



## OP06: The Lentil Genome – from the sequencer to the field

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**Kirstin Bett** is Professor of Plant Breeding and Genetics in the Department of Plant Sciences, University of Saskatchewan in Canada. She is an experienced pulse breeder and currently responsible for the common bean breeding program at the University. CDC WM-1, developed by Dr. Bett, was the first slow darkening pinto bean variety in commercial production in Canada and second in the world after the Mexican variety Pinto Saltillo. Dr. Bett leads the pulse crop genomics and bioinformatics program where she uses both classical and molecular techniques to better understand the traits that lead to the development of superior pulse crop cultivars. This has included work in seed quality, disease resistance and cold tolerance and has extended to the use of wild species as a source of useful variability. Dr. Bett is a project lead of an \$8.5-million Genome Canada project to investigate the genetics of domestication and adaptation in lentil. She led the international effort to sequence the lentil genome and released the assembly to the international research community in early 2016.

Lentil (*Lens culinaris* ssp. *culinaris*; genome size 4.3 Gb) plays a significant role in supporting sustainable agriculture worldwide. Its nutrition value has also been recognized as part of the solution to combat global food and nutritional security. The lentil genome assembly v1.0, based on the Canadian variety CDC Redberry, was released in January 2016. The assembly consists of 7 pseudomolecules anchored through the use of 6 high-density genetic linkage maps, with the total assembled bases representing approximately half of the 4.3 Gb lentil genome. It was assembled from genomic and RNA sequencing results carried out by several institutions across the world using different technologies. The assembly, with putative genes identified, can be visualized on a genome browser (JBrowse) and queried using BLAST via the Knowpulse web portal (<http://knowpulse.usask.ca>). Having the full genome sequence of lentil has provided tools that facilitate in-depth genetic studies. Markers and candidate genes that control several agronomic and quality traits have been identified and we have implemented marker-assisted selection for several traits of importance to the breeding program at the University of Saskatchewan. To assess the breadth of genetic potential present within the *L. culinaris* gene pool, a lentil diversity panel (~ 400 accessions from several lentil germplasm collections) has been re-sequenced using a restriction site associated DNA (RAD) genotyping-by-sequencing (GBS) approach. Sequencing results suggest 4 populations based on adaptation to specific growing environments and altitude. The distinctness of the temperate and South Asian populations is striking and demonstrates the lack of intermating that is occurring between germplasm from these distinct regions. To fully understand the genetic basis of adaptation characteristics in lentils, we plan to conduct field phenotyping of the diversity panel in different lentil growing regions. We will then develop molecular markers and other breeder-friendly resources that will allow the breeders to better use exotic germplasm while reducing the negative impacts usually associated with maladaptation to the local environment. This will enable breeders to develop better lentil varieties through systematic use of diverse cultivated germplasm.