

## CANADIAN GENOMICS PROJECT IS LEADING THE WAY IN WHEAT BREEDING INNOVATION



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Wheat farmers have reason to celebrate, as the Canadian Triticum Applied Genomics (CTAG2) project is about to step up its contribution to the global effort to decipher the wheat genome, led by the [International Wheat Genome Sequencing Consortium](#) (IWGSC). The expected outcome is a new generation of wheat cultivars with higher yields and better resistance to stresses.

The CTAG2 project, led by Dr. Curtis Pozniak of the University of Saskatchewan, in collaboration with Dr. Andrew Sharpe of the National Research Council Canada, recently received \$8.5 million from [Genome Canada](#) and the [Western Grains Research Foundation](#), with co-funding from the Saskatchewan Wheat Development Commission, Alberta Wheat Development Commission, SeCan, the Saskatchewan, Manitoba, and Ontario provincial governments, and DuPont Pioneer.

The CTAG2 team will work with the IWGSC to generate a high quality reference sequence of wheat chromosome 2B, a necessary foundation to discover genes of agricultural importance and to drive innovation in wheat breeding. Chromosome 2B is known to contain genes involved in drought tolerance, antibiotic resistance to wheat midge, control of pre-harvest sprouting and yield increase.

Curtis Pozniak, a Professor and Wheat Breeder at the Crop Development Centre, has released 11 new wheat cultivars in the past eight years and is a leader in application of genomic technologies to wheat improvement. “The CTAG2 project aims to exploit advances in sequencing technologies to continue development of a high quality reference sequence of wheat with the outcome of the next generation of DNA markers to enhance the rate of wheat improvement. This work will continue our collaboration with IWGSC where we have nearly completed the assembly of a gold-standard reference for chromosome 1A.”

Dr. Andrew Sharpe is no stranger to genome sequencing. He has played a critical role in genome assemblies of multiple crops, including *Brassica oleracea*, canola and camelina, and he is now applying this experience to wheat. “The development of a high quality reference genome is a proven pathway to enable rapid progress in genetic improvement and functional characterization of the gene complement in multiple crops. Fortunately, we are now able to take advantage of the latest technological advances in sequencing platforms and new bioinformatics tools to enable us to achieve this goal for the large wheat genome.”

Of the 21 wheat chromosomes, only one – chromosome 3B – is currently sequenced to high quality. Reference sequencing of 13 other chromosomes, in addition to the 2B project, is currently underway in 12 countries and will be completed in the next two years.

The IWGSC is still seeking funding for reference sequencing of six wheat chromosomes. Provided that additional funding is secured soon, the IWGSC anticipates that a high-quality genome sequence for bread wheat could be publicly available by 2018.

The sequencing strategy adopted by the IWGSC is a chromosome-by-chromosome approach that is based on physical maps. This strategy efficiently delivers a high quality, ordered sequence comparable to the gold standard reference sequence of rice. The physical map that will be used for reference sequencing of chromosome 2B was produced as part of a €1 million contribution from Bayer Crop Science aimed at delivering the remaining physical maps needed to advance the bread wheat sequencing project.

Wheat is the most widely grown cereal crop in the world and the staple food for more than 35% of the global human population. It accounts for 20% of all calories consumed throughout the world. As global population grows, so too does its dependence on wheat. To meet future demands of a projected world population of 9.6 billion by 2050, wheat productivity needs to increase by 1.6% each year. Since availability of new land is limited to preserve biodiversity and water and nutrient resources are becoming scarcer, the majority of this increase has to be achieved via crop and trait improvement on land currently cultivated. A high quality reference genome sequence would greatly contribute to achieving this goal.

### **About the CTAG2 project**

The CTAG2 project's goal is to better understand the wheat genome and to apply this research to improve wheat breeding efficiency. The end result will be the development of tools and strategies for wheat breeders to accelerate breeding programs and to develop improved cultivars that are more productive and resistant to biotic and abiotic stresses such as diseases, pests, heat and drought. With this new generation of wheat varieties, wheat farmers will be able cultivate more productive, profitable and environmentally sustainable wheat.

### **About the IWGSC**

The IWGSC, with more than 1,100 members in 55 countries, is an international, collaborative consortium, established in 2005 by a group of wheat growers, plant scientists, and public and private breeders. The goal of the IWGSC is to make a high quality genome sequence of bread wheat publicly available, in order to lay a foundation for basic research that will enable breeders to develop improved varieties.

The IWGSC is a U.S. 501(c)(3) Non-Profit organization

[www.wheatgenome.org](http://www.wheatgenome.org)

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