



BARCODING LIFE



TAKES FLIGHT

ALL BIRDS BARCODING INITIATIVE

Needs and Resources Statement

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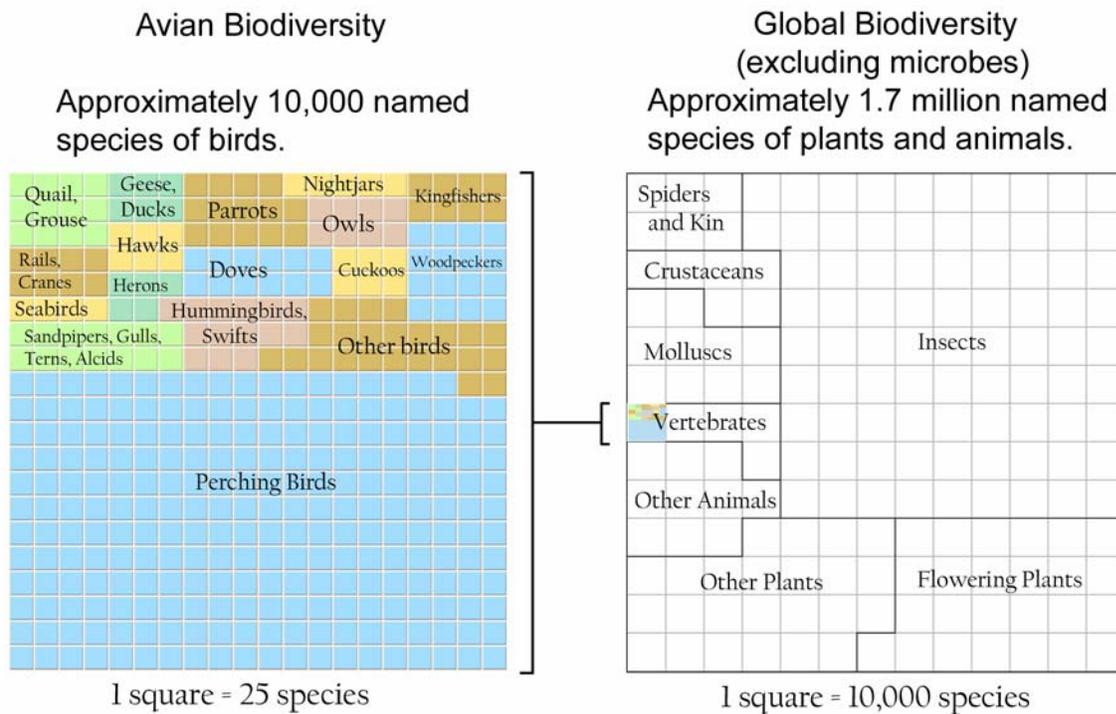
CONSORTIUM FOR THE BARCODE OF LIFE



The All Birds Barcoding Initiative (ABBI) aims to establish a public archive of DNA barcodes for all birds, approximately 10,000 species, by 2010.

Beginning with Darwin’s finches, avian study has led to powerful insights into evolution, speciation, and population biology. Birds are an ideal group for exploring the efficacy of barcodes in species identification because avian taxonomy is so well-established: species limits are better understood in birds than in any other large group of animals. ABBI will help identify possible limitations to barcoding, such as newly emerged species or those that hybridize regularly. As a global avian survey, ABBI will likely contribute to the recognition of many new bird species.

ABBI is a flagship project of the Consortium for the Barcode of Life (CBOL), an international initiative devoted to developing DNA barcoding. ABBI was launched at the First International Conference on Barcoding Life, held at The Natural History Museum, London, 7-9 February 2005.



A comprehensive library of avian barcodes linked to identified specimens will be an enduring resource for ornithologists, ecologists, public health officials, and the interested public. DNA barcoding can be applied equally to intact specimens, single feathers collected from live birds in banding or customs operations, or fragments of birds involved in aircraft collisions, for example.

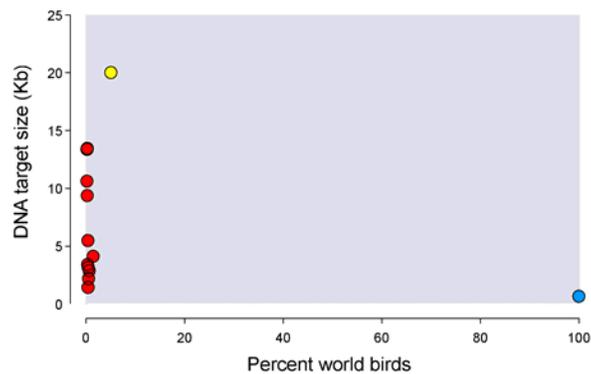


Photos courtesy Carla Dove

According to the FAA, avian strikes cost civil aviation an estimated \$1.2 billion annually, including \$500 million in damage to aircraft and 500,000 hours of civil aircraft downtime. Identification of bird species involved in airstrikes enables targeted interventions aimed at minimizing presence of these species around airfields and provides information to aircraft manufacturers relevant to aircraft design.

ABBI is one of the first “broad and shallow” explorations of the genomic landscape of biodiversity, and will create a high-resolution genomic map of a large sector of animal life. The enormous data set of sequences and associated specimen information will be of interest to those studying evolution, population biology, and biodiversity, as well as to avian experts. One challenge for ABBI is to develop efficient strategies for obtaining and processing large numbers of tissue specimens. It is anticipated that about 50,000 specimens will be analyzed, representing an average of five for each of 10,000 species.

Depth and breadth of avian genomic projects:
DNA target size and percent world birds



- recent large scale avian phylogenetic studies
- Early Bird-Assembling the Tree of Life
- ABBI projected

What does ABBI need to do and what resources are available to accomplish the goal of barcoding all bird species by 2010?

Need 1. Establish list of target species.

Resources: Several recent expert taxonomic compilations of world birds are available. Establishing a target list will enable ABBI to distribute tasks, track progress, and avoid duplication of effort. The reference list can be updated regularly and shared online.

	Checklists of world birds	Updated
Books		
1	Clements 2000. Birds of the World: A Checklist, 5th ed.	2005
2	Dickinson 2003. Howard and Moore Complete Checklist of the Birds of the World, 3rd ed.	2003
3	Wells 1998. World Bird Species Checklist	1998
4	Monroe and Sibley 1993. Checklist of World Birds.	1993
Databases		
5	Zoological Nomenclature Resource for World Birds at www.zoonomen.net .	2005

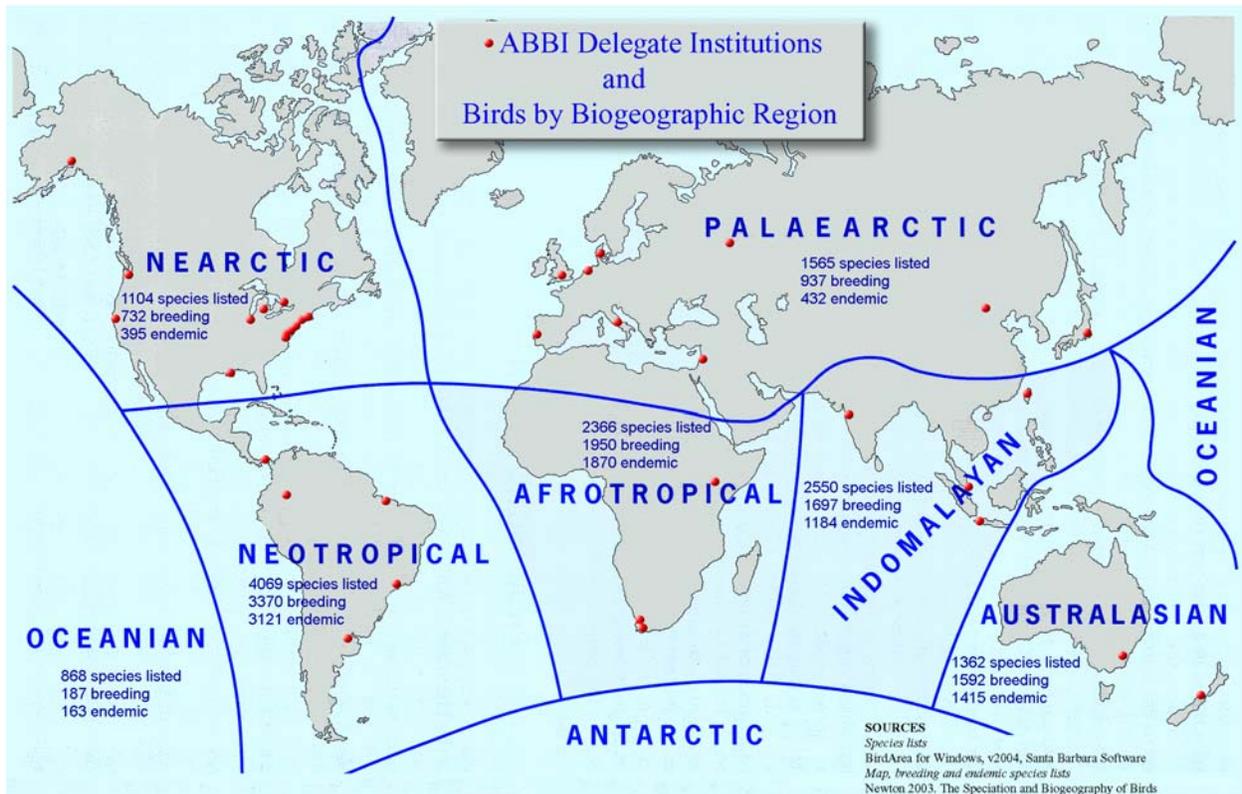
Need 2. Locate specimens.

Resources: At least half of the world's bird species are already represented in tissue collections. A spreadsheet prepared for ABBI compiles holdings in frozen tissue collections and compares these to a world checklist. Expanding and regularly updating this list will enable efficient organization of barcoding efforts and will help determine if and when museum skins need to be sampled or new collecting is needed.

Collection	Tissue specimens	Species represented
Australian Museum	1,433	308
Burke Museum	21,699	1817
Field Museum	20,485	2056
Indonesian Museum	861	211
Louisiana State University	34,766	3282
Museo Argentino	376	99
Museum of Comparative Zoology	286	286
Museum of Vertebrate Zoology	8,900	432
Philadelphia Academy of Natural Sciences	2,245	1937
Smithsonian Institution	20,000	1709
Smithsonian Tropical Research Institute	9,033	716
Zoological Museum of Copenhagen	24,000	2409
Totals	144,084	5,765

Need 3. Establish organizational framework.

Resources: Organization by biogeographic region, with regional teams and team leaders, and region-specific species lists will enable ABBI to accomplish its goals efficiently.



Need 4. Establish sampling strategies within species.

Resources: Results so far show that barcode differences within bird species are much smaller than between species and that overlaps between species are uncommon. This indicates that for most species, a small sample of specimens can be used to establish diagnostic barcodes. More detailed sampling may be needed in some cases, particularly for wide-ranging species, species that hybridize regularly, closely related sister species, and those with well-marked subspecies or geographic variation. Experts in avian taxonomy and population biology can help establish scientific sampling strategies that reliably capture differences within and among species.

Need 5. Identify permit issues.

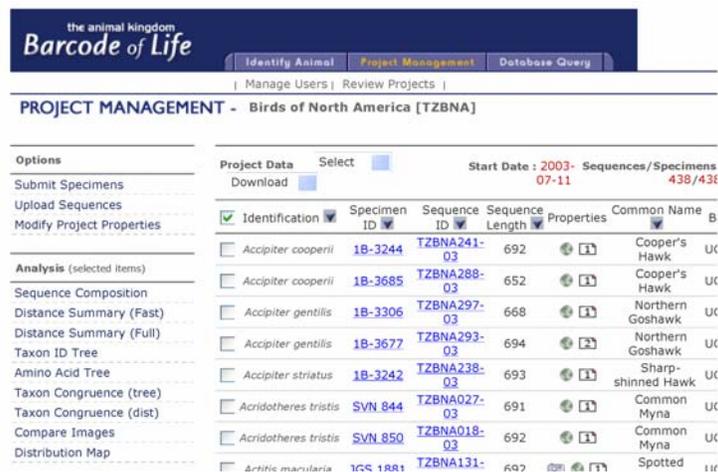
Resources: Analysis of museum specimens is governed by a host of regulations, both within institutions and by governments, often with multiple agencies involved. In some cases, it is not possible to transport specimens. Regional ABBI leaders can help identify permit issues on a collection by collection basis to determine the best strategy, with speed and cost being the considerations. Outreach efforts to institutions and regulatory agencies in advance of specimen requests may help speed the process.

Need 6. Steer specimens to sequencing facilities.

Resources: Sequencing facilities are available in many localities. The most efficient strategy will likely combine centralized sequencing at high-throughput centers and more local analysis of specimens where permitting limits sample movement. Efficient processing of large numbers of specimens requires close communication between collection and sequencing facility personnel so that possible problems, such as mislabeling of specimens or inability to amplify DNA, are quickly detected and corrected.

Need 7. Establish a shared software platform and standards for data submission and access.

Resources: A shared software platform is essential for managing ABBI as a global distributed project. The Barcode of Life Database (BoLD) offers a software platform that could be used for assembling, integrating, tracking, and analyzing the data coming in from all the biogeographic regions. Shared access among ABBI researchers as the database is populated will help speed the project along. BoLD is directly linked to GenBank, providing a stable, permanent home for barcode data. Strict data standards for barcode records have already been established by CBOL and GenBank, including a requirement that each record be linked to a voucher specimen and validated species name.



the animal kingdom
Barcode of Life

Identify Animal | Project Management | Database Query

Manage Users | Review Projects

PROJECT MANAGEMENT - Birds of North America [TZBNA]

Options

Submit Specimens

Upload Sequences

Modify Project Properties

Analysis (selected items)

Sequence Composition

Distance Summary (Fast)

Distance Summary (Full)

Taxon ID Tree

Amino Acid Tree

Taxon Congruence (tree)

Taxon Congruence (dist)

Compare Images

Distribution Map

Project Data Select Start Date : 2003- Sequences/Specimens
Download 07-11 438/438

Identification	Specimen ID	Sequence ID	Sequence Length	Properties	Common Name	B
<input type="checkbox"/>	Accipiter cooperii 1B-3244	TZBNA241-03	692		Cooper's Hawk	UC
<input type="checkbox"/>	Accipiter cooperii 1B-3685	TZBNA288-03	652		Cooper's Hawk	UC
<input type="checkbox"/>	Accipiter gentilis 1B-3306	TZBNA297-03	668		Northern Goshawk	UC
<input type="checkbox"/>	Accipiter gentilis 1B-3677	TZBNA293-03	694		Northern Goshawk	UC
<input type="checkbox"/>	Accipiter striatus 1B-3242	TZBNA238-03	693		Sharp-shinned Hawk	UC
<input type="checkbox"/>	Acridotheres tristis SVN 844	TZBNA027-03	691		Common Myna	UC
<input type="checkbox"/>	Acridotheres tristis SVN 850	TZBNA018-03	692		Common Myna	UC
<input type="checkbox"/>	Artibeus maritima 1CC 18A1	TZBNA131-	692		Spotted	UC

Barcode of Life Database (BoLD) can provide an accessible repository for analyzing and tracking ABBI data.

Need 8. Identify funding strategies.

Resources: The project will be widely distributed and can therefore seek funding from a variety of sources. The high visibility of birds suggests that support from individual donors and private foundations can make a major contribution. Regulatory agencies involved in airline safety, wildlife management, trade in endangered species, or public health authorities interested in control of West Nile virus in avian reservoirs, for example, may be interested in supporting the project. Finding ways to lower unit costs and including support for collections that provide specimens will help the project succeed. High volume sequencing centers can analyze tissue specimens for approximately \$5/specimen, suggesting a unit cost of \$10/specimen is feasible. Costs may be substantially greater in low volume centers, for analysis of dried specimens, or where new collecting is needed. Where new specimens are needed, efforts can be made to utilize ongoing collecting operations.

Need 9. Publication strategy.

Resources: ABBI is expected to be a high profile research project because it will likely suggest the presence of many new species of birds and is the first large-scale exploration of the fine structure of genomic biodiversity. At least three types of publications are envisioned: All Birds by geographic area (e.g. All Birds of Oceania), All Birds by taxonomic category (e.g. All Woodpeckers), and analytic studies that focus on nucleotide and protein sequence data independent of avian biology. These papers can be submitted as the effort moves along. In addition, ABBI can plan a multi-author All Birds paper to be published in a major scientific journal in 2010. Exploring publication strategy at the outset will help guide collaborations.

Need 10. Timeline.

Resources: Tangible, realistic goals of barcodes compiled by region and taxon will provide concrete evidence of progress, help attract public interest, and recruit private and public support.

Background

Barcode of Life is a short DNA sequence, from a uniform locality on the genome, used for identifying species. DNA barcoding can be used to help discover, characterize, and distinguish species, and to assign unidentified individuals to species.

“**Ten Reasons for Barcoding Life**” are described in a brief illustrated brochure available at <http://phe.rockefeller.edu/barcode/docs/TenReasonsBarcoding.pdf>. The goals, rationale, and results so far of this new technology for biodiversity science are described in “**Barcoding Life, Illustrated**”, available at http://phe.rockefeller.edu/PDF_FILES/BLIllustrated26jan04print%20v1-3.pdf.

Consortium for the Barcode of Life (CBOL) (<http://barcoding.si.edu/>) is an international initiative whose mission is to explore and develop the potential of DNA barcoding as a practical tool for species identification in taxonomic research, biodiversity studies and conservation, and diverse applications that use taxonomic information in service to science and society. CBOL is an alliance of natural history museums, herbaria, zoos, botanical gardens; research organizations devoted to biodiversity, conservation, bioinformatics, genetics and related topics; government agencies, NGOs, and other organizations that rely on taxonomic information; and private sector companies.

More information on DNA barcoding is available at University of Guelph’s Barcode of Life website (<http://www.barcodinglife.org/>) and The Rockefeller University barcode site (<http://phe.rockefeller.edu/BarcodeConference/>).