PROJECT DETAILS

- **Title**: Canadian Canola Clubroot Cluster Pillar 4: Surveillance and pathotype monitoring
- **Funders:** Alberta Canola
- **Research program:** Canola Agronomic Research Program
- **Principal investigator:** Stephen (Steve) Strelkov and Sheau-Fang Hwang
- **Collaborators/additional investigators:** Rudolph Fredua-Agyeman, Michael (Mike) Harding, Mary-Ruth McDonald and Bruce Gossen
- **Year completed:** 2019

Abstract

Clubroot is an important soilborne disease of canola caused by the pathogen *Plasmodiophora brassicae*. While clubroot was first detected in just a few fields in central Alberta in 2003, it has spread relatively quickly over the past 15 years. The most effective management strategy is the planting of clubroot resistant (CR) canola cultivars. Recently, however, new strains of the pathogen have emerged that can overcome this resistance.

This project represented the first year of a 5-year work plan that had four specific objectives:

1) clubroot surveillance and detection of new pathogen strains overcoming resistance, including the isolation and characterization of single-spore isolates and field populations;
2) refinement of the current clubroot differential set;
3) examination of the genetic and virulence relationships between pathotypes and their interactions; and
4) development of molecular tests to distinguish between pathotypes.

Clubroot surveillance activities identified 300 new clubroot infestations in Alberta in 2018, for a grand total of 3044 documented field infestations since 2003. In Saskatchewan, 37 canola crops were found with visible clubroot symptoms, while in Manitoba, 17 cases of clubroot were detected in 2018.

A total of 119 *P. brassicae* populations, each representing a different field, were tested for pathotype classification on the differentials of Williams and the Canadian Clubroot Differential (CCD) Set. These included 103 populations recovered from Alberta, 10 from Saskatchewan and 6 from Manitoba.

Pathotype 3A was most common in Alberta followed by pathotype 3D, both of which are highly virulent on CR canola. Eighty seven of the 103 populations collected from Alberta in 2018 could overcome clubroot resistance, bringing the total number of confirmed fields with resistance issues to 191 in the province. Of the 10 samples evaluated from Saskatchewan, eight were pathotype 3H and two were 5L (neither pathotype overcomes first

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generation clubroot resistance). The populations from Manitoba included two pathotype 3H, one pathotype 5L, and two classified as pathotype 2 on the system of Williams but representing a novel virulence pattern on the CCD Set. A sixth population from Manitoba was classified as pathotype 3A and could overcome resistance. This was the first confirmed case of a clubroot resistance-breaking pathotype detected on canola outside of Alberta.

Methodologies for the recovery of single-spore isolates of *P. brassicae* were refined, with 39 single-spore isolates obtained and characterized for their virulence on the CCD Set and a suite of CR canola cultivars. Many of the pathogen populations analyzed consisted of mixtures of virulent and avirulent single-spore isolates, underscoring the fact that field isolates can be heterogeneous. In total, 13 pathotypes were identified amongst the 39 single-spore isolates.

The genomes of these 39 isolates plus 6 field populations were sequenced and high quality reads used to generate individual assemblies. An initial analysis of the variation among the 45 full genomes identified 131 potential polymorphisms which can be used for PCR-based discriminatory assays. Primers based on Indel polymorphisms have been designed for three genomic regions and are currently being tested.

Screening of a large collection of Brassicas identified 19 accessions with good potential as differential hosts for refinement of the clubroot differential set, and crosses were made with selected hosts to begin development of advanced generations.

Collectively, the research conducted as part of this project will help growers and the canola industry to mitigate the impact clubroot by improving understanding of the outbreak and pathogen population structure.

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