

BRE1607: Marker-Assisted Introgression of Useful New Diversity into the Pea Genome for Rapid Cultivar Improvement

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. *Researchers acknowledge the funding support for this project from Saskatchewan Pulse Growers, Western Grains Research Foundation, Saskatchewan Agriculture Development Fund, and the University of Saskatchewan.*