

Cluster 2 – Non-confidential Summary

1. CLUSTER PROJECT DETAILS

Project number: AIP- CL03- Pulse Activity T1.G6.V1

Name of Project: Pea Root Rot: Distribution, genetic variability, resistance, and management

Project research period: 2013-04-01 to 2018-03-31

Period covered by this report: 2013-04-01 to 2018-03-31

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NON-CONFIDENTIAL ABSTRACT/SUMMARY (For use in publications and pulse grower websites)

- Overall project objectives, methodology, research design & findings from project start to March 31, 2017.
- **500 words** in lay language.

Assessment of more than 1,000 commercial fields of peas and lentils across all three provinces demonstrated that root rot on peas and lentils 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 peas and only small differences for lentils, which is slightly less susceptible than field peas. The study also demonstrated that root rot can be an important problem of pulse crops even in dry regions.

Sets of primers 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 that were 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. In a companion study, 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 peas 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 peas and lentils (alternatives are soybeans, faba beans, or chickpeas). 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.