

Genomic atlas of gene switches in plants provides roadmap for crop research

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What allows certain plants to survive freezing and thrive in the Canadian climate, while others are sensitive to the slightest drop in temperature? Those that flourish activate specific genes at just the right time—but the way gene activation is controlled remains poorly understood.

A major step forward in understanding this process lies in a genomic map produced by an international consortium led by scientists from McGill University and the University of Toronto and published online today in the journal *Nature Genetics*.

The map, which is the first of its kind for plants, will help scientists to localize [regulatory regions](#) in the genomes of [crop species](#) such as canola, a major crop in Canada, according to researchers who worked on the project. The team has sequenced the genomes of several crucifers (a large plant family that includes a number of other [food crops](#)) and analyzed them along with previously published genomes to map more than 90,000 [genomic regions](#) that have been highly conserved but that do not appear to encode proteins.

"These regions are likely to play important roles in turning genes on or off, for example to regulate a plant's development or its response to environmental conditions," says McGill computer-science professor Mathieu Blanchette, one of the leaders of the study. Work is currently underway to identify which of those regions may be involved in controlling traits of particular importance to farmers.

The study also weighs in on a major debate among biologists, concerning how much of an organism's [genome](#) has important functions in a cell, and how much is "junk DNA," merely along for the ride. While stretches of the genome that code for proteins are relatively easy to identify, many other 'noncoding' regions may be important for regulating genes, activating them in the right tissue and under the right conditions.

While humans and plants have very similar numbers of protein-coding genes, the map published in *Nature Genetics* further suggests that the regulatory sequences controlling plant genes are far simpler, with a level of complexity between that of fungi and microscopic worms. "These findings suggest that the complexity of different organisms arises not so much from what genes they contain, but how they turn them on and off," says McGill biology professor Thomas Bureau, a co-author of the paper.

More information: An atlas of over 90,000 conserved non-coding sequences yields detailed insight into crucifer regulatory regions, [DOI: 10.1038/ng.2684](https://doi.org/10.1038/ng.2684)

Provided by McGill University

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