

Pea root rot: Distribution, genetic variability, resistance and management

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SPG Contributions	Duration/Timeline of Project (Year to Year)	Co-funders	Total Project Cost
\$109,970.00	April 2013 – March 2018	Agriculture and Agri-Food Canada; Manitoba Pulse & Soybean Growers	\$706,274.00

Project Description

To develop and assess molecular diagnostic procedures for rapid, specific and sensitive detection of new and emerging root rot pathogens in symptomatic field pea roots; to identify new sources of resistance to prevalent root rot pathogens and develop molecular markers closely linked to resistance genes for aphanomyces root rot; to develop a risk assessment tool for Fusarium species causing root rot of field pea.

Outcome

Assessment of more than 1000 commercial fields of pea and lentil across all three provinces demonstrated that root rot in pea and lentil was prevalent across the Canadian Prairies. Also, Aphanomyces root rot (caused by Aphanomyces euteiches) was shown to be present across the Prairie region. There were no differences in root rot severity or frequency of A. euteiches with soil zone for field pea and only small differences for lentil, which is slightly less susceptible than field pea. The study also demonstrated that root rot can be an important problem of pulse crops even in dry regions.

Primer sets for a molecular assay that can identify several root rot pathogens in a single analysis (multiplex qPCR) were developed and validated. A second molecular test (ddPCR) to identify minute quantities the most important root rot pathogens was designed and validated. These tests were used to identify the root rot pathogens present in each field that was surveyed, which had not previously been possible using standard culturing techniques.

A greenhouse study demonstrated that there is a synergistic interaction between A. euteiches and several Fusarium spp. Assays for F. avenaceum and F. solani were used to correlate inoculum dose in soil or on stubble to root rot severity and DNA quantity. These assays were then applied to field soils collected from healthy and diseased patches in 14 commercial pea fields, assessed using the quantities of pathogen DNA and by greenhouse bioassay. Pathogen DNA was detected in almost all soil samples, but there was no correlation between pathogen DNA in soil and root rot severity in each pea field.

New sources of resistance to root rot of pea were identified and information was obtained on the genetics of resistance / tolerance to aphanomyces root rot. Several adapted field pea cultivars with some resistance to components of the root rot complex in Western Canada were identified. These will be used as sources of resistance in field pea breeding programs. New information on the precise location of the genes governing resistance to aphanomyces root rot in the pea line 00-2067 should facilitate marker-assisted selection for that trait in breeding programs.

Management recommendations are limited. Producers should continue to use standard seed treatment fungicide cocktails, which provide early-season reduction of seed decay and seedling blight for all root rot pathogens except A. euteiches. Where levels of A. euteiches are low, use a seed treatment with activity against A. euteiches and extend rotations away from pea and lentil (alternatives are soybean, faba bean, or chickpea). When partially resistant cultivars become available, producers will still need to avoid heavily infested fields, because this resistance will likely break down quickly under high disease pressure.

Research Objective

OBJECTIVE 1

To develop and assess molecular diagnostic procedures for rapid, specific and sensitive detection of new and emerging root rot pathogens in symptomatic field pea roots.

OBJECTIVE 2

To identify new sources of resistance to prevalent root rot pathogens and develop molecular markers closely linked to resistance genes for aphanomyces root rot.

OBJECTIVE 3

To develop a risk assessment tool for Fusarium species causing root rot of field pea.