

Marker-assisted selection for Aphanomyces resistance in pea for rapid development of adapted pea varieties with improved Aphanomyces resistance

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SPG Contributions	Project Status	Duration/Timeline of Project (Year to Year)	Total Project Cost
\$308,360.00	Completed	April 2016 – March 2019	\$308,360.00

Project Description

To complement back-crossing and pathogenicity testing with marker-assisted selection that is feasible owing to the work conducted by US and French scientists, who have identified quantitative trait loci (QTLs) and developed markers for Aphanomyces root rot (ARR) resistance in pea.

Aphanomyces root rot has emerged as an economically important disease of field peas, which has already restricted pea production in some areas of Saskatchewan. Disease management options are very limited and the most efficacious one is an extended rotation away from susceptible peas and lentils. All pea cultivars currently grown in Saskatchewan are susceptible to the disease, but sources of resistance have been identified in France and the USA. Resistance to Aphanomyces root rot is incomplete and controlled by many genes (QTLs). Tracing as many as possible of those genes through the breeding program is difficult through traditional pathogenicity testing, but can be substantially improved through marker-assisted selection, where the genes or gene regions are tagged and can thus be traced through molecular markers. Genetic information enabling such tagging was published by French colleagues in 2015, enabling us to add this tool to our efforts to develop partially Aphanomyces root rot resistant pea varieties.

Outcome

An intensive backcrossing program was initiated to move resistance from the two main sources of aphanomyces root rot resistance into two yellow and four green adapted pea varieties. In the course of three years, molecular markers were developed to trace QTLs, a total of 75 crosses were made, more than 9,000 plant tissue or seed samples were screened with the molecular markers in addition to pathogenicity testing of close to 100 lines. The resistance QTLs of the two main sources of aphanomyces root rot have been combined in the background of the two yellow and four green pea varieties, but require one additional screening with molecular markers and pathogenicity testing before seeds of selected lines of these varieties can be increased for agronomic assessment. That will be followed by entering them into the co-op trials for the variety registration process regulated by CFIA.

Research Objective

OBJECTIVE 1

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