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Life's Bar Code: Genetic Tests Unveil 15 New Species of North American Birds

A bird in the taxonomic hand may actually be two in the bush, according to the results of a genetic survey of all North American avians

The common raven may not be so common anymore, according to the results of the largest DNA bar coding effort to date. Despite hundreds of years of observation and examination by countless experts and amateurs, *Corvus corax*, as the genus and species name goes under the Linnaean taxonomic system, may actually harbor two distinct species, indistinguishable to the eye but not in the makeup of its mitochondrial DNA. "[DNA] barcodes are giving us a direct signal of where species boundaries lie," says Paul Hebert, an evolutionary biologist at the University of Guelph in Ontario and a progenitor of the genetic bar code effort. "We have very low levels of variation within a species and this deep divergence between species."

This May marks the 300th anniversary of the birth of Carl Linnaeus, the Swedish naturalist who established the conventions for naming living organisms as well as the system of scientific classification that, with a few modifications, are still used today. Under his system each new (to science) living thing is included in a genus—a general grouping of that particular type of bird or fish, for example—and then given a specific species name. But distinguishing a new genus or a new species requires fulfilling a host of criteria—and the designation sometimes responds to popularity. For example, nematodes—flat worms that thrive on the bottom of the ocean—are numerous but largely uncatalogued whereas colorful birds do not lack for designation and sometimes are overdesignated. White-headed gulls are currently split into at least eight different species, though they are quite difficult to tell apart.

By using a portion of one gene—cytochrome c oxidase I (COI)—contained in the energy-producing mitochondria of cells in all eukaryotic life, researchers can now distinguish between species that look identical because this particular stretch of DNA mutates frequently. "Mitochondria [are] a good place for mutation because there is a lot of damaging stuff produced just in the course of respiration," Hebert explains. And, because it is present in every living cell, it becomes possible to use it to distinguish. "This tiny gene region will allow me to tell apart fish, birds, every insect, protozoan and every fungus," he adds.

These differences do not have to be much. Some fish differ by just one arrangement of the various amino acids in the DNA while disparate species can vary by nearly one quarter of the genetic sequence. By surveying all the birds of North America, bar code proponents aimed to demonstrate the efficacy and accuracy of the technique. After all, although there are 643 bird species on the continent, there are vastly more bird enthusiasts. "There are nearly as many birders in North America as there are birds," Hebert says. "If you're going to ground-truth a system it's nice to have a ground system that has been well-surveyed."

The researchers sampled tissue from stored specimens to tease out genetic samples and ended up producing 15 new distinct species and revealing several genetic twins, triplets and even one octuplet (the aforementioned white-headed gulls), according to the study in *Molecular Ecology Notes*. Of course, the vast majority of DNA bar coding merely served to



confirm the original Linnaean taxonomy. "In the groups that we have looked at we are able to place 98 percent of known species accurately," Hebert says.

The bird study is part of a much larger effort to create such genetic bar codes for all life. To date, researchers have catalogued 200,000 specimens and at least 25,000 species, including a study of tropical bats in Guyana that uncovered six new bat species among 840 specimens. "We targeted the bats specifically because they are the most diverse mammal on the planet," Hebert says. "It makes us feel quite comfortable that bar coding can tackle the tropics."

But it is in less glamorous precincts that bar coding may prove its true worth. "We can deliver maybe not names for every organism but we can recognize all the genetically divergent ones. We can have them waiting in small vials until there is a taxonomist waiting to describe them," Hebert notes. "You wait a very long time for people to rise up who will categorize the nematodes at the bottom of the ocean." Already, new species of butterfly have been taxonomically described after being discovered by such genetic bar coding.

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"We are fairly ambitious in terms of our long term goals: a digital identification system for eukaryotic life," Hebert says. "Closure for life on the planet will be a difficult task. There will always be a nematode lurking under a rock."

"But now I'm getting worried that there isn't enough to keep me busy," he adds. "This job is going to get done." Assuming, of course, that there is sufficient interest and funding for the work of testing the DNA of the estimated five million species on the planet. Already, the fish and mammals of the world will soon be complete and there is an extra urgency to the task, in Hebert's view: "For \$100 million we can register life on the planet while it's still here."

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