

DNA sequencing of noninvasively collected hair expands the field of conservation genetics

July 21 2015



An American pika (*Ochotona princeps*) calling. Credit: Philippe Henry, CC BY 4.0

Information embedded within DNA has long contributed to biodiversity

conservation, helping to reconstruct the past history of species, assess their current status, and guide strategies for their protection. A new study shows that the entire genome of hard to study species may now be available to scientists without the need to handle or even see their study organism, opening up the field of conservation genomics to the use of non-invasive sampling techniques.

Endangered and elusive species by definition may be both rare and difficult to locate. As a result, conservation geneticists typically have to rely on sources of DNA collected non-invasively, such as from hair, feathers or feces. Up until now, these approaches have been quite successful in obtaining genetic information from a handful of markers across the genome. However, so-called 'next-generation DNA sequencing' (NGS) now allows researchers to collect massive volumes of genetic data on the scale of entire genomes, yet the necessary requirements for harnessing such technology may not be available in most cases for [endangered species](#). For example, NGS typically requires high quality and large quantities of starting DNA extracted from fresh tissues or blood. Acquiring such materials is trivial for humans; a mere cheek swab will usually do. This is not the case, say, for the Amur leopard, which is both rare and elusive. In such cases, scientists and managers must rely on non-invasively collected sources of DNA that typically yield low quality and low quantity of starting material.



An American pika (*Ochotona princeps*) foraging. Credit: Philippe Henry, CC BY 4.0

The new study published in the open access journal *PeerJ* by researchers at the University of British Columbia (UBC) and SNPsaurus LLC demonstrates that the non-invasive sampling that is essential for many conservation-related studies is now compatible with the minimum requirements for harnessing NGS technologies. As a result, it will now be possible to further expand the field of conservation genetics in the genomics era.

"We were able to collect genome-wide data from natural populations of the elusive and climate-sensitive American pika on a scale unheard of just a few years ago" says Dr. Michael Russello, an Associate Professor at UBC and principal investigator of the study. The innovative data

collection approach pioneered by Dr. Eric Johnson and Dr. Paul Etter of SNPsaurus LLC, both co-authors of the study, enabled the sampling of almost 10,000 variable sites in the American pika genome using, in some cases, as little as 1 nanogram (one billionth of a gram) of starting DNA extracted from hair. "There are tremendous benefits for expanding our coverage of the genome when studying species of conservation concern, as it vastly improves our inferences of key genetic characteristics of populations and opens up new avenues for inquiry in the form of potentially identifying those parts of the [genome](#) that are involved in organisms' ability to adapt to changing environments" adds Dr. Russello. The use of NGS on non-invasively collected samples is not without its challenges, but can be overcome with a host of careful considerations pointed out by the authors.

In an era in which global biodiversity continues to decline at rates consistent with a mass extinction, conservation scientists and managers can now add genomics to their toolkit for attempting to document and reverse this trend.

More information: Russello et al. (2015), From promise to practice: pairing non-invasive sampling with genomics in conservation. *PeerJ* 3:e1106; [DOI: 10.7717/peerj.1106](https://doi.org/10.7717/peerj.1106)

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Citation: DNA sequencing of noninvasively collected hair expands the field of conservation genetics (2015, July 21) retrieved 23 April 2024 from <https://phys.org/news/2015-07-dna-sequencing-noninvasively-hair-field.html>

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