Avena sterilis L. Genotypes as a Potential Source of Resistance to Oat Powdery Mildew

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Abstract

Okoń S., Paczos-Grzęda E., Ociepa T., Koroluk A., Sowa S., Kowalczyk K. and Chrzastek M. *Avena sterilis* L. genotypes as a potential source of resistance to oat powdery mildew. Plant Dis. 100:2145-2151.

The aim of the present study was to identify *Avena sterilis* genotypes demonstrating a high level of resistance against oat powdery mildew, using host-pathogen tests. The study was conducted on 350 *A. sterilis* genotypes from different parts of the world. Six single-spore isolates of *Blumeria graminis* (DC.) f. sp. *avenae*, which demonstrated different levels of virulence to control lines and cultivars, were used in host-pathogen screening tests. To confirm the resistant response of selected genotypes, 13 other isolates were used. Reactions to the isolates were grouped into three classes: resistant, intermediate, and susceptible. Susceptible

cultivars Sam and Fuchs were used as controls to estimate the degree of infection. The results of the screening test showed that 10 genotypes were classified as resistant. The second test based on 13 other isolates revealed that only four of the 10 genotypes were a valuable source of resistance against powdery mildew. The identified genotypes may be used in oat breeding programs to increase the level of resistance against powdery mildew. First, however, further studies aimed at identifying whether this resistance is conditioned by a single gene or combinations of different genes are required.

The genus *Avena* contains about 27 different species from diploid to hexaploid plants with different genome compositions, including several important crop or pasture weeds, occurring throughout the world. *Avena sterilis* L., also known as sterile oat, is one of the most important wild relatives of cultivated oat that has a global geographical distribution (Thurston and Phillipson 1976). This species is a major component of herbaceous formations in the oak park and forest vegetation. It is an aggressive weed that massively colonizes road sides, crops, and cultivated field edges (Wahl 1970). Moreover, it can also severely reduce crop yields (Balyan et al. 1991, Dhima et al. 2000).

The development of *A. sterilis* is highly dependent on temperature and rainfall (Fernandez-Quitanilla et al. 1986). The optimal regions for this species are the Mediterranean countries, such as France, northern Spain, northern Greece, Albania, Serbia, and northern Italy. Central and northern Europe are climatically unsuitable for its growth, as a result of excessive cold stress (Castellanos-Frías et al. 2014).

Due to their adaptation to different environmental conditions, wild and weedy oat species, including *A. sterilis*, are characterized by high genetic diversity (Paczos-Grzęda et al. 2007, 2009). Identification of this diversity is very important for the efficient use of wild species in breeding programs. At present, a number of wild *Avena* species with different ploidy levels are used as donors of valuable traits (Loskutov 1998).

Hybridization with *Avena sterilis* L. can be used to increase oat genetic variability (Gupta et al. 1986; Lawrence and Frey 1975). *A. sterilis* genotypes are a valuable source of different agronomically important traits, such as abundant tillering and leaf growth or good adaptation for grazing, which are very important in breeding oat varieties suited for sheep (Brown and Patterson 1992). Sterile oats were also used as a source of genes conditioning the high yield potential of *Avena sativa* cultivars and better adaptation to different environmental conditions (Lawrence and Frey 1975). *A. sterilis* also could serve

as a donor of genes determining high protein and fat content (Thro and Frey 1985). Genes responsible for resistance to nematodes and herbicides have been found in the *A. sterilis* genome (Rivoal and Cook 1993). Effective resistance genes for oat crown rust and powdery mildew have also been found in sterile oat (Herrmann and Roderick 1996; Kiehn et al. 1976; Roderick et al. 2000; Sebesta et al. 1993).

Powdery mildew, caused by fungus *Blumeria graminis* (DC.) f. sp. *avenae* Em. Marchal, is one of the most harmful fungal diseases of oat. This pathogen has been reported as a serious problem in many parts of the world. Oat powdery mildew is common in northwestern Europe, and South America (Aung et al. 1977; Roderick et al. 2000). Crop losses caused by this disease in western Europe range from 5 to 10% every year (Clifford 1995; Hsam et al. 1997). It also occurs in eastern Europe, including Poland, Austria, Czech Republic, Germany, and Greece (Roderick et al. 2000; Sebesta et al. 1991). The most effective method of controlling and limiting the consequences of powdery mildew is the introduction of crop cultivars containing effective resistance genes. To date, eight genes conferring resistance to oat powdery mildew have been characterized, but only three, *Pm1*, *Pm3*, and *Pm6*, were used in breeding programs (Hsam et al. 1997, 1998; Okoń 2012; Sánchez-Martín et al. 2011). Okoń (2015) showed that most of these genes are not effective against the existing powdery mildew populations. The author demonstrated that only two genes, *Pm4* and *Pm7*, are still effective.

Resistance to powdery mildew is decreasing due to the emergence of new pathotypes; therefore, there is a need to search for novel and effective sources of resistance to powdery mildew in oat. Wild oat species seem to be an enormous reservoir of resistance to this pathogen (Hsam et al. 1997, 1998). Because of this fact, the objective of the present study was to identify *Avena sterilis* genotypes with high levels of resistance to oat powdery mildew.

Materials and Methods

The plant materials used in this study were 350 *Avena sterilis* genotypes from different parts of the world (Fig. 1). Oat accessions were provided by the following gene banks: Genebank IPK Gatersleben (Germany), genotype symbol AVE; Plant Gene Resources of Canada (Saskatoon, Canada), genotype symbol CN; National Germplasm Resources Laboratory (Beltsville, MD, U.S.A.), genotype symbol PI; and the National Center for Plant Genetic Resources (IHAR) (Poland), without symbol. Powdery mildew susceptible cultivars (Fuchs

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Accepted for publication 16 May 2016.

and Sam) and lines with known resistance genes (Bruno, *Pm6*; Jumbo, *Pm1*; Mostyn, *Pm3*; AV1860, *Pm4*; and APR122, *Pm7*) were used as controls in host-pathogen tests. Control plant materials were supplied by S. L. K. Hsam from the Technical University of Munich, Germany.

Single-spore *Blumeria graminis* DC. f. sp. *avenae* isolates were obtained according to the method described by Okon and Kowalczyk (2012). Pathogen populations were collected from random fields located in different parts of Poland. Single colonies from each collected leaf were transferred to the susceptible cultivar Fuchs. More than 100

Fig. 1. Distribution of *Avena sterilis* genotypes used in host-pathogen tests to search for new sources of resistance to powdery mildew in oat.

Table 1. Reaction of control cultivars and lines carrying known resistant genes to powdery mildew after inoculation with *Blumeria graminis* f. sp. *avenae* isolates selected for screening tests

Powdery mildew Isolates	Control lines and cultivars ^a						Fuchs
	Bruno <i>Pm6</i>	Jumbo <i>Pm1</i>	Mostyn <i>Pm3</i>	Av1860 <i>Pm4</i>	APR122 <i>Pm7</i>	Sam	
MCh2010/3	S	S	S	R	S	S	S
MCh2011/1	S	S	R	R	R	S	S
MCh2011/4	I	R	I	R	I	S	S
MCz2013/1	S	I	S	R	R	S	S
MSt 2012/1	R	S	I	R	R	S	S
MSt2012/4	S	S	S	R	I	S	S

^a R = resistant, I = intermediate, and S = susceptible.

Table 2. Reaction of control cultivars and lines carrying known resistant genes to powdery mildew after inoculation with *Blumeria graminis* f. sp. *avenae* isolates selected to confirm the results obtained in screening tests

Powdery mildew Isolates	Control lines and cultivars ^a						Fuchs
	Bruno <i>Pm6</i>	Jumbo <i>Pm1</i>	Mostyn <i>Pm3</i>	Av1860 <i>Pm4</i>	APR122 <i>Pm7</i>	Sam	
MBi2014/1	4	0	4	0	1	4	4
MCh2010/2	3	3	3	0	0	4	4
MCh2014/4	4	4	4	0	2	4	4
MCi2014/2	4	4	4	0	2	4	4
MCz2013/4	4	0	4	0	1	4	4
MCz2014	4	4	4	0	0	4	4
MCu2014/2	4	4	4	0	1	4	4
MMk2014	4	4	4	1	1	4	4
MPI2014/1	0	4	4	0	2	4	4
MSk2014	4	4	4	0	0	4	4
MSt2013/2	4	4	4	0	0	4	4
MSt2013/3	4	4	4	0	0	4	4
MZb2014/1	4	3	4	0	2	4	4

^a Scale 0 to 4, where 0 means lack of powdery mildew symptoms and 4 means powdery mildew mycelium takes up over 50% of leaf surface.

single-spore isolates were obtained. Virulence of these isolates was defined on the basis of the host-pathogen tests carried out on a set of control lines and cultivars (data not shown).

For screening tests of *A. sterilis* genotypes, six single-spore isolates with different levels of virulence to the control lines and cultivars were used (Table 1.). In a follow-up test, 13 of the most virulent isolates were used to confirm the resistance of selected resistant genotypes from the first test (Table 2.). Host-pathogen tests were carried out on the first leaves of 10-day-old seedlings, according to the method described by Okoń and Kowalczyk (2012). Two leaf fragments of each of the *A. sterilis* genotypes were placed on 12-well culture plates amended with benzimidazole agar (6 g of agar per 1 liter of water and 35 mg of benzimidazole per liter). Control genotypes were put into the first and last well of each dish. The plates with the leaf fragments were inoculated in an inoculation tower by applying about 500 to 700 spores of powdery mildew per square centimeter. The dishes were then incubated in a phytotron at about 17°C and light intensity of approximately 4 kLx. Inoculated leaves were rated 10 days after inoculation and reactions were grouped into three classes: resistant, in which leaf area with visible pustules ranging from 0 to 20% relative to Fuchs, intermediate, in which leaf area with visible pustules ranging from 20 to 50%, and susceptible, in which the powdery mildew pustules are visible on more than 50% of the leaf area (Hsam et al. 1997). To confirm the reliability of the results, every test was repeated twice.

The selected resistant genotypes from the phytotron assay were tested in experimental plots under natural infection to gather additional information on their reaction to powdery mildew. The experimental plots

were located in the eastern part of Poland. Grains from all *A. sterilis* genotypes and the set of control cultivars and lines were densely sown (approximately 200 grains per square meter) in two-row plots, with a row spacing of 20 cm. The same cultivars and lines used in host-pathogen tests, with defined resistance genes against powdery mildew, were used as controls in field experiments. Plant response to the attack of powdery mildew under natural conditions was rated on a 0 to 4 scale, where 0 means lack of powdery mildew symptoms and 4 means powdery mildew pustules occupy over 50% of the leaf surface. All plots were rated for powdery mildew twice, once when the first symptoms were detected and, again, two weeks later when the disease developed.

Results

Of the 350 genotypes evaluated, 10 were characterized as being total resistant to the powdery mildew isolates used in the first screening tests. A total of 137 genotypes showed a moderate level of resistance against the selected isolates; among them, 52 genotypes were resistant to a single isolate used in host-pathogen tests.

Genotypes originating from African countries showed a low level of resistance to the powdery mildew isolates tested. Only two genotypes from Tunisia, out of the 108 tested from this region, were resistant to powdery mildew isolates (Fig. 2; Table 3).

Four genotypes from Libya were resistant to one or two isolates, the rest of the genotypes from this region were totally susceptible (Fig. 2; Tables 3 and 4).

Almost all genotypes derived from Middle East countries were susceptible to powdery mildew. Only one genotype from Israel

Fig. 2. Reaction of *Avena sterilis* genotypes from different countries to powdery mildew isolates used in host-pathogen tests.

Table 3. *Avena sterilis* genotypes resistant to all powdery mildew isolates used in screening tests

Accession number	Country of origin	Source ^a	Powdery mildew isolates ^b					
			MCh2010/3	MCh2011/1	MCh2011/4	MCz2013/1	MS2012/1	MS2012/4
CN 67383	France	GRIN-CA	R	R	R	R	R	R
52280	Unknown	IHAR	R	R	R	R	R	R
CN 66606	United Kingdom	GRIN-CA	R	R	R	R	R	R
CN 22667	Tunisia	GRIN-CA	R	R	R	R	R	R
CN 22668	Tunisia	GRIN-CA	R	R	R	R	R	R
CN 58106	Sweden	GRIN-CA	R	R	R	R	R	R
CN 113554	Italy	GRIN-CA	R	R	R	R	R	R
PI 287211	Israel	GRIN-NPGS	R	R	R	R	R	R
CN 113536	Italy	GRIN-CA	R	R	R	R	R	R
CN 67349	Greece	GRIN-CA	R	R	R	R	R	R

^a GRIN-CA = Plant Gene Resources of Canada (Saskatoon, Canada), IHAR = National Center for Plant Genetic Resources (Radzików, Poland), GRIN-NPGS = National Germplasm Resources Laboratory (Beltsville, MD, U.S.A.).

^b R = resistant, I = intermediate, and S = susceptible.

Table 4. *Avena sterilis* genotypes resistant for one to three powdery mildew isolates

Accession number	Country of origin	Source ^a	Powdery mildew isolates ^b					
			MCh2010/3	MCh2011/1	MCh2011/4	MCz2013/1	MS12012/1	MS12012/4
AVE 2055	Belgium	IPK	S	S	I	I	S	R
CN 67381	France	GRIN-CA	I	I	I	I	I	R
CN 21790	France	GRIN-CA	R	S	R	I	I	R
CN 21792	France	GRIN-CA	I	I	R	I	R	I
AVE 1510	France	IPK	I	S	I	I	R	R
CN 21872	Gibraltar	GRIN-CA	I	S	I	I	R	S
CN 67451	Gibraltar	GRIN-CA	R	I	I	I	I	I
CN 67350	Greece	GRIN-CA	I	S	R	I	I	I
CN 67345	Greece	GRIN-CA	R	I	I	R	I	I
CN 67343	Greece	GRIN-CA	R	S	R	I	I	I
CN 67351	Greece	GRIN-CA	I	S	I	I	I	R
CN 67344	Greece	GRIN-CA	R	I	I	I	I	I
AVE 245	Greece	IPK	S	S	I	I	S	R
AVE 446	Greece	IPK	S	S	I	I	S	R
AVE5009	Iran	IPK	I	S	I	I	S	R
CN 113537	Italy	GRIN-CA	R	I	R	I	I	I
CN 113539	Italy	GRIN-CA	I	I	R	I	S	I
CN 113549	Italy	GRIN-CA	R	R	R	I	S	I
CN 113550	Italy	GRIN-CA	R	I	I	S	I	I
CN 113552	Italy	GRIN-CA	I	I	R	S	I	I
CN 113553	Italy	GRIN-CA	I	S	R	I	R	I
AVE 531	Italy	IPK	I	S	I	I	I	R
CN 45569	Jordan	GRIN-CA	S	S	I	R	I	I
CN 21811	Libya	GRIN-CA	S	R	S	S	S	S
CN 21821	Libya	GRIN-CA	S	S	R	R	S	S
CN 67409	Libya	GRIN-CA	S	S	S	R	R	S
AVE 2116	Libya	IPK	I	S	R	I	I	I
AVE 534	Morocco	IPK	R	S	I	I	S	R
CN 64606	Portugal	GRIN-CA	I	I	R	I	R	I
CN 26489	Portugal	GRIN-CA	R	S	I	I	S	R
AVE 2561	Portugal	IPK	I	I	I	I	I	R
CN 23006	Spain	GRIN-CA	I	S	R	S	I	I
CN 23007	Spain	GRIN-CA	I	S	R	S	I	S
CN 23008	Spain	GRIN-CA	I	S	R	S	I	I
CN 21873	Spain	GRIN-CA	I	S	R	I	I	S
AVE 1895	Spain	IPK	S	S	R	I	S	R
CN 58107	Sweden	GRIN-CA	R	I	I	I	I	S
CN 20301	Syria	GRIN-CA	S	S	R	I	I	S
AVE 2532	Tajikistan	IPK	S	S	R	I	S	R
AVE 2919	Tunisia	IPK	S	S	S	I	S	R
CN 53851	United Kingdom	GRIN-CA	I	S	R	I	I	R
CN 58097	United Kingdom	GRIN-CA	R	I	R	I	I	R
CN 65881	United Kingdom	GRIN-CA	S	S	R	I	I	I
51557	Unknown	IHAR	R	S	R	I	S	I
52337	Unknown	IHAR	S	S	S	I	S	R
51834	Unknown	IHAR	S	S	S	I	S	R
51857	Unknown	IHAR	S	S	I	I	I	R
51822	Unknown	IHAR	S	S	I	S	S	R
51851	Unknown	IHAR	S	S	S	R	S	R
51840	Unknown	IHAR	R	S	I	I	S	R
51555	Unknown	IHAR	I	S	I	I	S	R
51557	Unknown	IHAR	I	S	I	I	R	R

^a IPK = Genebank IPK Gatersleben (Germany), GRIN-CA = Plant Gene Resources of Canada (Saskatoon, Canada), IHAR = National Center for Plant Genetic Resources (Radzików, Poland).

^b R = resistant, I – intermediate, and S = susceptible.

Table 5. Reaction of selected *Avena sterilis* genotypes to 13 powdery mildew isolates used in the second host-pathogen test

Accession number	Country of origin	Source ^a	Powdery mildew isolates ^b				
			MBi2014/1	MCh2010/2	MCh2014/4	MCi2014/2	MCz2013/4
CN 67383	France	GRIN-CA	R	R	R	R	R
52280	Unknown	IHAR	R	R	R	I	I
CN 66606	United Kingdom	GRIN-CA	I	R	I	I	S
CN 22667	Tunisia	GRIN-CA	R	S	R	I	S
CN 22668	Tunisia	GRIN-CA	R	S	R	I	S
CN 58106	Sweden	GRIN-CA	I	R	I	I	S
CN 113554	Italy	GRIN-CA	R	I	R	I	I
PI 287211	Israel	GRIN-NPGS	R	I	I	I	I
CN 113536	Italy	GRIN-CA	R	R	R	R	R
CN 67349	Greece	GRIN-CA	I	I	I	I	S

(continued on next page)

^a GRIN-CA = Plant Gene Resources of Canada (Saskatoon, Canada), IHAR = National Center for Plant Genetic Resources (Radzików, Poland), GRIN-NPGS = National Germplasm Resources Laboratory's (Beltsville, MD, U.S.A.).

^b R = resistant, I = intermediate, and S = susceptible.

proved to be resistant to the tested powdery mildew isolates (Fig. 2; Table 3).

Genotypes derived from North America and Australia had very low levels of resistance. Genotypes from Asian countries exhibited moderate levels of resistance or were completely susceptible to the powdery mildew isolates used in the present study (Fig. 2; Table 4).

The highest levels of resistance were demonstrated by genotypes derived from European countries. Among these genotypes, six were identified as resistant to all powdery mildew isolates used in the host-pathogen tests (Fig. 2; Table 3). Fifteen genotypes were resistant to single isolates (Fig. 2; Table 4). Other genotypes were susceptible or exhibited a moderate level of resistance.

Ten *A. sterilis* genotypes selected as resistant to powdery mildew based on the first screening tests were retested, using 13 additional isolates characterized as being more virulent than those used in the first screening assay (Table 2). These tests were performed to confirm the resistance of the selected genotypes. The test results showed that, among the selected genotypes, only four (CN 67383, CN 113536, CN 22667, and CN 22668) were resistant to powdery mildew. These genotypes showed a resistant response to all isolates used (Table 5). Genotypes CN 67349, CN 113554, and PI 287211 showed resistant or intermediate response to the isolates (Table 5). The remaining genotypes selected in screening tests showed an intermediate or susceptible response to new isolates.

In 2015, genotypes selected as resistant in screening tests were tested in the field under natural infection. Powdery mildew symptoms first appeared on the susceptible cultivars Fuchs and Sam. Among *A. sterilis* genotypes, CN 66606, PI 287211, 52280, CN22667, and CN 22668 were infected first. Two weeks after the first observation, symptoms of powdery mildew were visible on the genotypes CN 66606, PI 287211, CN 113554, CN 22667, and CN 22668. Accessions CN 67383, CN 58106, CN 113536, and CN 67349 were highly resistant under natural infection, without visible symptoms of powdery mildew (Table 6). Intensification of symptoms caused by powdery mildew were not observed until the end of the plant growing period.

Discussion

Wild relatives of cultivated crops are valuable sources of many important traits, including resistance to fungal diseases. Breeding for disease resistance often involves the transfer of resistance factors from related wild species and genera into the cultivated species. Wild relatives of cultivated wheat and barley have been used as donors of many resistance genes for powdery mildew and crown rust (McIntosh et al. 1998; Pickering et al. 1995; Reader and Miller 1991; Shi et al. 1998; Xu and Kasha 1992). Moreover, wild *Avena* species have also been used as donors of genes for many important traits, such as resistance to pest and fungal diseases (Sánchez-Martín et al. 2012; Sebesta et al. 1993; Tan and Carson 2013). Wild relatives of *A. sativa* were also used as donors of resistance to powdery

mildew. Many sources of resistance to this pathogen have been identified in lower ploidy *Avena* species (Aung et al. 1977; Herrmann and Roderick 1996; Hoppe and Kummer 1991; Okoń et al. 2014; Thomas et al. 1975; Yu and Herrmann 2006). Due to strong sterility barriers that isolate species of lower ploidy levels from the cultivated forms, the transfer of resistant genes cannot be carried out by means of a similar backcrossing program. More effective transfer of resistant genes can be achieved using species that share all genomes with *A. sativa*. *A. sterilis* genotypes have been used repeatedly as donors of resistant genes to powdery mildew and crown rust (Hayes and Jones 1966; Wahl 1970), Okoń et al. (2014) tested genotypes belonging to different oat species and demonstrated that, among hexaploid *Avena* species, *A. sterilis* seems to be the most promising source of resistance to powdery mildew. The current study screened 350 *A. sterilis* accessions to identify genotypes with high levels of resistance to powdery mildew. The study showed that some of the tested genotypes could be used as donors of effective resistance. Some of these genotypes were resistant to all powdery mildew isolates used in host-pathogen tests. The present study also showed that the identification of effective and reliable sources of resistance requires multiple assays using a variety of pathogen races. Considering the high variability of the pathogen, it is necessary to screen a wide range of pathogens from different regions. In the present study, the first test showed that 10 genotypes were fully resistant to six selected isolates. However, follow-up tests conducted using a more virulent set of isolates of diverse origin (different years and regions) showed that only four genotypes are, in fact, resistant.

Table 6. Powdery mildew infection of adult plants of *Avena sterilis* genotypes in field conditions under natural infection

Accession number	Country of origin	Source ^a	Field observations ^b	
			First	Second
CN 67383	France	GRIN-CA	0	0
52280	Unknown	IHAR	1	3
CN 66606	United Kingdom	GRIN-CA	2	4
CN 22667	Tunisia	GRIN-CA	1	3
CN 22668	Tunisia	GRIN-CA	1	3
CN 58106	Sweden	GRIN-CA	0	0
CN 113554	Italy	GRIN-CA	0	2
PI 287211	Israel	GRIN-NPGS	2	4
CN 113536	Italy	GRIN-CA	0	0
CN 67349	Greece	GRIN-CA	0	0

^a GRIN-CA = Plant Gene Resources of Canada (Saskatoon, Canada), IHAR = National Center for Plant Genetic Resources (Radzików, Poland), GRIN-NPGS = National Germplasm Resources Laboratory (Beltsville, MD, U.S.A.).

^b Scale 0 to 4, where 0 means lack of powdery mildew symptoms and 4 means powdery mildew mycelium takes up over 50% of leaf surface.

Table 5. (continued from preceding page)

Powdery mildew isolates ^b							
MCz2014	MCu2014/2	MMk 2014	MPi2014/1	MSk2014	MSt2013/2	MSt2013/3	MZb2014/1
I	R	R	R	R	R	R	R
R	I	R	R	I	I	R	R
S	S	I	S	I	R	I	R
R	R	R	S	R	R	R	S
R	R	R	S	R	R	R	S
S	S	I	S	S	R	I	I
I	I	R	I	I	R	I	I
R	I	S	I	I	R	I	I
R	R	R	R	R	R	R	R
R	I	I	I	I	R	I	I

Resistance of adult plants is very important for breeders. Therefore, determination of the adult plant response to stress caused by pathogens plays a crucial role in the selection of disease resistance donors. Resistance in the seedling stage does not always translate into adult plant resistance. In the present study, selected genotypes of *A. sterilis* were tested in the field under natural conditions. The observations revealed that some of the genotypes with a high level of resistance at the seedling stage showed a moderate response as adult plants. Disease symptoms appeared on these plants relatively late in comparison with susceptible checks. Similarly, Tan and Carson (2013), in addition to the host-pathogen test at the seedling stage, estimated the resistance of wild *Avena* species at the adult plant stage. As in our study, those authors demonstrated that the genotypes resistant at the seedling stage often demonstrated moderate response or were susceptible to the pathogen as adult plants. These authors pointed out that the genotypes resistant at the seedling stage and the adult stage are the most valuable source of resistance. Carson (2009, 2010), who identified *A. barbata* genotypes with a broad-spectrum of resistance to crown rust, came to similar conclusions. The current study showed that the two genotypes selected in host-pathogen tests as being resistant at the seedling stage were also resistant in the field. These results suggest that these two genotypes, CN 67383 and CN 113536 carry valuable sources of resistance against oat powdery mildew.

A. sterilis genotypes tested in the present study came from different parts of the world and different geographic regions and climatic conditions. The results showed that the genotypes identified as resistant to powdery mildew were acquired from countries located in the Mediterranean region. This observation indicates that the Mediterranean region may be the most suitable to seek for sources of resistance to powdery mildew and, possibly, other biotic and abiotic stresses. In his research, Loskutov (2004) also highlighted the fact that the Mediterranean was the best region to search for the genotypes resistant to fungal diseases, concluding that the resistance most frequently occurred in accessions from North African countries such as Tunisia, Algeria, and Morocco. In addition, *A. barbata* genotypes identified by Carson (2009, 2010) as resistant originated from western Mediterranean countries. Tan and Carson (2013) selected genotypes derived from Morocco to search for new sources of resistance to crown rust. They demonstrated that among the tested genotypes, 67% were resistant. In the current study, 140 analyzed genotypes came from the Mediterranean countries, of which only six were resistant to the isolates used in host-pathogen tests. Differences in the number of resistant genotypes may result from the fact that the present study tested genotypes belonging only to species *A. sterilis*. Tan and Carson (2013) tested accessions belonging to different species, and the most resistant genotypes were diploid and tetraploid species. Okoń et al. (2014) also demonstrated that the group of tetraploid species has a higher level of resistance than the group of hexaploid species.

Many studies indicated the need to search for new and effective sources of resistance to fungal disease, due to high variability of pathogens (Hsam et al. 1997, 1998; Okoń 2015; Okoń et al. 2014; Tan and Carson 2013). This work indicates new potential sources of resistance that can be incorporated into oat cultivars to improve the level of resistance to powdery mildew. The results from the current study demonstrated that the most promising sources of resistance among the tested *A. sterilis* accessions were genotypes CN 67383 and CN 113536 (Plant Gene Resources of Canada, Saskatoon, Canada) from France and Italy.

Acknowledgments

This work was carried out in the framework of the Programme LEADER V project number: LIDER V/21/p325/L-5/13/NCBR/2014 "Identification of new and effective resistance genes to fungal diseases in oats and development of DNA markers for their identification", supported by the National Research and Development Center.

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