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RESISTANCE AND GENES OF RESISTANCE AGAINST POWDERY MILDEW OF SELECTED WHEAT GENETIC RESOURCES

ODOLNOSŤ A GÉNY REZISTENCIE VOČI MÚČNATKE TRÁVOVEJ VO VYBRANÝCH GENETICKÝCH ZDROJOCH PŠENICE LETNEJ

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Quantitative resistance of wheat genetic resources to powdery mildew expressed by the AUDPC values was assessed under field conditions in Slovakia in 2006 and 2007. The range of AUDPC values was from 10 to 1872. Genetic resources with lower AUDPC values in comparison with control cultivar Torysa were analyzed in laboratory conditions using a set of differential powdery mildew isolates possessing different virulence. Eight specific resistance genes, namely *Pm2, Pm3a, Pm4b, pm5, Pm6, Pm7, Pm8* and *Pm17* were detected in genetic resources singly or in combination. Among the observed genetic resources, genotypes were found possessing partial effective specific resistance gene (*Pm17* in combination with *pm5* in Century and *Pm3a* in combination with *pm5* in Vercors) along with the genotypes in which the defence against powdery mildew was provided by the adult plant resistance (genetic resources with the least AUDPC values – Harrow, Chequer, Century, Narion, Smuggler, Belcast, Acclaim, MV Kodmon, Ines (HE 5727), Maverick, MV Suveges and Eros).

Key words: *Blumeria graminis*, powdery mildew, *Triticum aestivum*, wheat, disease, resistance

Powdery mildew of wheat (*Triticum aestivum* L.), caused by the obligate biotrophic ectoparasitic fungus *Blumeria graminis* (DC) Speer f. sp. *tritici* Marchal, is of economic importance in regions with high rainfall and with maritime or semi-continental climate. With the spread of irrigation, the use of semi-dwarf cultivars, chemical growth regulators and the increased application of nitrogen fertilizers, powdery mildew has also moved into areas with hotter and dries climates (Bennett 1984). Pathogen of powdery mildew causes grain yield reductions up to 10–15% and can significantly reduce flour yield and adversely affect other aspects of grain quality (Perugini et al. 2008). The use of resistant cultivars is an effective, economical and environmentally safe approach to eliminate the use of fungicides and to reduce production losses due to this disease. However, since several wheat resistance genes tend to become ineffective within a short period due to frequent changes in the pathogen population, it is necessary to search for new sources of resistance and to use available genes in combinations that will provide effective and more durable resistance. So far, 37 genes for resistance to wheat powdery mildew (*Pm1-Pm37*) have been identified and assigned to specific chromosomes or chromosome arms (Huang and Röder 2004; Zhu et al. 2005, Miranda et al. 2006; Miranda et al. 2007; Perugini et al. 2008). The poor durability of race-specific resistances has led in many cases to the view that race non-specific resistance can bring a more satisfactory answer

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to disease control problems, and this with or without the supplementary use of pesticides (Keller et al. 1999). This quantitative resistance is generally observed at the adult stage and it delays infection, development and the reproduction of the pathogens (Chantret et al. 2001). Calculation of the area under disease-progress curve (AUDPC) as a suitable measure of quantitative resistance provides an equivalent amount of information about repeated assessments (Jeger and Viljanen-Rollinson 2001). Breeding for quantitative resistance to powdery mildew is more promising, but is difficult to select on a phenotypic basis. The impact of quantitative resistance is more significant when the selection pressure is extended over a longer period in the season and/or a wide geographical region. Selective progress of quantitative resistance is measured as continuous variation in the level of resistance and results are compared as relative values of different lines and cultivars. In this paper, the results of the assessment of resistance to powdery mildew in large number of wheat genetic resources are presented. Interesting genotypes in term of resistance under field conditions were tested using the isolates of powdery mildew in laboratory conditions.

MATERIAL AND METHODS

Ninety-six genetic sources of wheat were evaluated in 2006 and 2007. The genetic resources are a part of the wheat collection in Gene bank Piešťany, Slovakia, the samples were provided by Dr. Hauptvogel, the curator of genetic resources of cereals (wheat and progenitors) and wild species.

Field assessment

The plot experiments were established under natural disease infection in Piešťany. The region of Piešťany is the maize-wheat growing region. Satisfactory infective pressure of pathogen was obtained by sowing susceptible spreader cultivar Carsten V at regular distances. The field trial was established with a two-replicated randomized block design in plot size 1 m^2. The attack by powdery mildew was first observed during the tillering. At 10-days intervals thereafter, powdery mildew severity, as percentage of leaf area covered, was recorded for each plot of wheat genetic resources. Quantitative resistance was expressed in term of area under the disease progress curve (AUDPC) which was calculated according to Broers et al. (1996) from observed mildew severity data. Data were analyzed by analysis of variance using SPSS Base 13.0. For the field experiments, Astella (K1) – sensitive commercial cultivar without genes of resistance to powdery mildew, Bardotka (K4) – resistant commercial cultivar without resistance genes, Torysa (K3) – moderately resistant commercial cultivar possessing two resistance genes *Pm2* and *Pm6* and Ilona (K2) – moderately resistant cultivar possessing one recessive resistance gene *pm5* were used as control cultivars.

Laboratory tests

Genetic resources with lower AUDPC values in comparison with control cultivars were tested in laboratory conditions using a set of differential powdery mildew isolates possessing different virulence. Tests for powdery mildew response were carried out on primary leaves segments of wheat genetic resources. For each experiment, ten leaf segments of each genotype of 3 cm length were placed in Petri dishes on agar (4 $g.l^{-1}$ agar and 35 $mg.l^{-1}$ benzimidazole) and were attacked by one mildew isolate. The methods of inoculation and incubation were according to Lutz et al. (1992). Disease reactions were assessed 10 days after inoculation according to Király et al. (1970). Three major classes of host reactions were distinguished: r = resistant, i = intermediate, s = susceptible.

RESULTS AND DISCUSSION

Field assessment

Quantitative resistance of wheat genetic resources is presented by mean AUDPC values that were calculated from obtained data (two years and two plot repetitions per genetic resource). Data are shown in Table 1. The range of this values was from 10 (Harrow) to 1872 (Genio). Significant differences among genetic resources and between years were found at 95% probability using the analysis of variance of AUDPC values (Table 2). The homological series as well as significant differences accord-

ing to Tukey test (P=0.05) are given in Table 1. When comparing the genetic resources to the control cultivars, significantly resistant genetic resources were found by comparing to the control Astella only. Significantly the most resistant were genotypes Harrow, Chequer, Century, Na-

T a b l e 1

Resistance of wheat genetic resources to powdery mildew (*Blumeria graminis* f. sp. *tritici*) expressed by AUDPC values

Genotype	Origin	AUDPC		Genotype	Origin	AUDPC
Harrow	USA	10^{a1}		Paradon	FRA	548^{a-m}
Chequer	USA	40^{ab}		Magnet	DEU	552^{a-m}
Century	USA	91^{a-c}		Lurre	NLD	552^{a-m}
Narion	FRA	169^{a-d}		Iglo	FRA	553^{a-m}
Smuggler	GBR	211^{a-e}		Nectar	FRA	564^{a-m}
Belcast	FRA	219^{a-f}		Trakos	DEU	600^{a-m}
Acclaim	GBR	224^{a-g}		Vergain	FRA	615^{a-m}
MV Kodmon	HUN	249^{a-g}		Ina	FRA	635^{a-n}
Ines	CZE	276^{a-g}		Danubius	AUT	685^{a-n}
Maverick	GBR	290^{a-g}		Versailles	NLD	686^{a-n}
MV Suveges	HUN	295^{a-g}		Mirleben	UKR	688^{a-n}
Eros	DEU	302^{a-g}		Sisley	FRA	699^{a-n}
Maris Fundin	GBR	306^{a-h}		Andalou	FRA	725^{a-n}
Slawa	POL	306^{a-h}		Valda	SVK	735^{a-o}
Nutka	POL	311^{a-h}		Aurele	FRA	754^{a-p}
Pastor	SVK	315^{a-h}		Occitan	FRA	769^{a-r}
Dublo	DNK	324^{a-i}		Manella	NLD	772^{a-r}
Electron	FRA	329^{a-i}		Conte Marzotto	ITA	784^{b-r}
Novara	FRA	332^{a-i}		Ritmo	NLD	801^{b-s}
Vector	GBR	336^{a-i}		Villanova	ITA	806^{c-s}
Storm	GBR	340^{a-i}		Winetou	DEU	817^{c-t}
Bardotka	CZE	344^{a-i}		Delta	RUS	817^{c-t}
KO-IN	HUN	349^{a-i}		Barb	USA	823^{c-t}
Carera	FRA	350^{a-i}		Anouk	BEL	837^{c-u}
Zorba	RUS	350^{a-i}		Lely	NLD	885^{d-v}
Augustus	AUT	361^{a-i}		Glutinoso	ITA	903^{d-v}
Solstice	GBR	361^{a-i}		Knyzhma	RUS	912^{d-v}
Bocquiau	FRA	362^{a-i}		Bellevue	FRA	917^{d-v}
Bastide	FRA	363^{a-i}		GK Kalalka	HUN	928^{d-v}
Kornett	DEU	375^{a-i}		Ekho	RUS	970^{e-v}
Pavla	SVK	383^{a-j}		Winzi	DEU	978^{f-v}
Exquisit	AUT	385^{a-j}		Must	FRA	982^{g-v}
Vercors	FRA	386^{a-j}		Astella	SVK	1067^{h-v}
Marshal	GBR	397^{a-k}		Dorico	ITA	1081^{i-v}
Edison	AUT	410^{a-k}		Witington	POL	1138^{j-x}
Catalan	FRA	410^{a-k}		Lampo	ITA	1158^{k-x}
Aubusson	FRA	441^{a-k}		Hector	NLD	1207^{l-x}
Verdon	FRA	442^{a-k}		Lira	RUS	1209^{m-x}
Ilona	SVK	444^{a-l}		Juna	RUS	1211^{m-x}
Bonitus	AUT	444^{a-l}		Moldavska L 1052	SUN	1385^{n-x}
Markola	SVK	461^{a-m}		Pippo	ITA	1493^{o-x}
Veldava	SVK	463^{a-m}		Mac Vicar	USA	1501^{p-x}
Ariete	ITA	491^{a-m}		Golia	ITA	1522^{r-x}
Adam	AUT	493^{a-m}		Libellula	ITA	1552^{s-x}
Mila	SVK	493^{a-m}		Purcell	USA	1574^{t-x}
Mieti	ITA	503^{a-m}		Passarinka	FRA	1587^{u-x}
Torysa	SVK	525^{a-m}		Nugaines	USA	1628^{v-x}
Dominus	AUT	534^{a-m}		Genio	ITA	1872^{x}

AUDPC values are significant different according Tukey ($P < 0.05$)

rion, Smuggler, Belcast, Acclaim, MV Kodmon, Ines, Maverick, MV Suveges and Eros based by the lowest AUDPC values. Significantly more sensitive compared to the control cultivars were Moldavska L 1052, Pippo, Mac Vicar, Golia, Libellula, Purcell, Passarinka, Nugaines and Genio.

Laboratory tests

Forty-five genetic resources which gave lower AUDPC values in comparison with control cultivar Torysa were tested in laboratory conditions. The twenty-three differential powdery mildew isolates were used for genetic analysis of specific resistance genes. The specific interactions between the powdery mildew isolates and 16 near-isogenic lines / differential cultivars with known resistance genes are given in Table 3. The reactions of genetic resources after inoculation with pathogen isolates are presented in Table 4. The specific resistance genes involved in the genetic resources were identified by comparing the responses of near-isogenic lines / differential cultivars and genetic resources. The presence of specific resistance genes to powdery mildew was not confirmed in twenty among forty-five tested genetic resources. Specific resistance genes *Pm2, Pm3a, Pm4b, pm5, Pm6, Pm7, Pm8* and *Pm17* were found in tested genotypes singly or in combination. The response pattern of genotype Century did not correspond to 16 differential lines / cultivars in many cases (Table 3). The results show that in two genotypes only (Century and Vercors) partial effective resistance genes were detected, namely *Pm17* and *Pm3a* in combination with other resistance gene (*pm5*) what is overcome on the present – the information about efficiency of monitored specific resistance genes is not published in this paper.

T a b l e 2

Analysis of variance of AUDPC values

Source	df	Mean Square	F
Model	192	1260793[1]	20.654^{++}
Genotype	95	654040	10.714^{++}
Year	1	4347334	71.217^{++}
Genotype × Year	95	104248	1.708^{++}
Error	192	61044	
Total	384		

[1] R^2 = 0.954 (Adjusted R^2 = 0.908)

T a b l e 3

Differential reactions of 16 wheat cultivars / lines possessing known powdery mildew resistance genes (*Pm*) after inoculation with 23 isolates of *Blumeria graminis* f. sp. *tritici* pathogen

Cultivar/Line	*Pm* – resistance gene	*Blumeria graminis* f. sp. *tritici* isolates																						
		1	3	4	5	7	8	10	11	14	16	17	18	19	20	21	23	24	25	26	27	30	31	32
Axminster/8*CC[1]	*1a*	r[2]	s	s	r	r	s	r	r	s	r	s	r	s	s	r	s	s	r	s	s	s	s	s
Ulka/8*CC	*2*	r	r	r	r	r	s	r	r	r	r	r	s	s	r	s	s	s	r	r	s	s	s	s
Asosan/8*CC	*3a*	r	r	r	r	s	s	s	r	r	s	s	s	s	r	s	s	s	s	s	r	s	s	s
Chul/8*CC	*3b*	r	r	r	r	r	r	s	s	r	s	r	s	r	r	s	s	r	s	r	s	s	s	s
Sonora/8*CC	*3c*	r	r	r	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Kolibri	*3d*	r	r	r	s	r	r	s	s	r	s	s	s	r	s	s	s	s	s	s	r	s	s	s
Michigan Amber/8*CC	*3f*	r	r	r	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Khapli	*4a*	s	r	s	r	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Armada	*4b*	s	r	s	r	s	r	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Hope	*5a*	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	r	s	s	s	s	s	s	s
Timgalen	*6*	s	s	s	s	s	s	r	s	s	s	r	s	s	s	r	s	s	s	s	s	s	s	s
Transfed	*7*	s	s	s	s	r	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Salzmünde 14-44	*8*	s	s	s	s	s	s	s	s	s	s	s	r	s	s	s	s	r	s	s	s	s	s	s
Amigo	*17*	r	r	r	s	s	s	s	s	s	s	r	r	r	s	s	s	s	s	s	s	s	r	s
Maris Dove	*2,Mld*	r	r	r	r	s	r	r	r	r	r	s	s	s	s	s	r	s	s	s	s	r	s	s
Normandie	*1,2,9*	r	s	s	r	r	s	r	r	s	r	s	s	s	s	r	s	s	r	r	s	s	s	s

[1]eight times backrossed to cv. Chancelor

[2]r = resistant, s = susceptible

The genetic diversity of specific resistance genes to powdery mildew was very low in monitored genetic resources. Similarly, low genetic diversity of specific resistance genes was obtained among wheat cultivars registered in the Slovak Republic in 1994–1994 (Švec et al. 1999). Smith et al. (1989) detected *Pm17* in Century. Our study found the presence of *Pm17* in this

T a b l e 4

Reactions of 54 wheat genetic resources after inoculation with 23 isolates of *Blumeria graminis* f. sp. *tritici* pathogen

Cultivar/Line	*Pm* – resistance gene	*Blumeria graminis* f. sp. *tritici* isolates																						
		1	3	4	5	7	8	10	11	14	16	17	18	19	20	21	23	24	25	26	27	30	31	32
Adam	–	s[1]	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Augustus	*2, 6*	r	s	r	s	r	s	r	r	s	s	r	r	r	s	s	s	s	s	s	s	s	s	s
Bonitus	*2, 6*	r	i	r	i	r	s	r	r	s	s	r	r	r	s	s	i	s	s	s	s	s	s	s
Edison	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Exquisit	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Ines	*2, 6*	r	s	r	s	r	s	r	r	s	s	r	r	r	s	s	i	s	s	s	s	s	s	s
Eros	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Kornett	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Dublo	*2, 4b, 6*	i	r	r	r	i	s	r	r	s	s	r	r	r	s	s	i	s	s	s	s	s	s	s
Aubusson	*4b, 5*	s	r	s	r	i	i	s	s	s	s	s	s	s	s	s	s	r	s	s	s	s	s	s
Bastide	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Belcast	*2, 4b, 6*	r	r	r	r	r	s	i	r	s	s	i	r	s	s	s	i	s	s	s	s	s	s	s
Bocquiau	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Carera	*8*	s	s	s	s	s	s	s	s	s	r	s	s	s	s	s	s	s	r	s	s	s	s	s
Catalan	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Electron	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Narion	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Novara	*2, 6*	r	s	r	s	r	s	i	r	s	s	r	r	r	s	s	i	s	s	s	s	s	s	s
Vercors	*3a, 5*	r	r	r	r	s	r	s	s	r	s	s	i	s	s	i	r	r	s	s	s	s	s	s
Verdon	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Acclaim	*4b, 8*	s	r	s	r	s	s	s	s	s	r	s	s	s	s	s	s	s	r	s	s	s	s	s
Maris Fundin	*2, 6*	i	s	r	s	r	s	i	r	s	s	i	r	r	s	s	s	s	s	s	s	s	s	s
Marshal	*4b, 8*	s	r	s	r	s	s	s	s	s	r	s	s	s	s	s	s	s	r	s	s	s	s	s
Maverick	–	i	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Smuggler	*6, 7*	i	s	r	s	r	s	s	r	s	s	r	s	r	s	s	s	s	s	s	s	s	s	s
Solstice	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Storm	*2, 6, 7*	i	s	r	s	r	s	i	r	s	s	r	r	r	s	s	i	s	s	s	s	s	s	s
Vector	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
KO-IN	*2, 4b, 5*	r	r	r	r	r	s	r	i	s	s	s	r	s	s	s	r	r	s	s	s	i	s	s
MV Kodmon	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
MV Suveges	–	s	s	s	s	s	i	s	i	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Ariete	–	i	s	s	s	i	i	s	s	s	s	s	s	s	s	s	s	s	s	i	s	s	s	i
Nutka	*2, 6*	i	s	r	s	i	i	r	r	s	s	r	r	r	s	s	i	s	s	s	s	s	s	s
Slawa	*8*	s	s	s	s	s	s	s	s	s	r	s	s	s	s	s	s	s	r	s	s	s	s	s
Zorba	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Ilona	*5*	s	s	i	i	s	s	s	s	s	s	s	s	i	s	s	i	r	s	s	s	s	s	s
Markola	*2*	r	s	r	s	s	s	r	r	s	s	i	r	s	s	s	i	s	s	s	s	s	s	s
Mila	–	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s	s
Pastor	*4b*	i	r	i	r	i	s	s	s	s	s	i	i	s	s	s	i	s	s	s	i	s	s	i
Pavla	*2, 6*	r	i	r	s	i	s	r	r	s	s	r	r	r	s	s	r	s	s	s	s	s	s	s
Veldava	*2*	r	s	r	s	i	s	i	r	s	s	i	r	s	s	s	s	s	s	s	s	s	s	s
Century	*5, 17, ?*	r	r	r	r	r	i	r	i	i	r	r	i	i	r	i	i	r	i	r	i	r	i	r
Harrow	*8*	i	i	s	s	i	s	s	i	s	r	s	s	s	s	s	s	s	r	s	s	s	s	s
Chequer	*2, 6, 8*	r	i	r	i	r	s	r	r	s	r	r	r	r	r	i	i	s	r	s	s	r	s	s

[1]r = resistant, s = susceptible, i = intermediate

genotype, too, however in combination with *pm5*. Presence of one or more resistance genes in combination with described genes in Century is possible but it is not possible to detect this resistance using the set of powdery mildew isolates used in this study. Genetic resources with ineffective specific resistance genes and genetic resources without specific resistance genes were found, however, these expressed a good level of resistance under field conditions. They are not as susceptible as expected pursuant to the specific resistance genes expressed at the seedling stage. Therefore, the defence to powdery mildew in adult plant stage was provided by quantitative resistance. Jeger and Viljanen-Rollinson (2001) recommended the use of calculated AUDPC for assessing the quantitative resistance. Similarly, Yu et al. (2001) evaluated sixty Chinese wheat varieties during two cropping seasons and two locations in central China and found out that AUDPC was highly correlated with final disease severity. Navabi et al. (2003) concluded from the results of their study that breeding for the adult plant resistance (quantitative resistance generally observed at the adult plant stage) would be possible by selection for disease severity at the critical stage of growth. Selection must be done under epidemic of pathogen with a high spectrum of virulence for any known seedling resistance genes that may act epistatically and mask the effect of adult plant resistance linked by non-specific genes. In this connection, Mingeot et al. (2002) and Paillard et al. (2002) discovered that some ineffective specific resistance genes (*Pm3c, Pm3g, Pm4b*) influenced by residual effect on resistance at adult stage. Similarly, Hsam et al. (2001) reported the specific gene *pm5a* to be possible source of adult plant resistance in combination with other *Pm* genes cultivation. Narion, MV Kodmon, Maverick, MV Suveges and Eros without specific resistance genes belonged to the significantly most resistant genetic resources but these did not possess any specific resistance genes. The quantitative resistance of these genotypes could not be caused by residual effect of ineffective specific genes, therefore, it is assumed that resistance in adult plant stage was provided by non-specific genes.

CONCLUSIONS

Availability of suitable sources of resistance is a basic prerequisite for successful breeding of disease resistance. In order to protect successfully against powdery mildew along with the ephemeral persistence of specific gene efficiency and existing and generating new more virulent pathotypes of powdery mildew pathogen, there is an urgent need to search novel sources of powdery mildew resistance. Genotypes with resistance genes that would provide defence during all development stages have not been found, however, results presented in this study in term of AUDPC are an useful information about adult plant resistance as well as a possibility to utilize the most resistant genetic resources Harrow, Chequer, Century, Narion, Smuggler, Belcast, Acclaim, MV Kodmon, Ines, Maverick, MV Suveges and Eros in the process of development of new wheat genotypes.

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SÚHRN

V dvoch vegetačných obdobiach v rokoch 2006 a 2007 bola sledovaná odolnosť genetických zdrojov pšenice letnej f. ozimnej (*Triticum aestivum* L.) voči obligátnemu patogénovi *Blumeria graminis* (DC) Speer f. sp. *tritici* Marchal (pôvodca múčnatky trávovej na pšenici). Hodnotených bolo 96 genetických zdrojov, ktoré sú súčasťou kolekcie pšenice Génovej banky Slovenskej republiky Piešťany. V prirodzených poľných podmienkach bolo hodnotené napadnutie patogéna percentom napadnutej plochy na rastlinách v dvoch opakovaniach v pravidelných časových intervaloch. Tieto hodnoty boli použité na stanovenie AUDPC (plochy napadnutia pod krivkou vývoja choroby). Analýzou variancie boli zistené rozdiely medzi genetickými zdrojmi aj medzi rokmi. Hodnoty AUDPC sa pohybovali v rozmedzí od 10 (Harrow) po 1872 (Genio). Ako kontrolné odrody boli použité slovenské registrované odrody Astella – bez špecifických génov rezistencie, Bardotka - so silnou nešpecifickou rezistenciou, Ilona – so špecifickým génom rezistencie *pm5* a Torysa – so špecifickými génmi rezistencie *Pm2, Pm6*. Porovnaním s kontrolnými odrodami boli nájdené genetické zdroje, ktoré boli preukazne odolnejšie len voči Astelle: Harrow, Chequer, Century, Nation, Smuggler, Belcast, Acclaim, MV Kodmon, Ines, Maverick, MV Suveges a Eros. Genetické zdroje s hodnotami AUDPC nižšími ako kontrolná odroda Torysa boli testované v laboratórnych podmienkach. Na testovanie boli použité izoláty patogéna so stanoveným virulenčným spektrom proti najfrekventovanejším špecifickým génom rezistencie. Vybranými zbierkovými monospórickými izolátmi boli inokulované listové segmenty. Na základe reakcií na listových segmentoch boli stanovené špecifické gény rezistencie v jednotlivých genetických zdrojoch. Boli detegované špecifické gény *Pm2, Pm3a, Pm4b, pm5, Pm6, Pm7, Pm8* a *Pm17*, z toho len gény *Pm3a* a *Pm17* zabezpečujú čiastočnú ochranu proti múčnatke trávovej. Výsledné hodnoty AUDPC poukazujú na skutočnosť, že dobrú až veľmi uspokojivú úroveň odolnosti, ktorú genetické zdroje s neúčinnými špecifickými génmi rezistencie a genetické zdroje bez génov špecifickej rezistencie v poľných podmienkach vykazovali, môže zabezpečovať aj odolnosť podmienená nešpecifickými génmi rezistencie, ktorá môže byť podporená reziduálnym vplyvom prekonaných génov špecifickej rezistencie.

Kľúčové slová: *Triticum aestivum*, pšenica, *Blumeria gramnis*, múčnatka trávová, odolnosť, gény odolnosti