

Marker-assisted introgression of useful new diversity into the pea genome for rapid cultivar improvement

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SPG Contributions	Project Status	Duration/Timeline of Project (Year to Year)	Co-funders	Total Project Cost
\$175,880.00	Completed	November 2015 – December 2019	Saskatchewan Ministry of Agriculture – Agriculture Development Fund (ADF); Western Grains Research Foundation	\$505,699.00

Project Description

To introduce new diversity into pea breeding material to improve the crop in key traits, and to combine these traits into individual varieties.

The goal of the project is to expand the diversity in pea germplasm. Without diversity, plant breeders cannot make progress. In this project, we are bringing in (introgressing) diversity by crossing a Saskatchewan-grown pea cultivar called CDC Amarillo with five different pea varieties, each of which carries interesting traits for pea breeding. The traits we are attempting to bring in include higher seed protein concentration, greater tolerance to high temperatures during the flowering period, increased resistance to root rot, and increased resistance to Ascochyta blight. The donors of these traits include a common pea variety, breeding lines, and land races. The unique approach being used is the development of 'introgression lines' which carry approximately one quarter of a chromosome from each of the five donors with the remainder of the chromosomes from CDC Amarillo. This technically challenging approach is being achieved through a combination of conventional plant breeding and marker assisted selection methods. In the coming year the arising introgression lines will be grown in the field for the first time and evaluated for the key traits. The initial testing will be on a very limited scale due to the small number of seeds that will be available, however after this project formally ends, further testing of the introgression lines will be conducted in replicated tests at multiple key locations on the Canadian prairies. Data arising from the field trials, and subsequent seed analyses, will help us determine the key chromosomal regions affecting the traits of interest.

Outcome

Three diverse varieties identified as donors of heat stress resistance, high seed protein content, and improved Aphanomyces root rot resistance were introgressed as short chromosomal segments into a common genetic background. This diversity was introgressed into CDC Amarillo which is a high yielding pea cultivar. Three recombinant inbred line (RIL) populations and three chromosome segment substitution line (CSSL) libraries were generated using a combination of traditional crossing and marker-assisted selection. The RILs and CSSLs are being tested in repeated field trials for key traits related to pea performance in Western Canada over the coming years. The genetic resources created in this project will be useful for functional genomics studies and pyramiding of genes associated with heat stress resistance, high seed protein content, and Aphanomyces root rot resistance in pea.

Research Objective

OBJECTIVE 1

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