

SNP marker panel for profiling pea lines and its effectiveness in breeding for high seed protein concentration

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SPG Contributions	Project Status	Duration/Timeline of Project (Year to Year)	Co-funders	Total Project Cost
\$221,691.25	Active	December 2017 – April 2022	Saskatchewan Ministry of Agriculture – Agriculture Development Fund (ADF)	\$414,466.25

Project Description

To identify trait linked SNP markers for multiple phenotypes; to validate identified trait linked markers; to fine map QTLs for identification of markers closely linked to traits; to convert key SNP markers to Taqman assays for routine screening of breeding lines; to breed for high seed protein concentration.

The goal of the project was to identify single nucleotide polymorphism (SNP) markers linked to various agronomic and seed quality traits important for pea breeding using diverse mapping populations. We assembled a panel of 34 unique SNP markers associated with 18 traits of pea.

The selected traits include:

- 1) Agronomic – days to flowering, days to maturity, lodging resistance, plant height, seed dimpling, seed weight, and grain yield;
- 2) Heat stress – SPAD (chlorophyll measurement), leaf wax, and stem thickness;
- 3) Seed quality – concentration of Iron (Fe), zinc (Zn), phytate, starch, and protein, and;
- 4) Disease resistance – Aphanomyces root rot, Mycosphaerella blight, and powdery mildew, for use in marker-assisted selection (MAS) in a breeding program.

The identified SNP markers were converted to Kompetitive allele specific PCR (KASP) assays and the assays were validated under laboratory conditions. We have used the SNP markers for MAS of high seed protein concentration and other traits in two mapping populations. The panel of SNP markers reported in this project will be useful for MAS in pea breeding as they will enrich the germplasm reaching yield trials with fixed alleles of importance.

Outcome

Research Objective

OBJECTIVE 1

To identify trait linked SNP markers for multiple phenotypes.

OBJECTIVE 4

To convert key SNP markers to Taqman assays for routine screening of breeding lines.

OBJECTIVE 2

To validate identified trait linked markers.

OBJECTIVE 5

To breed for high seed protein concentration.

OBJECTIVE 3

To fine map QTLs for identification of markers closely linked to traits.