

# Characterizing Fusarium Species in Manitoba: Genetic Diversity and Detection

Molecular tools have been developed for rapid, accurate detection of *Fusarium* species. It is now possible to differentiate between three important pathogens associated with root rot in soybeans – *F. graminearum*, *F. poae* and *F. avenaceum*.

**ACCURATE IDENTIFICATION OF** fungal phytopathogens is essential for disease management. More specifically, rapid, accurate detection and differentiation between *Fusarium* pathogens can lead to the development of improved control options. Several different *Fusarium* species are recognized as soybean pathogens. Approximately 20 *Fusarium* species are associated with soybean root rot. However, little is known regarding the genetic diversity of these species and how to detect and differentiate them.

The objectives of this study were to:

1. examine the genetic diversity of the *Fusarium* community associated with soybean root rots in Manitoba and
2. design molecular markers to detect and differentiate these pathogens.

Plant diseases have traditionally been identified by culture-based morphological approaches that are time-consuming, laborious and require extensive knowledge of taxonomy. Using this method, diseases may be difficult to culture, identify and quantify. Molecular methods, on the other hand, offer faster, more specific,

more sensitive and more accurate results. In this study, 11 different species of *Fusarium* were identified by molecular techniques and assessed for diversity. The information gathered across *Fusarium* species was sequenced and made publicly available to other researchers for future studies.

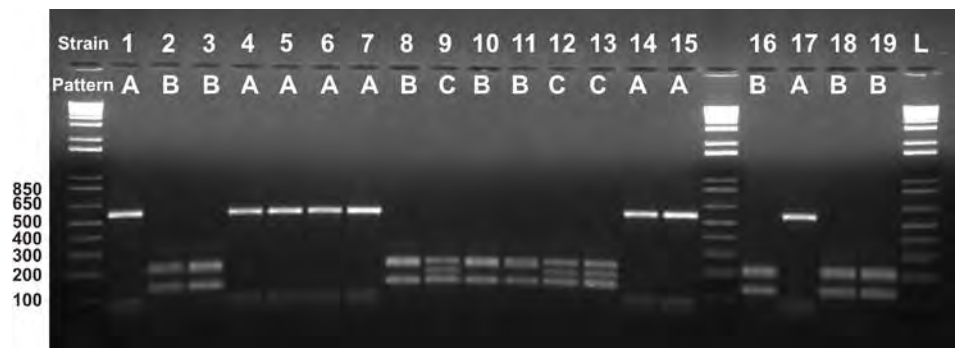
Several molecular tools were developed during this project for rapid detection of *Fusarium* pathogens that cause root rot in soybeans. One highlight is the development of a polymerase chain reaction (PCR) restriction fragment length polymorphism (RFLP) protocol, which is considered one of the most sensitive methods for accurate species characterization. With the PCR-RFLP protocol developed, it is now possible to differentiate between three important soybean *Fusarium* pathogens: *F. graminearum*, *F. poae* and *F. avenaceum*.



Another highlight of the study is that the first molecular marker for specific detection of *F. graminearum* was developed. This genetic marker allows for differentiation among closely-related pathogens in the *F. graminearum* species complex and among other *Fusarium* species that can cause head blight in cereals and root rot in soybeans.

The results of this study can be used in future basic and applied research to accurately identify, understand and manage various *Fusarium* species. Further investigation is needed for *Fusarium* species associated with soybean seed. Due to the cross-pathogenicity across crop types and widespread production of legume and cereal crops, *Fusarium* management will become increasingly important. ▀

Figure 1. Differentiation between *Fusarium* species according to the PCR restriction fragment length polymorphism (PCR-RFLP) method. Pattern A is *F. avenaceum*, pattern B is *F. graminearum* and *F. cerealis*, and pattern C is *F. poae*.



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