

Development of improved markers for mycosphaerella blight resistance in pea

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SPG Contributions	Project Status	Duration/Timeline of Project (Year to Year)	Co-funders	Total Project Cost
\$185,150.00	Completed	May 2013 – January 2016	Saskatchewan Ministry of Agriculture – Agriculture Development Fund (ADF); Western Grains Research Foundation	\$356,882.00

Project Description

A recombinant inbred line (RIL) population (PR-19) developed from a cross between Alfetta (*Pisum sativum*) and P651 (*P. fulvum*) was evaluated for disease resistance and was genotyped using 1536 SNPs Illumina GoldenGate array. A wide range of variation was observed for mycosphaerella blight scores and other agronomic traits. A high density genetic linkage map consisting of 733 SNP markers covering a genetic distance of 682.1 cM was used for QTL analysis.

Outcome

Six QTLs were identified for mycosphaerella blight under field and 3 additional QTLs were identified under greenhouse conditions. Individually, these QTLs explained 10 to 28% of phenotypic variation. In addition, five QTLs each were identified for plant height, days to maturity, and grain yield, four QTLs for days to flower, and two QTLs for lodging. QTLs mbIII-1 and mbl-IV-2 were consistent across locations and/or years and selected for HIFs development. HIF-173 and HIF-224 were developed from lines PR-19-173 and PR-19-224 for fine mapping, respectively. HIFs evaluated under field conditions in 2015 at Saskatoon showed a wide range of variation in disease scores and other traits. Phenotyping of HIFs in 2016 at two locations is in progress. Genotyping of HIFs was conducted using eight markers designed from an Illumina GoldenGate array. Based on Kompetitive Allele Specific PCR (KASP) assay, PsC27225p371 for HIF-173 was used for association study. However, this marker was not significantly associated with disease scores. Research is in progress to genotype HIFs using markers (30) generated from genotyping by sequencing (GBS) to identify closely linked markers associated with disease resistance.

Research Objective

OBJECTIVE 1

To identify quantitative trait loci (QTL), develop heterogeneous inbred families (HIFs), and then fine map QTLs segregating for mycosphaerella blight resistance to identify closely linked markers and/or candidate genes.