Research

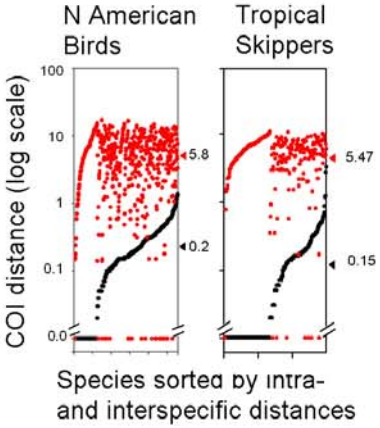
Growing mitochondrial DNA libraries pose and help address research questions. For example, many avian species have been analyzed for other mitochondrial regions, such as cytochrome b. Do COI sequences predict differences elsewhere in mitochondrial genomes?

mtDNA clusters usually correspond to recognized species, suggesting that mtDNA differences are representative of changes in the nuclear genome. To what extent do nuclear and mitochondrial genes co-vary within and between species?

Most species analyzed so far are temperate zone migrants. Do these results hold for tropical and non-migratory fauna?

In Anseriformes (ducks, geese, swans), nearest neighbor differences are lower than in other orders analyzed so far. Is this finding particular to anseriformes and what does this indicate about their biology?

Results so far show low mitochondrial sequence variation within most species, including vertebrates and invertebrates in tropical, temperate, terrestrial, and marine environments. What constrains mitochondrial diversity?



average values for minimum interspecific (red) and intraspecific (black) distances are indicated

Links

All Birds Barcoding Initiative (ABBI)
http://www.barcodingbirds.org
Barcode of Life Data Systems (BOLD)
http://www.barcodinglife.org
Consortium for the Barcode of Life (CBOL)
http://www.barcoding.si.edu
DNA Barcode Blog
http://phe.rockefeller.edu/barcode/blog

Applications

DNA barcoding can be equally applied to intact specimens, feathers collected during banding operations, fragments recovered by wildlife enforcement agencies, or tissue remnants collected after aircraft birdstrike collisions, for example.

In the U.S., over 10,000 birdstrike collisions with civilian and military aircraft occur yearly, resulting in estimated costs of $1.2 billion due to aircraft damage and downtime. Worldwide, 195 deaths due to birdstrikes have occurred since 1988. Identification of species is the first step in mitigation efforts to reduce bird presence near airports and aids in improvements in aircraft design to reduce potentially catastrophic effects of birdstrikes.

Feather Identification Laboratory, Smithsonian Institution

Until recently, identification of birdstrike tissue specimens required expert training to recognize feather characteristics under high-powered microscopy. DNA barcoding is a widely-accessible method for identifying tissue remnants, including those collected after birdstrikes.

Some live birds are difficult for experts to identify, even in the hand. DNA sequencing of feathers offers a practical method that can be applied regardless of age, sex, or plumage.

COI sequencing of a breast feather helped confirm the identity of this newly banded Alder flycatcher (*Empidonax alnorum).*

This *Selasphorus* hummingbird wintering in Ontario was revealed as *S. rufus* by COI sequencing of a feather found at a feeder.

All Birds Barcoding Initiative Update

v2.0 2 April 2008

Mark Stoeckle, The Rockefeller University

What is DNA barcoding?

Distinguishing species is the first step in understanding the living world. **DNA barcoding describes a standardized approach to identifying species by their DNA.** Standardizing on one or a few gene segments enables a universal reference library and promotes inexpensive technologies for species identification that can be employed by a wide variety of interested persons.

What is All Birds Barcoding Initiative (ABBI)?

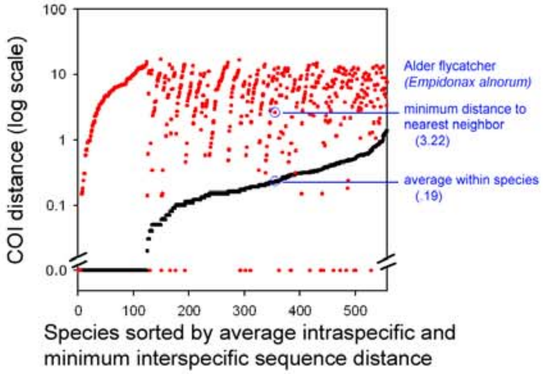
ABBI is an international effort that aims to establish a public reference library of DNA barcodes for the approximately 10,000 known species of world birds. **The ABBI library of avian sequences linked to museum specimens will speed discovery of new species and aid societal and scientific efforts to preserve biodiversity.**

Results so far

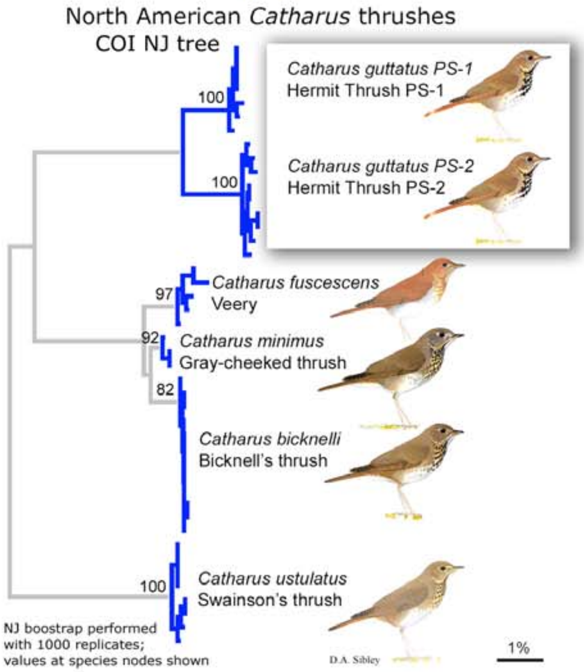
1. COI sequence differences are generally much smaller within species than between species.

As a result, most bird species examined so far are represented as single sequence clusters distinct from those of other species, enabling precise assignment of specimens to species by COI barcode.

COI sequence distances within species (black) and minimum sequence distances between species (red) among 557 North American birds. As an example, results for Alder flycatcher are highlighted.

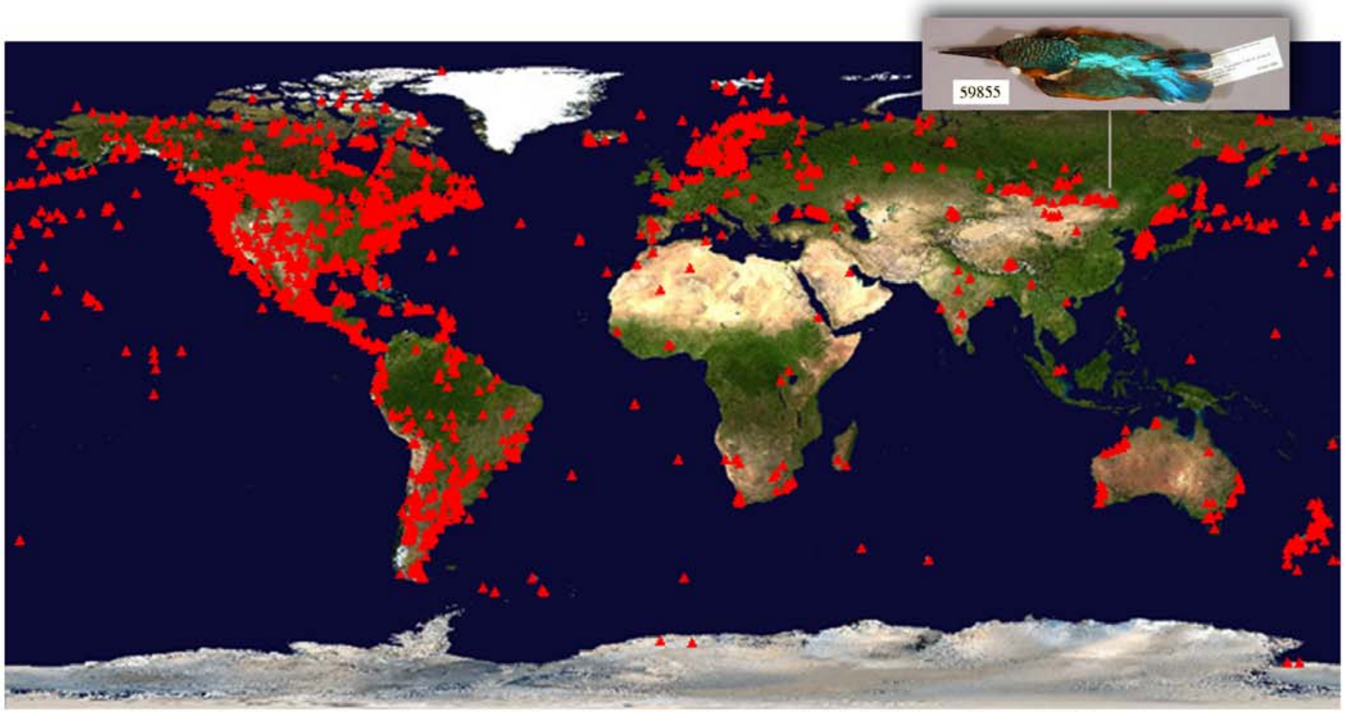


2. COI barcodes reveal provisional new species even in well-studied groups.



3. Approximately 12,000 individuals from 2,200 species have been barcoded so far.

Wherever possible, the reference library utilizes specimens from museum tissue collection backed up by study skins, enabling full specimen data to accompany the sequence record and allowing puzzling results to be investigated further.



Collection locations for avian specimens with COI barcode sequences in Barcode of Life Data Systems database (BOLD) are shown.

4. Some bird species share COI sequences.

So far, most appear to be very young species or species that hybridize regularly. Some may represent populations within a single species.

In approximately 6% of North American birds, COI barcode clusters correspond to small sets of closely related species. For example, Ross's goose (*Chen rossii*) and Snow goose (*C. caerulescens)* have overlapping COI barcode clusters. This may reflect reproductive mixing, as mixed pairs and intermediate individuals are found in some breeding colonies and F1 hybrid offspring are fertile.

5. Population size and species age appear to have only modest effects on mitochondrial DNA sequence differences within species.

Intraspecific COI sequence variation is low in most North American birds, although their population sizes range from a few thousand to several hundred million individuals.