



Population structure of yellow rust (*Puccinia striiformis* f. sp. *tritici*) in Poland in 2024

Piotr Słowacki, Urszula Piechota, Magdalena Radecka-Janusik, Dominika Piaskowska, Paweł Czembor

Plant Breeding and Acclimatization Institute – National Research Institute
Department of Applied Biology
Radzików, 05-870 Błonie

INTRODUCTION

Yellow rust caused by the fungus *Puccinia striiformis* f. sp. *tritici* (Pst) is considered one of the most important pathogens of wheat. 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 44 single uredinium Pst isolates derived from both spring and winter wheat and triticale from six localizations in Poland in year 2024 were investigated. Analysis of the isolates was carried out using two molecular methods: analysis of SSR profiles for 19 loci and MARPLE (Mobile And Real-time PLant disEase). In addition, selected isolates were phenotyped using a differential test.

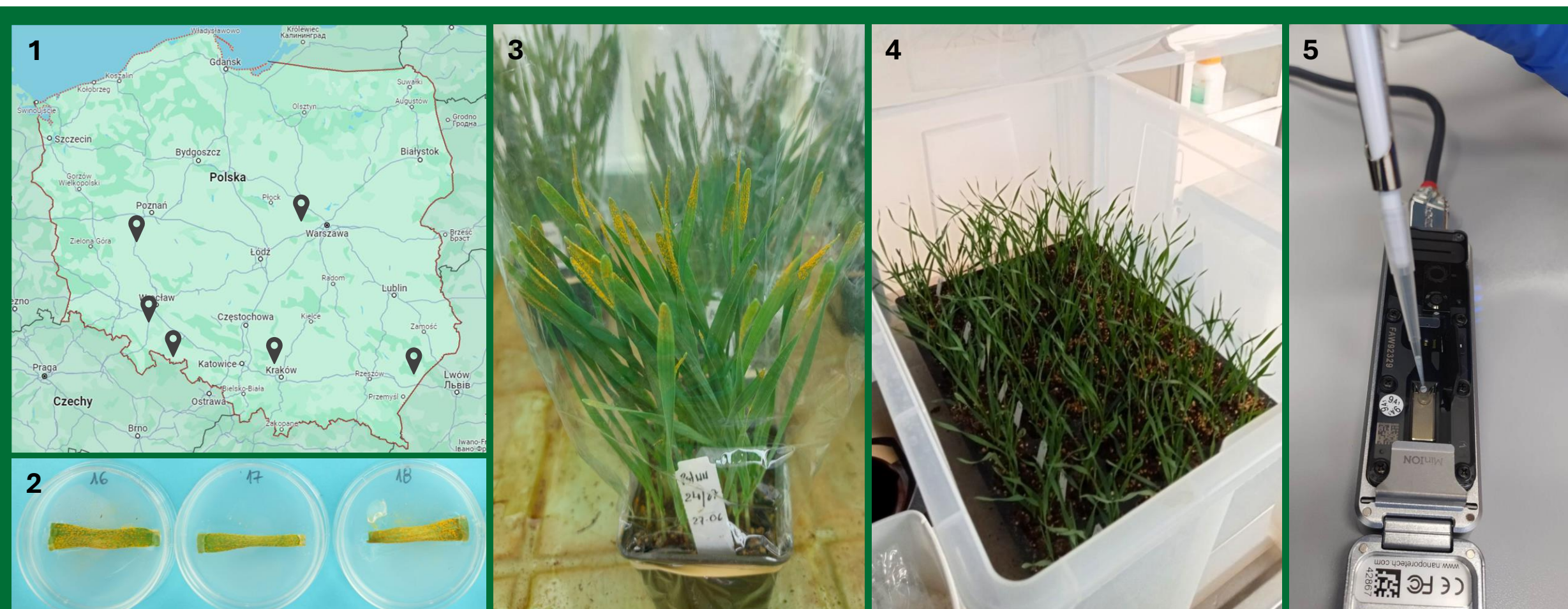


Figure 1. Collection and testing of Pst isolates. 1 – Collection of Pst-infected leaves from different sites in Poland, 2 – Maintenance of infected leaf segments on media, 3 – Inoculum production, 4 – Virulence tests on a differential panel comprising wheat and triticale lines with known Pst resistance genes, 5 – Molecular analysis.

RESEARCH FINDINGS AND CONCLUSIONS

The SSR method is robust to characterize isolate races. MARPLE provides more detailed data on isolates but requires greater resources, including reagents, computing power, and data storage. Phenotyping is inexpensive regarding materials but is labor-intensive, time-consuming, and requires sufficient rust spores for infection assays.

The analysis indicates that genetic group PstS10 (including Warrior(-) race) is dominant on both wheat and triticale. Specifically, group PstS10 had the largest number of isolates, with 20 isolates from wheat and 8 isolates from triticale, clearly highlighting its predominance. Additionally, wheat exhibited slightly greater genetic diversity, with isolates belonging to genetic groups: PstS7 (6 isolates), PstS8 (1), PstS10 (20), and PstS13 (1). In contrast, triticale had isolates identified only from genetic groups: PstS8 (1 isolate), PstS10 (8), and PstS13 (7).

ACKNOWLEDGEMENTS

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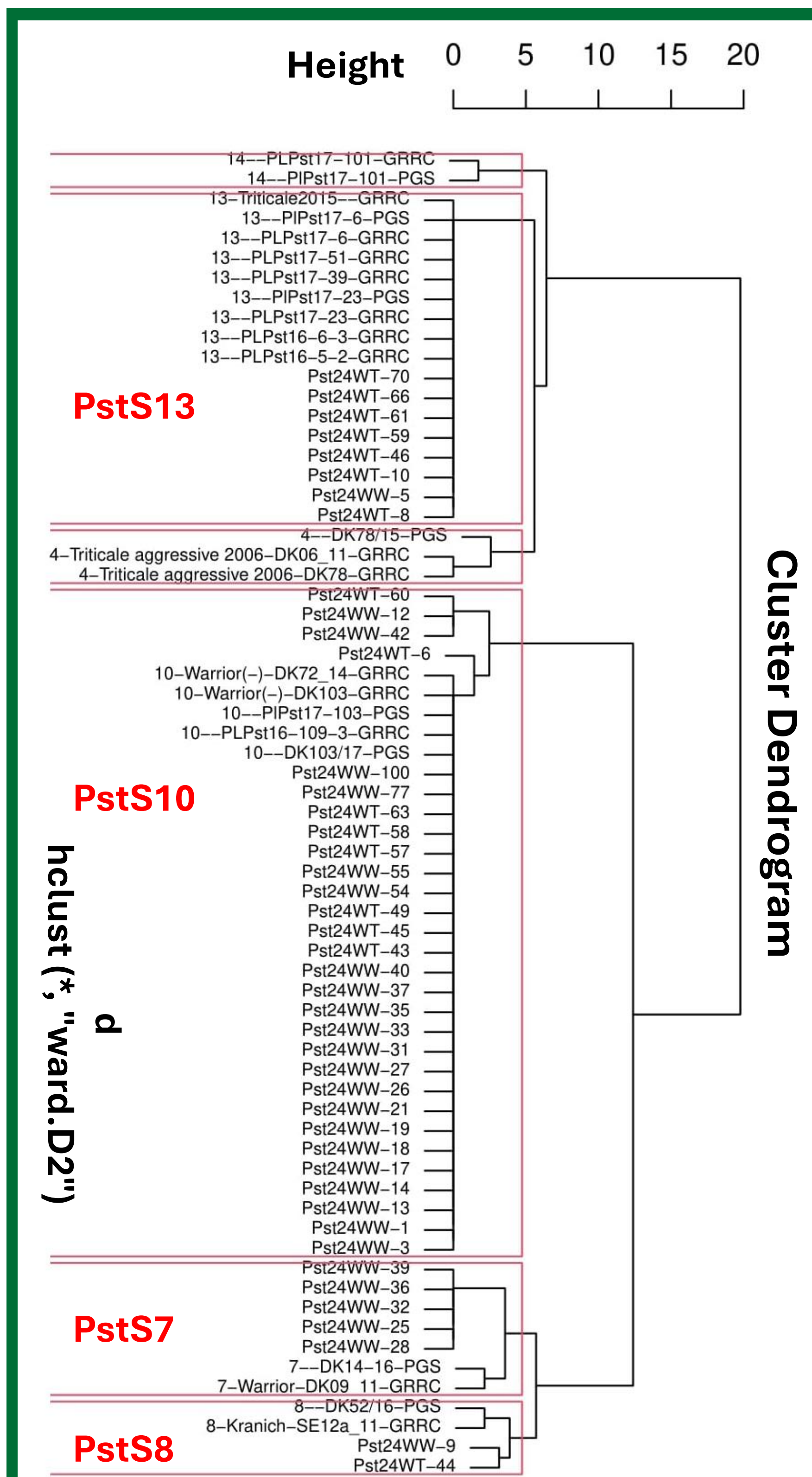


Figure 2. Cluster dendrogram for 48 Pst isolates collected in Poland in the year 2024. The number of isolates in each genetic group is as follows: PstS7 – 6, PstS8 – 2, PstS10 – 28, PstS13 – 8.