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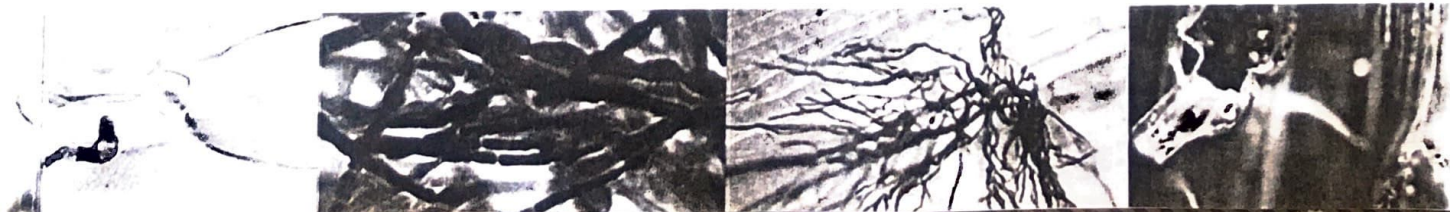
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ABSTRACT BOOK



P10. Virulence of *Blumeria graminis tritici* in Serbia (2000-2009)

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Blumeria graminis tritici, the causal agent of powdery mildew is a regular and economically important disease of wheat in Serbia. Infection intensity varies depending on wheat variety, climate conditions and agricultural practices. Although there have been no epiphytotics in Serbia yet, this disease can play a significant role in the formation of yield. Successful wheat breeding for resistance to causal agent of powdery mildew is based on the identification of virulence and changes in the pathogen population. In Serbia, continual population surveys started in 1961, when physiological races were identified, and they continued up to date. In the early 1970s, conventional investigations of physiological races were improved by introducing a survey of the virulence of pathogen populations, based on the interaction between resistance alleles and virulence according to the "gene-for-gene" theory.

The sexual generation of the population was studied for ten years (2000-2009). Wheat samples containing cleistothecia of the fungus were collected in 46 locations in Serbia. Fungal cultures were produced by the standard method. Pathogenicity of 288 isolates (cultures) of *Blumeria graminis tritici* was determined by comparing them with wheat varieties and lines that possess resistance genes: Axminster/8*CC (Pm1), Ulka/8*CC (Pm2), Idaed 59b/8*CC (Pm2+), Asosan/8*CC (Pm3a), Chul/8*CC (Pm3b), Sonora/8*CC (Pm3c), Khapli/8*CC (Pm4a), Weihenstephan M-1 (Pm4b), Hope/8*CC (pm5), Michigan Amber/8*CC (Pm6), Transec (Pm7), Kavkaz (Pm8), Amigo (Pm17), Normandie (Pm1+Pm2+Pm9), CI 12633 (Pm2+Pm6), Coker 983 (Pm5+Pm6), Halle Stamm 13471 (Mld), Granada (Pm5+Pm8), Dolomit (Mli), C-39 (Pm2+Pm4b+Pm6). (* - eight-times backcrossed to Chancellor). Reaction of seedlings was assessed 8-10 days after inoculation, on the 0-9 scale.

The 288 isolates analyzed rendered 259 virulence formulae. The results showed that numerous genotypes had V7, V6, V5+8, V8, V3c, v5, Vi and V4a virulence alleles. Most efficient among the sexual populations of the parasite was the gene combination Pm5+6 from the variety Coker 983. A large number of the pathotypes produced by sexual reproduction cannot exist in nature, or their frequencies in the population are very low.

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