Plant Breeding and Acclimatization Institute – National Research Institute (PBAI-NRI)

Assessing stripe rust (*Puccinia striiformis* f. sp. *tritici*) population structure using molecular methods

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), 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 45 single uredinium Pst isolates obtained from winter wheat and triticale from four localizations in Poland in year 2025 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).

Figure 1. Collection and testing of Pst isolates. 1 – Collection of Pst-infected leaves form 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.

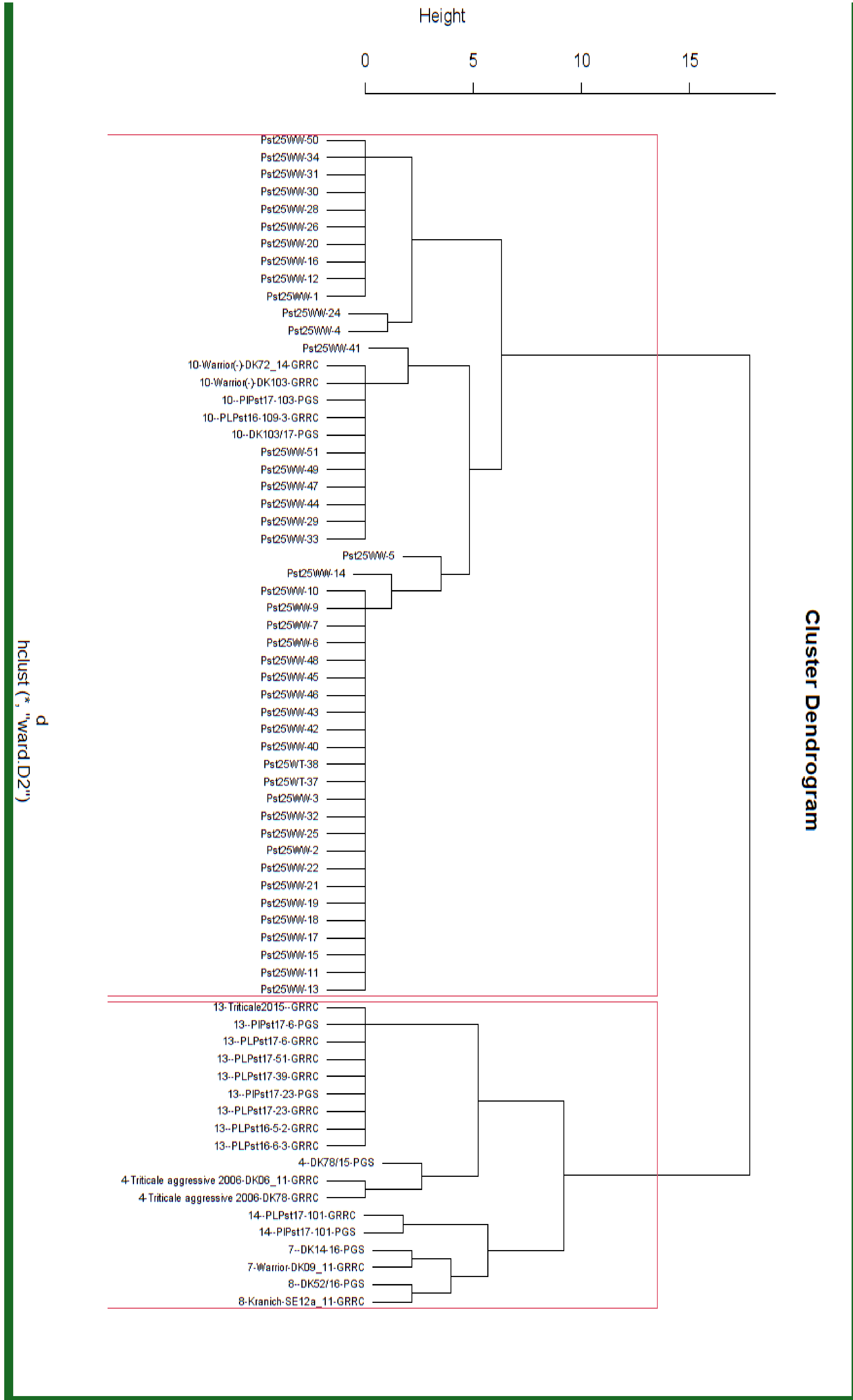

Figure 2. Cluster dendrogram for 45 Pst isolates collected in Poland in the year 2025. Only PstS10 genetic group was identified

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 not diverse in 2025. We managed to identify only PstS10 genetic group. Yellow rust in 2025 was very scarce in Poland. Monitoring of the pathogen population and knowledge of its genetic structure is very important for crop protection and resistance breeding.

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