

# Genetic control of powdery mildew resistance in common wheat (*Triticum aestivum* L.)

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Several common wheat cultivars and lines were analyzed for resistance to powdery mildew disease by using the method of aneuploid monosomic analysis and differential isolates of *Erysiphe graminis* f. sp. *tritici*. Disease response patterns and the mode of inheritance were determined, and new resistance genes have been located and identified. Monosomic analysis revealed that powdery mildew resistance of the Italian cultivar 'Virest' was conferred by a single dominant gene, *Pm22*, located on chromosome 1D. Resistance to pathogen in the introgressive line 146-155-T, derivative of *Triticum timopheevii*, was controlled by one dominant gene, *Pm27*, located on the 6B chromosome. Restriction fragment length polymorphism and microsatellite analyses detected the presence of a *T. timopheevii* segment translocated to the 6B chromosome, with breakpoints between the loci *Xpsr 8/Xpsr 964* on 6B<sup>s</sup> arm and *Xpsr 154/Xpsr 546* on 6B<sup>l</sup> arm. The powdery mildew resistance of the Estonian/Finland cultivar 'Meri' was controlled by one major dominant gene, *Pm28*, located on the 1B chromosome.

**Key words:** monosomic analysis, powdery mildew resistance, *Triticum aestivum*, *Triticum timopheevii*

## INTRODUCTION

Powdery mildew, caused by *Erysiphe graminis* f. sp. *tritici*, is one of the most important diseases of common wheat, *Triticum aestivum*, in the Baltic countries and in almost all temperate regions of the world. Up to now, 28 genes for mildew resistance have been designated [1, 2], however, only few major resistance genes are currently in use in commercial wheat cultivars, because the efficiency of the most of them has already been overcome by new virulent strains of the pathogen. Therefore it is necessary to search for and identify new resistance ge-

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Table 1. Segregation for seedling reaction to mildew isolates Nos. 2 and 6 in monosomic F<sub>2</sub> populations from crosses of 21 'Chinese Spring' monosomics with common wheat cultivar 'Virest'

Monosomic line	Powdery mildew isolate No. 2		$\chi^2$ 3 : 1	Powdery mildew isolate No. 6		$\chi^2$ 3:1
	Resistant	Susceptible		Resistant	Susceptible	
1A	112	38	0.01	114	36	0.08
2A	12	4	0.00	11	5	0.33
3A	101	31	0.16	101	31	0.16
4A	72	32	1.84	75	29	0.46
5A	91	25	0.74	89	27	0.19
6A	99	34	0.02	108	25	2.73
7A	52	16	0.08	54	14	0.71
1B	110	36	0.01	106	40	0.45
2B	89	30	0.00	88	31	0.07
3B	93	28	0.23	95	26	0.80
4B	98	28	0.52	95	31	0.01
5B	101	27	1.04	100	28	0.67
6B	106	39	0.28	109	36	0.00
7B	26	9	0.01	25	10	0.24
1D	92	12	10.05**	93	9	11.54**
2D	109	39	0.15	113	35	0.15
3D	41	13	0.02	43	11	0.61
4D	112	34	0.23	112	34	0.23
5D	83	27	0.01	89	21	2.05
6D	94	37	0.73	100	31	0.12
7D	56	16	0.30	56	16	0.30

\*\*P < 0.01.

nes for ensuring the diversification of gene combinations in wheat breeding.

The present report deals with the localization and identification of genes conferring resistance to powdery mildew in cultivars 'Virest' and 'Meri' and in breeding line 146-155-T, derivative of *Triticum timopheevii*, on the basis of disease response patterns, the mode of inheritance and monosomic analysis.

## MATERIALS AND METHODS

A set of 21 Chinese Spring monosomic lines was crossed as female with the common wheat cultivars 'Virest' and 'Meri' and with the introgressive line 146-155-T selected in the progeny of crosses between the mutant line 146-155 (induced by NMU in wheat cv. 'Norröna') and tetraploid wheat *Triticum timopheevii* [3]. Cytologically verified monosomic plants  $F_1$  ( $2n = 41$ ) were grown in greenhouse and selfed to determine the segregation ratios for the  $F_2$  generations. The powdery mildew isolates Nos. 2, 6 and 9 were used to test segregating  $F_2$  populations in the seedling stage. Methods applied for inoculation of leaf segments and disease assessment were as described by J. Lutz et al. [4].

## RESULTS AND DISCUSSION

The  $F_2$  populations from the crosses of the 21 'Chinese Spring' (CS) monosomics with cv. 'Virest' were inoculated with powdery mildew isolates Nos. 2 and 6. Twenty of the  $F_2$  populations segregated in ratios of 3 resistant: 1 susceptible, but hybrid combination between CS mono- 1D and 'Virest' significantly deviated from the expected 3:1 ratio (Table 1). This indicated that the major dominant gene conferring resistance to powdery mildew was located on chromosome 1D. The new gene was designated *Pm 22* [1, 5].

The  $F_2$  progenies from the crosses of CS monosomics with introgressive wheat line 146-155-T, inoculated with powdery mildew isolate No. 9, showed a ratio of 3:1 resistant to susceptible plants in 20

Table 2. Segregation for seedling reaction to mildew isolates No. 9 in monosomic  $F_2$  populations from crosses of 21 'Chinese Spring' monosomics with the hybrid line 166-155-T

Monosomic line	Powdery mildew isolate No. 2		$\chi^2$ 3 : 1
	Resistant	Susceptible	
1A	54	17	0.08
2A	114	26	2.76
3A	66	24	0.10
4A	161	51	0.09
5A	166	55	0.00
6A	177	62	0.08
7A	176	54	0.36
1B	73	26	0.09
2B	79	25	0.04
3B	110	36	0.02
4B	189	57	0.48
5B	106	37	0.02
6B	180	15	31.5*
7B	120	26	4.17
1D	185	59	0.08
2D	134	37	1.01
3D	178	49	1.49
4D	107	44	1.25
5D	107	43	0.96
6D	155	68	3.43
7D	71	22	0.05

\*P < 0.01.

Table 3. Segregation for seedling reaction to mildew-isolates Nos. 2 and 9 in monosomic  $F_2$  populations from crosses of 21 'Chinese Spring' monosomics with common wheat cultivar 'Meri'

Monosomic line	Powdery mildew isolate No. 2		$\chi^2$ 3 : 1	Powdery mildew isolate No. 6		$\chi^2$ 3:1
	Resistant	Susceptible		Resistant	Susceptible	
1A	114	32	0.74	110	36	0.01
2A	57	17	0.16	111	41	0.31
3A	102	37	0.19	106	33	0.12
4A	113	39	0.03	116	36	0.14
5A	90	33	0.22	88	35	0.78
6A	90	33	0.22	93	30	0.02
7A	92	27	0.34	87	32	0.23
1B	127	10	22.89*	121	16	12.96*
2B	71	25	0.05	70	26	0.22
3B	112	40	0.14	117	35	0.31
4B	113	35	0.14	112	36	0.04
5B	109	33	0.23	103	39	0.46
6B	111	36	0.02	104	43	1.42
7B	106	43	1.18	117	32	0.99
1D	117	33	0.72	113	37	0.01
2D	101	43	1.81	108	36	0.00
3D	117	37	0.08	112	42	0.42
4D	85	27	0.05	78	34	1.71
5D	110	39	0.11	110	39	0.11
6D	54	17	0.04	50	21	0.79
7D	81	24	0.26	78	27	0.03

\*P < 0.05.

cross-combinations. The  $F_2$  population from the cross between CS mono- 6B and wheat line 146-155-T significantly deviated from the expected ratio 3:1 (Table 2).

A monosomic and marker molecular analysis has shown that the powdery mildew resistance in line 146-155-T is controlled by a single gene located on a segment from *Triticum timopheevii* chromosome that has been transferred into chromosome 6B of common wheat. This new powdery mildew resistance gene has been designated *Pm 27* [6].

The  $F_2$  population from the crosses of the 21 monosomic lines of CS and cv. 'Meri' were tested with isolates Nos. 2 and 9 (Table 3). The segregation of the cross between CS mono- 1B with cv. 'Meri' deviated in a highly significant way from the expected ratio 3:1. Such great deviations from the Mendelian ratios of segregation with a significant decrease of the susceptible plant amount indicates the location of the dominant resistance gene on the

"critical" chromosome 1B. The segregation ratios for disomic and all other monosomic crosses in ratios of 3 resistant: 1 susceptible satisfactorily conformed with a single gene segregation for both isolates. The new dominant gene located on chromosome 1B was designated *Pm 28* [2].

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