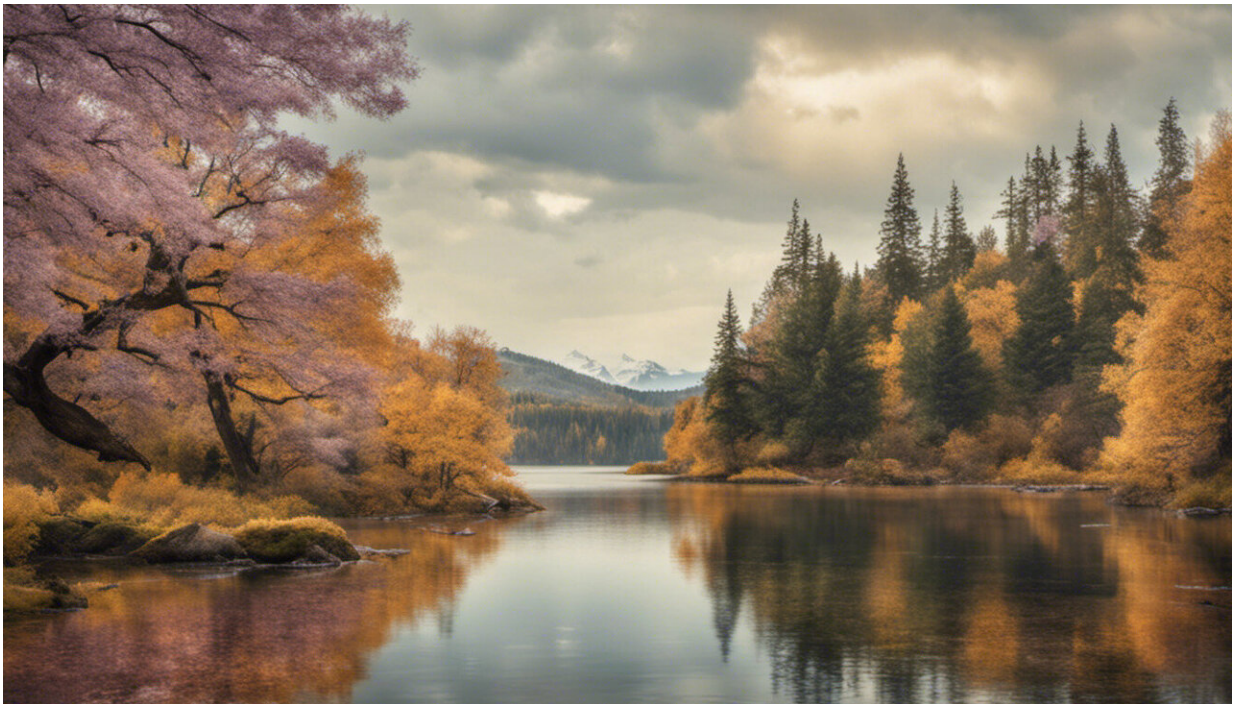


# Why we're sequencing the genomes of Canada's iconic species

June 28 2018, by Stephen W. Scherer

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Credit: AI-generated image ([disclaimer](#))

Last year, to commemorate Canada's 150th birthday —and to lay a foundation for Canadian research excellence for the next 150 years—a group of scientists in our country embarked upon the Canada 150 Sequencing Initiative (CanSeq150).

Motivated by our nation's curiosity about the animal that most shaped our history, [we sequenced the genome —the genetic instruction book —of the Canadian beaver \(\*Castor canadensis\*\)](#) in time for Canada's sesquicentennial. We've also begun sequencing 34 other species, including the Canada jay (*Perisoreus canadensis*) and the Canada lynx (*Lynx canadensis*).

Our goal is to sequence the genomes of 150 organisms important to Canada —and Canadians.

We are accepting proposals from researchers who present the best cases for the historical or immediate importance to Canada of each proposed organism. As new species are chosen, Canada's Genomics Enterprise (CGEn) will announce [additional species selected to undergo whole genome sequencing on its website](#).

Some of these genomes will be sequenced in a way that allows us to develop and test new technologies or methods to analyze the genetic sequence. We also hope that by better understanding the genomes of other species —and our own —we can better understand ourselves and our place in natural history.

Scientists learn and teach [Theodosius Dobzhansky's famous 20th century concept](#): "Nothing in biology makes sense except in the light of evolution."

In the 21st century, with the vision that genomic sequences will enable better biological and medical studies, we might consider updating Dobzhansky's insight to include [genome sequence](#) as well as evolution.

The CanSeq150 approach builds on past experience and provides inspiration for new submissions. For example, when the severe acute respiratory syndrome (SARS)-associated coronavirus threatened the

health of Canadians in 2003, [researchers mobilized to sequence the viral genome to aid in diagnosis and vaccine development.](#)

## **No bird brain**

We're now working on generating a genomic sequence of *Perisoreus Canadensis* —the Canada jay —that can be used as a reference for other studies. (Known as the gray jay for 60 years, the [American Ornithologist's Union recently reverted to its original name.](#))

The Canada jay inhabits all 13 provinces and territories, and figures strongly in First Nations folklore, where it is called the Wisakedjak, or whiskey jack. There is strong support for its designation as Canada's national bird.

A fascinating attribute of the Canada jay is its superior intelligence. It has developed a highly complex food-stockpiling strategy across widely scattered sites that keeps the bird alive through the winter breeding season. Each Canada jay can retrieve thousands of saliva-coated food caches each season by memory and pattern recognition —all hard-wired by its brain structure and encoded by its [genome](#).

## **Nature and nurture**

Long before Canada was a country, early accounting ledgers of the Hudson Bay Company show the Canada lynx and the snowshoe hare were in an obligate relationship.

The two animals share identical geographic range, covering the Canadian boreal forest. Deduced from historical fur harvest records, [hare and lynx populations were found to oscillate in tightly linked 10-year cycles.](#)

The genomes of the lynx and the hare can enlighten researchers on how the changing environment induces hormones and contributes to the cyclical declines in reproductive fitness in the hare population.

The genetic changes encoding the environmental sensors that underlie seasonal coat colour changes in the [snowshoe hare](#), among other physiological and environmental relationships, will be revealed.

## **Life's code**

The genome provides cells with directions like a blueprint, or orchestral score, for all aspects of development throughout the life of the organism.

Humans inherit half of their DNA from each parent, as they did from their parents, and so on, right back to the origin of Homo sapiens. The genomic information embedded in this DNA ties together the millions of species of Charles Darwin's tree of life.



A pair of Canada jays feed their nestlings in Algonquin Park, Ontario. Credit: [Dan Strickland/Wikimedia, CC BY-SA](#)

We have ample examples demonstrating how decoding human genomes can reveal the underpinnings of diseases and disorders, such as [cancer](#) and [autism](#), and [enable diagnostics for early detection](#). Medical or pharmaceutical treatments [increasingly target specific features of a disease](#), such as the proteins a cell expresses on its surface.

By definition, [genome sequencing](#) provides far better coverage of a genome's genetic markers than earlier technologies. We will be sequencing whales and trout, bear and sheep, maple trees and fungus, in order to discover genomic [DNA bar codes](#) —DNA markers covering all the cell's chromosomes —that are important for selection and

adaptation, and can be used in breeding and conservation.

## Gift to science

I teach my own students that as some applications of genomic science are becoming rather effortless, we are now only limited by our creativity.

To encourage such creativity, we believe that the first crack at studying a given new genome sequence [should be made by researchers who best understand the organism's unique biological, cultural, economic, societal and historical role.](#)

For CanSeq150, we will sequence the genomes of 150 organisms brought forward by Canadian researchers.

We believe that those same scientists can best harness the genome sequence information for our country —and for the world.

These experiences will influence decisions for future projects, including those related to human disease. The typical cost of a genome project will be \$3,000, and while this cost will be borne by CGEn and its partners, the studies will be led by the researchers who submit the genomes for sequencing.

Results from CanSeq150 will be available to researchers worldwide through public databases, such as the [National Center for Biotechnology Information.](#)

With our "updated" (genome-based) view of Dobzhansky's evolutionary biology concept, we aspire to promote scientific discovery altruistically. Understanding the intersections among the CanSeq150 species —and others —will surely help us become wiser custodians of our heritage.

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