

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. Because species limits are better understood in birds than in any other large group of animals, birds are an ideal group for exploring the efficacy of barcodes. **ABBI** will help identify possible limitations to barcoding, such as emerging 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.

Avian Biodiversity

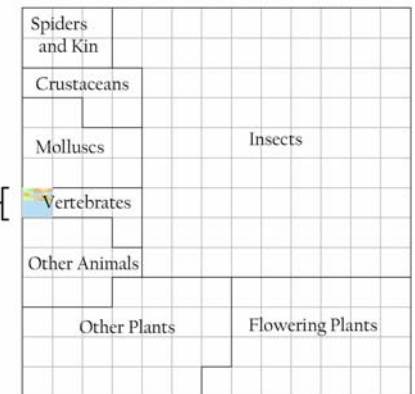
Approximately 10,000 named species of birds.



1 square = 25 species

Global Biodiversity (excluding microbes)

Approximately 1.7 million named species of plants and animals.



1 square = 10,000 species

CONSORTIUM FOR THE BARCODE OF LIFE (CBOL) is an international alliance of natural history museums, herbaria, zoos, botanical gardens; research organizations devoted to biodiversity, conservation, bioinformatics, and genetics; and government agencies, NGOs and private sector companies.

CBOL's mission is to develop the potential of DNA barcoding as a practical tool for species identification in taxonomic research, biodiversity studies and conservation, and in diverse applications that use taxonomic information in service to science and society. For more information, see <http://barcoding.si.edu/>.

BARCODE OF LIFE: A short DNA sequence, from a uniform locality on the genome, used for identifying species.

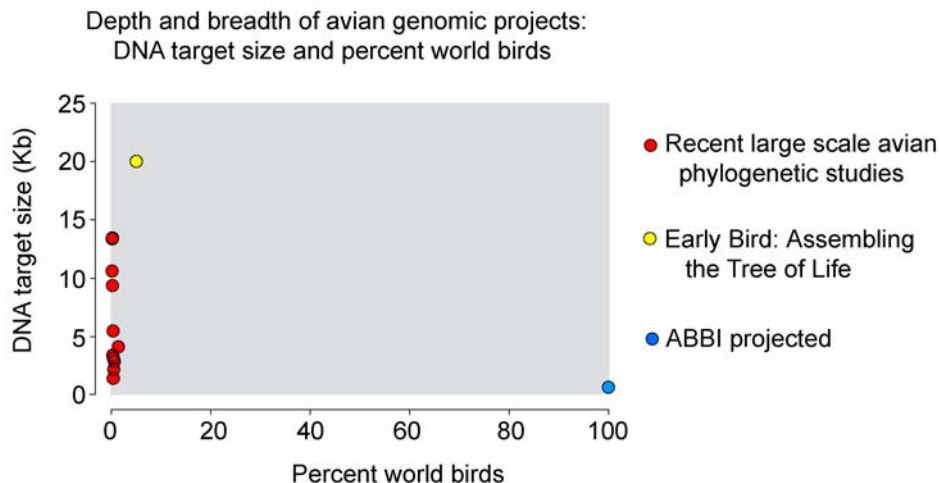
ABBI's comprehensive library of avian barcodes linked to identified specimens will be an enduring resource for ornithologists, ecologists, public health officials, and the interested public. DNA barcoding can be applied equally to intact specimens, single feathers collected from live birds in banding 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 that reduce presence of these species near airfields and helps manufacturers improve aircraft design.

ABBI is one of the first “broad and shallow” explorations of the genomic landscape of biodiversity. 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. ABBI will help drive development of efficient strategies for processing tissue specimens. It is anticipated that about 50,000 specimens will be analyzed, representing an average of five for each of 10,000 species.



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 the 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
Monroe and Sibley 1993. Checklist of World Birds.	1993
Wells 1998. World Bird Species Checklist	1998
Dickinson 2003. Howard and Moore Complete Checklist of the Birds of the World, 3 rd edition.	2003
Clements 2000. Birds of the World: A Checklist, 5 th edition	2005
Zoological Nomenclature Resource for World Birds (www.zoonomen.net)	2005

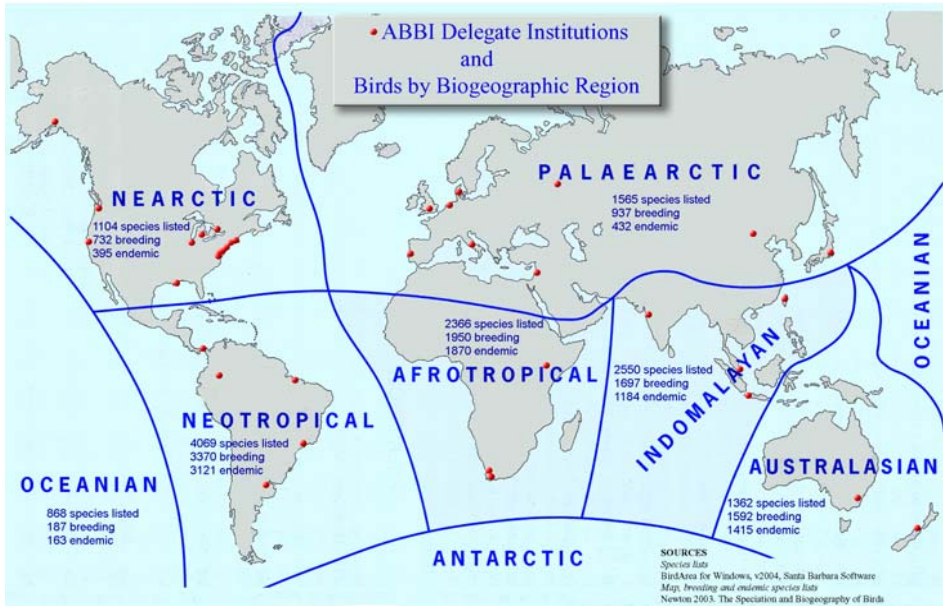
Need 2. Locate specimens.

Resources: A compilation of avian tissue collections prepared for ABBI shows that at least two-thirds of the world's bird species are already represented in tissue collections. Expanding this list will enable efficient organization of barcoding efforts and 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	340
Burke Museum	21,699	1,873
Field Museum	20,485	2,056
Indonesian Museum	1,037	258
Louisiana State University	34,766	3,282
Museo Argentino	376	114
Museum of Comparative Zoology	1,660	456
Museum of Vertebrate Zoology	8,945	441
Philadelphia Academy of Natural Sciences	13,000	2,102
Royal Ontario Museum	27,470	960
Smithsonian Institution	20,000	1,902
Smithsonian Tropical Research Institute	9,033	764
Swedish Museum of Natural History	12,140	912
University of Kansas	10,000	1,730
Zoological Museum of Copenhagen	24,000	2,646
Totals	206,044	6,320

Need 3. Establish organizational framework.

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



Need 4. Establish sampling strategies within species.

Resources: Results so far show barcode differences within bird species are much smaller than between species, and overlaps between species are uncommon. Thus 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 will 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 determine the fastest and least expensive strategy for processing specimens. Outreach efforts to institutions and regulatory agencies in advance of specimen requests and providing support for collections 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 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: The Barcode of Life Database (BoLD) offers a software platform that can be used for assembling, integrating, tracking, and analyzing the data. 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. 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

PROJECT MANAGEMENT - Birds of North America [TZBNA]

Options	Project Data	Select	Start Date	Sequences/Specimens		
Submit Specimens	Download	<input type="checkbox"/>	2003-07-11	438/438		
Upload Sequences						
Modify Project Properties						
<input checked="" type="checkbox"/> Identification	Specimen ID	Sequence ID	Sequence Length	Properties	Common Name	B
<input type="checkbox"/> <i>Accipiter cooperii</i>	1B-3244	TZBNA241-03	692		Cooper's Hawk	UC
<input type="checkbox"/> <i>Accipiter cooperii</i>	1B-3685	TZBNA288-03	652		Cooper's Hawk	UC
<input type="checkbox"/> <i>Accipiter gentilis</i>	1B-3306	TZBNA297-03	668		Northern Goshawk	UC
<input type="checkbox"/> <i>Accipiter gentilis</i>	1B-3677	TZBNA293-03	694		Northern Goshawk	UC
<input type="checkbox"/> <i>Accipiter striatus</i>	1B-3242	TZBNA238-03	693		Sharp-shinned Hawk	UC
<input type="checkbox"/> <i>Acridotheres tristis</i>	SVN 844	TZBNA027-03	691		Common Myna	UC
<input type="checkbox"/> <i>Acridotheres tristis</i>	SVN 850	TZBNA018-03	692		Common Myna	UC
<input type="checkbox"/> <i>Artibeus marularia</i>	1CC 18R1	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.

SOURCES

- Clements J. 2000. *Birds of the World: A Checklist*, 5th edition. 867 pp. Ibis Publishing Company.
- Cracraft J, Barker FK, Braun M, Harshman J, Dyke GJ, et al. 2004. Phylogenetic relationships among modern birds (Neornithes). In *Assembling the Tree of Life*, pp. 468-489. Oxford University Press.
- Hebert PDN, Stoeckle MY, Zemlak TS, Francis CM. 2004. Identification of birds through DNA barcodes. *PLoS Biol* 2:e312.
- Tudge C. 2000. *The Variety of Life*. 684pp. Oxford University Press.
- Edwards SV, Jennings WB, and Shedlock AM. 2005. Phylogenetics of modern birds in the era of genomics. *Proc Royal Soc London B* 272: 979–992.
- Newton I. 2003. *The Speciation and Biogeography of Birds*. 668 pp. Academic Press.

ADDITIONAL INFORMATION

Ten Reasons for Barcoding Life are described in a brief illustrated brochure (<http://phe.rockefeller.edu/barcode/docs/TenReasonsBarcoding.pdf>)

Barcoding Life, Illustrated outlines the goals, rationale, and results so far of this new technology for biodiversity science (http://phe.rockefeller.edu/PDF_FILES/BLIllustrated26jan04print%20v1-3.pdf.)

More information on DNA barcoding is available at <http://barcoding.si.edu> (CBOL), <http://www.barcodinglife.org/> (University of Guelph), and <http://phe.rockefeller.edu/BarcodeConference/> (The Rockefeller University).



Photo courtesy Stuart Mackenzie

The library of avian barcodes is anchored in collections of identified specimens archived in museums and other biological repositories. Linking sequence data to named specimens adds value to museum collections and ensures that both sequences and specimens can be re-analyzed in cases of discordant results. Once a reference library is established, DNA barcoding can provide an independent, inexpensive method for verifying identifications of tissue specimens, intact skins, or birds monitored in banding operations.