

## Assessing stripe rust (*Puccinia striiformis* f. sp. *tritici*) population structure in Poland in 2023

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Yellow rust, caused by the fungus *Puccinia striiformis* f. sp. *tritici* (Pst), can lead to significant reductions in crop yields under favorable conditions. It is considered one of the most important wheat pathogens. The risk of decreased yields depends on the frequency and speed at which new fungal races spread. Understanding the genetic composition of the pathogen population is crucial for developing resistant wheat varieties and promoting sustainable agricultural practices.

In this study, 48 single uredinium *Pst* isolates from spring and winter wheat, as well as triticale, were collected from eight locations in Poland in 2023. DNA was extracted from these isolates using the CTAB method. The isolates were assessed using two molecular techniques: analysis of SSR profiles at 19 loci (Ali et al., 2011) and MARPLE (Mobile And Real-time PLant disEase; Radhakrishnan et al., 2019). Additionally, selected isolates were phenotyped using a differential test.

The SSR method can be easily implemented in most laboratories with existing equipment and is a robust tool for characterizing isolate races. MARPLE provided extensive data and information about the isolates but required more resources, including consumables, computing power, and data storage. Phenotyping, although very time-consuming and labor-intensive as it requires a substantial number of rust spores for infection testing, is relatively inexpensive in terms of material costs.

The *P. striiformis* population in Poland was diverse. We identified genetic groups PstS7, PstS8, PstS10, and PstS13, along with two samples that contained a mix of more than one race. The dominant pathotype was PstS10. Monitoring the pathogen population and understanding its genetic structure are vital for effective crop protection and resistance breeding.