Virulence and Genetic Diversity of *Puccinia* spp. Infecting Switchgrass in the United States

Background/Objective

- Rust, caused by *Puccinia* spp., is the most predominant disease of switchgrass, affecting biomass yield and thus representing a threat for the use of switchgrass as a biomass feedstock. This project thus examined genetic diversity and virulence of *Puccinia* spp. on switchgrass in the United States.

Approach

- Fourteen single-spore rust isolates of *Puccinia* spp., collected from field samples across seven U.S. states, were evaluated for virulence on 38 diverse switchgrass genotypes.
- Genetic diversity was characterized based on single nucleotide polymorphism (SNP) variation in 720 cloned amplicons, representing 654 base pairs of the elongation factor 1-α (EF-1α) gene.

Results

- **Virulence pattern:** The 14 *Puccinia* spp. isolates were distinguished based on their infection profiles on nine switchgrass accessions, resulting in the identification of eight races that differed by one to three virulence factors.
- **Genetic diversity:** Five major haplotypes were detected. STRUCTURE analysis, principal coordinate analysis, and phylogenetic methods grouped the isolates into two distinct genetic clusters. Among the sampled locations, Virginia showed the highest rust genetic diversity, while Georgia showed the lowest.

Significance/Impacts

- This study provides a comprehensive analysis of virulence patterns and genetic diversity in *Puccinia* spp. infecting switchgrass across the U.S. Despite evidence of migration, the rust populations exhibit strong local adaptation and clonal reproduction, with distinct regional genetic structure. These findings highlight the need for region-specific breeding strategies and long-term monitoring to manage rust disease and support the cultivation of switchgrass as a bioenergy crop.

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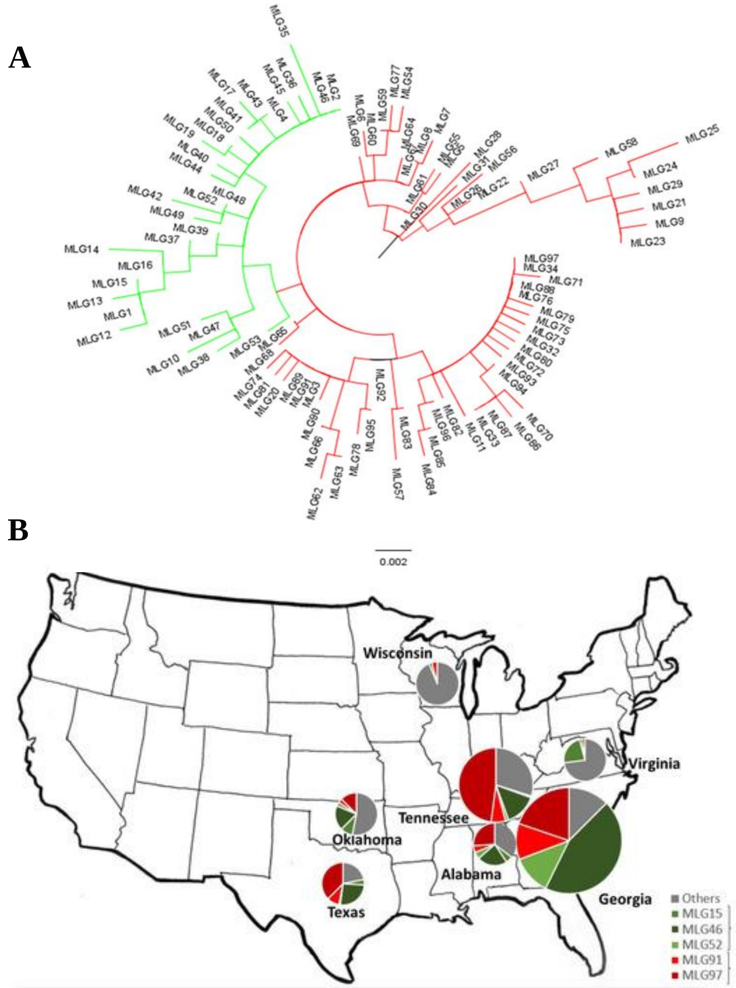

Population structure of *Puccinia* spp. on switchgrass in the U.S. (A) Phylogenetic relationships (ML tree) between 97 *Puccinia* spp. haplotypes show two genetic clusters: Pop1 (red) and Pop2 (green). (B) Geographic location of the five major haplotypes of switchgrass rust populations in seven U.S. states.