



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

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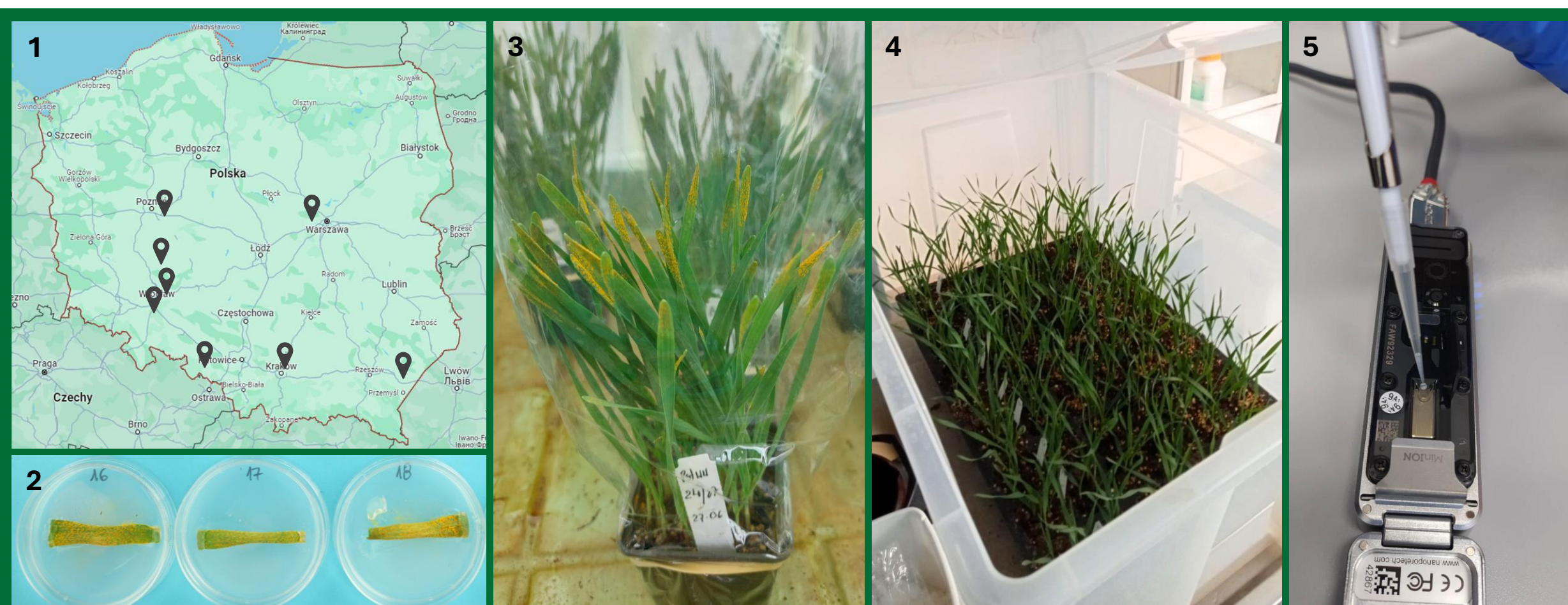
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## INTRODUCTION

Yellow rust caused by the fungus *Puccinia striiformis* f. sp. *tritici* (Pst), can lead to significant reductions in crop yields when conditions are favorable. It is considered one of the most important pathogens of wheat. The risk of the decreasing quantity of yield depends on the frequency and speed of spreading of new fungus races. Understanding the genetic makeup of the pathogen population is essential for developing resistant varieties and promoting sustainable agricultural practices.

## MATERIALS AND METHODS

In this study 48 single uredinium Pst isolates obtained from both spring and winter wheat and triticale from eight localizations in Poland in year 2023 were assessed. DNA from Pst isolates was extracted using CTAB method. Assessment of the isolates was carried out using two molecular methods: analysis of SSR profiles for 19 loci (Ali et al. 2011) and MARPLE (Mobile And Real-time PLant disEase; Radhakrishnan et al. 2019). In addition, selected isolates were phenotyped using a differential test.



**Figure 1. Collection and testing of Pst isolates.** 1 – Collection of Pst-infected leaves from various plant breeding stations across Poland, 2 – Growth of Pst on disinfected leaves placed in 1% agar, 3 – Inoculum production, 4 – Virulence tests on a differential panel comprising wheat and triticale lines with known Pst resistance genes, 5 – Molecular analysis.

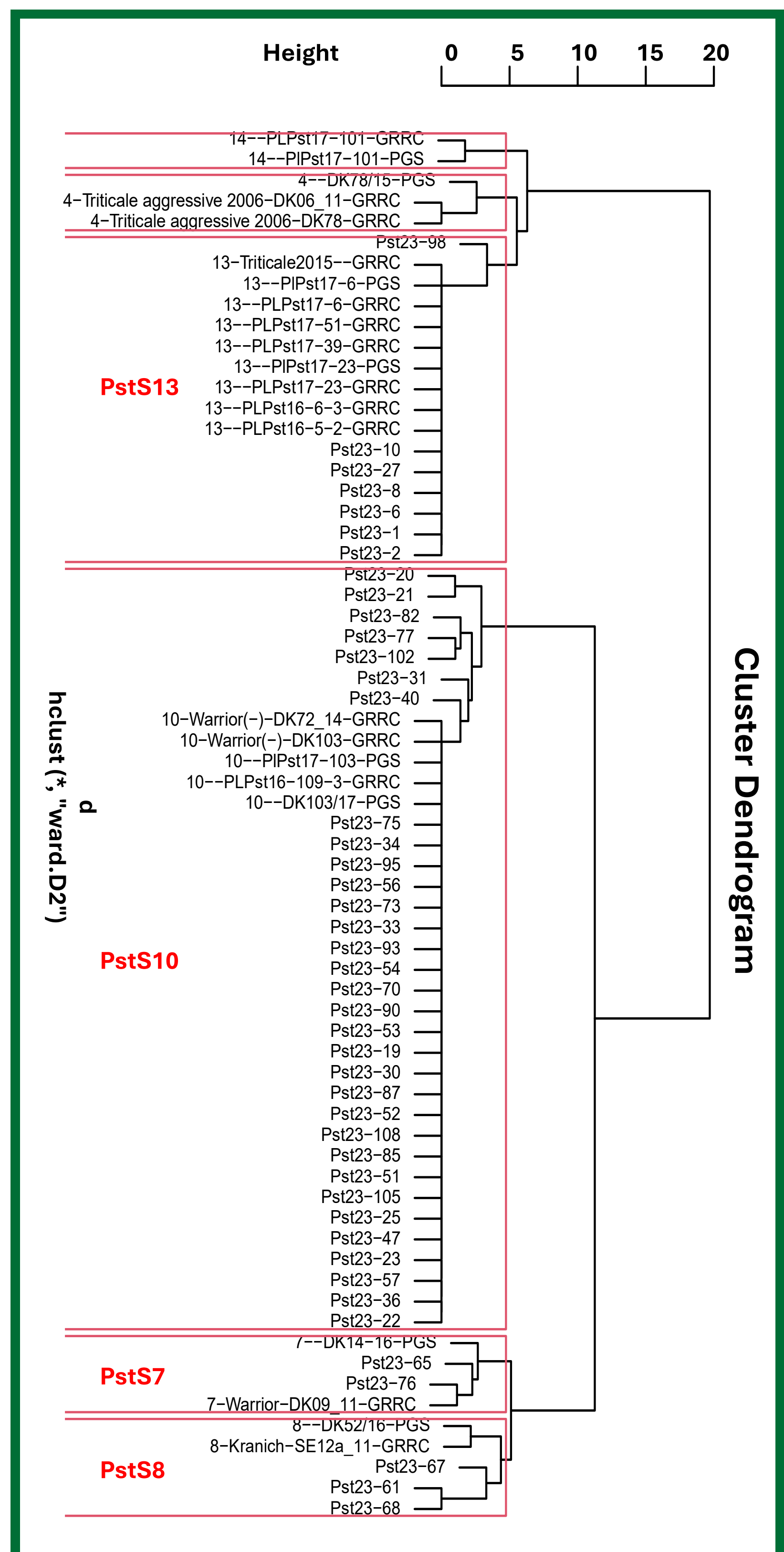
## RESEARCH FINDINGS AND CONCLUSIONS

The SSR method can be easily implemented in most laboratories using existing equipment and is a robust tool used to characterize isolate races. MARPLE allowed us to obtain much more data and information about the isolates, however it takes up more resources, both in consumable reagents as well as computing power and data disc storage. Phenotyping is very time consuming and labor intensive, as it needs to have a fair amount of rust spores for differentials infection, it is however cheap when cost of materials is considered.

The *P. striiformis* population in Poland was diverse. We managed to identify PstS7, PstS8, PstS10 and PstS13 genetic groups along with two samples containing a mix of more than one race. The dominant pathotype was PstS10. Monitoring of the pathogen population and knowledge of its genetic structure is very important for crop protection and resistance breeding.

## ACKNOWLEDGEMENTS

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**Figure 2.** Cluster dendrogram for 48 Pst isolates collected in Poland in the year 2023. The number of isolates in each genetic group is as follows: PstS7 – 2, PstS8 – 3, PstS10 – 32, PstS13 – 7, mixed – 2.