Вид и видообразование, tree of life, новые методы секвенирования,

Прикладная генетика для зоологов, лекция 9, последняя.

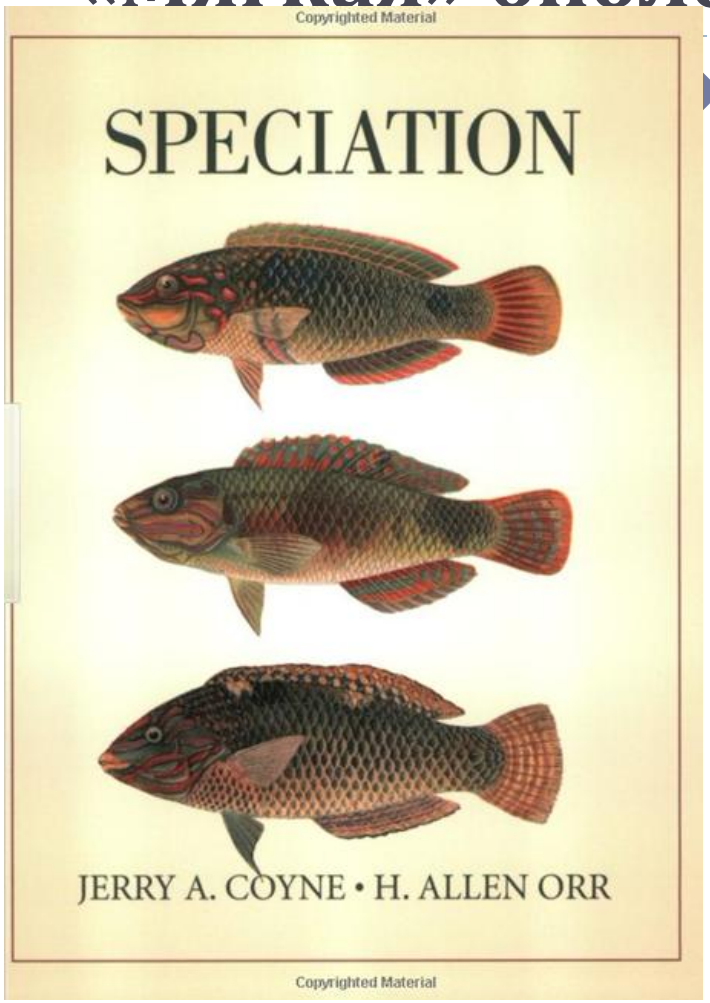
Мюге Н.С.

Что такое вид

- **Биологическая концепция вида** - концепция, по которой основным критерием вида есть нескрещиваемость (репродуктивная изоляция). Ф. Добжанский (1937), Майр, 1995.

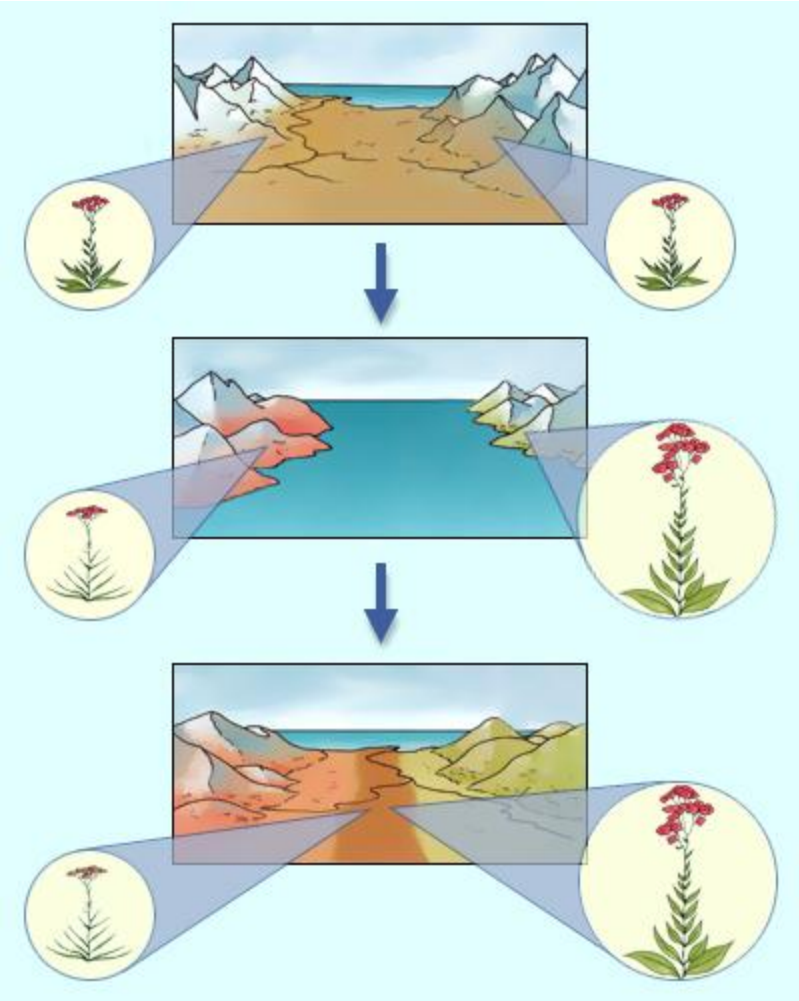
Концепция	Определение
Концепция Биологического вида	Вид-группа скрещивающихся природных популяций репродуктивно изолированных от других групп. (Mayr 1995)
Концепция генотипических кластеров	Вид-это совокупность организмов, образующих (морфологически или генетически) непересекающийся с другими кластер. (Mallet, 1995)
Концепция видо-распознования	Вид – совокупность особей, имеющих одинаковую систему спаривания (Paterson, 1985)
Экологическая концепция вида	Вид – совокупность особей, занимающих минимально отличающуюся от других экологическую нишу (Van Valen, 1976)
Филогенетическая концепция вида	Вид – наиболее базальный кластер организмов, диагностически отличный от других и имеющий монофилетичное происхождение (Cracraft, 1989)

«Мягкая» биологическая концепция вида



- **Вместо полной репродуктивной изоляции допускается наличие «изолирующих барьеров», затрудняющих обмен генами с другими видами. (Coyne, Orr, 2004)**

Аллопатрическое видообразование



Политипическая концепция вида

- **Политипическая концепция вида** - концепция, согласно которой вид может включать в себя несколько подвидов.
- Бурый медведь имеет 8 подвидов, лисица - 17, соболь - 6, горностай - 11, ласка - 8, белка - 29, заяц-беляк - 10. Наличие подвидов - результат микроэволюции. Признание того факта, что многие виды политипичны, стало важнейшим событием в таксономии XX века, т. к. концепция политипичности позволила упростить классификацию многих групп организмов.
- К 1910 г. было зарегистрировано около 19 тыс. монотипических видов птиц, политипичность позволила свести их к 8600 видам.

Переход от типологической концепции вида к биологической позволил значительно упростить систематику птиц
К 1910 г. было зарегистрировано около 19 тыс. монотипических видов птиц, политипичность позволила свести их к 8600 видам.

Симпатрическое видообразование у рыб в озере Апойо (Никарагуа)

Vol 439|9 February 2006|doi:10.1038/nature04325 nature

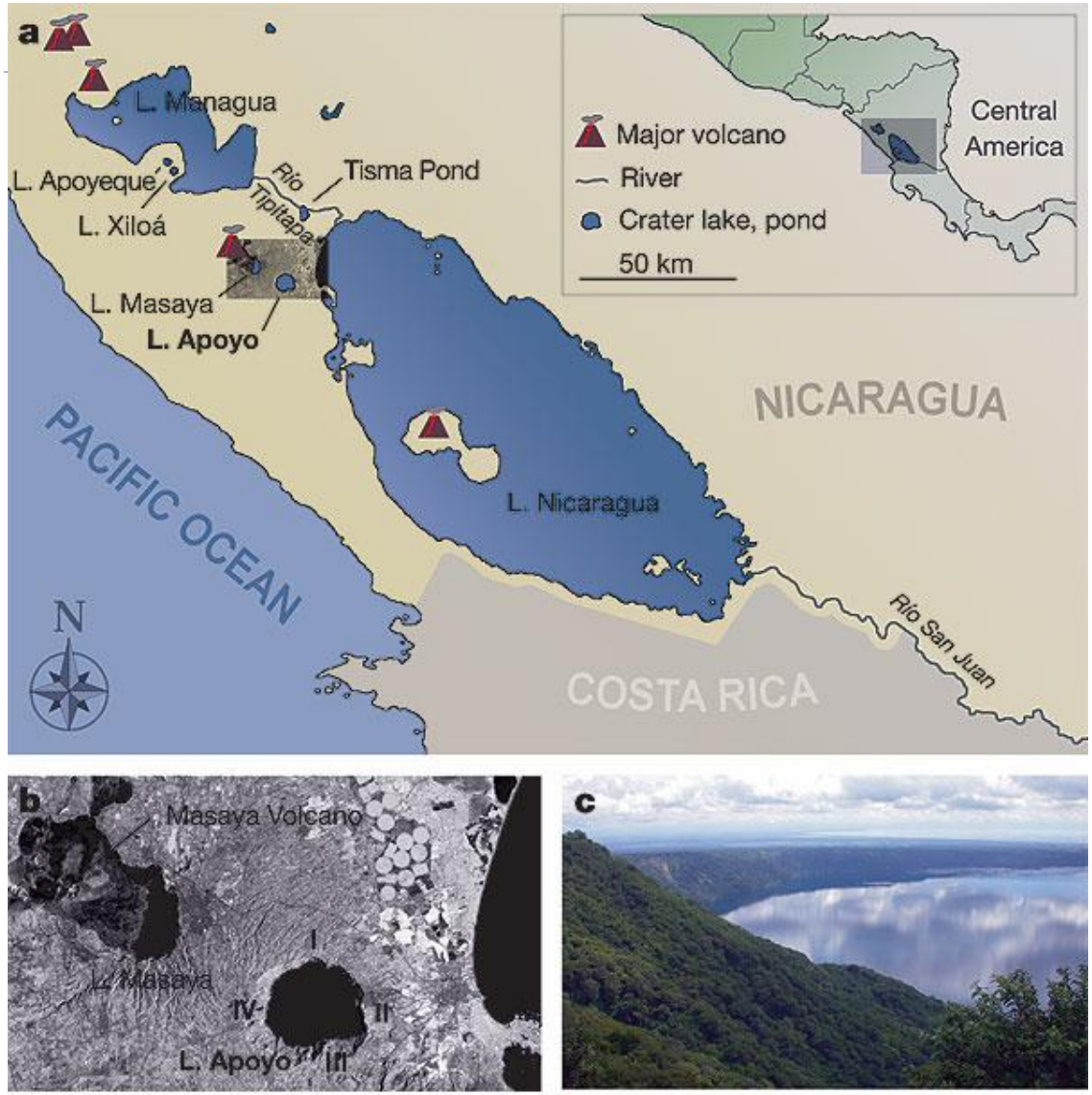
LETTERS

Sympatric speciation in Nicaraguan crater lake cichlid fish

Marta Barluenga[1]*, Kai N. Stölting[1]*, Walter Salzburger[1,2]*, Moritz Muschick[1] & Axel Meyer[1]

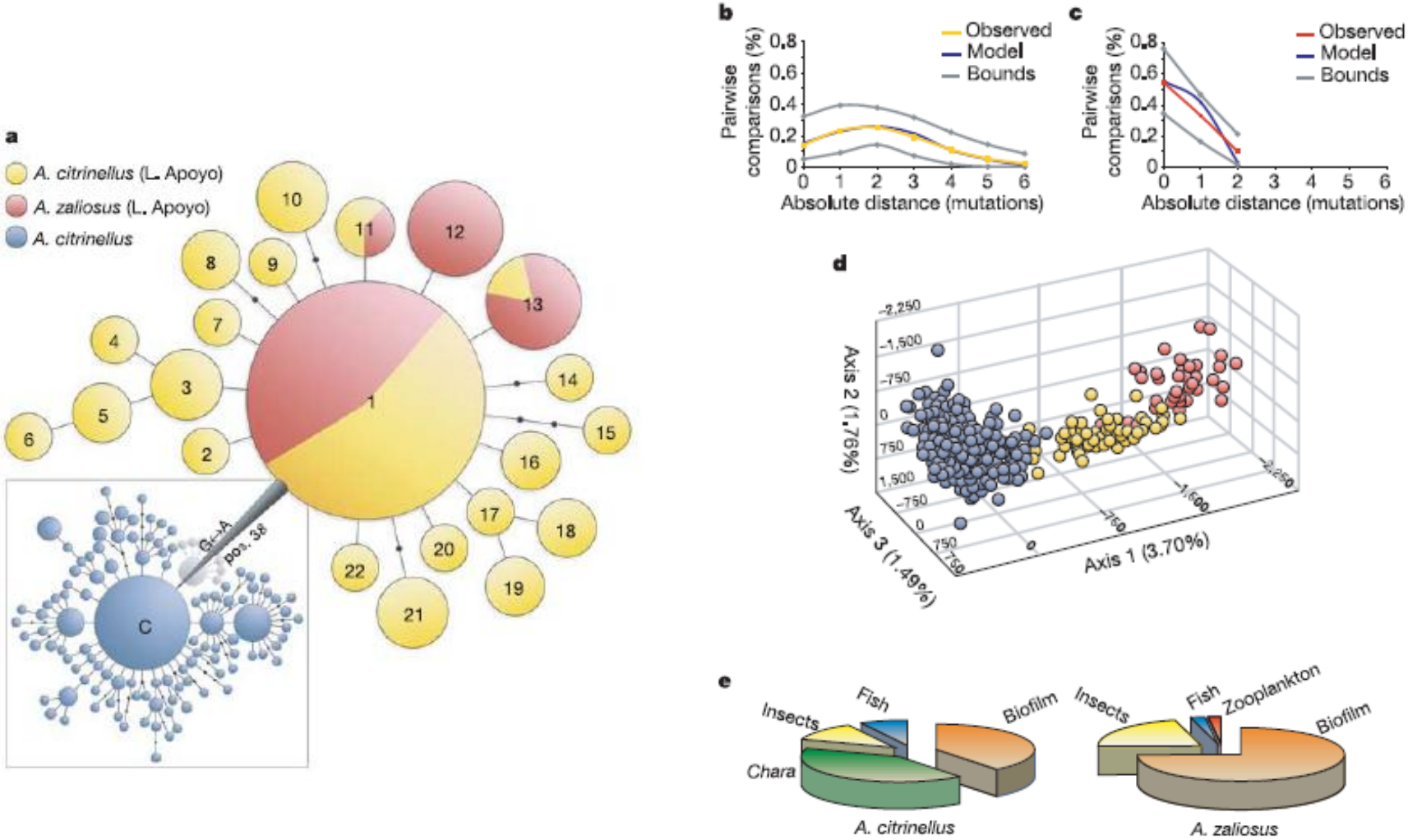
Sympatric speciation, the formation of species in the absence of geographical barriers, remains one of the most contentious concepts in evolutionary biology. Although speciation under sympatric conditions seems theoretically possible[1–5], empirical studies are scarce and only a few credible examples of sympatric speciation exist[6]. Here we present a convincing case of sympatric speciation in the Midas cichlid species complex (*Amphilophus* sp.)

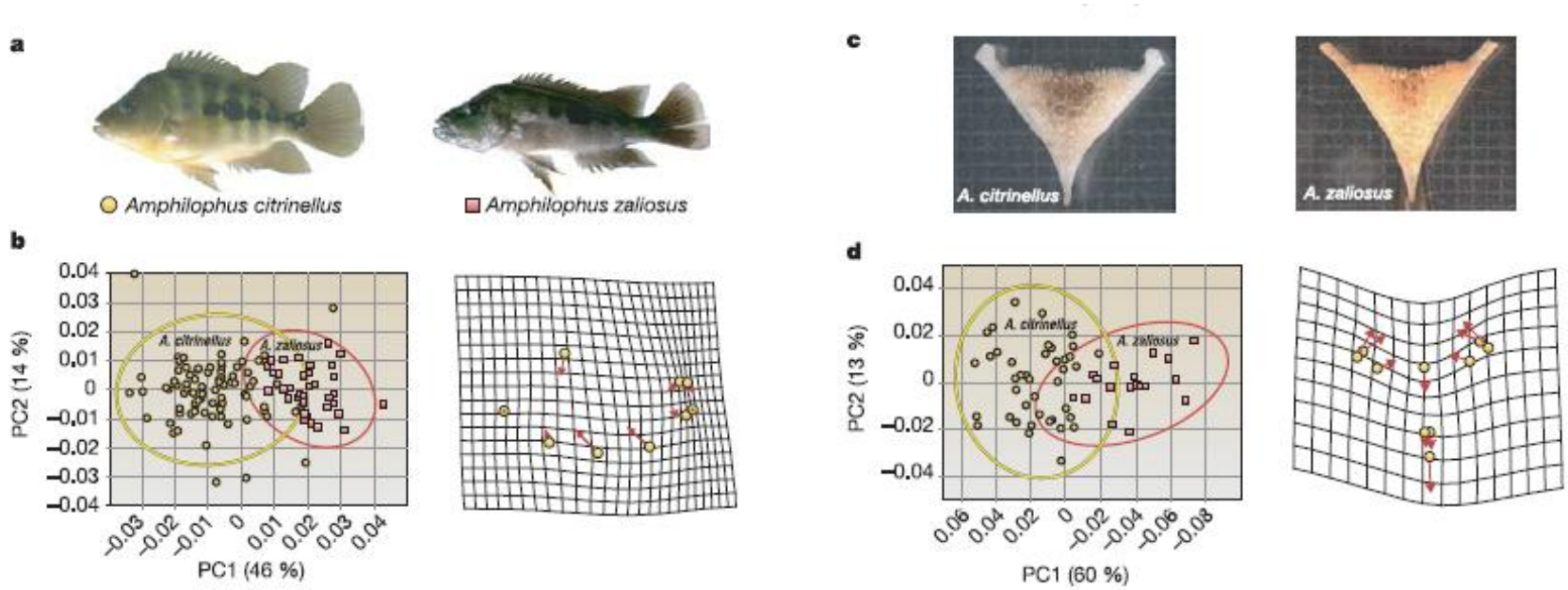
north of Costa Rica. In *A. citrinellus* of other lakes and in *A. labiat*
two colour morphs are recognized, but such polymorphism has r
been described in Lake Apoyo. To examine whether the enden
Arrow cichlid emerged in Lake Apoyo from an ancestral stock
Midas cichlids under fully sympatric circumstances, we adopted
comprehensive approach including phylogeographic, populatio
genetic, morphometric and ecological analyses. We included abo


a
L. Managua
L. Apoyeque
L. Xiloá
Río Tipitapa
Tisma Pond
L. Masaya
L. Apoyo
L. Nicaragua
PACIFIC OCEAN
NICARAGUA
COSTA RICA
Río San Juan
N
Major volcano
River
Crater lake, pond
50 km
Central America
b
Masaya Volcano
La Masaya
I
II
III
IV
L. Apoyo
c

Amphilophus citrinellus

Amphilophus zaliosus


a
A. citrinellus (L. Apoyo)
A. zaliosus (L. Apoyo)
A. citrinellus
G->A
pos. 38
b
Pairwise comparisons (%)
Observed
Model
Bounds
Absolute distance (mutations)
c
Pairwise comparisons (%)
Observed
Model
Bounds
Absolute distance (mutations)
d
Axis 2 (1.76%)
Axis 3 (1.49%)
Axis 1 (3.70%)
e
Insects
Fish
Biofilm
Chara
A. citrinellus
Insects
Fish
Zooplankton
Biofilm
A. zaliosus


a
Amphilophus citrinellus
Amphilophus zaliosus
b
A. citrinellus
A. zaliosus
PC2 (14 %)
PC1 (46 %)
c
A. citrinellus
A. zaliosus
d
A. citrinellus
A. zaliosus
PC2 (13 %)
PC1 (60 %)

http://www.barcodinglife.org/

BARCODE OF LIFE DATA SYSTEMS

Advancing species identification and discovery through the analysis of short, standardized gene regions

SEARCH

About BOLD Contact Us

Published Projects | Taxonomy Browser | Request an Account | Identify Specimen | Introductory Tutorial | Documentation | Citation

The Barcode of Life Data Systems (BOLD) is an online workbench that aids collection, management, analysis, and use of DNA barcodes. It consists of 3 components (MAS, IDS, and ECS) that each address the needs of various groups in the barcoding community.

MANAGEMENT & ANALYSIS

BOLD-MAS provides a repository for barcode records coupled with analytical tools. It serves as an online workbench for the DNA barcode community.

Username

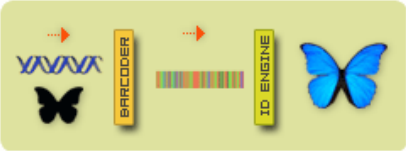
Password

Login

- Request a new user account
- Forgot your username or password?

IDENTIFICATION ENGINE

BOLD-IDS provides a species identification tool that accepts DNA sequences from the barcode region and returns a taxonomic assignment to the species level when possible.



EXTERNAL CONNECTIVITY

BOLD-ECS provides web developers and bioinformaticians the ability to build tools and workflows that can be integrated with the BOLD framework. We welcome the addition of new analytical modules.

BARCODE COUNTS

Formally Described Species With Barcodes	54,738
Total Barcode Records	572,075
Source	Breakdown
GenBank	77,638
Canadian Centre	448,550
Others	45,887

SYSTEM UPDATES

Sept-23-2008 - **Merging Private Data with Public Projects (MAS)**
The Project List page now displays all public projects as a distinct part of a user's access list. Users can view, merge, and analyze this data along with their own.

Aug-8-2008 - **Performance Upgrade (MAS)**
The BOLD data access modules have been upgraded to be more efficient and caching mechanisms have been integrated to improve user experience.

Apr-30-2008 - **Primer Registry Interface (MAS)**
A primer registry is now available from both the Project List page and the Project Console. The registry allows users to access and get information on all publicly available primers. A new form has been added to allow users to modify and maintain their own registered primers.

Mar-2-2008 - **BOLD Integration with LIMS (MAS)**
BOLD users that make use of our standard Laboratory Information Management System (LIMS) now have access to LIMS progress reports and audit trails directly from the specimen page of a record. Gel electrophoresis images are also available for each sample through this interface.

Jan-12--2007 - **Support for ITS Marker (MAS & IDS)**
BOLD now supports the storage and limited analysis of records utilizing ITS as a barcode marker. Selection of ITS as the primary marker when instantiating a project activates features specific to non-coding markers. A separate ID engine has been incorporated into BOLD to support the identification of ITS barcode markers. BLAST is utilized to generate a list of high scoring matches to query sequences. Due the difficulty in aligning ITS, treeing of results have been deactivated for this pipeline.

BOLDSYSTEMS | Management & Analysis

Project Options

- Merge Projects
- Search All Records
- View All Primers

Campaigns

- ACG Parasitoids
- All Birds Barcoding Initiative
- Ants Of The World
- Arctic Life (PROBE)
- Barcoding Canadian Animals
- Barcoding Fish (FishBOL)
- Barcoding Mammals of the World
- Fauna Bavarica
- Fungal Barcoding
- Genbank Animals (COI)
- GenBank Fungi (COI)
- General Projects
- Global Geometridae
- Lepidoptera of Eastern North America
- Lepidoptera of NA Phase II
- Lepidoptera of the ACG
- Marine Life (MarBOL)
- Mosquitos of the World
- Pests and Invasive Species
- Saturniidae - Global
- Sphingidae - Global

	Code	ACG Parasitoids	Sequences	Specimens	Species	Species with Seq	Pub	Primary Marker
☐	ASTAZ	ACG Generalist Tachinidae	712	2134	78	0	✔	COI-5P/ITS/28S-D2
☐	ASMG	ACG Microgastrinae	1298	2575	323	6	✔	COI-5P/ITS
☐	ASMIN	ACG Microgastrinae (Braconidae) - minimalist barcode	11	22	15	0	✔	COI-5P/ITS
☐	HCIC	ACG Tachinidae (Belvosia)	246	736	32	0	✔	COI-5P/ITS/28S-D2

	Code	All Birds Barcoding Initiative	Sequences	Specimens	Species	Species with Seq	Pub	Primary Marker
☐	AAPR	ABBI additional public records	140	140	86	86		COI-5P
☐	BARG	Birds of Argentina - Phase I	1594	1594	500	500	✔	COI-5P
☐	ABNA	Birds of North America - Phase II	2586	2586	657	657	✔	COI-5P
☐	TZBNA	Birds of North America	437	437	263	263	✔	COI-5P
☐	BNACA	Birds of North America, Canadian geese	141	141	2	2	✔	COI-5P
☐	BNABS	Birds of North America, Canadian passerines	120	120	38	38	✔	COI-5P
☐	BNAUS	Birds of North America, General sequences	1871	1871	594	594	✔	COI-5P
☐	BNADU	Birds of North America, SI Duplicates	17	17	13	13	✔	COI-5P
☐	BWA	Birds of Western Australia	75	78	31	31		COI-5P
☐	KBBI	DNA Barcoding Korean Birds	255	255	102	102	✔	COI-5P
☐	AROM	Royal Ontario Museum - Birds 1	352	352	79	79	✔	COI-5P
☐	AROMB	Royal Ontario Museum-Birds2	128	128	10	10		COI-5P
☐	AROMC	Royal Ontario Museum - Birds 3 Rostratula	9	9	3	3	✔	COI-5P
☐	AGBF	Selected GenBank Birds Folder	640	640	330	330		COI-5P
☐	AGWEB	AGB 2005 MPE 36:233	34	34	34	34		COI-5P
☐	AGFEL	AGB 2005 ZS 34:145	9	9	4	4		COI-5P
☐	AGFLE	AGB 2006 BL 2:466	5	5	5	5		COI-5P
☐	AGBA	AGB 2007 MPE 42:665	34	34	14	14		COI-5P
☐	AGBLO	AGB 2007 MPE 44:1031	101	101	88	88		COI-5P
☐	AGNYA	AGB 2007 MPE 44:154	41	41	5	5		COI-5P

BOLDSYSTEMS | Management & Analysis

BOLD - ID

Cytochrome Oxidae Subunit 1 [COX1] | Internal Transcribed Spacer Region [ITS]

The BOLD Identification System (IDS) accepts sequences from the 5' region of the mitochondrial gene COI and returns a species-level identification when one is possible. Further validation with independent genetic markers will be desirable in some forensic applications.

The reference database of validated records is used by default and is recommended for all identification purposes.

Search Databases:

- (●) **All Barcode Records on BOLD (552,411 sequences)**
  Every COI barcode record on BOLD with a minimum sequence length of 500bp (warning: unvalidated database and includes records without species level identification). This includes many species represented by only one or two specimens as well as all species with interim taxonomy. This searchonly returns a list of the nearest matches and does not provide a probability of placement to a taxon.
- ( ) **Species Level Barcode Records (495,770 sequences/37,849 Species)**
  Every COI barcode record with a species level identification and a minimum sequence length of 500bp (warning: unvalidated dataset). This includes many species represented by only one or two specimens as well as all species with interim taxonomy.
- ( ) **Reference Barcode Database (234,588 Sequences/13,774 Species)**
  Validated subset of the full database with a minimum sequence length of 500bp and containing only those species represented by three or more individuals showing less than 2% sequence divergence

Enter sequences in fasta format:

Submit | Cancel