

Post-2020 Global Biodiversity Framework Input from The International Barcode of Life Consortium

Recognizing the urgent need to assess the impacts of environmental changes on biodiversity, the International Barcode of Life Consortium (iBOL) has established an innovative DNA-based science and technology program to monitor biodiversity on a planetary scale. With a participatory approach from a global network of scientists, collaborators, and citizens (including indigenous peoples and local communities), iBOL is building a library of life which will provide a first-ever baseline of biodiversity for Earth. This data will allow assessments of shifts in species distributions under the impact of climate change with implications for science-based decision-making. Data generated by iBOL can be freely accessed through the Barcode of Life Data Systems (boldsystems. org), an online platform for molecular biodiversity information which contributes to the Global Biodiversity Information Facility (GBIF). iBOL's long-term goal is to establish an Earth observation system for biodiversity, akin to the weather monitoring system that alerted us to global warming.

Starting in 2019 and going beyond 2020, iBOL will oversee a collaborative project, BIOSCAN, which will transform biodiversity science, improve citizens' understanding of species and their interactions, and build capacity for biodiversity conservation. BIOSCAN will provide the data and tools to address urgent questions relating to food security, water and soil health, human health, and climate change.

iBOL believes that it is vital for our society to protect global biodiversity and that active participation by all sectors of our society is essential to build a bio-literate world and attain the 2050 Vision of 'Living in Harmony with Nature'.

Addressing Planetary Biodiversity

Our planet is in transition; air temperatures are rising, rainfall patterns are shifting, and ice is retreating. These changes are restructuring ecosystems around the world, creating the need for approaches to track biodiversity change at large geographic scales. Because of the exponential rise in the power of both DNA sequencers and computational technology, DNA-based identification systems can meet this need and more. They can also disclose the intensity, nature, and flux of interactions among the constellation of species present at each locality.

The shift to DNA-based identification systems makes it possible to ascertain the species composition of mass collections, permitting biodiversity surveys with unprecedented taxonomic resolution and at hitherto impossible temporal and spatial scales. It also enables a rapid answer to a previously intractable question – how many species share our planet? Finally, it provides a new pathway, symbiome analysis, to both reveal and investigate interactions among species. It achieves this by linking every sequence recovered from a particular specimen to its source, be it commensal, parasite or mutualist.



Applications of DNA-based Identification

DNA-based identification methods, such as DNA barcoding, have many practical applications beyond species inventories for biodiversity assessment. Reliable identification of organisms, across all life stages, is of paramount importance for species such as invasive alien species, protected species, bioindicator species, species of economic importance, or pests/pathogens/vectors. Early detection allows a rapid response in cases of species with a negative impact on biodiversity, human health and well-being. Consequently, a DNA-based identification system will be an invaluable tool for food security, international trade of goods, and advancing the implementation of national strategies and action plans for biodiversity conservation as well as contributing to achieving the Aichi Biodiversity Targets and Sustainable Development Goals.

At COP13 in 2016 (CBD/COP/DEC/XIII/31), the Parties to the Convention on Biological Diversity (CBD) recognized DNA barcoding as a useful tool to implement the Strategic Plan for Biodiversity 2011-2020. Following this decision, a series of capacity-building activities in DNA barcoding took place in developing countries with support from iBOL and the Secretariat of the CBD. The need to continue training in DNA barcoding for rapid species identification was also acknowledged by COP 14 (CBD/COP/DEC/14/24) and welcomed by iBOL which sees capacity-building as an important component of its on-going and future programs.

International Organization

The International Barcode of Life Consortium, an alliance of research organizations in 30+ nations, began to lay the foundational elements for a DNA-based identification system for eukaryotes in 2010. By 2015, it had completed its first project, BARCODE 500K, a \$125 million effort that delivered DNA barcode coverage for 500,000 species. Among these, many invasive alien species, protected species, pests and species of economic importance were barcoded and the results are readily available to practitioners from the conservation and regulatory sectors. In June 2019, iBOL will launch BIOSCAN, a 7-year, \$180 million project that will ascertain species assemblages at 2,000 sites around the planet, while also examining the interactions among the species present at these locations.

Our understanding of the physical world has been revolutionized by technology; shifts in surface features are now sensed by satellite and hyperspectral imaging. High-throughput sequencers represent the technology that will transform our understanding of the biological world by detailing species interactions and by allowing ecosystem appraisal on a planetary scale. BIOSCAN lays the foundation for this transformation. Its successor, the PLANETARY BIODIVERSITY MISSION, will complete it; all species will be registered, all ecosystems will be monitored, and all species interactions will be codified.

Outcome

By registering patterns of biodiversity across ecoregions, BIOSCAN will make it possible to forecast changes in response to anthropogenic drivers such as shifting land use, pollution, and global warming. It will also deepen our understanding of species interactions by probing the symbiome – a new approach that employs the array of mitochondrial sequences recovered from any specimen to diagnose the species associated with it. Although BIOSCAN's initial studies will target terrestrial environments, the resultant protocols will soon see adoption in freshwater and marine ecosystems.

Tracking Ecosystems

Our planet is an island of life in the cosmos. We know its major domains, but the details are lacking, even for multicellular organisms. BIOSCAN will illuminate millions of dark species by metabarcoding assemblages from 2,000 sites, first targeting the most diverse compartment of terrestrial life, arthropods. As BIOSCAN's work will involve the analysis of at least 100 million specimens, millions of new species will be encountered. Their registration will be expedited by algorithms that translate sequence arrays into understanding of species diversity and distributions. It's not simply a matter of registering species; it's the capacity to study their dynamics. Over its duration, BIOSCAN will survey at least half the world's ecoregions, setting the stage for a subsequent push towards global coverage and the activation of a planetary biosurveillance system that will track biotic change. This system and the information generated will be paramount for science-based decisions to protect biodiversity in the context of climate change.

Revealing Symbiomes

No organism is an island; it is a complex ecosystem where multi-cellular parasites, parasitoids, commensals, and mutualists are joined by single-celled microbes. Lured by the prospect of discovering unknown domains of prokaryotic life, researchers are now probing the microbiome in diverse taxa. Until now, much less effort has been directed towards analyzing the associations of multi-cellular organisms. BIOSCAN will address this gap; it will use sequence variation in the mitochondrial genome to ascertain eukaryotic associations, the symbiome. Because third generation sequencers produce high-fidelity reads from single DNA molecules, they can reveal the full diversity of mitotypes associated with any specimen. When many individuals of a particular species are analyzed, the results provide a taxon-level perspective on the symbiome. For example, perhaps 10% of specimens will carry a particular parasite, 20% a particular commensal, and 95% a mutualist. That's the symbiome of a species.

1. What is iBOL?

iBOL is a consortium involving scientists and research organizations in 30+ nations. It is developing and employing the DNA-based identification systems required to deliver a detailed understanding of global biodiversity. It works in partnership with academic, government, and private sector organizations.

Activated in 2010, iBOL leads large-scale research programs in biodiversity genomics, and develops the sequencing facilities, informatics platforms, and analytical protocols required to support them. Its first program was BARCODE 500K; its second is BIOSCAN.

2. What is iBOL's mission?

Recognizing the urgent need for a capacity to assess the impacts of environmental changes on biodiversity, iBOL's mission is to deliver a DNA-based identification system for all animals, fungi, and plants. This approach will make it possible to rapidly complete the inventory of species and to track shifts in their distributions, abundances, and interactions. Its long-term goal is to establish an Earth observation system for biodiversity.

3. What did BARCODE 500K accomplish?

The \$125 million BARCODE 500K project met its goal of assembling barcode records for 500,000 species within five years (2010–2015). These results demonstrated that DNA barcoding is a very effective tool for species discrimination, one which is far more scalable and less expensive than traditional morphological approaches.

It also developed the BOLD informatics platform (boldsystems. org) that assembles barcode data into functional format, and delivers key analytical services. These collective achievements propelled DNA barcoding into a mainstream enterprise that now supports both basic and applied science.

4. What is BIOSCAN and what is its mission?

BIOSCAN is a seven-year (2019–2025), \$180 million research program that includes three lines of investigation. It will expand the DNA barcode reference library to provide coverage for two million species; it will probe interactions among these species; and it will scan species assemblages at 2,500 sites to lay the foundation for a global biomonitoring system.

5. Why is BIOSCAN being launched now?

BIOSCAN is being launched now because advances in sequencing technologies have reduced the costs to barcode a single specimen to \$1, while also introducing the capacity to analyze bulk samples. As a result, iBOL can now scale up past work, and launch new lines of investigation which will accelerate progress toward its mission.

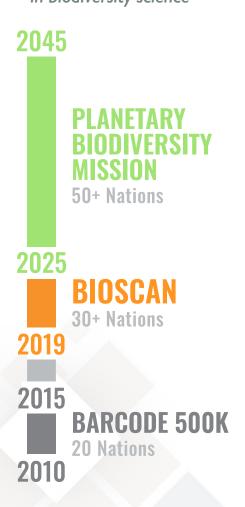
6. What are iBOL's longer-term plans?

iBOL will launch a 20-year research program, the Planetary Biodiversity Mission, in 2026. It will both aim to complete the inventory of multi-cellular life and document many of their interactions. It will also activate an Earth observation system for biodiversity.





BIOSCAN will help to establish the first-ever set of tools to monitor and understand changes in biodiversity on a planetary scale. Gaining this knowledge through **DNA-based** systems will have far-reaching benefits for addressing urgent societal and planetary issues and it will greatly contribute to the Post-2020 Global Biodiversity Framework towards the 2050 Vision. From food security to climate change, BIOSCAN is positioned to be one of the most crucial endeavours in biodiversity science



7. What is iBOL's data and resource sharing policy?

All specimens remain the property of their source nation, but DNA barcode sequences and information on their associated specimens become publically available after validation. DNA extracts are not available for genomic characterization without approval from their source nation.

iBOL works with the appropriate agency in each participating nation to ensure compliance with all regulations relating to the transfer of biomaterials.

8. Who will benefit from iBOL and how?

iBOL is laying the foundation for a global biodiversity observation system akin to the weather monitoring system that alerted us to global warming. By delivering the capacity to identify any species in any environment, iBOL will benefit science and society.

Consider just one axis of application – an enhanced capacity to recognize invasive species. Without early detection, financial losses linked to even a single invasive species can be massive. For instance, the Argentine fire ant has recurrently colonized Australia, but its establishment in Brisbane was overlooked for 20 years. If this species continues its spread, it will have a devastating impact on Australian environments, some \$45 billion in damage each year. Given this threat, the Australian government committed \$400 million in 2018 to launch an eradication program.

9. How does iBOL relate to other biodiversity initiatives?

iBOL is building a system for species identification based on the analysis of minimal sequence information, less than a millionth of the genome. Through this approach, it will provide a dynamic perspective on shifts in species distribution and abundance in a rapid, cost-effective way. By contrast, projects that seek to characterize whole genomes will deepen our understanding of evolutionary trajectories and nuclear gene arrays, but they are not suited for large-scale environmental monitoring.

Consider the following – does it make more sense to gain information on the species composition of an ecosystem by sequencing 500 base pairs of DNA in each of a million different specimens or 500 million base pairs in one? This dichotomy reveals why approaches targeting whole genomes are inefficient for scanning species composition.

iBOL will aid the push to establish a unified biodiversity information system by working in close collaboration with the Global Biodiversity Information Facility, the Secretariat for the Convention on Biological Diversity, and other initiatives that are extending knowledge of biodiversity.

10. Who can get involved in iBOL and how?

Each member nation in iBOL is represented by an institution which is the main point of contact at the national level for other institutions, researchers, or members of the public. Contact your national representative or email info@ibol.org for advice on the best path to involvement.

National Representatives:

Brazil

Argentina Pablo Tubaro (pltubaro@gmail.com)
Museo Argentino de Ciencias Naturales

Australia Mark Stevens (mark.stevens@samuseum.sa.gov.au)

South Australian Museum

Austria Nikolaus Szucsich (nikolaus.szucsich@nhm-wien.ac.at)

Natural History Museum Vienna

Belarus Tatsiana Lipinskaya (tatsiana.lipinskaya@gmail.com)

Scientific & Practical Center for Bioresources Guilherme Oliveira (guilherme.oliveira@itv.org)

Instituto Tecnológico Vale

Canada Mehrdad Hajibabaei (mhajibab@uoguelph.ca)

China Centre for Bíodiversity Genomics
Chenxi Liu (liuchenxi@caas.cn)
Institute of Plant Protection, CAAS

Colombia Mailyn González (magonzalez@humboldt.org.co)

Alexander von Humboldt Institute

Costa Rica José Alfredo Hernández Ugalde (bactris@gmail.com)

Consejo Nacional de Gestion de la Biodiversidad

Egypt Samy Zalat (samysinai@yahoo.com)
Nature and Science Foundation

Finland Marko Mutanen (marko.mutanen@oulu.fi)

University of Oulu

France Rodolphe Rougerie (rrougeri@gmail.com)
National Museum of Natural History, Paris

Avel Housean (houseann a@gach do)

Germany Axel Hausmann (hausmann.a@snsb.de)
Bavarian Natural History Collections - Zoology

Lebanon Magda Bou Dagher Kharrat (magda.boudagher@usj.edu.lb)

Universite Saint-Joseph

Mexico Manuel Elías-Gutiérrez (melias@ecosur.mx)

El Colegio de la Frontera Sur

Netherlands Edwin van Huis (edwin.vanhuis@naturalis.nl)

Naturalis Biodiversity Center

New Zealand Susie Wood (susie.wood@cawthron.org.nz)

Cawthron Institute

Norway Torbjørn Ekrem (torbjorn.ekrem@ntnu.no)

NTNU University Museum

Pakistan Nazeer Ahmed (nazeer.ahmed@buitms.edu.pk)

Balochistan University of Information Technology,

Peru Engineering & Management Sciences
Rina Ramírez (rina_rm@yahoo.com)
Universidad Nacional Mayor de San Marcos
Philippines lan Fontanilla (ianfontanilla@hotmail.com)

University of Phillippines Diliman

Poland Michal Grabowski (michal.grabowski@biol.uni.lodz.pl)

University of Lodz

Portugal Filipe Costa (fcosta@bio.uminho.pt)

University of Minho

Romania Mihael Cristin Ichim (cichim@hotmail.com)

National Institute of Research and Development

for Biological Sciences

Slovakia Ivona Kautmanov (kautmanova.ivona@gmail.com)

Slovak National Museum - Nature History Museum

South Africa Michelle van der Bank (vanderbank.michelle@gmail.com)

African Centre for DNA Barcoding

Thailand Buntika Butcher (buntika.a@chula.ac.th)

Chulalongkorn University

Turkey Emre Keskin (emre.keskin@ankara.edu.tr)

University of Ankara

United Kingdom Peter Hollingsworth (PHollingsworth@rbge.org.uk)

Royal Botanic Garden Edinburgh

United States Scott Miller (millerS@si.edu)

National Museum of Natural History, Washington

Scientific Director: Paul Hebert (phebert@ibol.org)

Executive Secretary: Donald Hobern (dhobern@ibol.org)

Media Contact: Hannah James (hjames@ibol.org)

General Information: Visit iBOL.org