 2013 (3)																		
R	R	R	R	R	R	R	R	R	R	R	S	S	S	R	R	R	R	S
Strzelce 2013 (6)																		
I	R	R	R	I	R	R	R	I	R	R	S	S	S	R	R	R	R	S
Strzelce 2015 (1)																		
R	R	R	R	I	S	I	R	I	I	I	S	S	S	R	R	R	R	R
Strzelce 2015 (1) PK																		
R	R	R	R	R	I	R	R	R	R	R	S	S	S	R	R	R	R	S
Strzelce 2016 2/2																		
R	R	R	R	R	S	R	R	R	R	R	S	S	S	R	R	R	R	S
Strzelce 2016 3/1																		
I	R	R	R	R	R	I	R	R	R	I	S	S	S	R	R	R	R	S
Strzelce 2017 (2)																		
S	R	R	R	R	S	S	R	R	R	S	S	S	R	R	S	R	R	S
Strzelce 2017 2/2																		
S	R	R	R	I	S	R	R	I	S	R	S	S	R	R	S	I	S	S
Zambrow 2014 (1)																		
S	R	R	R	R	I	R	R	R	I	R	S	S	S	R	R	I	S	S
Żalno 2015																		
R	R	R	R	S	R	R	R	R	R	R	R	S	S	R	R	R	R	S
Żalno 2015 PK																		
I	R	R	R	R	R	I	R	R	R	I	S	S	S	R	R	R	R	S

R resistant, S susceptible, I intermediate response to *Blumeria graminis* f. sp. *avenae* isolates

Fig. 2 The response of *A. sterilis* genotypes to *Blumeria graminis* f. sp. *avenae* isolates used



of resistance to all isolates collected in the years 2010–2017. The effectiveness of these resistance sources has not decreased in recent years; thus, we can speculate that it will persist in the coming years.

Based on the obtained results, we can postulate that the resistance identified in *A. sterilis* genotypes CN67383 and CN113536 is conditioned by not yet characterized resistance genes. These two genotypes can be used as new and effective sources of resistance against powdery mildew in oat.

Discussion

The identification of new sources of resistance to fungal diseases and their introduction into cultivated crops is a very important element of breeding programs. Selection of only the most effective sources of resistance is a significant factor determining the success of the breeding process (Pietrusińska and Czembor 2015). The resistance of crop plants to pathogens should be genetically diverse, durable, stable over time and effective in various environmental conditions. Therefore, the efficacy of sources of resistance depends on the dynamics of changes in the virulence of pathogen populations. Different levels of powdery mildew pathogen virulence, depending on geographical distribution, was observed by Shi et al. (2009), Xu et al. (2014), Liu et al. (2015), Rsaliyev et al. (2017). Okoń (2015) showed that the effectiveness of powdery mildew resistance genes in oat had changed after introducing isolates from different geographical regions. Okoń and Ociepa (2017) also observed that powdery mildew isolates collected in different parts of Poland overcame the resistance conditioned by the studied powdery mildew resistant genes with varying strength. The current work analyzed the effectiveness of new resistance genes against powdery mildew in oats based on a set of 50 powdery mildew isolates with varied level of virulence, collected in the year

2010–2017 in different geographical regions of Poland. The study underlines that it is necessary to perform tests based on a diverse set of pathogen isolates in order to obtain reliable results on the effectiveness of disease resistance. Observations based on isolates sampled in one region or in 1 year may be insufficient to draw reliable conclusions.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interests.

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