TRENDS OF THE CHANGES OF THE VIRULENCE GENES FREQUENCIES IN THE LATVIAN POPULATION OF BLUMERIA GRAMINIS F.SP. HORDEI

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Abstract

Samples of Blumeria graminis f.sp. hordei were collected in two different part of Latvia during 1996—2002. Frequencies of virulence genes Va6, Va7, Va9, Va12, Vk and Vla were high in both places. All years of investigation very low frequencies were found for virulences against resistance factors in the barley line SI1 and variety ‘Steffi’. Not any isolate virulent to mlo gene was found. During 1996—2002 considerable changes of frequencies of some virulence genes were detected. Firstly virulence genes Val, Va3 and Va13 appeared only in the Central part of Latvia with low frequencies and later their frequencies increased from 4—14% in 1996 to 33—53% in 2000. About 2—3 years later those virulence genes appeared in the South-eastern part of Latvia. In 2001—2002, considerable increasing of Val, Va3 and Va13 were detected also in this region: virulence frequencies against barley lines with Mla!, Mla3 and Mla13 resistance genes reached 23—30%. We postulated that mentioned changes of the population structure are result of spore spread which for the barley powdery mildew agent occurs generally in the West-East direction (Limpert et ai., 1999). The distance between places of the investigation (about 200 km) and difference in time of the virulence appearing corresponds to the approximately speed of pathogen spread 100 km per year

Key words: powdery mildew, barley, virulence genes, resistance.

Introduction

Barley (Hordeum vulgare L.) is one of the most important cereals in Europe (Bousset et al., 2002). There are many dangerous pathogens of barley, the biotrophic fungus Blumeria graminis f.sp. hordei, an ascomycete that is one of them. The fungus is the causal agent of barley powdery mildew, which can arise more than 25% of loses in yield (Czembor and Czembor, 2001). The disease spreads by conidiospores, which forms a numerous pustules on the leaf surface. Spores mostly dispersed by wind to neighbouring plants, where new infection establishes. Live spores of the Blumeria graminis f.sp. hordei were wind-transported over distances of 500 km or more with a speed approximately 100 km per year from West to East (Limpert, 1987; Limpert et ai., 1999; Brown, Hovmøller, 2002; Hovmøller et ai., 2002).

Long-distance dispersal, mutations and recombinations are the most important reasons for genotype or pathotype diversity in different populations of Blumeria graminis f.sp. hordei. The need to control of barley powdery mildew is a major stimulus for investigation of virulences of the pathogen in different countries where this disease is a problem.

Virulence genes and their frequencies may vary considerably between regions and years. The composition of virulence genes of the pathogen and their frequencies were detected in different parts of Europe (Torp et ai., 1978; Hovmøller et ai., 2000; Czembor, Blandenopolous, 2001). In Latvia, monitoring of the virulence genes frequencies in Blumeria graminis f.sp. hordei population was done since 1981, mainly in the central part of country (Rashal et ai., 1997). Since 1995, South-eastern part of Latvia was included in the research program. Data about virulence frequencies in Latvia were presented earlier (Rashal et ai., 1997; Kokina, Rashal, 2001; Kokina et ai., 2002; Kokina, Rashal, 2004).

The aim of this paper is to accentuate changes in the composition of virulence genes of Blumeria graminis f.sp. hordei and their frequencies in Latvia during several last years. We discuss here reasons of differences between those frequencies in different parts of Latvia.

Materials and Methods

In 1996—2002 samples of the pathogen were collected in the Southeastern part of Latvia. In the Central part of the country samples were collected in 1996—2000. In both cases the universally susceptible variety ‘Otra’ were used as a trap plant. Monopustules were isolated from collected samples both in sporulation and cleistothecia phases.

A set of differentials was used for the detection of monopustules (Table 1). Differentials were inoculated by microinoculation technique (Dreiseitl, 1998). Infection types of each isolate on the differentials were scored after 8—9 days according (Torp et ai., 1978) on a 0—4 scale.
Results and Discussion

The long-term observation of the pathogen population is necessary to get information about the pathogen spread direction and ability to overcome host resistance factors. This kind of knowledge is very important for resistance breeding programs, because any usage of chemicals for plant protection is increasingly criticized (Czembor, Blandenopoulos, 2001).

During 1996—2002 considerable changes of frequencies of some virulence genes were detected in the pathogen population in Latvia. Particularly interesting are data about virulence genes \( V_{a1}, V_{a3} \) and \( V_{a13} \) (Fig. 1). First mentioned virulences appeared in the Central part of Latvia with low frequencies and later their frequencies increased from 4—14% in 1996 to 33—53% in 2000. About 2—3 years later than in the Central part those virulence genes appeared in the Southeastern part of Latvia too. In 2001—2002, considerable increasing of \( V_{a1}, V_{a3} \) and \( V_{a13} \) were detected also in this region: virulence frequencies against barley lines with \( M_{la1}, M_{la3} \) and \( M_{la13} \) resistance genes reached 23—30%.

Most probably, that mentioned changes of virulences are result of spore spread which for the barley powdery mildew agent occur generally in the West-East direction (Limpert et al., 1999). The distance between places of the investigation (about 200 km) and difference in time in virulence appearing corresponds to the approximately speed of pathogen spread 100 km per year (Limpert et al., 1999; Brown, Hovmøller, 2002; Hovmøller et al., 2002).

Since 1999, barley line \( S_{II} \) and variety ‘Steffi’ were included in the research programs in Latvia. Some virulent isolates against \( S_{II} \) resistance factors were detected in both parts of Latvia in 1999 (Fig. 1). In 2000, such isolates were detected in the Southeastern part of Latvia only. Since 2001, not any virulent isolate against \( S_{II} \) was detected here. Gradual increasing of \( V(S_{II}) \) presence in population from 2% to 11% were observed in Southeastern part of Latvia in the opposite from the Central part, where it decreased from 32% in 1999 till 13% in 2000.

There are many virulence genes with high frequencies in Latvian population of barley powdery mildew: \( V_{a6}, V_{a7}, V_{a9}, V_{a12}, V_k \) and \( V_{la} \). Those virulence genes were presented in the both parts of the population with frequencies higher than 60—90% in all years of investigation. It is not any sense to use correspondent resistance genes in the commercial barley varieties.

Only \( mlo \) resistance gene was completely effective during all years of the investigation. This gene is very wide exploited in spring barley in the West and Central Europe and it is used also in contemporary barley breeding programs in Latvia. There are attempts to introduce \( mlo \) resistance into modern winter barley varieties. If \( mlo \) resistance will be presented on barley fields all year around the natural selection pressure in direction to broken down this resistance type will increase extremely.
Fig. 1. Virulence genes with low-medium frequencies in the Sourtheasern (a) and Central (b) parts of Latvia in 1996—2002

Taking in account the direction of the spore dispersal in Europe and our results we can predict that any new *Blumeria graminis* f.sp. *hordei* virulence which would occur in the Central or West Europe will come to Latvia in several years. It means that breeding programs should based not only on few resistance sources even they are highly effective at the moment. Therefore it is especially important to looking for the new resistance sources, especially from barley wild relatives, such as *Hordeum spontaneum*. 
Fig. 2. Virulence genes with high frequencies in the Southeaster (a) and Central (b) parts of Latvia in 1996—2002.
References


