

## **BRE1320: Lentil Genome Sequencing (LenGen): Establishing a Comprehensive Platform for Molecular Breeding**

The project goal was to sequence the lentil genome and utilize the sequencing information to accelerate lentil genetic improvement. We have sequenced the lentil variety CDC Redberry using different types of next generation DNA sequencing technologies. The resulting lentil assembly consists of seven pseudomolecules anchored through the use of six high-density genetic linkage maps, with the total assembled bases representing approximately half of the four Gb lentil genome. The remaining, unassembled fragments are made up of repetitive sequences. The assembly is accessible by the international research community through the KnowPulse web portal (<http://knowpulse.usask.ca/portal/>).

The completion of a draft lentil genome assembly represents a powerful enabling platform for lentil biology, as we have documented in studies of genome sequence-assisted dissection of agronomic traits. Through this project we have established a considerable plant bioinformatics capability at the University of Saskatchewan, which will facilitate future pulse genomics studies and the development of molecular marker selection tools. With the additional support from the Saskatchewan Pulse Growers, Genome Canada, and partner agencies, we were able to embark on a new project – Application of Genomics to Innovation in the Lentil Economy (AGILE). The goal of AGILE is to make use of the genome assembly to better understand evolution in the genus *Lens*, and the changes that have occurred during domestication and subsequent adaptation to different lentil growing regions of the world. Results from this project will enable lentil breeders to develop better lentil varieties through systematic use of diverse cultivated germplasm and wild relatives of the genus *Lens*.