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RESISTANCE TO POWDERY MILDEW IN BARLEY CULTIVARS AND BREEDING LINES INCLUDED IN 1998-2000 POLISH REGISTRATION TRIALS

ABSTRACT

A total of 46 barley cultivars and breeding lines (35 spring and 11 winter) tested in 1998 - 2000 Polish registration trials were tested for powdery mildew resistance with 23 differential isolates of *E. graminis* f. sp. *hordei*. The isolates were chosen according to differences in virulence spectra that were observed on 'Pallas' isoline differential set and on 8 additional differential cultivars. The experiment was conducted in the IHAR Radzików greenhouse 1999-2000.

From 35 tested spring cultivars and breeding lines 6 (17%) were composed of different lines carrying different genes for resistance. Eight different resistance alleles [*Mla1*, *Mla7*, *Mla12*, *Mla6*, *Mla14*, *Mlg*, *Ml (CP)* and *mlo*] were detected alone or in combinations. Among tested cultivars and breeding lines of spring barley, majority (94%) had combination of different genes for resistance. The most common resistance gene was *Mla12* and this gene was present in 12 (34%) spring breeding lines. Seven spring cultivars and breeding lines possessed Mlo resistance.

Seven different resistance alleles [*Mla12*, *Mla6*, *Mla14*, *Mla13*, *Ml (Ru3)*, *Ml (Bw)*, *Mlra*] were detected alone or in combination in tested winter cultivars and breeding lines. From 11 tested cultivars and breeding lines of winter barley 3 were composed of different lines carrying different genes for resistance. Majority (91%) of these cultivars and breeding lines had combination of different genes for resistance. Major strategies for control of powdery mildew using resistance genes are discussed.

Key words: barley, breeding lines, cultivars, *Erysiphe graminis* f. sp. *hordei*, genes, powdery mildew, resistance

INTRODUCTION

Barley (*Hordeum vulgare* L.) is the fourth most important cereal crop in the world, after wheat, maize and rice. In European Union (EU) barley is the second (after wheat) most important cereal crop with about 32% of EU cereals acreage (Rasmusson 1985, Atzema 1998). In Poland barley is grown on about 1, 300, 000 ha (spring on 1.0 - 1.1 millions ha and winter on about 150-200 thousands ha), (Anonymous 1999c). Over half of the world barley crop is used for animal feed, while about 10% is used for malt. Malting bar-

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ley is an especially important crop in the USA and Europe (Rasmusson 1985, Czembor 1996, Atzema 1998).

The powdery mildew caused by *Erysiphe graminis* f. sp. *hordei* (synamorph *Blumeria graminis* f. sp. *hordei*) is serious disease of barley in Poland. In countries where mildew is a problem, including Poland, yield losses may exceed 25%, although average losses are smaller and can reach about 10% (Zwatz 1987, Schally *et al.* 1995, Czembor 1996, Atzema 1998, Czembor and Czembor 1998, 1999). Yield reduction is due to loss of functional green leaf area, reduced root growth, reduced kernel weight, smaller numbers of kernels per spike and tillers per plant. Reduction in quality characteristics is particularly detrimental for malting barley (Balkema-Boomstra and Masterbroek 1995, Schally *et al.* 1995, Czembor 1996).

In Europe, the use of specific resistance genes to control barley powdery mildew began in the 1930s with the work of Honecker (Honecker 1938). Since that period, barley breeders commonly used such resistance genes as *Mla6*, *Mla7*, *Mla9*, *Mla12* and *Mla13* belonging to the *Mla* locus and the resistance alleles *Mlk*, *Mlg*, *Ml (La)*, *Mlh* and *Mlra* (Czembor and Czembor 1998, 1999). However, resistance conferred by most resistance genes used on large acreage has not been effective for more than a few years with the exception of genes *mlo* and *Ml (La)*. The *Ml (La)* resistance gene have been effective for more than 10 years. Despite the fact that since 1979 the *Mlo* resistance has been deployed in many barley cultivars throughout Europe there is no known virulence for *mlo* genes (Munk *et al.* 1991, Jørgensen 1994). This lack of durability of resistance genes was caused by high level of pathogenic variability encountered in natural populations of *E. graminis* f. sp. *hordei*. In many investigations it was proved that *E. graminis* f. sp. *hordei* is able to develop many new races and that its spores are spread by wind over the large distances across Europe (Brändle 1994, Limpert *et al.* 1999, Hovmøller *et al.* 2000).

In order to predict performance of specific powdery mildew resistance and to use it properly in different strategies of disease control it is essential to know the resistances of already registered cultivars and future registered cultivars (breeding lines and cultivars included in registration trials) and their reaction (effectiveness) to this fungus (Gacek and Czembor 1983, 1984, Czembor and Gacek 1990, Czembor and Czembor 1998, 1999). Therefore, frequent tests of new cultivars and breeding lines included in registration trials have to be carried out for identifying alleles for powdery mildew resistance. This is done on the basis of the gene-for-gene hypothesis (Flor 1956) by inoculation of plants with pathogen isolates that have a defined, well-known virulence spectrum. The subsequent scoring of infection types determines a reaction spectrum for each entry and than the possible resistance phenotype of tested plant material can be determined (Gacek 1990, Czembor and Gacek 1990, Czembor and Czembor 1998, 1999).

Table 1

List of spring barley cultivars and breeding lines (Anonym. 1998a, 1999a, 2000a, 2000b)

Cultivar	*Type of cultivar	Country of origin	Year of entry into		Breeder
			registration trials	the Register	
Sezam	M	PL	1997	2000	SHR Modzurów
Prosa	M	AU	1998	2000	Probsdorfer Saatzucht
Riviera	M	UK	1998		PBI
STH 2497	M	PL	1998		ZDHR Strzelce
NS 89-1132	F	DE	1998		Nordsaat Saatzucht
P5053.31A	F	AU	1998		Probsdorfer Saatzucht
BKH 3798	M	PL	1999		ZHR Bąków
NAD 2298	M	PL	1999		SHR Nagradowice
NAD 2398	M	PL	1999		SHR Nagradowice
NAD 2498	M	PL	1999		SHR Nagradowice
POA 2198	M	PL	1999		"Piast" HR Łagiewniki
POA 2298	M	PL	1999		"Piast" HR Łagiewniki
NS GS 1749	M	DE	1999		Nordsaat Saatzucht
POB 2998	M	PL	1999		HBP (DH Polanowice)
RAH 3198	F	PL	1999		ZDHR Radzików
STH 2998	F	PL	1999		ZDHR Strzelce
STH 3098	F	PL	1999		ZDHR Strzelce
LP2.2840	F	DE	1999		Lochow-Petkus
NS 96-1116	F	DE	1999		Nordsaat Saatzucht
P 6616	F	AU	1999		Probsdorfer Saatzucht
BKH 4099	M	PL	2000		ZHR Bąków
BKH 4199	M	PL	2000		ZHR Bąków
NAD 2699	M	PL	2000		SHR Nagradowice
NAD 2799	M	PL	2000		SHR Nagradowice
MOB 1899	M	PL	2000		SHR Modzurów
POA 2399	M	PL	2000		"Piast" HR Łagiewniki
STH 3199	M	PL	2000		ZDHR Strzelce
Jersey	M	NL	2000		Cebeco
LP 697-94	M	DE	2000		Lochow-Petkus
NS 96-1114	M	DE	2000		Nordsaat Saatzucht
P7020	M	AU	2000		Probsdorfer Saatzucht
BKH 3999	F	PL	2000		ZHR Bąków
NIB 1099	F	PL	2000		HR Nieznanice
STH 3499	F	PL	2000		ZDHR Strzelce
Pejas	F	CZ	2000		CEZEA Ceic

*Types of cultivars: M – Malting, F - Fodder

The aim of the present investigation was to identify the powdery mildew resistance genes in 46 barley cultivars and breeding lines included in Polish registration trials in 1998-2000.

MATERIALS AND METHODS

Plant material

A total of 46 barley cultivars and breeding lines (35 spring and 11 winter) included in 1998 - 2000 Polish registration trials were tested (Tables 1, 2). Among tested cultivars and breeding lines 18 (39%) were not of Polish origin. These cultivars and breeding lines were bred by companies from Germany, The Netherlands, Austria, United Kingdom, Sweden and Czech Republic. Seed samples of these cultivars or breeding lines were kindly provided by their breeders.

Table 2.
List of winter barley cultivars and breeding lines, their country of origin, breeder and year of entry into registration trials (Anonymous 1998b, 1999b, 2000c).

Cultivar	*Type of cultivar	Country of origin	Year of entry into registration trials	Breeder
Hampus	F	SE	1997	Svalof Weibull AB
Carola	F	DE	1999	Nordsaat
KRC 197	F	PL	1997	PHR (SHR Krzemlin)
BKH 2198	F	PL	1998	ZHR Bąków
LP 6-562	F	DE	1998	Lochow-Petkus
POA 1898	F	PL	1998	"Piast" HR Łagiewniki
BKH 2399	F	PL	1999	ZHR Bąków
LP 6-758	F	DE	1999	Lochow-Petkus
NIB 999	F	PL	1999	SHR Nieznanice
POA 2099	F	PL	1999	"Piast" HR Łagiewniki
CWB 96-9	M	UK	1999	PBI

*Type of cultivar: F – Fodder, M - Malting

Differential isolates

Twenty three differential isolates of *E. graminis* f. sp. *hordei* were used in this study (Table 3). The isolates were kindly provided by Dr. H. J. Schaerer (ETH, Zürich, Switzerland) and originated from collections of the Risø National Laboratory, Roskilde, Denmark; Danish Institute for Plant and Soil Science, Lyngby, Denmark and Edigenossische Technische Hochschule – ETH, Zürich, Switzerland. In addition five isolates coming from mildew collection of the Plant Breeding and Acclimatization Institute - IHAR, Radzików, Poland were used. The isolates were chosen according to differences in virulence spectra that were observed on 'Pallas' isoline differential set (Kølster *et al.* 1986)

Table 3

Differential isolates and their infection types on Pallas isolines set and on 8 additional cultivars

Differential set		Isolates							
Pallas isolines and cultivars	Gene	1	2	3	4	5	6	7	8
		58-74.1	59-12	63-1a	A6c	D17-1	EmA30.1	HL3/5.c	JEH11-2
Pallas	*Mla8*	4	4	4	4	4	4	4	4
P1	*Mla1*	0	0	4	4	4	0	0	0
P2	*Mla3*	0	0	0	0	0	0	0	0
P3	*Mla6, Mla14*	0	0	0	0	0	4	4	0
P4A	*Mla7, Mlk, +?*	4	4	4	0	0	0	0	4
P4B	*Mla7, +?*	4	4	4	0	1	0	0	4
P6	*Mla7, MlLG2*	4	4	4	0	0	0	0	4
P7	*Mla9, Mlk*	4	0	4	0	0	0	0	4
P8A	*Mla9, Mlk*	4	0	4	0	0	0	0	4
P8B	*Mla9*	4	0	4	0	0	0	0	4
P9	*Mla10, MlDu2*	4	4	4	0	0	0	0	4
P10	*Mla12*	0	0	4	0	0	4	0	0
P11	*Mla13, MlRu3*	4	0	4	0	0	0	0	0
P12	*Mla22*	4	4	0	4	4	4	4	0
P13	*Mla23*	1	1	1	1	1	1	1	1
P14	*Mlra*	4	4	4	0	4	4	4	4
P15	*Ml(Ru2)*	2	4	4	4	2	4	2	4
P17	*Mlk*	4	4	4	2	2	2	2	4
P18	*Mlnn*	4	4	4	4	4	4	4	4
P19	*Mlp*	2	2	2	2	2	2	2	2
P20	*Mlat*	0	2	2	4	2	2	2	4
P21	*Mlg, Ml(CP)*	4	4	4	0	0	0	4	0
P22	*mlo5*	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)	3	0(4)
P23	*Ml(La)*	0	4	4	4	4	4	4	4
P24	*Mlh*	4	4	4	2	4	4	4	4
Benedicte	*Mla9,Ml(IM9)*	0	0	4	0	0	0	0	0
Lenka	*Mla13,Ml(Ab)*	0	0	4	0	0	0	0	0
Gunnar	*Mla3, Ml(Tu2)*		0	3	0	0	0	0	0
Steffi	*Ml(St1),Ml(St2)*	0	0	2	0	0	0	4	0
Kredit	*Ml(Kr)*		2	4	0	0	0	0	2
Jarek	*Ml(Kr), +?*	4	4	4	4	4	4	4	4
Trumph	*Mla7, Ml(Ab)*	4	4	4	4	4	4	4	4
Borwina	*Ml(Bw)*	2	4	4	4	3	4	2	4
Manchuria	-	4	4	4	4	4	4	4	4

Table 3

Continued

Differential set		Isolates							
Pallas isolines and cultivars	Gene	9	10	11	12	13	14	15	16
		MH1-3	R189.1	R303a	Ru3.2	TR2-2	En1/A1	R303.2	E92-1
Pallas	*Mla8*	4	4	4	4	4	4	4	4
P1	*Mla1*	0	0	0	0	4	0	0	4
P2	*Mla3*	0	0	0	0	4	0	0	0
P3	*Mla6, Mla14*	2	4	0	4	0	0	0	4
P4A	*Mla7, Mlk, +?*	2	1	1	0	4	4	0	4
P4B	*Mla7, +?*	4	0	0	1	4	4	0	4
P6	*Mla7, MlLG2*	4	0	0	0	2	4	0	4
P7	*Mla9, Mlk*	0	0	0	0	4	0	0	0
P8A	*Mla9, Mlk*	0	0	0	0	4	0	0	0
P8B	*Mla9*	0	2	0	0	4	0	0	0
P9	*Mla10, MlDu2*	0	0	4	0	4	4	4	4
P10	*Mla12*	2	0	0	0	4	4	0	4
P11	*Mla13, MlRu3*	4	0	0	0	0	4	0	0
P12	*Mla22*	4	4	0	4	4	4	0	0
P13	*Mla23*	1	1	1	1	1	1	1	1
P14	*Mlra*	0	4	4	4	4	4	4	4
P15	*Ml(Ru2)*	2	4	4	4	4	4	4	4
P17	*Mlk*	2	2	0	2	4	4	2	4
P18	*Mlnn*	4	2	2	4	4	4	4	4
P19	*Mlp*	2	2	2	2	2	2	2	2
P20	*Mlat*	2	2	2	2	4	2	2	2
P21	*Mlg, Ml(CP)*	4	0	4	4	4	4	4	4
P22	*mlo5*	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)
P23	*Ml(La)*	4	4	4	4	4	4	4	4
P24	*Mlh*	4	4	4	4	4	4	4	2
Benedicte	*Mla9,Ml(IM9)*	4	0	4	0	4	4	0	4
Lenka	*Mla13,Ml(Ab)*	0	0	0	0	0	4	0	0
Gunnar	*Mla3, Ml(Tu2)*	0	0	0	0	3	3	0	0
Steffi	*Ml(St1),Ml(St2)*	4	4	4	0	2	4	0	0
Kredit	*Ml(Kr)*	4	0	4	1	2	4	2	4
Jarek	*Ml(Kr), +?*	4	4	4	4	4	4	4	4
Trumph	*Mla7, Ml(Ab)*	4	4	4	4	4	4	4	4
Borwina	*Ml(Bw)*	4	2	4	4	4	4	4	4
Manchuria	-	4	4	4	4	4	4	4	4

Table 3

Continued

Differential set		Isolates						
Pallas isolines and cultivars	Gene	17	18	19	20	21	22	23
		59-11.2	SZ/C10a	Ra7	Ra9-1	Ra10-2	Ra16a	Ra22-2
Pallas	*Mla8*	4	4	4	4	4	4	4
P1	*Mla1*	0	0	0	0	4	0	0
P2	*Mla3*	0	4	0	4	0	0	0
P3	*Mla6, Mla14*	0	4	4	4	4	4	4
P4A	*Mla7, Mlk, +?*	4	0	0	4	4	4	4
P4B	*Mla7, +?*	4	2	0	2	2	4	4
P6	*Mla7, MlLG2*	4	0	0	1	1	4	4
P7	*Mla9, Mlk*	0	0	0	0	0	4	0
P8A	*Mla9, Mlk*	0	0	0	0	0	4	0
P8B	*Mla9*	0	0	0	0	0	4	0
P9	*Mla10, MlDu2*	2	0	0	4	4	4	4
P10	*Mla12*	0	4	0	4	4	0	4
P11	*Mla13, MlRu3*	0	0	0	0	4	0	4
P12	*Mla22*	4	4	4	0	4	0	0
P13	*Mla23*	1	1	1	1	1	1	1
P14	*Mlra*	4	4	4	0	4	4	4
P15	*Ml(Ru2)*	4	4	4	0	4	4	4
P17	*Mlk*	4	2	2	4	4	4	4
P18	*Mlnn*	4	2	4	4	4	2	2
P19	*Mlp*	2	2	2	2	2	2	2
P20	*Mlat*	2	4	2	2	4	2	2
P21	*Mlg, Ml(CP)*	4	4	0	4	4	0	4
P22	*mlo5*	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)
P23	*Ml(La)*	4	4	4	4	4	4	4
P24	*Mlh*	4	4	4	4	4	4	4
Benedicte	*Mla9,Ml(IM9)*	0	0	0	4	4	0	4
Lenka	*Mla13,Ml(Ab)*	0	0	0	0	4	0	4
Gunnar	*Mla3, Ml(Tu2)*	0	0	0	0	0	0	
Steffi	*Ml(St1), Ml(St2)*	2	2	0	4	2	4	4
Kredit	*Ml(Kr)*	1	2	0	2	4	2	4
Jarek	*Ml(Kr), +?*	4	4	4	4	4	4	2
Trumph	*Mla7, Ml(Ab)*	4	4	4	4	4	4	4
Borwina	*Ml(Bw)*	2	4	2	4	4	4	4
Manchuria	-	4	4	4	4	4	4	4

(kindly provided by Dr. L. Munk from Royal Agricultural and Veterinary University, Copenhagen, Denmark) and on 8 additional differential cultivars (Benedicte, Lenka, Gunnar, Steffi, Kredit, Jarek, Trumph, Borwina). Isolates were purified by single pustule isolation. Young seedlings of the cultivar 'Manchuria' (CI 2330) were used to maintain and propagate all isolates used. Isolates were tested frequently on host differentials to assure their purity throughout the experiment.

Resistance tests

The experiment was conducted in the IHAR Radzików greenhouse 1999-2000. From 5 to 10 plants of each cultivar and breeding line were tested together with seedlings of cultivar 'Manchuria' (used as susceptible control) and differential set (to assure purity of isolates throughout the experiments). The plants were grown in 16 h light and 16-22°C range of temperature. The inoculation was carried out when plants were 10 – 12 days old (two leaf stage) by shaking or brushing conidia from diseased plants. After 8-10 days of incubation the disease reaction types showed by seedlings were scored.

Disease assessment

The reaction types exhibited by barley plants after infection with *E. graminis* f. sp. *hordei* were scored using a 0 through 4 scale adopted from Mains and Dietz (1930) (Table 4). This scale was broadened by including

Table 4.

Description of infection types and codes used (adapted from Mains and Dietz, 1930).

Infection type	Symptoms
0	No visible symptoms. (Immunity).
0(4)	Sparse small colonies originating from the stomatal subsidiary cells.
1	Necrotic flecks, usually minute. No mycelial growth. No sporulation. (Hypersensitivity).
2	Frequent chlorosis. Reduced mycelial growth. No or very scarce sporulation.
3	Moderate mycelial growth, moderate sporulation. Sometimes chlorosis.
4	Profuse sporulation of well developed colonies and sometimes green islands.

score 0 (4) describing infection type characteristic for gene *mlo*. Disease symptoms were assessed on the primary leaf of the seedlings. Plants with infection types 0 - 2 were classified as resistant, while plants that scored 3 and 4 were classified as susceptible.

Postulation of resistance alleles

Hypotheses about the specific resistance genes present were made from the comparison of the reaction spectra of the tested lines with those of differential lines. The lines giving the same reaction spectra with all isolates were classified in the same group. Identification of resistance

genes was made by eliminating resistance genes not present in tested lines. The next step was determination of postulated and possible resistance genes present and was done on the basis of the gene for gene hypothesis. In the case when a compatible reaction (scores 3 and 4) was observed with one given isolate, it meant that the cultivar did not possess the resistance alleles for which the isolate was avirulent. Incompatible reactions (scores 0-2) with isolates possessing only one avirulence allele among the remaining possible resistance alleles made it possible to postulate that the matching resistance allele was present (Flor 1956, Brown and Jørgensen 1991, Czembor and Czembor 1998, 1999).

RESULTS

Spring barley

From 35 tested cultivars and breeding lines of spring barley 6 (17%) (NAD 2498, POA 2198, BKH 4099, NAD 2799, STH 3499, Pejas) were composed of different lines carrying different genes for resistance (Table 5). In 6 cultivars and breeding lines (Riviera, NS 89-1132, P5053.31A, BKH 4199, NAD 2699, POA 2399) it was impossible to determine which specific gene or genes were present.

Eight different resistance alleles [*Mla1*, *Mla7*, *Mla12*, *Mla6*, *Mla14*, *Mlg*, *Ml (CP)* and *mlo*] were detected alone or in combination. Among tested cultivars and breeding lines majority (94%) had combination of different genes for resistance. Resistance genes at the Mla locus (*Mla7*, *Mla12*, *Mla6*, *Mla14*, *Mla1*) were present in 18 (51%) cultivars and breeding lines. The most common resistance gene was *Mla12*. This gene was present in 12 (34%) breeding lines. Resistance genes at *Mlg* and *Ml (CP)* were postulated to be present in 7 cultivars and breeding lines. Seven cultivars and breeding lines (POA 2298, NS 96-1116, STH 3199, Jersey, LP 697-94, NS 96-1114, P7020) possessed *Mlo* resistance.

Winter barley

Seven different resistance alleles [*Mla12*, *Mla6*, *Mla14*, *Mla13*, *Ml (Ru3)*, *Ml (Bw)*, *Mlra*] were detected alone or in combination in tested winter cultivars and breeding lines (Table 6). From 11 tested cultivars and breeding lines of winter barley 3 (KRC 197, BKH 2198 and POA 1898) were composed of different lines carrying different genes for resistance. Majority (91%) of these cultivars and breeding lines had combination of different genes for resistance. The most common combination of resistance genes was *Mla6*, *Mla14*. This combination was present in Hampus, Carola and LP 6-562. Resistance genes at the *Mla* locus (*Mla6*, *Mla14*, *Mla13* and *Mla12*) were present in 5 (45%) cultivars and breeding lines. Breeding line CWB 96-9 had only one

Table 5

Resistance alleles and infection types of 35 cultivars and breeding lines of spring barley to infection by 23 isolates of *E. graminis* f. Sp. *hordei.*

Cultivar or breeding line	Isolates					Postulated resistance alleles	Possible alleles[1]
	58-74.1	59-12	63-1a	A6c	D17-1		
Sezam	4	4	4	0	0	*Mla7, +?*[2]	
Prosa	0	0	4	0	0	*Mlg, Ml(CP), +?*	
Riviera	0	0	4	0	0	*?*	*Mlg, Ml(CP)*
STH 2497	0	0	4	0	0	*Mla12*	
NS 89-1132	0	0	4	0	0	*?*	*Mla12 or Mla13, +?*
P5053.31A	0	0	0	4	0	*?*	*Mla1, +?*
BKH 3798	4	4	4	0	0	*Mla7, +?*	
NAD 2298	0	0	4	0	0	*Mla12, +?*	
NAD 2398	0	0	0	0	0	*Mla6, Mla14, +?*	
NAD 2498	0	0	4	0	0	*Mix (Mla12, +?)*	
POA 2198	0	0	0	0	0	*Mix (Mla12, +?)*	
POA 2298	0	0	0(4)	0	0	*mlo, +?*	
NSGS 1749	0	0	1	0	0	*Mla12, Mlg, Ml(CP), +?*	
POB 2998	0	0	4	0	0	*Mla12*	
RAH 3198	0	0	4	0	4	*Mla1, +?*	
STH 2998	0	0	4	0	0	*Mla12, Mlg, Ml(CP), +?*	
STH 3098	2	0	4	0	0	*Mla12, Mlg, Ml(CP),+?*	
LP2.2840	0	0	4	0	0	*Mla12, +?*	
NS 96-1116	0	0	0	0	0	*mlo, +?*	
P 6616	0	0	4	0	0	*Mla7, +?*	
BKH 4099	0	0	4	4	0	*Mix (?)*	
BKH 4199	0	0	4	0	0	*?*	*Mla13 or Mla12, +?*
NAD 2699	0	0	4	0	0	*?*	*Mla12, +?*
NAD 2799	4	4	4	0	0	*Mix (Mla7, +?)*	
MOB 1899	0	0	4	0	0	*Mla12, Mlg, Ml(CP), +?*	
POA 2399	4	0	4	4	0	*?*	
STH 3199	0	0	0(4)	0	0	*mlo, +?*	
Jersey	0	0	0(4)	0	0	*mlo, +?*	
LP 697-94	0	0	0(4)	0	0	*mlo, +?*	
NS 96-1114	0	0	0	0	0	*mlo, +?*	
P7020	0	0	0(4)	0	0	*mlo, +?*	
BKH 3999	0	0	2	0	0	*Mla12, Mlg, Ml(CP), +?*	
NIB 1099	0	0	4	0	0	*Mla12, Mlg, Ml(CP), +?*	
STH 3499	0	0	4	0	0	*Mix (?)*	
Pejas	0	0+4	4	0	0	*Mix (?)*	

[1] Resistance alleles not eliminated from the reactions of susceptibility and not confirmed with the reactions of resistance [2] Unidentified resistance allele, not present in the 'Pallas' isolines set

Table 5

Continued

Cultivar or breeding line	Isolates					Postulated resistance alleles	Possible alleles[1]
	EmA30.1	HL3/5.c	JEH11-2	MH1-3	R189.1		
Sezam	0	0	4	4	0	*Mla7, +?*[2]	
Prosa	0	4	0	4	0	*Mlg, Ml(CP), +?*	
Riviera	0	3	0	4	0	*?*	*Mlg, Ml(CP)*
STH 2497	0	0	0	4	0	*Mla12*	
NS 89-1132	0	0	0	0	0	*?*	*Mla12 or Mla13,+?*
P5053.31A	0	0	0	0	0	*?*	*Mla1, +?*
BKH 3798	0	0	4	0	0	*Mla7, +?*	
NAD 2298	1	0	0	4	0	*Mla12, +?*	
NAD 2398	0	3	0	4	4	*Mla6, Mla14, +?*	
NAD 2498	0	0	0	0+4	0	*Mix (Mla12, +?)*	
POA 2198	0	4	0	0+4	0	*Mix (Mla12, +?)*	
POA 2298	0	0	0	0	0	*mlo, +?*	
NSGS 1749	0	0	0	0	0	*Mla12,Mlg,Ml(CP),+?*	
POB 2998	4	0	0	4	0	*Mla12*	
RAH 3198	0	2	0	0	0	*Mla1, +?*	
STH 2998	0	0	0	0	0	*Mla12,Mlg, Ml(CP),+?*	
STH 3098	0	0	0	2	0	*Mla12, Mlg, Ml(CP),+?*	
LP2.2840	0	0	0	2	0	*Mla12, +?*	
NS 96-1116	0	0	0	0	0	*mlo, +?*	
P 6616	0	0	0	4	0	*Mla7, +?*	
BKH 4099	4	0	0	4	0	*Mix (?)*	
BKH 4199	0	0	0	0	0	*€?*	*Mla13 or Mla12,+?*
NAD 2699	0	0	0	0	0	*?*	*Mla12, +?*
NAD 2799	0	0	0+4	0+4	0	*Mix (Mla7, +?)*	
MOB 1899	0	0	0	4	0	*Mla12, Mlg, Ml(CP),+?*	
POA 2399	0	4	4	4	4	*?*	
STH 3199	0	0	0(4)	0	0	*mlo, +?*	
Jersey	0	0	0	0	0	*mlo, +?*	
LP 697-94	0	0	0	0	0	*mlo, +?*	
NS 96-1114	0	0	0	0	0	*mlo, +?*	
P7020	0	0	0	0	0	*mlo, +?*	
BKH 3999	0	0	0	0	0	*Mla12, Mlg, Ml(CP),+?*	
NIB 1099	0	0	0	2	0	*Mla12, Mlg, Ml(CP), +?*	
STH 3499	0	0	0	0+4	0	*Mix (?)*	
Pejas	0	0+4	0	0	0	*Mix (?)*	

[1] Resistance alleles not eliminated from the reactions of susceptibility and not confirmed with the reactions of resistance [2] Unidentified resistance allele, not present in the 'Pallas' isolines set

Table 5

Continued

Cultivar or breeding line	Isolates					Postulated resistance alleles	Possible alleles[1]
	R303a	Ru3.2	TR2-2	En1/A1	R303.2		
Sezam	0	0	4	4	0	*Mla7, +?*[2]	
Prosa	4	4	4	4	4	*Mlg, Ml(CP), +?*	
Riviera	0	4	3	4	4	*?*	*Mlg, Ml(CP)*
STH 2497	0	0	4	4	0	*Mla12*	
NS 89-1132	0	0	0	4	0	*?*	*Mla12 or Mla13, +?*
P5053.31A	0	0	0	0	0	*?*	*Mla1, +?*
BKH 3798	0	0	4	4	0	*Mla7, +?*	
NAD 2298	0	0	4	4	0	*Mla12, +?*	
NAD 2398	0	4	0	0	0	*Mla6, Mla14, +?*	
NAD 2498	0	0	0+4	0+4	0	*Mix (Mla12, +?)*	
POA 2198	0	0	4	4	0	*Mix (Mla12, +?)*	
POA 2298	0	0	0	0	0	*mlo, +?*	
NSGS 1749	0	0	0	0	0	*Mla12, Mlg, Ml(CP), +?*	
POB 2998	0	0	4	4	0	*Mla12*	
RAH 3198	0	0	4	0	0	*Mla1, +?*	
STH 2998	0	0	0	1	0	*Mla12, Mlg, Ml(CP), +?*	
STH 3098	0	0	0	1	0	*Mla12, Mlg, Ml(CP), +?*	
LP2.2840	0	0	4	4	0	*Mla12, +?*	
NS 96-1116	0	0	0	0	0	*mlo, +?*	
P 6616	0	0	2	2	0	*Mla7, +?*	
BKH 4099	0	0	4	0+4	0	*Mix (?)*	
BKH 4199	0	0	0	4	0	*?*	*Mla13 or Mla12, +?*
NAD 2699	0	0	4	0	0	*?*	*Mla12, +?*
NAD 2799	0	0	0+4	0+4	0	*Mix (Mla7, +?)*	
MOB 1899	0	0	4	4	0	*Mla12, Mlg, Ml(CP), +?*	
POA 2399	4	4	4	4	4	*?*	
STH 3199	0	0	0	0	0	*mlo, +?*	
Jersey	0	0	0(4)	0	0	*mlo, +?*	
LP 697-94	0	0	0(4)	0(4)	0	*mlo, +?*	
NS 96-1114	0	0	0	0	0	*mlo, +?*	
P7020	0	0(4)	0(4)	0(4)	0	*mlo, +?*	
BKH 3999	0	0	0i4	1	0	*Mla12, Mlg, Ml(CP), +?*	
NIB 1099	0	0	0	0	0	*Mla12, Mlg, Ml(CP), +?*	
STH 3499	0+4	0	4	0+4	0	*Mix (?)*	
Pejas	0	0+4	0	0	0+4	*Mix (?)*	

[1] Resistance alleles not eliminated from the reactions of susceptibility and not confirmed with the reactions of resistance [2] Unidentified resistance allele, not present in the 'Pallas' isolines set

Table 5

Continued

Cultivar or breeding line	Isolates				Postulated resistance alleles	Possible alleles[1]
	E92-1	59-11.2	SZ/C10a	Ra7		
Sezam	4	4	4	0	*Mla7, +?*[2]	
Prosa	4	4	4	0	*Mlg, Ml(CP), +?*	
Riviera	0	0	4	0	*?*	*Mlg, Ml(CP)*
STH 2497	4	0	4	0	*Mla12*	
NS 89-1132	0	0	0	0	*?*	*Mla12 or Mla13, +?*
P5053.31A	0	0	0	0	*?*	*Mla1, +?*
BKH 3798	4	4	0	2	*Mla7, +?*	
NAD 2298	4	0	4	2+4	*Mla12, +?*	
NAD 2398	0	0	4	0	*Mla6, Mla14, +?*	
NAD 2498	0	0	0+4	0	*Mix (Mla12, +?)*	
POA 2198	0+4	0	4	0	*Mix (Mla12, +?)*	
POA 2298	0	0	0	0	*mlo, +?*	
NSGS 1749	0	0	0	0	*Mla12, Mlg, Ml(CP), +?*	
POB 2998	4	0	4	0	*Mla12*	
RAH 3198	4	0	0	0	*Mla1, +?*	
STH 2998	1	0	1	0	*Mla12, Mlg, Ml(CP), +?*	
STH 3098	1	2	2	0	*Mla12, Mlg, Ml(CP), +?*	
LP2.2840	4	0	4	2	*Mla12, +?*	
NS 96-1116	0	0	0	0	*mlo, +?*	
P 6616	1	4	2	0	*Mla7, +?*	
BKH 4099	4	0	0+4	0	*Mix (?)*	
BKH 4199	0	0	0	0	*?*	*Mla13 or Mla12, +?*
NAD 2699	4	0	0	0	*?*	*Mla12, +?*
NAD 2799	0i4	4	0+4	0	*Mix (Mla7, +?)*	
MOB 1899	4	0	4	0	*Mla12, Mlg, Ml(CP), +?*	
POA 2399	4	4	4	4	*?*	
STH 3199	0	0	0	0	*mlo, +?*	
Jersey	0	0	0	0	*mlo, +?*	
LP 697-94	0	0	0(4)	0	*mlo, +?*	
NS 96-1114	0	0	0	0	*mlo, +?*	
P7020	0(4)	0	0	0	*mlo, +?*	
BKH 3999	1	0	0	0	*Mla12, Mlg, Ml(CP), +?*	
NIB 1099	1	2	0	0	*Mla12, Mlg, Ml(CP), +?*	
STH 3499	4	4	0+4	0	*Mix (?)*	
Pejas	0	0	0	0	*Mix (?)*	

[1] Resistance alleles not eliminated from the reactions of susceptibility and not confirmed with the reactions of resistance [2] Unidentified resistance allele, not present in the 'Pallas' isolines set

Table 5

Continued

Cultivar or breeding line	Isolates				Postulated resistance alleles	Possible alleles[1]
	Ra9-1	Ra10-2	Ra16a	Ra22-2		
Sezam	4	4	4	4	*Mla7, +?*[2]	
Prosa	4	4	0	2	*Mlg, Ml(CP), +?*	
Riviera	0	4	0	0	*?*	*Mlg, Ml(CP)*
STH 2497	4	4	0	4	*Mla12*	
NS 89-1132	0	4	0	4	*?*	*Mla12 or Mla13, +?*
P5053.31A	0	0	0	0	*?*	*Mla1, +?*
BKH 3798	4	4	4	4	*Mla7, +?*	
NAD 2298	4	4	0	4	*Mla12, +?*	
NAD 2398	4	4	4	4	*Mla6, Mla14, +?*	
NAD 2498	0+4	4	0	0+4	*Mix (Mla12, +?)*	
POA 2198	0+4	4	0	0+4	*Mix (Mla12, +?)*	
POA 2298	0	0(4)	0	0	*mlo, +?*	
NSGS 1749	4	4	0	4	*Mla12, Mlg, Ml(CP), +?*	
POB 2998	4	4	0	4	*Mla12*	
RAH 3198	0	4	0	0	*Mla1, +?*	
STH 2998	4	4	0	4	*Mla12, Mlg, Ml(CP), +?*	
STH 3098	4	4	0	4	*Mla12, Mlg, Ml(CP), +?*	
LP2.2840	4	4	2	4	*Mla12, +?*	
NS 96-1116	0(4)	0	0	0	*mlo, +?*	
P 6616	4	4	4	4	*Mla7, +?*	
BKH 4099	0	4	0	4	*Mix (?)*	
BKH 4199	0	4	0	4	*?*	*Mla13 or Mla12, +?*
NAD 2699	0	4	0	0	*?*	*Mla12, +?*
NAD 2799	2	4	0+4	4	*Mix (Mla7, +?)*	
MOB 1899	4	4	0	4	*Mla12, Mlg, Ml(CP), +?*	
POA 2399	4	4	4	4	*?*	
STH 3199	0	0(4)	0	0	*mlo, +?*	
Jersey	0(4)	0(4)	0	0(4)	*mlo, +?*	
LP 697-94	0	0(4)	0	0	*mlo, +?*	
NS 96-1114	0	0(4)	0	0(4)	*mlo, +?*	
P7020	0(4)	0(4)	0	0(4)	*€mlo, +?*	
BKH 3999	4	4	0	4	*Mla12, Mlg, Ml(CP), +?*	
NIB 1099	4	4	0	4	*Mla12, Mlg, Ml(CP), +?*	
STH 3499	0+4	4	0	4	*Mix (?)*	
Pejas	0	0	0	2	*Mix (?)*	

[1] Resistance alleles not eliminated from the reactions of susceptibility and not confirmed with the reactions of resistance [2] Unidentified resistance allele, not present in the 'Pallas' isolines set

Table 6

Resistance alleles and infection types of 11 cultivars and breeding lines of winter barley to infection by 23 isolates of *E. graminis* f. sp. *Hordei*.

Cultivar or breeding line	Isolates												Postulated resistance alleles
	58-74.1	59-12	63-1a	A6c	D17-1	EmA30.1	HL3/5.c	JEH11-2	MH1-3	R189.1	R303a	Ru3.2	
Hampus	0	0	0	0	0	0	4	0	0	4	0	4	*Mla6, Mla14*
Carola	0	0	0	0	0	0	4	0	0	4	0	2	*Mla6, Mla14, +?*[1]
KRC 197	4	4	4	0	0+4	0	4	0+4	0	0+4	0	0	*Mix (?)*
BKH 2198	4	4	4	0+4	4	0	0+4	1+4	4	0	0	0+4	*Mix (?)*
LP 6-562	0	0	0	0	0	0	4	0	0	4	0	4	*Mla6, Mla14*
POA 1898	2	0+4	4	0	0+4	0	0	0+4	0	0+4	0+4	0	*Mix (?)*
BKH 2399	4	4	4	4	4	4	4	4	4	4	4	4	*Ml(Bw), +?*
CWB 96-9	4	4	4	0	4	0	4	4	0	4	4	4	*Mlra*
LP 6-758	4	4	4	4	4	4	4	4	4	4	4	4	-
NIB 999	4	0	4	0	0	0	0	0	4	0	0	0	*Mla13, Ml(Ru3)*
POA 2099	0	0	4	0	0	0	0	0	4	0	0	0	*Mla12, +?*

[1] Unidentified resistance allele, not present in the 'Pallas' isolines set

Table 6

Continued

Cultivar or breeding line	Isolates											Postulated resistance alleles
	TR2-2	En1/A1	R303.2	E92-1	59-11.2	SZ/C10a	Ra7	Ra9-1	Ra10-2	Ra16a	Ra22-2	
Hampus	0	0	0	4	0	4	4	4	4	4	4	Mla6, Mla14
Carola	0	0	0	2	0	4	4	4	4	4	4	Mla6, Mla14, +?1
KRC 197	4	4	0+4	0+4	4	4	0+4	4	4	4	4	Mix (?)
BKH 2198	0	4	1	2	4	0+4	4	4	4	4	4	Mix (?)
LP 6-562	0	0	0	2	0	4	4	4	4	4	4	Mla6, Mla14
POA 1898	0+4	4	0	0+4	0	4	0	0+4	4	4	4	Mix (?)
BKH 2399	4	4	4	2	4	4	4	4	4	4	4	Ml(Bw), +?
CWB 96-9	4	4	4	4	4	4	4	4	4	4	4	Mlra
LP 6-758	4	4	4	4	4	4	4	4	4	4	4	-
NIB 999	0	4	0	0	0	0	0	0	4	0	4	Mla13, Ml(Ru3)
POA 2099	4	4	0	4	0	4	0	4	4	0	4	Mla12, +?

[1] Unidentified resistance allele, not present in the 'Pallas' isolines set

gene (*Mlra*) for resistance. None gene for resistance was detected in breeding line LP 6-758.

DISCUSSION

Currently powdery mildew is one of the most common and most widespread disease of barley. However it was, for a long time, not important factor in barley production. The first devastating epidemic of barley powdery mildew was observed in Europe on winter barley in 1901 and on spring barley in 1903 (Wolfe and Schwarzbach 1978). It happened at the advent of modern agricultural methods such as the large scale cultivation of uniform varieties, the use high crop densities and the application of nitrogen fertilizers (Wolfe and Schwarzbach 1978, Wolfe 1984). The main means of control of powdery mildew are using of fungicides and growing of resistant varieties. However, future strategies for the control of powdery mildew will have to focus increasingly on ecologically sound methods because any usage of chemicals (pesticides, fungicides, herbicides, and mineral fertilizers) in agriculture is increasingly criticized in societies of many countries. This possible method is breeding for resistance. Application of resistance is considered also as relatively inexpensive and convenient for the farmer because the use of fungicides requires investments in machinery, labour and special training (Czembor and Gacek 1990, 1995, Gullino and Kuijpers 1994, Brown 1996, Jacobsen 1997).

A number of genes for specific resistance have been used in commercial barley cultivars. However from 33 the most common alleles 28 are closely linked or allelic (Jørgensen 1992b, 1994). This limits the possible number of combination in breeding of new cultivars and all these genes were successively overcome by the appearance of pathotypes with matching virulence (Gacek 1990, Czembor and Gacek 1990, Czembor and Czembor 1998, 1999). This was confirmed in this study by presence of genes in *Mla* locus in 51% of spring and in 45% of winter barley cultivars and breeding lines. Because of this situation the durability of resistance genes may be increased by use of multiline cultivars or by combining ('pyramiding') different resistance genes into one cultivar (Gacek and Czembor 1983, 1984, Czembor and Gacek 1990). Obtained results indicated that these strategies are commonly used by barley breeders. Multiline strategy of deploying resistance genes was used in 6 spring and 3 winter barley cultivars and breeding lines, respectively. In majority (94% of spring and 91% of winter) of tested cultivars 'pyramiding' different resistances into one cultivar was observed.

Also deploying many cultivars with different resistance genes in space (e. g. cultivar mixtures, growing different cultivars in different regions) or time (spring versus winter) may be used (Czembor and Gacek 1990, 1996, Finckh *et al.* 1996, 1997, 1999, Gacek *et al.* 1996, 1997, Czembor and Czembor 1998, 1999). For effectiveness of these strategies many

cultivars with different resistance genes and use of different resistance genes in spring and winter barley cultivars are needed. Presence of 12 different resistance genes from which only 3 are common for spring and winter cultivars and breeding lines is making possible to use successfully these two strategies.

Very important for resistance to powdery mildew in spring barley is presence of *Mlo* resistance in seven cultivars and breeding lines (POA 2298, NS 96-1116, STH 3199, Jersey, LP 697-94, NS 96-1114, P7020). The *Mlo* resistance has become very important source of powdery mildew resistance in barley because there is no known virulence for these genes (Hovmøller *et al.* 2000). However, in Europe in order to prolong effectiveness of the *Mlo* resistance it is proposed to use this resistance only in cultivars of spring barley (Jřrgensen 1994, Dreiseitl 1996, Atzema 1998). The *Mlo* resistance is a unique kind of resistance because it is monogenic, non-race-specific. Negative pleiotropic effects that were common when *mlo* was used in earlier crosses have been overcome by recent breeding and this type of resistance is at present utilized with increasing intensity in spring barley production. In the last couple of years 20-30% spring barley cultivars grown in EU and in Poland carry Mlo resistance (Jørgensen 1992a, 1994, Atzema 1998, Czembor and Czembor 1998, Anonymous 2000a). Obtained results indicate that 20% of spring cultivars and breeding lines tested in 1998-2000 Polish registration trials have *mlo* genes. These cultivars and breeding lines are very good sources for breeding for durable powdery mildew resistance.

Powdery mildew on barley is one of the most clearly characterized systems of host-pathogen genetic interactions. Since 1907, when Biffen started genetic studies of barley resistance to powdery mildew, in barley more than 100 mildew resistance genes have been identified (Biffen 1907, Jørgensen 1994, Czembor 2000a, 2000b, Czembor and Czembor 2000). The many resistance loci detected in barley make it increasingly difficult to apply the gene-for gene hypothesis for identification of resistance genes in newly released cultivars. It is especially difficult when Mlo resistance and other race-specific resistance genes are combined in the same cultivar (Czembor and Czembor 1998). The results presented here come from tests performed on seedlings, which does not necessarily predict adult plant resistance and field performance of the selected resistant lines. However, determination of powdery mildew resistance genes based on tests performed on seedlings is effective and sufficient for breeders and pathologist needs (Jensen and Jørgensen 1991, Brown and Jřrgensen 1991, Jensen *et al.* 1992, Czembor and Czembor 1998, 1999, Dreiseitl and Jørgensen 2000). Also different levels of partial resistance in tested lines may have influence on conclusions concerning postulation of presence of specific resistance genes (Jørgensen 1994, Czembor 1996).

Based on this study it may be concluded that in 1998-2000 Polish registration trials is a sufficient number of barley cultivars and breeding

lines with different resistance genes to use them, after their eventual registration, in different gene deploying strategies for efficient control of powdery mildew.

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