# Genetic structure peculiarities of the *Blumeria graminis* f. sp. *hordei* population in the north-eastern part of Lithuania

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In 2000, ascospores of *Blumeria graminis* f. sp. *hordei* were sampled in the north-eastern part of Lithuania, near Zarasai. Pathogen isolates were tested for virulence genes *Va1, Va3, Va6, Va7, Va9, Va12, Va13, Vk, Vla,* $V_{SI}$, $V_{ST}$, $V_{GO}$, $V_{ME}$. Virulence frequencies of *Va6, Va7, Va9, Va12, Vk, Vla* were high (60–80%). Virulence frequencies of *Va1, Va3, Va13,* $V_{SI}$, $V_{ST}$, $V_{GO}$, $V_{ME}$ were low (1–8%). Differences between pathogen populations in the north-eastern part of Lithuania and eastern part of Latvia (Latgale region, Daugavpils) were not detected.

**Key words:** *Blumeria graminis,* barley, virulence, resistance

## INTRODUCTION

Barley powdery mildew caused by *Blumeria graminis* f. sp. *hordei* is one of the widespread barley diseases. The use of host resistance for disease control is widely recommended [1].

No information on the virulence pattern of *Blumeria graminis* f. sp. *hordei* has been available in Lithuania till now. The genetic particularities of this pathogen are studied actively in many of European countries (see for review [1]). In the Baltic States, *Blumeria graminis* f. sp. *hordei* was studied only in Latvia [2]. The aim of this investigation was to get information on the frequencies of most important virulence genes in *Blumeria graminis* f. sp. *hordei* population in North-Eastern Lithuania.

## MATERIALS AND METHODS

Pathogen samples in the phase of cleistothecia were collected from leaves of barley of unknown genotype from commercial fields near Zarasai in August 2000. Monopustule isolates were tested for virulence by a set of differentials (Table 1) on detached leaves placed on agar with 0.004% benzimidazol. Inoculation was done by the microinoculation technique. Each isolate was designated by infection type on a 0–4 scale [3] under laboratory conditions (0–3 – avirulence, 4 – virulence). The frequencies of the particular virulences and pathotypes were calculated.

Table 1. **List of differentials used for detection of virulence genes**

| Differentials | Main resistance genes |
|---|---|
| P01 | *Mla1* |
| P02 | *Mla3* |
| P03 | *Mla6* |
| P04B | *Mla7* |
| P08B | *Mla9* |
| P10 | *Mla12* |
| P11 | *Mla13* |
| P17 | *Mlk* |
| P23 | *MlLa* |
| SI1 | *Ml(SI1)* |
| Steffi | *Ml(St1), Ml(St2)* |
| Goldie | *Mla12, MlLa, U* |
| Meltan* | *Mla13, Ml(IM9), Ml(Hu4)* |

* Three genes commonly are designated as $Ml_{ME}$.

## RESULTS AND DISCUSSION

Frequencies of virulence genes in the pathogen population in 2000 are presented in Table 2. All virulences can be divided into two sets. The first one included genes with high and the second with low frequencies.

High frequencies were detected for the virulences *Va6, Va7, Va9, Va12, Vk, Vla*: they exceeded 60–80%. It means that the corresponding resistance

Table 2. **Virulence frequencies of *Blumeria graminis* f. sp. *hordei* population of north-eastern part of Lithuania in 2000**

| Virulences | N | A | Γ |
|---|---|---|---|
| *Va1* | 75 | 2 | 2.6 |
| *Va3* | 75 | 3 | 4.0 |
| *Va6* | 75 | 62 | 82.6 |
| *Va7* | 75 | 58 | 77.3 |
| *Va9* | 75 | 62 | 82.6 |
| *Va12* | 75 | 52 | 69.3 |
| *Va13* | 75 | 6 | 8.0 |
| *Vk* | 75 | 59 | 78.6 |
| *Vla* | 75 | 56 | 74.6 |
| $V_{SI}$ | 75 | 4 | 4.0 |
| $V_{ST}$ | 75 | 1 | 1.3 |
| $V_{GO}$ | 75 | 2 | 2.6 |
| $V_{ME}$ | 75 | 5 | 6.6 |

N – number of tested isolates, A – number of isolates with particular virulence, V – virulence frequency.

genes *Mla6, Mla7, Mla9, Mla12, Mlk, MlLa* are ineffective in the north-eastern part of Lithuania. These genes lost their effectiveness in the neighbouring Latvia [2, 4] as well as in other parts of Europe [1].

The frequency of the virulence $V_{ME}$ in the pathogen population reached approximately only 6%. The corresponding resistance of the variety 'Meltan', which in fact is controlled by three genes *(Mla13, Ml(Im9), Ml(Hu4))*, was high. The more genes in a variety, the higher its resistance.

The frequencies of the virulences *Va1, Va3, Va13* were also low (2.6–8.0%) in North-Eastern Lithuania, implying that the race-specific resistance genes *Mla1, Mla3, Mla13* were effective at the moment. However, during the recent years a clear tendency was observed to higher frequencies of the virulences *Va1, Va3, Va13* in Europe. In some countries these virulences reached a middle-high level [1]. The pathogen spores spread generally in the west-east direction according to the main wind direction with an average speed of 110 km per year [5]. Thus, there is a high probability that the corresponding resistance genes will lose their effectiveness also in Lithuania and in other Baltic States, for example, in Latvia [2], in some years. Therefore it is very important to look for the new sources of resistance.

Only some sporadic isolates were found to overcome *SI1,* 'Goldie' and 'Steffi' resistance genes. The corresponding virulence genes $V_{SI}$, $V_{GO}$, $V_{ST}$ were of low frequencies (1–4%) in the pathogen population in Lithuania. Resistance genes from differentials *SI1,* 'Steffi' and 'Goldie' were highly effective as in other parts of Europe. *SI1* is a new source of resistance [1].

Pathotypes and their virulences in Lithuania in 2000 are presented in Table 3. A rather large number of pathotypes was detected: 10 alleles occurred in 34 different combinations. The most common pathotype in the pathogen population with a frequency 24.0% was *a6 a7 a9 a12 k la.* The same dominant pathotype was detected also in the eastern part of Latvia in 2000 [6]. All virulences presented in this pathotype had high frequencies in the both populations of the pathogen.

The frequencies of other pathotypes which comprised mainly the virulences *Va6, Va7, Va9, Va12, Vk, Vla* were low in the pathogen population (Table 3). The dominance of single (or few) patho-

Table 3. **Pathotypes and their frequencies in the pathogen population of North-Eastern Lithuania in 2000 (calculated for genes *Va1, Va3, Va6, Va7, Va9, Va12, Va13, Vk, Vla,* $V_{ME}$)**

| Pathotypes | Number of pathotypes | Frequencies, % |
|---|---|---|
| a1 a6 a7 a12 a13 k me | 1 | 1.3 |
| a1 a6 a7 a9 a12 | 1 | 1.3 |
| a12 k la | 1 | 1.3 |
| a3 a6 a7 a9 | 1 | 1.3 |
| a3 a6 a9 k la | 1 | 1.3 |
| a3 a7 a9 a12 a13 k la me | 1 | 1.3 |
| a6 a12 | 1 | 1.3 |
| a6 a12 k | 1 | 1.3 |
| a6 a12 k la | 1 | 1.3 |
| a6 a12 la | 1 | 1.3 |
| a6 a7 a12 la | 4 | 5.3 |
| a6 a7 a9 a12 a13 k la | 1 | 1.3 |
| a6 a7 a9 a12 k la me | 1 | 1.3 |
| a6 a7 a9 a12 la | 2 | 2.7 |
| a6 a7 a9 | 1 | 1.3 |
| a6 a7 a9 a12 k | 3 | 4.0 |
| a6 a7 a9 a12 k la | 18 | 24.0 |
| a6 a7 a9 a12 | 3 | 4.0 |
| a6 a7 a9 a12 la | 1 | 1.3 |
| a6 a7 a9 k | 4 | 5.3 |
| a6 a7 a9 k la | 6 | 8.0 |
| a6 a7 a9 la | 1 | 1.3 |
| a6 a7 k la | 1 | 1.3 |
| a6 a9 a12 k la | 6 | 8.0 |
| a6 a9 k | 1 | 1.3 |
| a6 k la | 1 | 1.3 |
| a7 a9 a12 a13 k la | 1 | 1.3 |
| a7 a9 a12 a13 k | 1 | 1.3 |
| a7 a9 a12 k la me | 2 | 2.7 |
| a7 a9 a13 k la | 1 | 1.3 |
| a7 a9 k la | 3 | 4.0 |
| a9 a12 k la | 1 | 1.3 |
| a9 k | 1 | 1.3 |
| k la | 1 | 1.3 |

types and a large number of pathotypes with low frequencies is a typical feature of powdery mildew fungi, proved by European-wide research data [7].

In 2000, particular pathotypes that consist of virulences with low frequency (*Va1, Va3, Va13,* $V_{ME}$) were detected in Lithuania. Such pathotypes were detected also in Latvia in 2000, and their frequencies were also low [6].

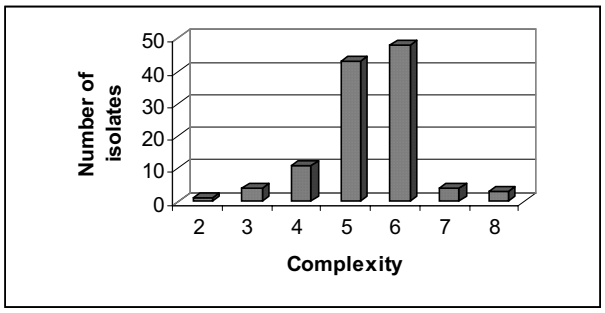


Figure. Distribution of virulence complexity in *Blumeria graminis* f. sp. *hordei* population of North-Eastern Lithuania in 2000

The distribution of virulence complexity in Lithuania in 2000 is presented in Figure. The complexity in all isolates tested varied from 2 to 8 virulences per genotype. Only one isolate with the maximal complexity was detected. The mean number of virulences per genotype was approximately 5, which proved the pathogen ability to accumulate virulences in particular genotypes.

Data obtained in the north-eastern part of Lithuania and the eastern part of Latvia in 2000 show a similarity of particular virulence frequencies, despite the fact that the grown host commercial varieties on these territories are different. The similarity of populations is most probably conditioned by their geographical proximity and similar climatic factors.

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