

BRE1319: Sequencing the Pea Genome: Creating a Solid Foundation for Long-Term Pea Genetic Improvement

The overall objective of the project was to support pea genome sequencing as part of a global research partnership. The vast genomic resources developed will be used to accelerate pea varietal improvement at Crop Development Centre (CDC) and internationally, through marker-assisted selection and/or introgression of useful genetic variation. Results from this project will create a strong foundation for long-term pea genetic improvement and also to maintain the competitiveness of the Canadian pea industry.

We have developed a bacterial artificial chromosome (BAC) library based physical map of peas. Five hundred and sixty RILs of five mapping populations PR-2 (Orb x CDC Striker), PR-11 (CDC Sage x CDC Centennial), PR-7 (Carerra x CDC Striker), PR-15 (1-2347-144 x CDC Meadow), and POP-9 (Cameor x China) were genotyped using 'genotyping by sequencing' (GBS) approach. High-density linkage maps of these mapping populations were constructed and used for identification of quantitative trait loci (QTL) for important traits such as lodging, phytate, and seed mineral content. We have also genotyped a panel of 177 diverse pea lines using GBS method and phenotypic characterization of these lines is in progress for future identification of trait-linked markers through association mapping.