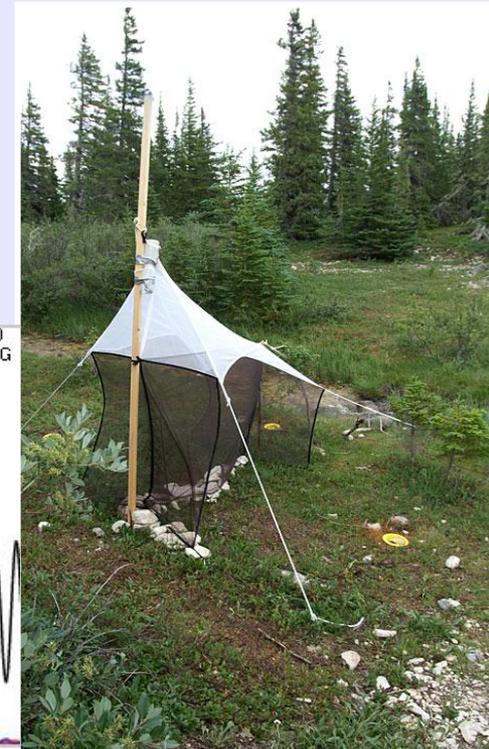
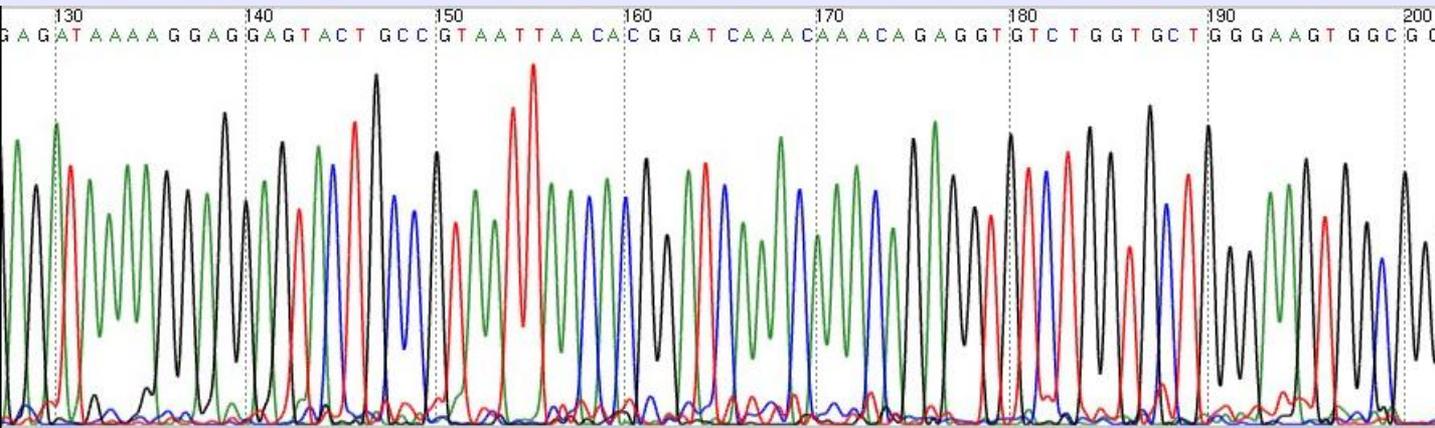


All-taxa Inventories: Are they getting serious?

Gordon Jarrell
25 October 2010



Conventional inventories

The Great Smokey Mtns. Inventory

Global Ocean Sampling Expedition

Churchill, Manitoba - Barcode of Life

Coastal Marine Biolabs – Bringing in students.

Some vocabulary...

ATBI = All-Taxa Biological Inventories

DLIA = Discovering Life in America (Non-profit coordinator of Great Smokies NP inventory)

BioBlitzes = Used variously. Generally, an intense, short-term effort to work a constrained area for a constrained set of taxa.

Rapid Assessment Inventories = Inventories in which relative diversity is estimated, often from the diversity of vertebrates and flowering plants, or from diversity of invertebrates as scored by counting the number of “recognizable (but undetermined) taxonomic units” (RTUs).

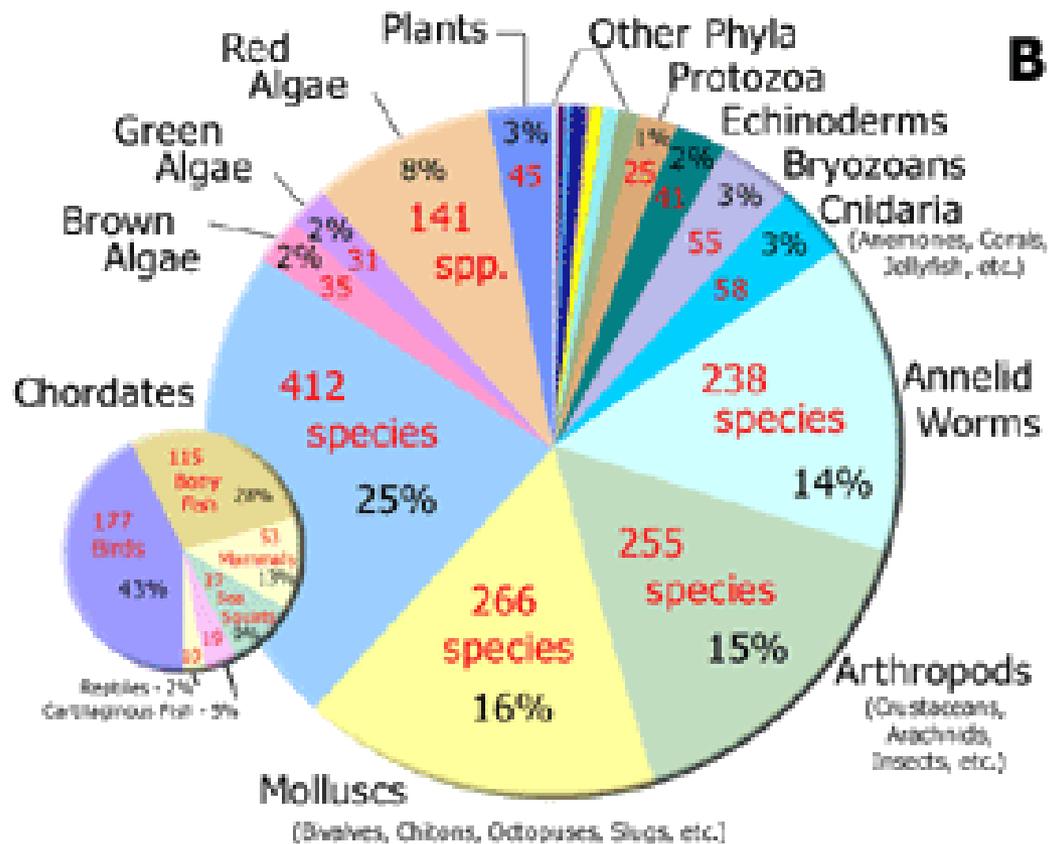


All Taxa Biodiversity Inventory

ATBI Alliance

- .Acadia NP
- .Adirondak Biodiversity Project
- .Big Thicket Association
- .Boston Harbor Islands Nat. Rec. Area
- .Canyon de Chelly NP
- .Congaree NP
- .Great Smokies NP
- .Mammoth Cave NP
- .Nantucket Biodiversity Initiative
- .Rock Creek Park
- .Tennessee State Parks
- .Tomales Bay Biodiversity Partnership
- .Yellowstone NP

Some ATBI members have no web page, others have obviously stagnated...



Biodiversity of Tomales Bay

This chart reflects the composition of species documented in the bay as of the end of 2003. As more study is performed on obscure or microscopic organisms, the percentage of Chordates will shrink and the percentages of invertebrate phyla will gain larger slices of the bay's biodiversity pie.



Big Thicket Association

Founded 1964

[Home](#) > [Scientists Information](#) >

- Home
- BTA
- ATBI
- Scientists Information
- Volunteer
- Donations
- Products for Sale
- Photo Galleries
- Contact Us

Online Database - Thicket of Diversity

ATBI data can now be entered online. Website address: atbi.thicketofdiversity.org/

[Volunteer](#)

[Support](#)



[Buy BTA Products](#)



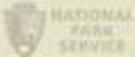


Username:

Password:

Remember Me [Forgot password?](#)






Contact Information

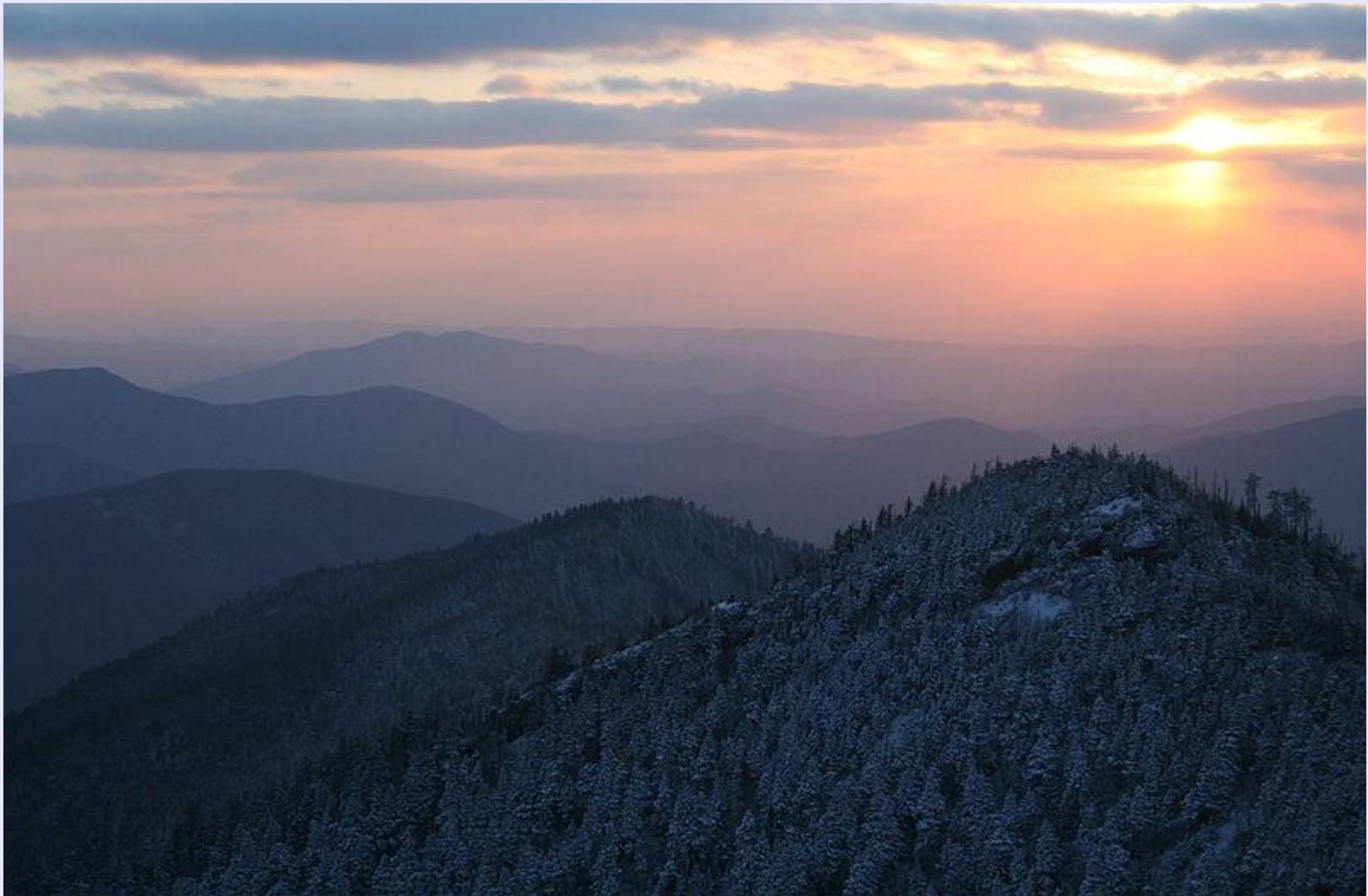


The connection has timed out

The server at atbi.thicketofdiversity.org is taking too long to respond.

- The site could be temporarily unavailable or too busy. Try again in a few moments.
- If you are unable to load any pages, check your computer's network connection.
- If your computer or network is protected by a firewall or proxy, make sure that Firefox is permitted to access the Web.

Try Again



Great Smoky Mountains

- Appalachian crest on the Tennessee & North Carolina border
- International Biosphere Reserve
- Largest stand of old-growth forest east of the Mississippi
- High biodiversity in lower-elevation hardwood forests



Discover Life in America

Great Smoky Mountains National Park All Taxa Biodiversity Inventory



~100,000 species in GSMNP?

9,552 previously documented species

6,582 species previously unknown

907 species new to science

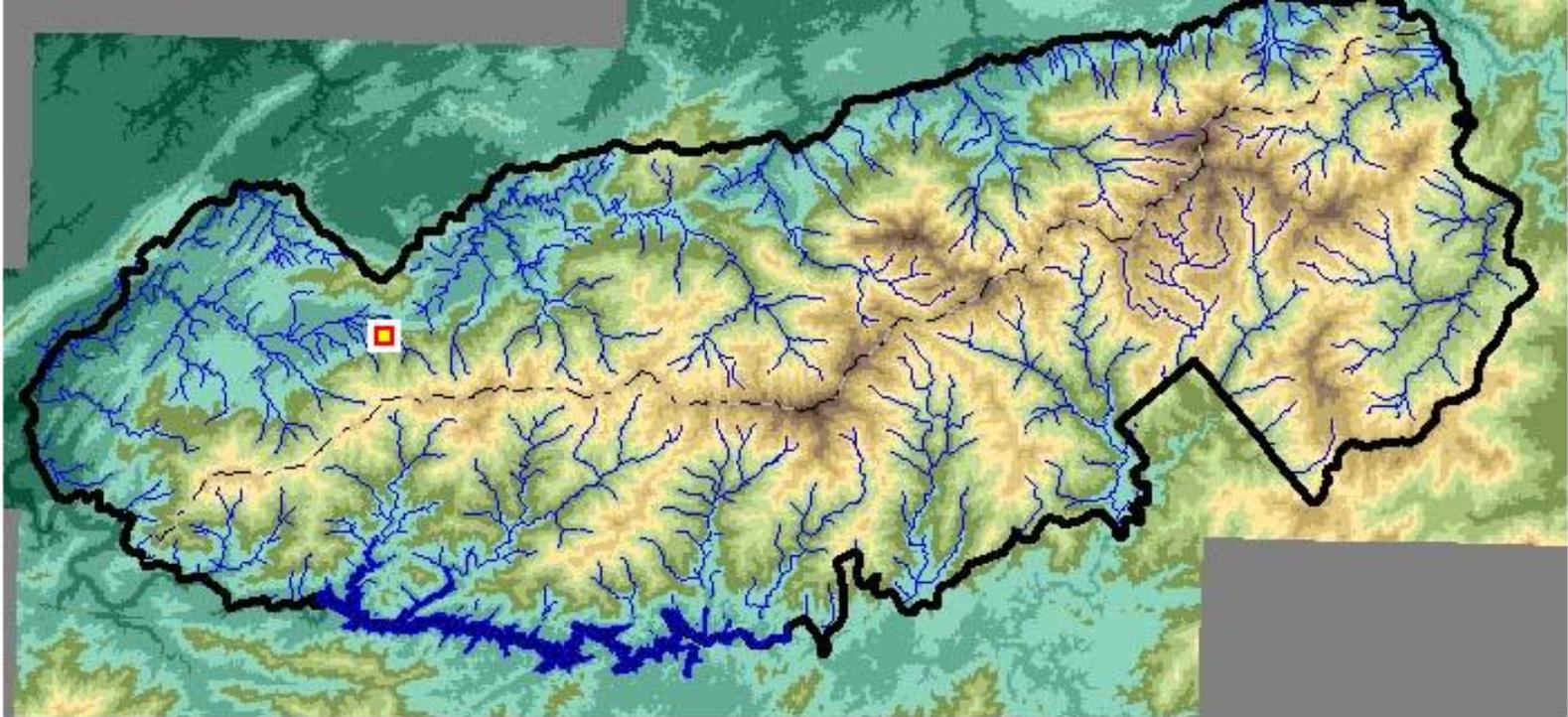
17,042 total discovered

~17% completion?

\$30,000 - \$100,000 per year in awards of \$5,000 and less

67 refereed publications as of 2007





SpecimenID: WKR-500011

Species: *Myotis lucifugus* (LeConte)

[Literature for this Species](#)

Common Name: Little brown bat

[Taxonomy:](#) Kingdom: Animalia, Division: Deuterostomia, Phylum: Chordata, Class: Mammalia, Order: Chiroptera, Family: Vespertilionidae

Determiner: WGrogan

Depository: none, specimen not collected (notcollect)

Description: 1 individual(s)

Preservation: Not Collected

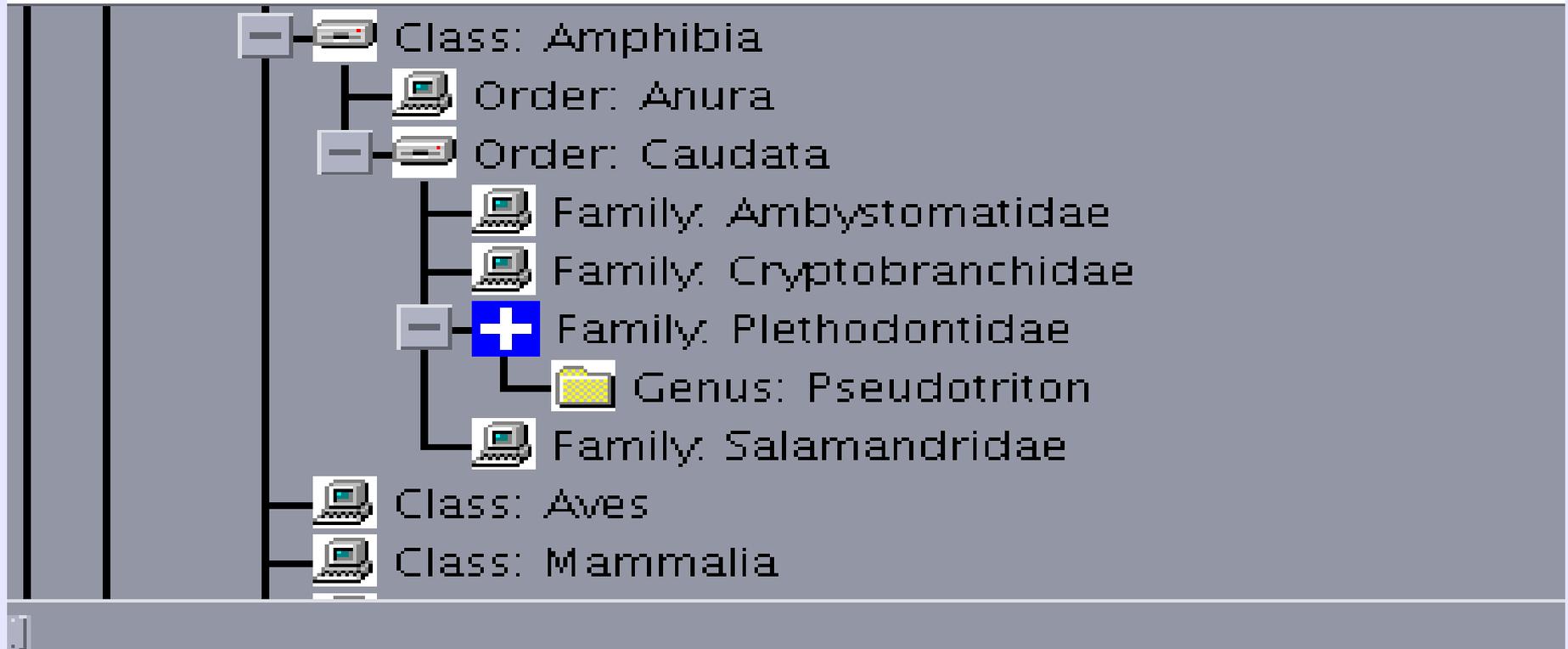
Notes:

Project: ATBI Reeves DLIA 1999

One *Myotis*, not collected, determined to species, in an area with about six species of *Myotis*?

Tree Representation

Please select a taxon node to expand, or type a taxon name to



The park holds ~6% of the world's salamander diversity, most of which are in Plethodontidae. There is one genus represented in the DLIA database.

Feature Location

Scientific Name **Plethodon jordani**

Verbatim Date 17 Jul 1967

Specific Locality 1 mi SE (by road) Clingman's Dome, Great Smokies National Park

Coordinate 3411.80928

Uncertainty In Meters

Great Smoky Mountains National Park

Tennessee
North Carolina

441



Discover Life in America

Great Smoky Mountains National Park All Taxa Biodiversity Inventory



Not incorporating data from other sources.

Not exporting data to GBIF.

Some work with vertebrate ectoparasites, none with endoparasites.

Emphasis (appropriately) arthropods.

No work with Prokaryota.

Mostly, they work with the taxa that are proposed by specialists.

A reasonably serious effort!

Metagenomics = sequencing environmental samples

About eight years old, uses “Shotgun” Sanger sequencing or “massively parallel pyrosequencing.”

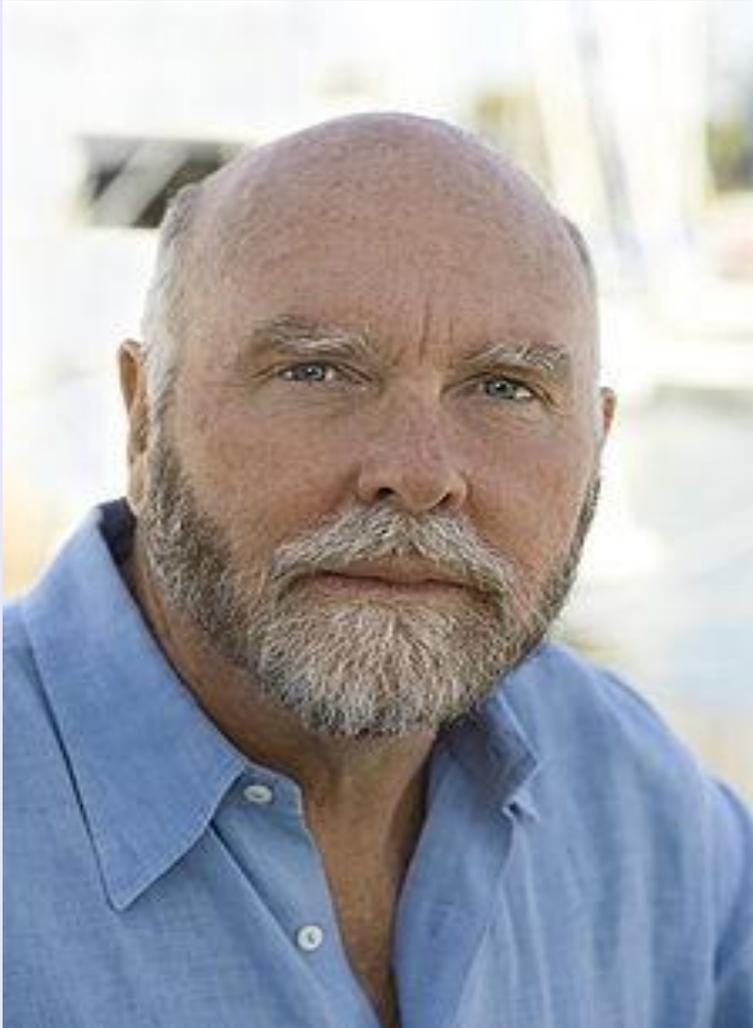
Human stool contains over 1,000 viral species.

200 liters of sea water contains over 5,000.

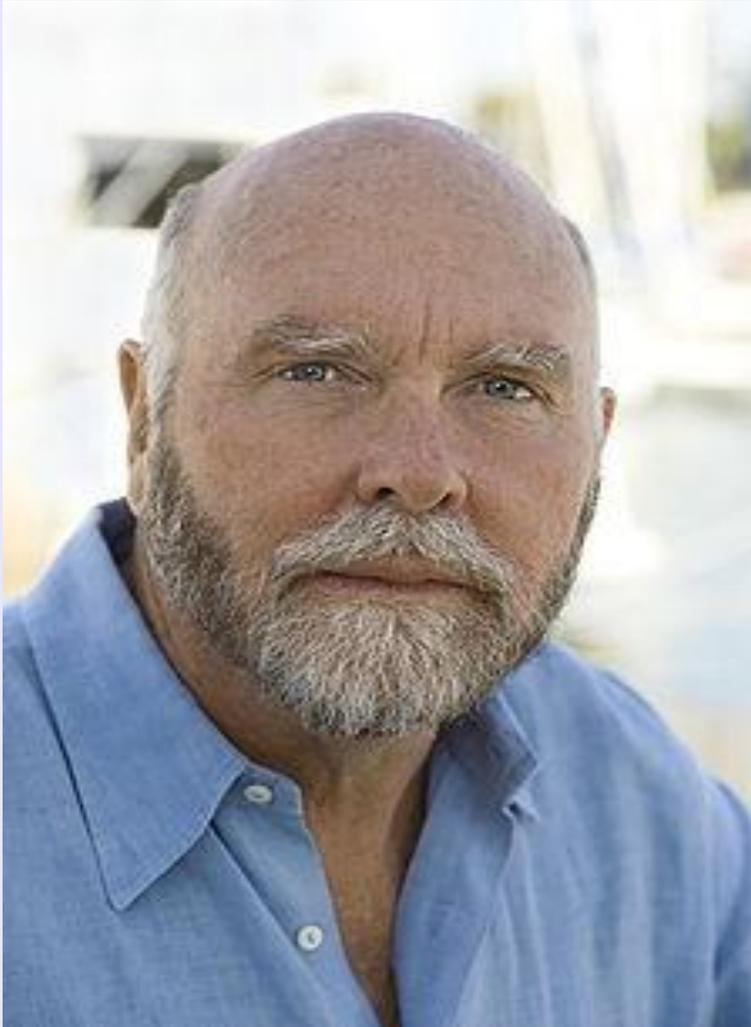
One liter of marine sediment contains perhaps 1,000,000.

All of above essentially new species.

Possible to study whole genomes of single-celled organisms without culturing.



Do you recognize this famous biologist?



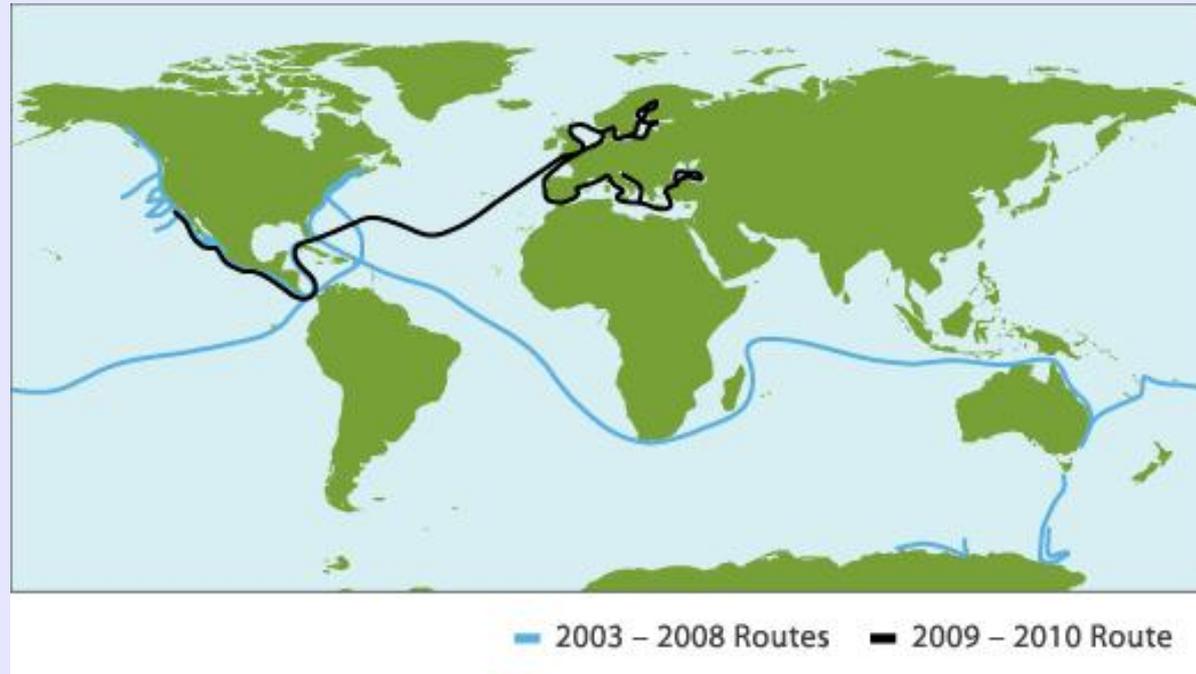
J. Craig Venter

2000 - 1st sequencing of human genome (three years ahead of NIH's proposed finish)

2003 - 2010 – Global Ocean Sampling Expedition

2010 – *Mycoplasma laboratorium*, 1st synthetic life form

Global Ocean Sampling Expeditions



- 200-400 liter water sample every 200 miles.
- Filter through progressively smaller filters to capture various sized organisms.
- Freeze filters, and apply metagenomic tools.

Pilot study:

1.2 million (now 6 million) new genes from 1,800 “genomic species.”

All data in GenBank, no patents sought.

Originally published in *Science Express* on 4 March 2004

Science 2 April 2004:

Vol. 304. no. 5667, pp. 66 – 74

DOI: 10.1126/science.1093857

[< Prev](#) | [Table of Contents](#) | [Next >](#)

RESEARCH ARTICLES

Environmental Genome Shotgun Sequencing of the Sargasso Sea

J. Craig Venter,^{1*} Karin Remington,¹ John F. Heidelberg,³ Aaron L. Halpern,² Doug Rusch,² Jonathan A. Eisen,³ Dongying Wu,³ Ian Paulsen,³ Karen E. Nelson,³ William Nelson,³ Derrick E. Fouts,³ Samuel Levy,² Anthony H. Knap,⁶ Michael W. Lomas,⁶ Ken Nealson,⁵ Owen White,³ Jeremy Peterson,³ Jeff Hoffman,¹ Rachel Parsons,⁶ Holly Baden-Tillson,¹ Cynthia Pfannkoch,¹ Yu-Hui Rogers,⁴ Hamilton O. Smith¹

We have applied "whole-genome shotgun sequencing" to microbial populations collected en masse on tangential flow and impact filters from seawater samples collected from the Sargasso Sea near Bermuda. A total of 1.045 billion base pairs of nonredundant sequence was generated, annotated, and analyzed to elucidate the gene content, diversity, and relative abundance of the organisms within these environmental samples. These data are estimated to derive from at least 1800 genomic species based on sequence relatedness, including 148 previously unknown bacterial phylotypes. We have identified over 1.2 million previously unknown genes represented in these samples, including more than 782 new rhodopsin-like photoreceptors. Variation in species present and stoichiometry suggests substantial oceanic microbial diversity.

**Can we use metagenomic tools
to inventory “real” organisms?**

**Sure. Apply massively parallel
pyrosequencing to samples
from things such as:**

Malaise traps

plankton trawls

stomach contents

**whole host organisms
(for parasites)**

etc., etc.

But first...



...Develop a reference sequence for known species.

BARCODE OF LIFE DATA SYSTEMS v 2.5

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



[Published Projects](#) | [Taxonomy Browser](#) | [Request an Account](#) | [Identify Specimen](#) | [Documentation](#) | [D](#)

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.

F
T
S

Standardized gene region for animals is 650 base pairs of mitochondrial cytochrome oxidase I.

Sequences for the identification engine's reference series must be vouchered specimens, preferably with expert taxonomic determinations.

Addresses the shortage of taxonomic expertise.

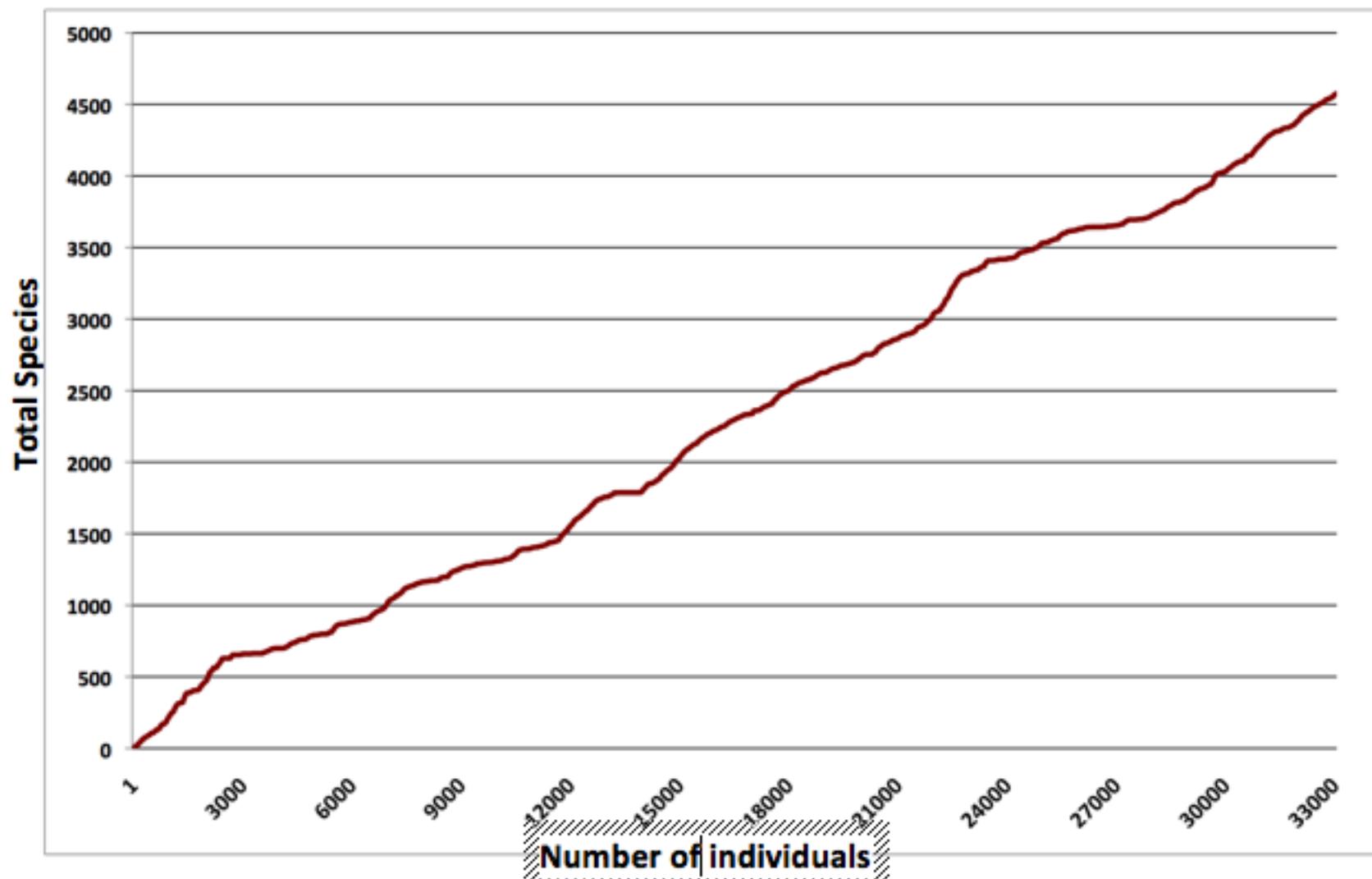
Provides reliable determinations to management agencies.

Is proving to be a powerful tool for discovery.



Barcoding Biotas
the Canadian Barcode of Life Initiative's effort to inventory and barcode all taxa at Churchill, Manitoba.

Barcoding All Eukaryotes at Churchill





87,187 named species are barcoded.

1,023,244 barcode records.

Fishes 25% complete.

Birds 14% complete.

North American freshwater fish 99% complete.

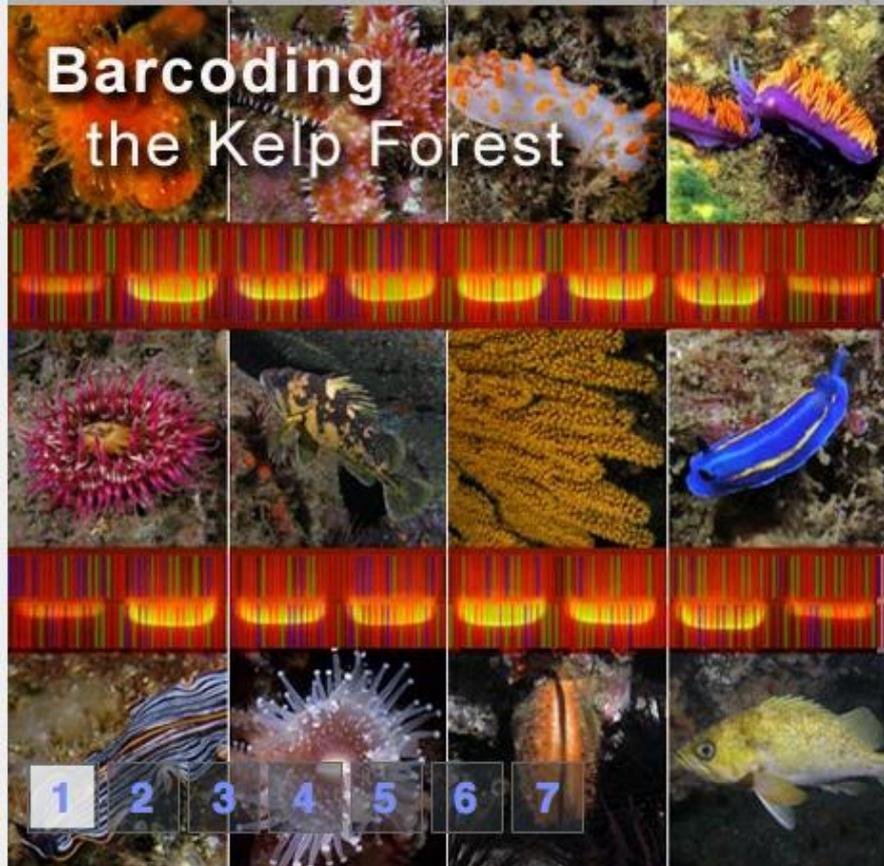
Romania's Lepidoptera complete.

**Many groups far more diverse than indicated by formal taxonomy.
Necessary to assign numbers to unnamed clusters.**





Barcoding the Kelp Forest



Interdisciplinary, Research-Based Science Education

Located in Ventura Harbor, Coastal Marine Biolabs is a private, research-based science education organization that provides innovative field and laboratory-based learning experiences for high school students. Under the mentorship of CMB scientists, students use many of the key technological cornerstones of modern scientific discovery to explore contemporary questions that lie at the frontiers of scientific knowledge.

Featured Students



Colin Crilly
Senior
Foothill Technology High School
Ventura, CA

- [News & Events](#)
- [Perspectives](#)
- [Recent Student Work](#)
- [Intro Video](#)

Page tools



Call for Applications

CMB is now accepting applications for the 2011 resident program sessions.

- [session dates](#)
- [apply here](#)



COASTAL MARINE BIOLABS
INTEGRATIVE BIOSCIENCES PROGRAM



ONE WORLD...ONE SCIENCE

Barcoding the Kelp Forest is the most popular of three nine-day courses offered by CMB. (All involve hands-on work with unanswered research questions.)

Tuition is \$2,470. 50% of last year's students received scholarships.

~8 upper division high-school students are dive certified.

Third day is first open-water collecting dive.

Collecting rock fish (~40 species) and various invertebrates.

Students do extraction, PCR, and electrophoretic fragment-size Verification.

Samples submitted to Guelph for COI sequencing trace files returned.



COASTAL MARINE BIOLABS
INTEGRATIVE BIOSCIENCES PROGRAM



ONE WORLD...ONE SCIENCE

Students analyze trace files and submit COI sequence to BoLD and to GenBank under their own name.

Frozen tissue vouchers are at the Ocean Genome Legacy.

Conventional vouchers at Santa Barbara Museum of Natural History.

Student success rate nearly 100%.

Conclusions:

- **No all-taxa inventories have been completed.**
- **We are fast gaining the tools to complete all-taxa inventories with realistic amounts of effort.**
- **How might a serious ATBI might work?**

