

# Scientists look to map the genes of thousands of animals

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In this Feb. 22, 2018 photo provided by the Massachusetts Division of Fisheries & Wildlife, scientists Jen Vashon, left, and Tanya Lama pose with a Canada lynx that was used to source genetic material for the Canada lynx reference genome at Cummings School of Veterinary Medicine in Worcester County, Mass. A consortium of scientists on Thursday, Sept. 13 unveiled the first results of an ambitious effort to map the genetics of tens of thousands of animal species, ranging from the Canada lynx to the kakapo, a flightless parrot native to New Zealand. (Bill Byrne/MassWildlife/Massachusetts Division of Fisheries & Wildlife via AP)

A group of scientists unveiled the first results Thursday of an ambitious effort to map the genes of tens of thousands of animal species, a project they said could help save animals from extinction down the line.

The scientists are working with the Genome 10,000 consortium on the Vertebrate Genomes Project, which is seeking to map the genomes of all 66,000 species of mammal, bird, reptile, amphibian and fish on Earth. Genome 10,000 has members at more than 50 institutions around the globe, and the Vertebrate Genomes Project last year.

The consortium on Thursday released the first 15 such maps, ranging from the Canada lynx to the kakapo, a flightless parrot native to New Zealand.

The genome is the entire set of genetic material that is present in an organism. The release of the first sets is "a statement to the world that what we want to accomplish is indeed feasible," said Harris Lewin, a professor of evolution at University of California, Davis, who is working on the project.

"The time has come, but of course it's only the beginning," Lewis said.

The work will help inform future conservation of jeopardized species, scientists working on the project said. The first 14 species to be mapped also include the duck-billed platypus, two bat species and the zebra finch. The zebra finch was the one species for which both sexes were mapped, bringing the total to 15.

Sequencing the genome of tens of thousands of animals could easily take 10 years, said Sadye Paez, program director for the project. But giving scientists access to this kind of information could help save rare species

because it would give conservationists and biologists a new set of tools, she said.

Paez described the project as an effort to "essentially communicate a library of life."

Tanya Lama, a doctoral candidate in environmental conservation at the University of Massachusetts at Amherst, coordinated the effort to sequence the lynx genome. The wild cat is the subject of debate about its conservation status in the United States, and better understanding of genetics can better protect its future, Lama said.

"It's going to help us plan for the future—help us generate tools for monitoring population health, and help us inform conservation strategy," she said.

The project has three "genome sequencing hubs," including Rockefeller University in New York, the Sanger Institute outside Cambridge, England, and the Max Planck Institute of Molecular Cell Biology and Genetics in Dresden, Germany, organizers said.

The work is intriguing because it could inform future conservation efforts of jeopardized species, said Mollie Matteson, a senior scientist with the Center for Biological Diversity who is not involved in the project. More information about animals' genetics could lead to better understanding of how animals resist disease or cope with changes in the environment, she said.

"I think what's interesting to me from a conservation aspect is just what we might be able to discern about the genetic diversity within a species," Matteson said.

The project has similarities with the Earth BioGenome Project, which

seeks to catalog the genomes for 1.5 million species. Lewin chairs that project's working group. The Vertebrate Genomes Project will contribute to that effort.

**More information:** [www.sanger.ac.uk/science/data/ ... e-genomes-sequencing](http://www.sanger.ac.uk/science/data/...e-genomes-sequencing)

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