

Association mapping of Aphanomyces root rot resistance in a pea GWAS panel

Dr. Tom Warkentin

University of Saskatchewan – CDC

SPG Contributions	Project Status	Duration/Timeline of Project (Year to Year)	Co-funders	Total Project Cost
\$56,991.00	Active	January 2022 – June 2025	Saskatchewan Ministry of Agriculture – Agriculture Development Fund; Western Grains Research Foundation	\$213,094.00

Project Description

Phenotyping of the GWAS-2 pea panel for Aphanomyces root rot resistance; association mapping for identification of SNP markers associated with Aphanomyces root rot resistance; in silico comparison of identified loci with known QTLs of Aphanomyces resistance; field evaluation of selected GWAS-2 accessions for resistance to root rot complex.

Outcome

A Genome-Wide Association Study (GWAS) panel, GWAS-2, was assembled by the pea breeding program at the Crop Development Centre (CDC). The GWAS-2 panel consists of 233 diverse pea (*Pisum sativum*) accessions selected for their genotypic diversity from among international pea core germplasm collections, breeding lines, and commercial cultivars released in Canada. The panel also includes 22 *Pisum fulvum* accessions. During the current reporting period, the 233 *P. sativum* accessions of GWAS-2 were evaluated for Aphanomyces root rot (ARR) resistance in a controlled environment, using *Aphanomyces euteiches* isolate AE11. New sources of moderate resistance to Aphanomyces root rot were identified among the GWAS-2 accessions. The GWAS-2 panel was genotyped using an Axiom® 90K SNP array. The phenotypic and genotypic information of the GWAS-2 panel will be used to identify the SNP markers associated with ARR resistance.

Research Objective

OBJECTIVE 1

Phenotyping of the GWAS-2 pea panel for Aphanomyces root rot resistance.

OBJECTIVE 4

Field evaluation of selected GWAS-2 accessions for resistance to root rot complex.

OBJECTIVE 2

Association mapping for identification of SNP markers associated with Aphanomyces root rot resistance.

OBJECTIVE 3

In silico comparison of identified loci with known QTLs of Aphanomyces resistance.