Research Computing Across the Tree of Life

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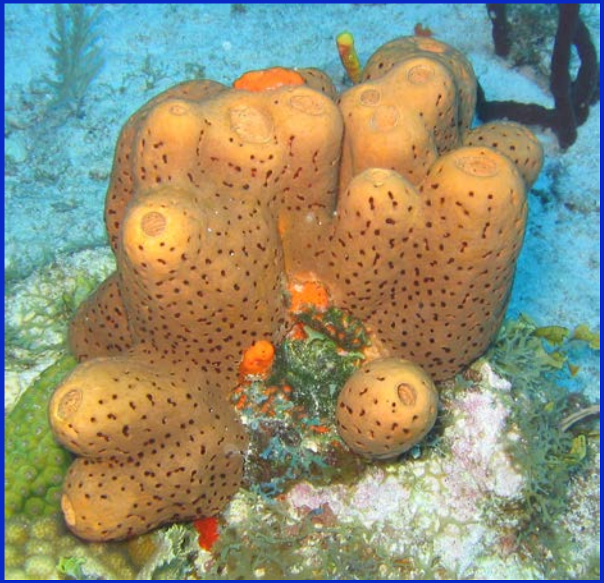
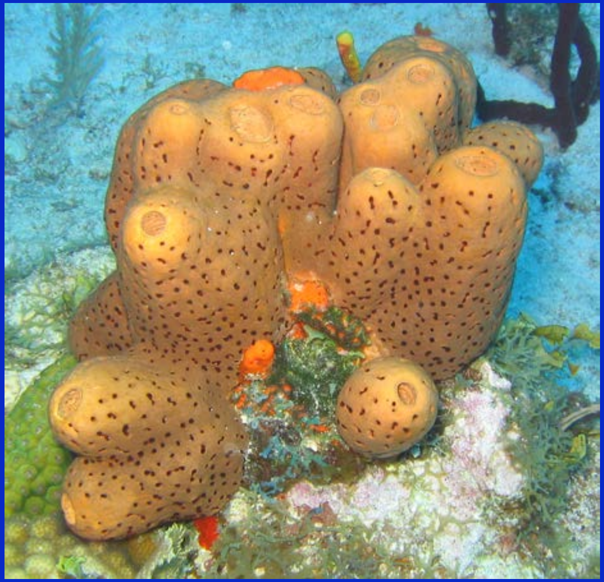
www.portol.org

Ecology & Evolution of Sponges



Ecology & Evolution of Sponges



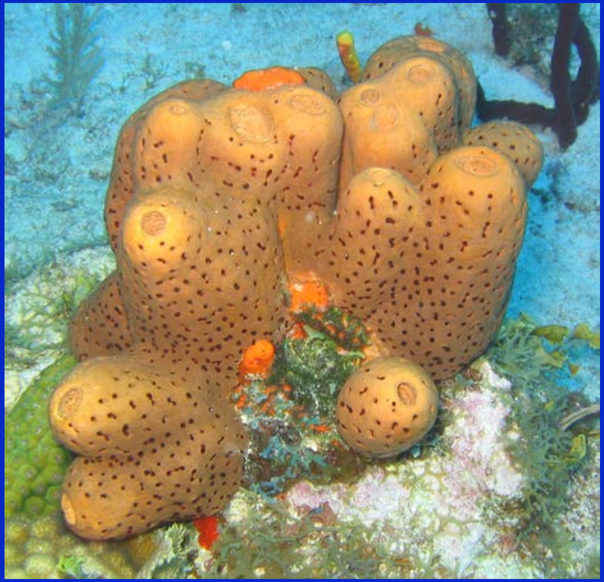
Biodiversity:

Species Discovery
& Systematics

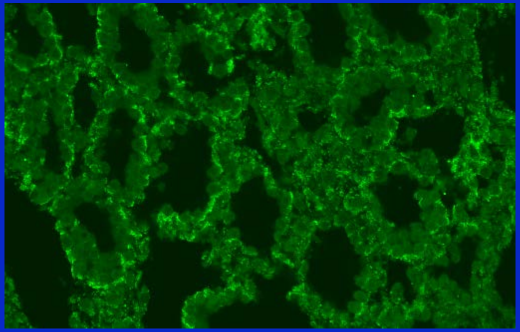
CONSERVATION INTERNATIONAL

Smithsonian

Ecology & Evolution of Sponges



Symbiotic
Interactions



Biodiversity:
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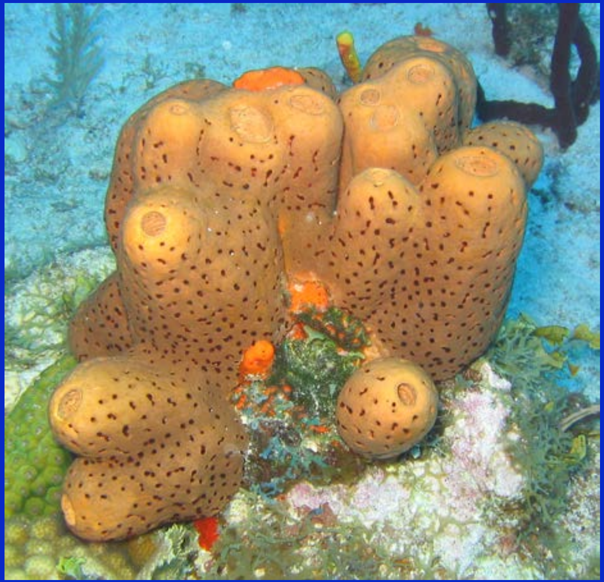
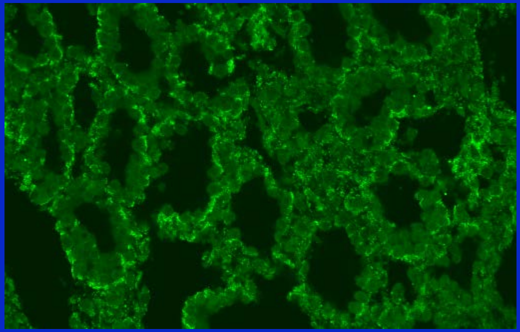
NSF

Ecology & Evolution of Sponges



Symbiotic Interactions



PorToL

Porifera Tree of Life

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Biodiversity:

Species Discovery & Systematics

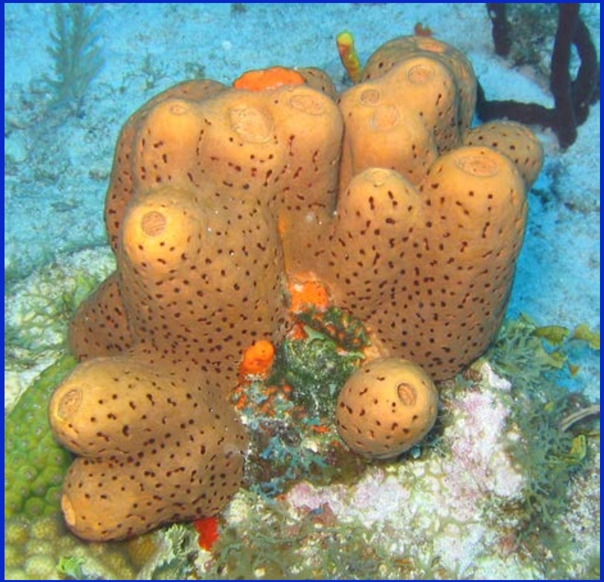
Large-Scale Phylogenetics

CONSERVATION INTERNATIONAL

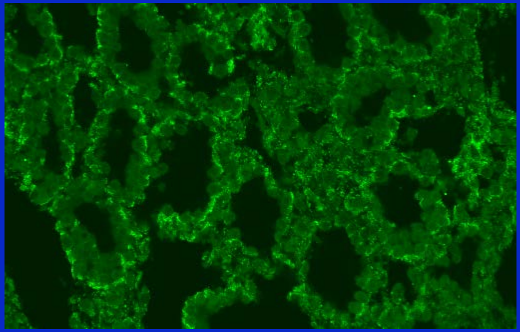
Smithsonian

NSF

Ecology & Evolution of Sponges



Symbiotic Interactions



PorToL

Porifera Tree of Life

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Biodiversity:

Species Discovery & Systematics

Large-Scale Phylogenetics

CONSERVATION INTERNATIONAL

Smithsonian

NSF

Arbor

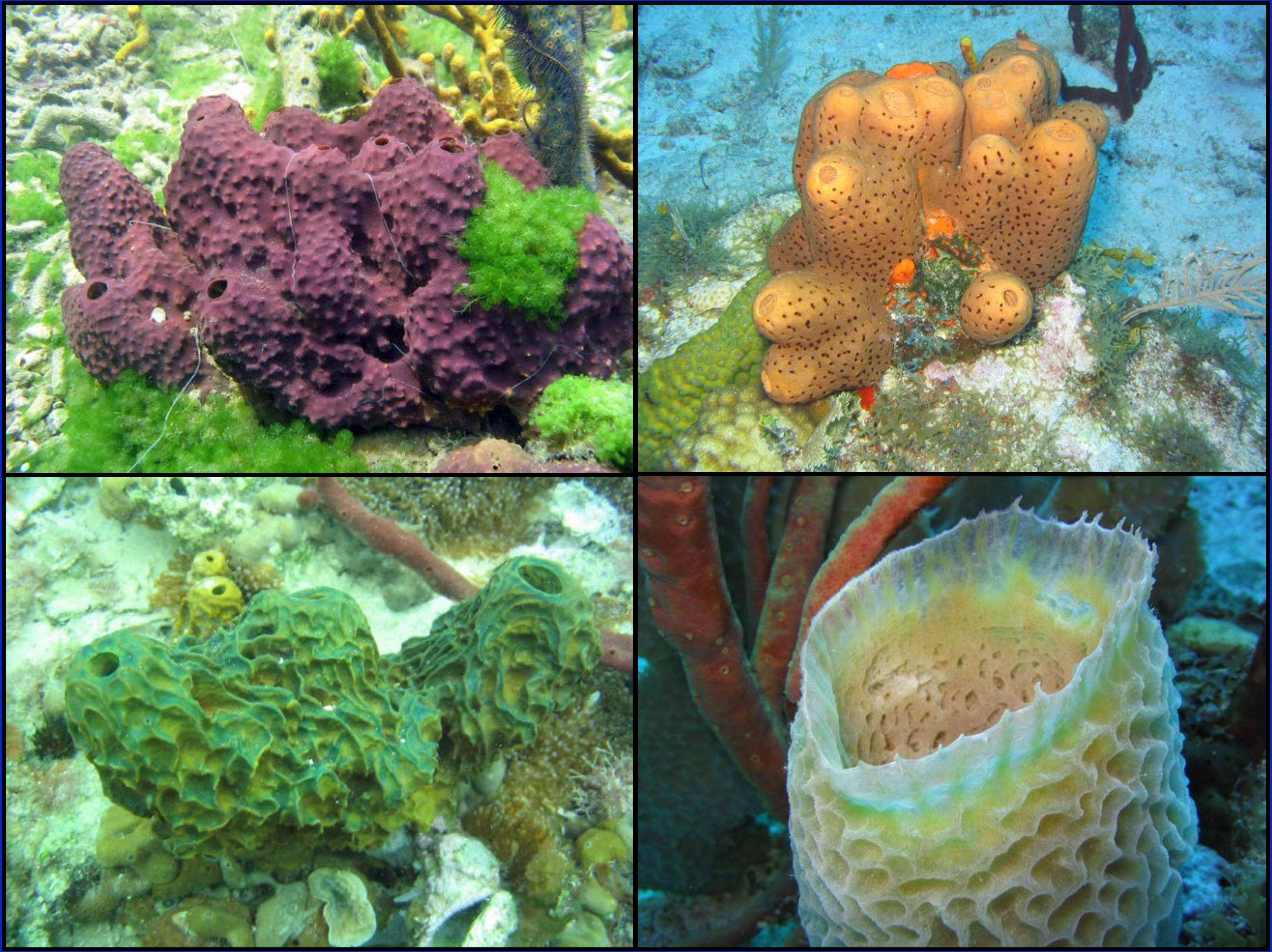
Sponge Biodiversity

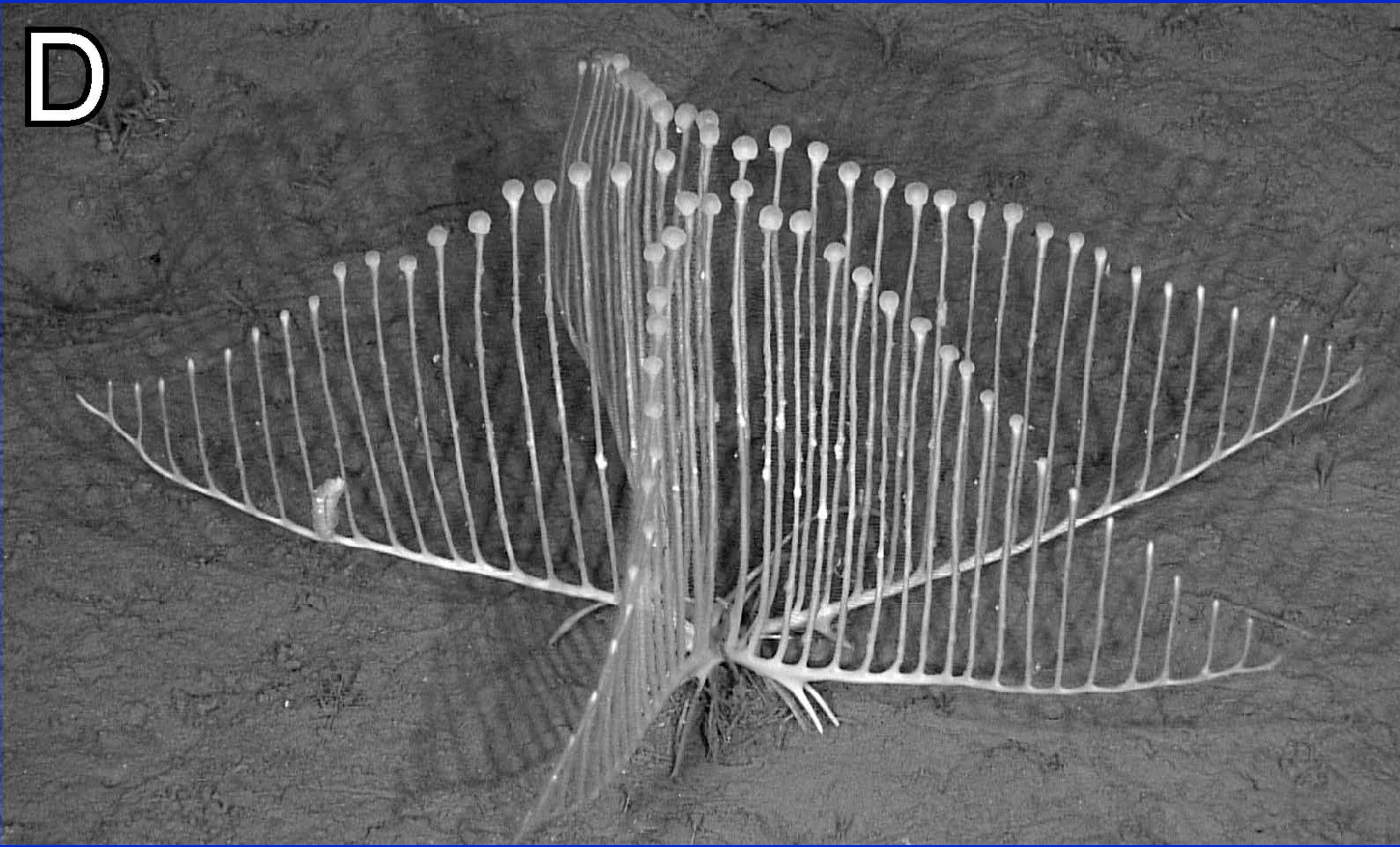
Porifera are distributed in

3 traditional classes + 1 new class = 4 classes
25 orders
127 families
682 valid genera (700+ proposed)
8,261 recognized species + estimated 8,000 to be named

ICZN sponge taxonomy is maintained as the
World Porifera Database (www.marinespecies.org/porifera)

Sponge Biodiversity

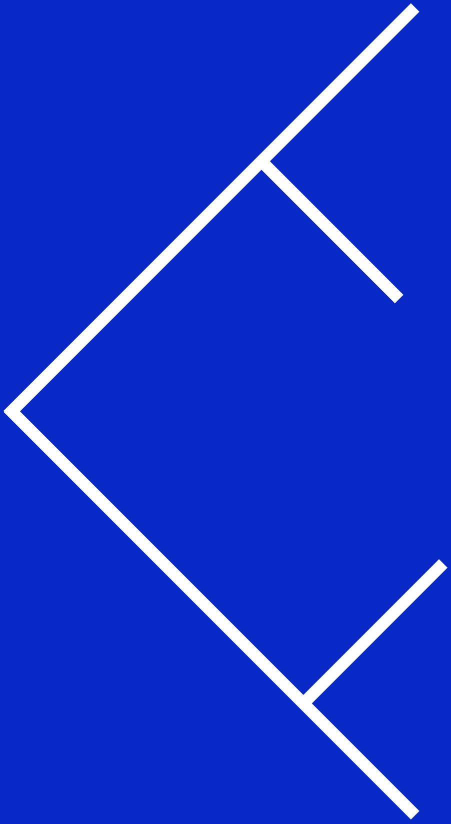




Chondrocladia lyra, a new species of carnivorous sponge from northern California (Demospongiae, Poecilosclerida, Cladorhizidae)

Welton Lee, California Academy of Sciences

A phylogeny is used to visualize evolutionary relationships among groups of organisms



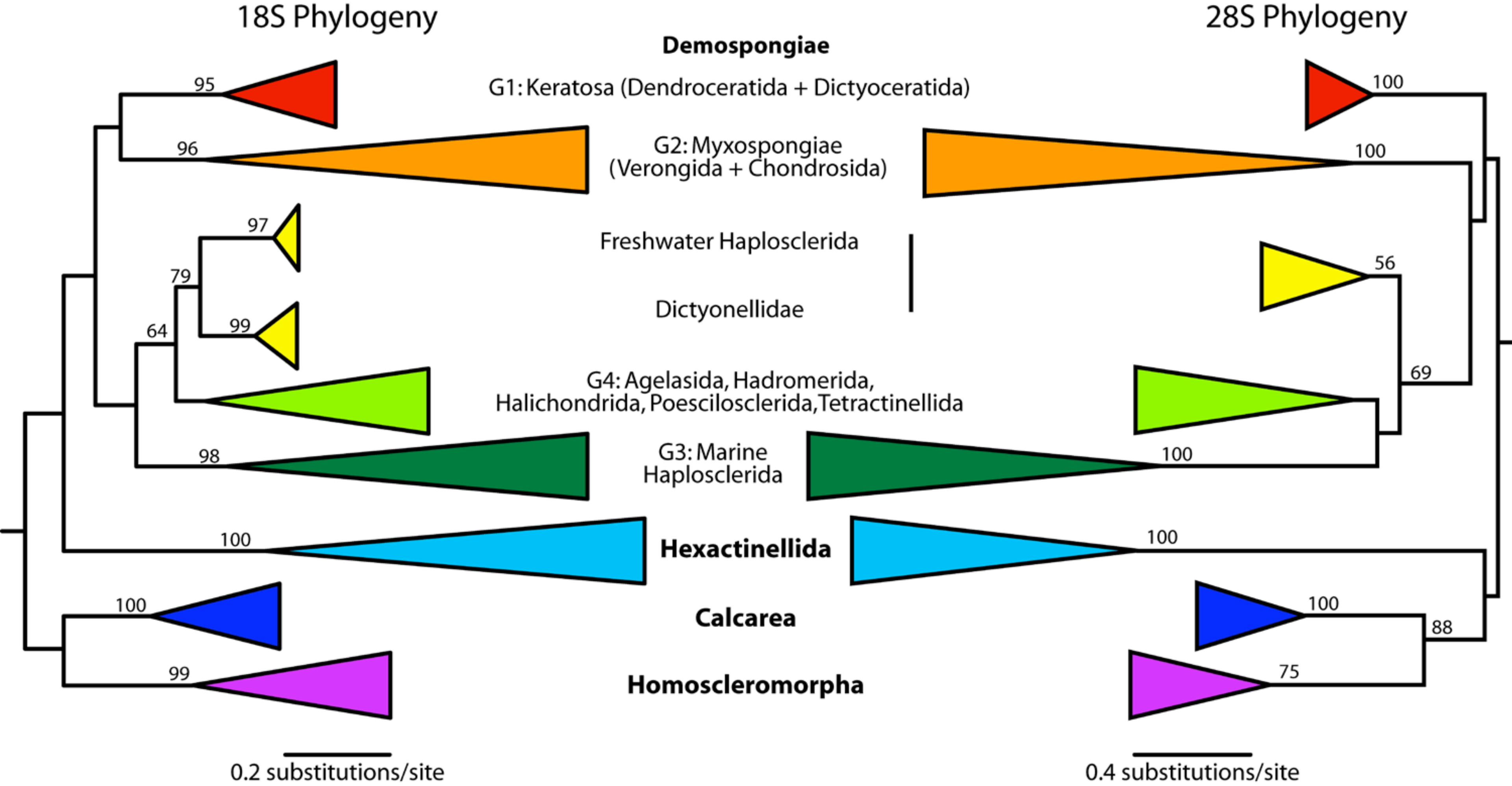
Demospongiae

Hexactinellida

Calcarea

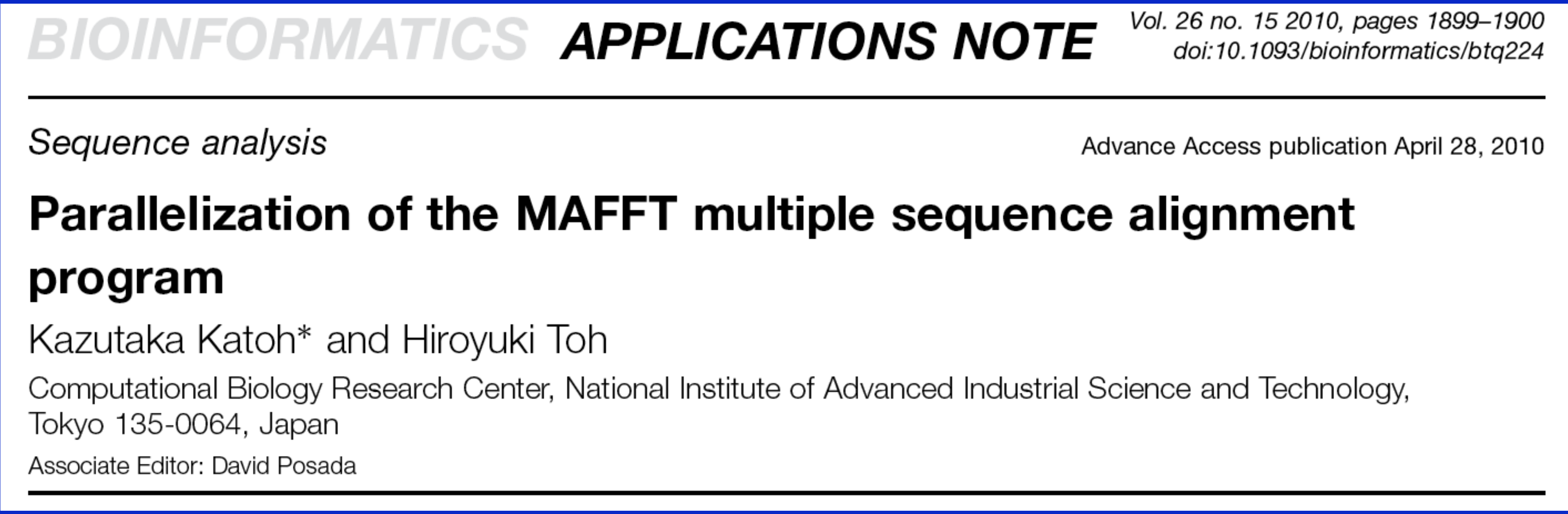
Homoscleromorpha

NSF Assembling the Tree of Life: Porifera Tree of Life (PorToL), >1300 species



Computational Needs for Phylogenetics

- Secondary Structure Alignments
  - Parallel MAFFT



BIOINFORMATICS **APPLICATIONS NOTE**
Vol. 26 no. 15 2010, pages 1899–1900
doi:10.1093/bioinformatics/btq224

Sequence analysis

Advance Access publication April 28, 2010

Parallelization of the MAFFT multiple sequence alignment program

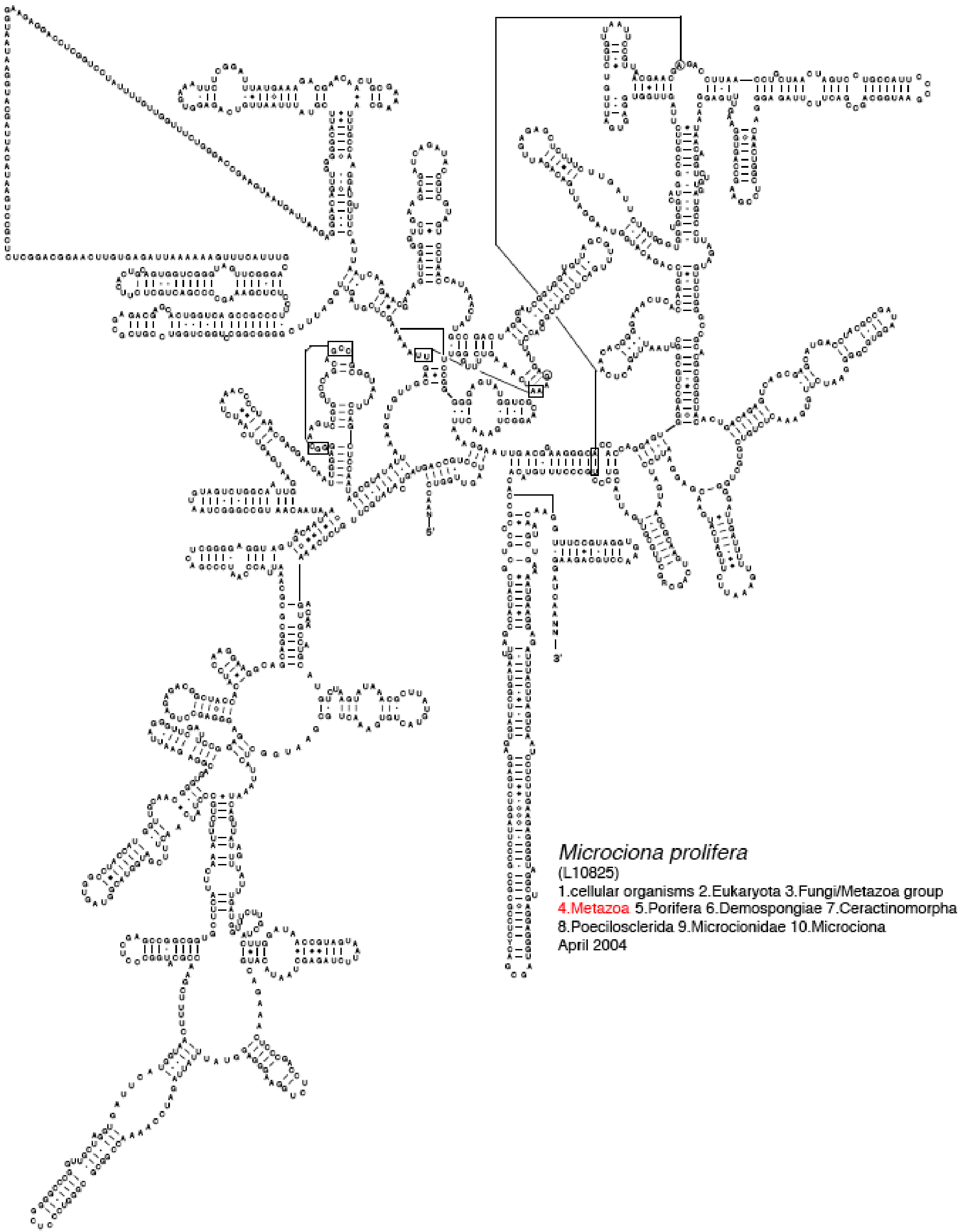
Kazutaka Katoh* and Hiroyuki Toh
Computational Biology Research Center, National Institute of Advanced Industrial Science and Technology, Tokyo 135-0064, Japan

Associate Editor: David Posada

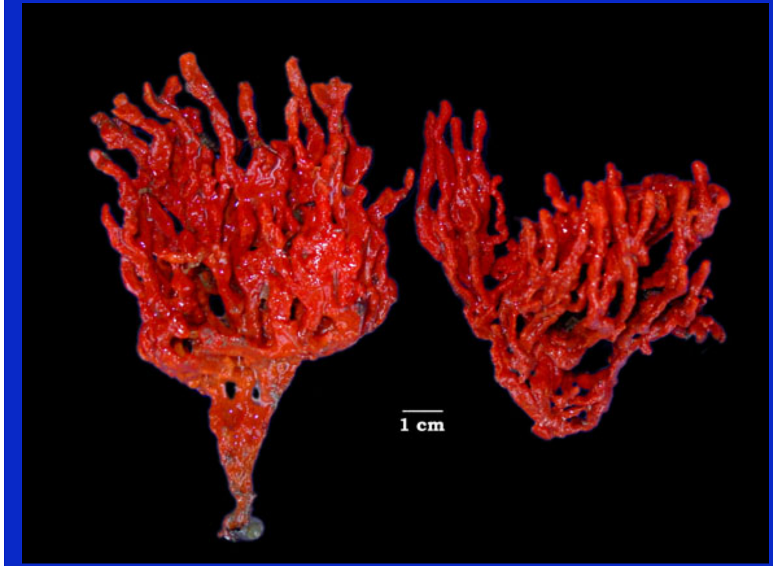
Analysis of Ribosomal Gene Sequences

Alignments based on folding of secondary structure are most accurate, but computationally complex

Secondary Structure: small subunit ribosomal RNA



Microciona prolifera
(L10825)
1.cellular organisms 2.Eukaryota 3.Fungi/Metazoa group
4.Metazoa 5.Porifera 6.Demospongiae 7.Ceractinomorpha
8.Poecilosclerida 9.Microcionidae 10.Microciona
April 2004

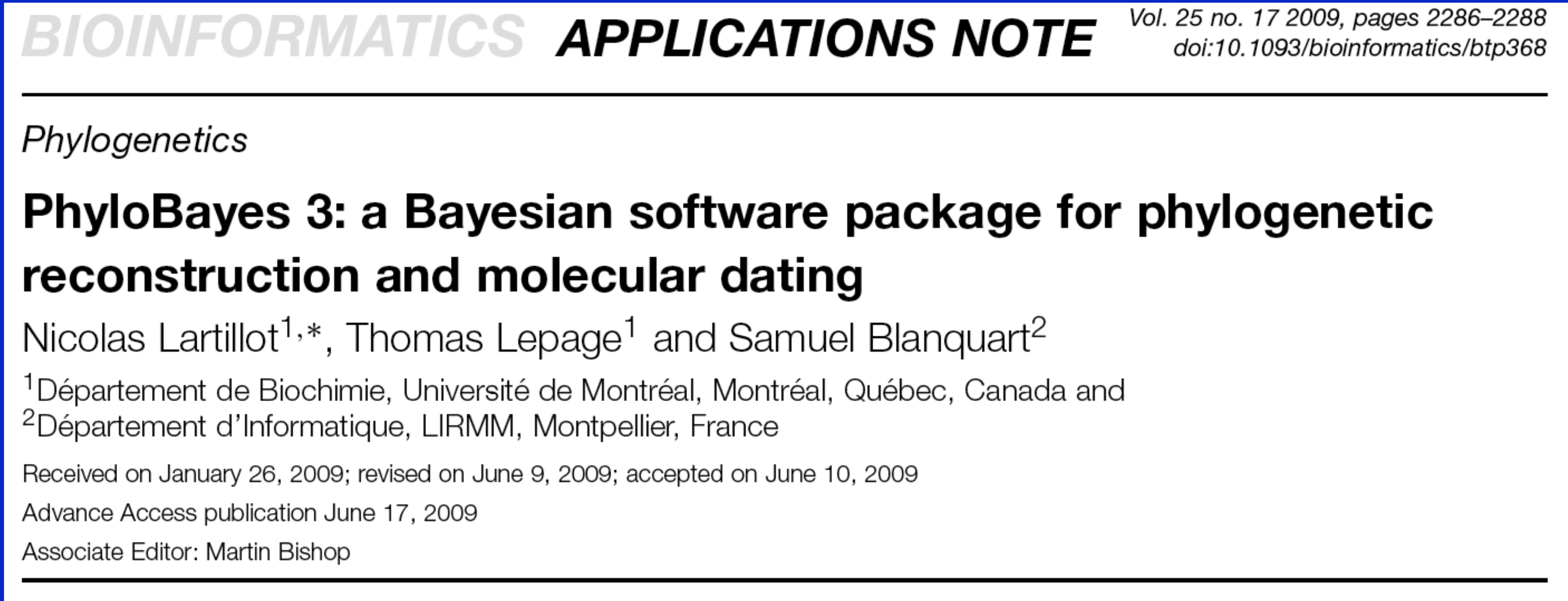


Dr. Robin Gutell
http://www.rna.ccbb.utexas.edu/
www.calacademy.org

Computational Needs for Phylogenetics

- Secondary Structure Alignments
  - Parallel MAFFT

- Bayesian Algorithms
  - Parallel PhyloBayes



BIOINFORMATICS **APPLICATIONS NOTE**
Vol. 25 no. 17 2009, pages 2286–2288
doi:10.1093/bioinformatics/btp368

Phylogenetics

PhyloBayes 3: a Bayesian software package for phylogenetic reconstruction and molecular dating

Nicolas Lartillot[1,*], Thomas Lepage[1] and Samuel Blanquart[2]

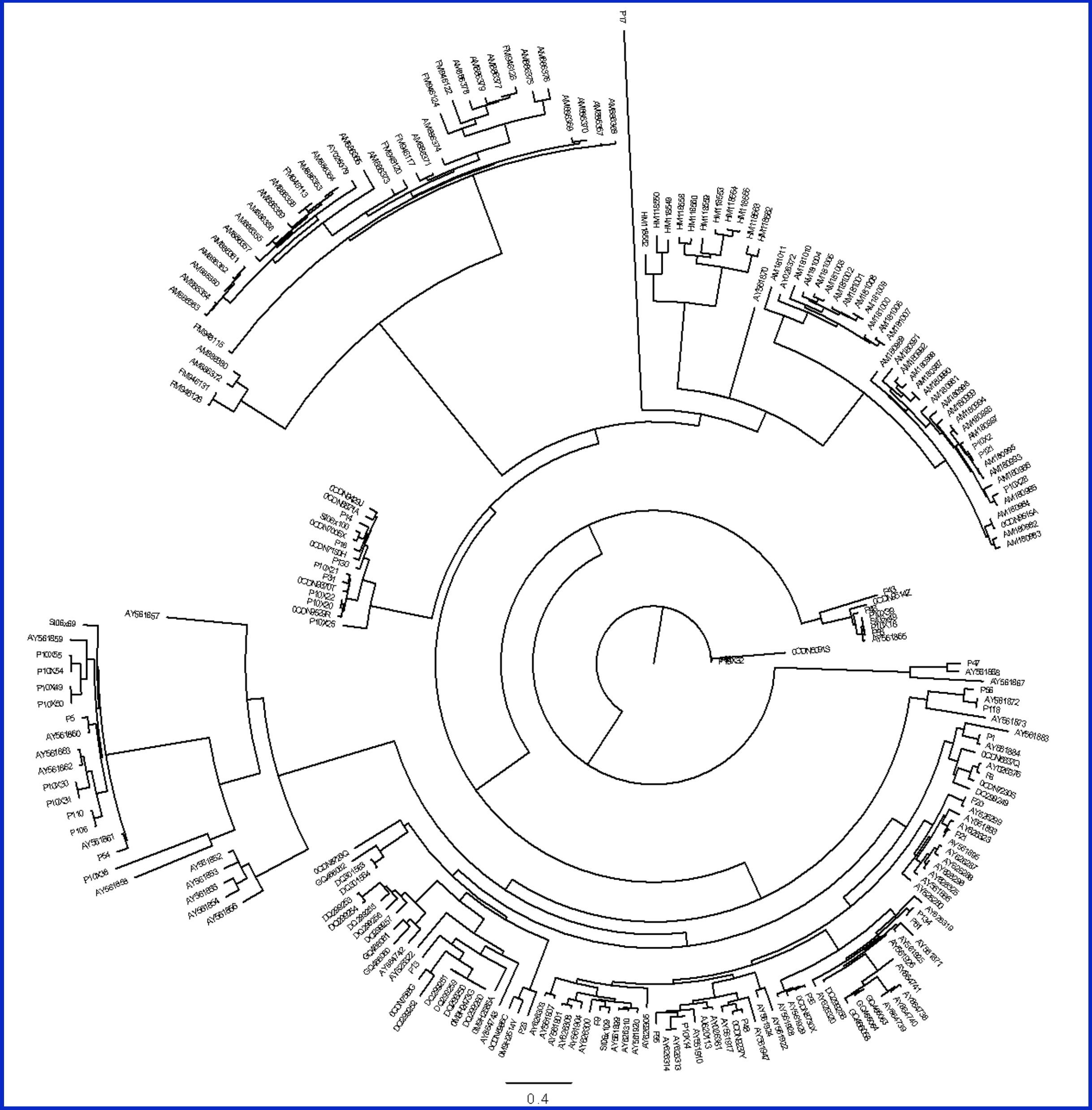
[1]Département de Biochimie, Université de Montréal, Montréal, Québec, Canada and
[2]Département d'Informatique, LIRMM, Montpellier, France

Received on January 26, 2009; revised on June 9, 2009; accepted on June 10, 2009
Advance Access publication June 17, 2009
Associate Editor: Martin Bishop

PhyloBayes

New parallel version implemented by Puri Bangalore

CAT-GTR model of sequence evolution, with over 50 different models specified across 3500 bp alignment of 250 taxa



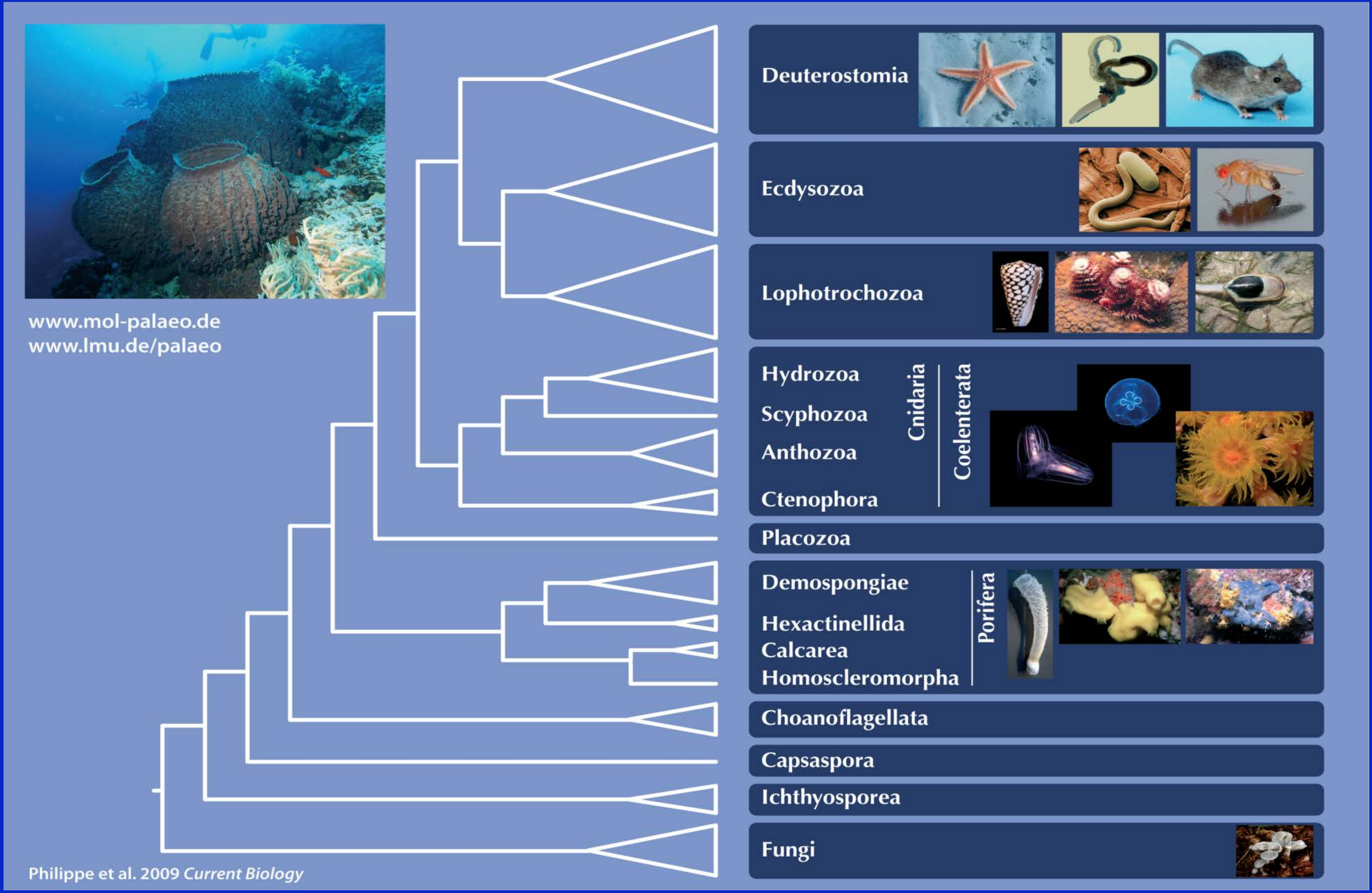
Computational Needs for Phylogenetics

- Secondary Structure Alignments
  - Parallel MAFFT

- Bayesian Phylogenies
  - Parallel PhyloBayes

- EST Libraries
  - Custom Software to Select Homologous Genes
    - 55 species
    - 128 nuclear-encoded proteins
    - 30,257 aligned amino acid positions

Sponges are an ancient lineage of metazoans.



www.mol-palaeo.de
www.lmu.de/palaeo

Philippe et al. 2009 *Current Biology*

PorToL team members contributed to a recent phylogenomic study of metazoan relationships that places sponges in a monophyletic clade that is basal to other animals (Philippe et al. 2009). Bayesian tree obtained from the analysis of 128 nuclear-encoded proteins (30,257 aligned amino acid positions) for 55 terminal taxa with the CAT model of evolution.

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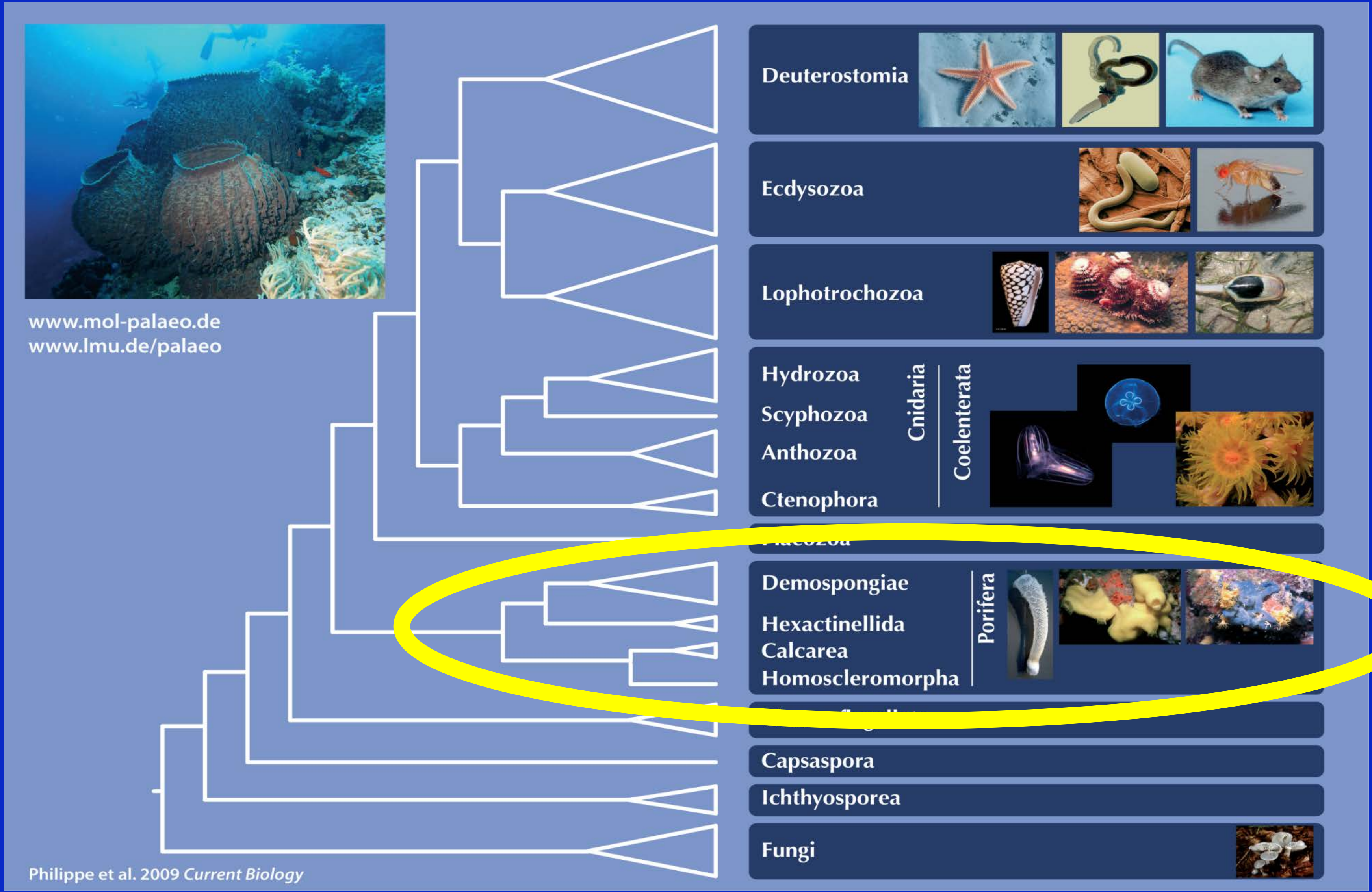

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Computational Needs for Phylogenetics

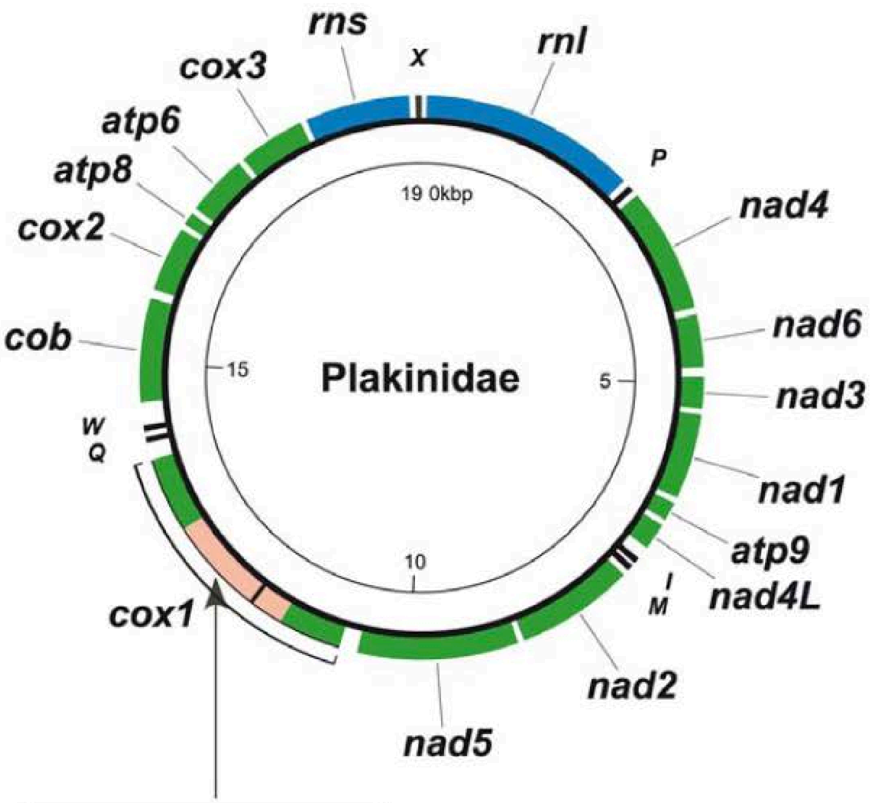
- Secondary Structure Alignments
  - Parallel MAFFT

- Bayesian Phylogenies
  - Parallel PhyloBayes

- EST Libraries
  - Custom Perl Scripts to Select Homologous Genes

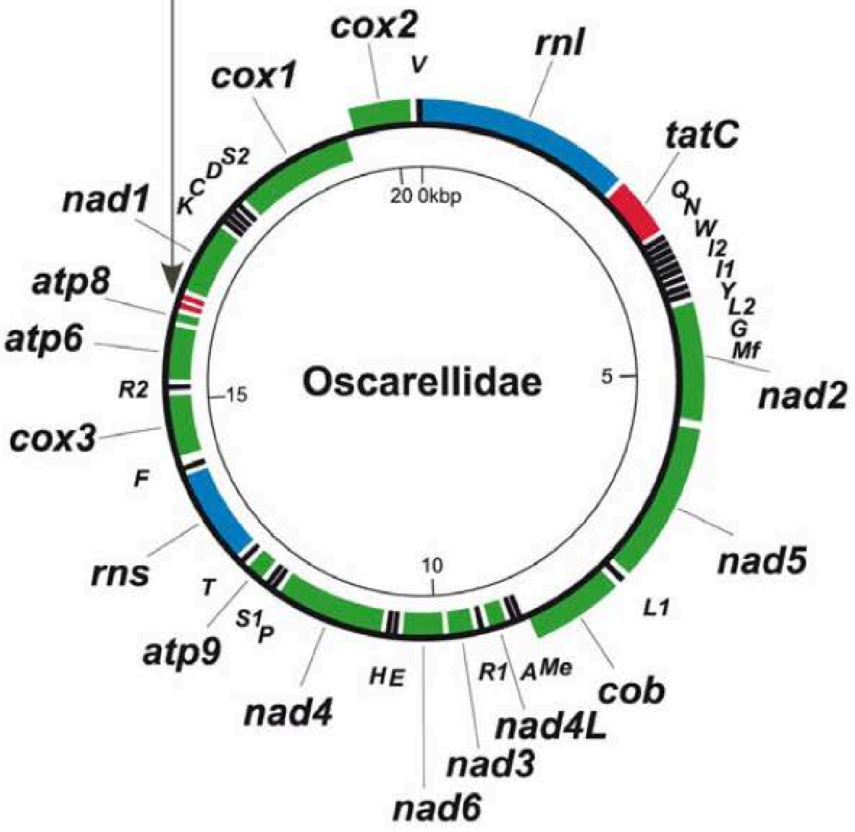
- Illumina Sequencing of Mitochondrial Genomes
  - Galaxy

Homoscleromorpha: Plakinidae vs. Oscarellidae

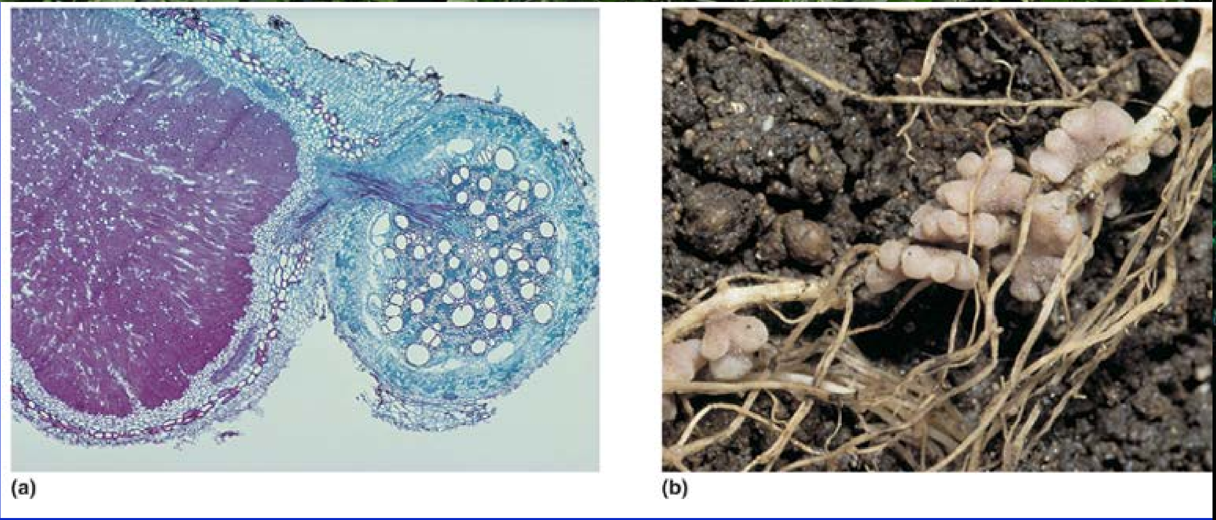


Introns:	
Plakinastrella sp.:	++
Plakina crypta:	++
Plakina trilopha:	+
Otherwise:	-

Oscarella microlobata:	*+trnY+trnT'*
Pseudocorticium jarrei:	*+trnV+trnX*
Otherwise:	*+trnV'+trnT'*



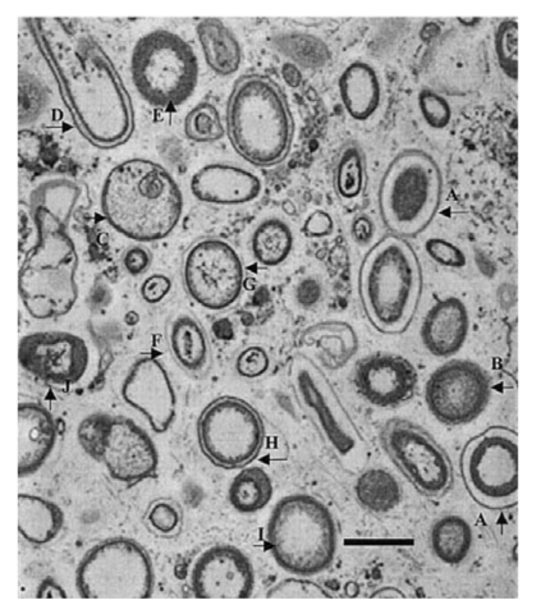
Symbiotic Interactions



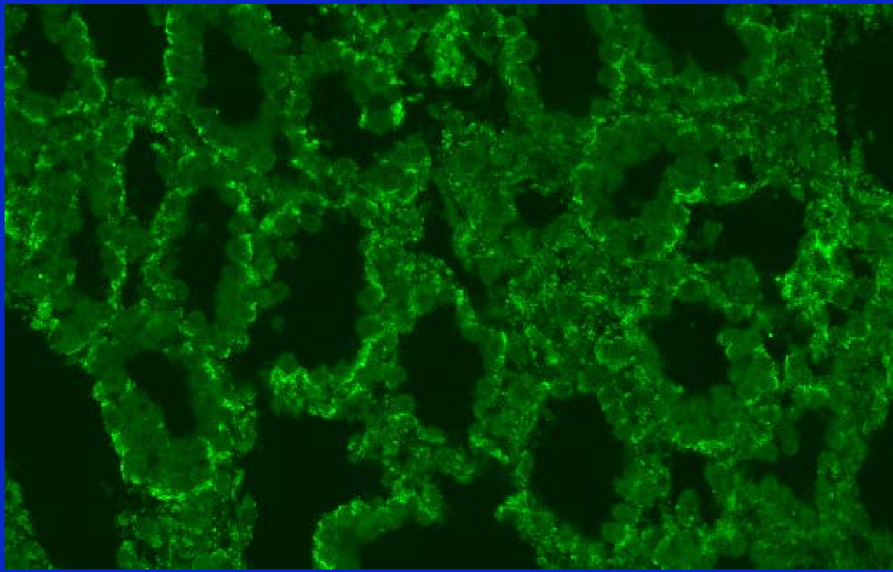
Sponge Microbiology

Sponges can host abundant and diverse communities of symbiotic microbes.

- How common are these associations?
- How diverse are these associations?
- How do microbial symbionts interact with the host sponge?



Webster et al. (2001) TEM of mesohyl of *Rhophaloeides odorabile*, with exclusively bacterial cells in this image.



Eubacterial FISH probe in the mesohyl of *Hyrtios violaceus* (Thacker et al. in prep)

Earth Microbiome Project

300 TAYLOR ET AL. MICROBIOL. MOL. BIOL. REV.

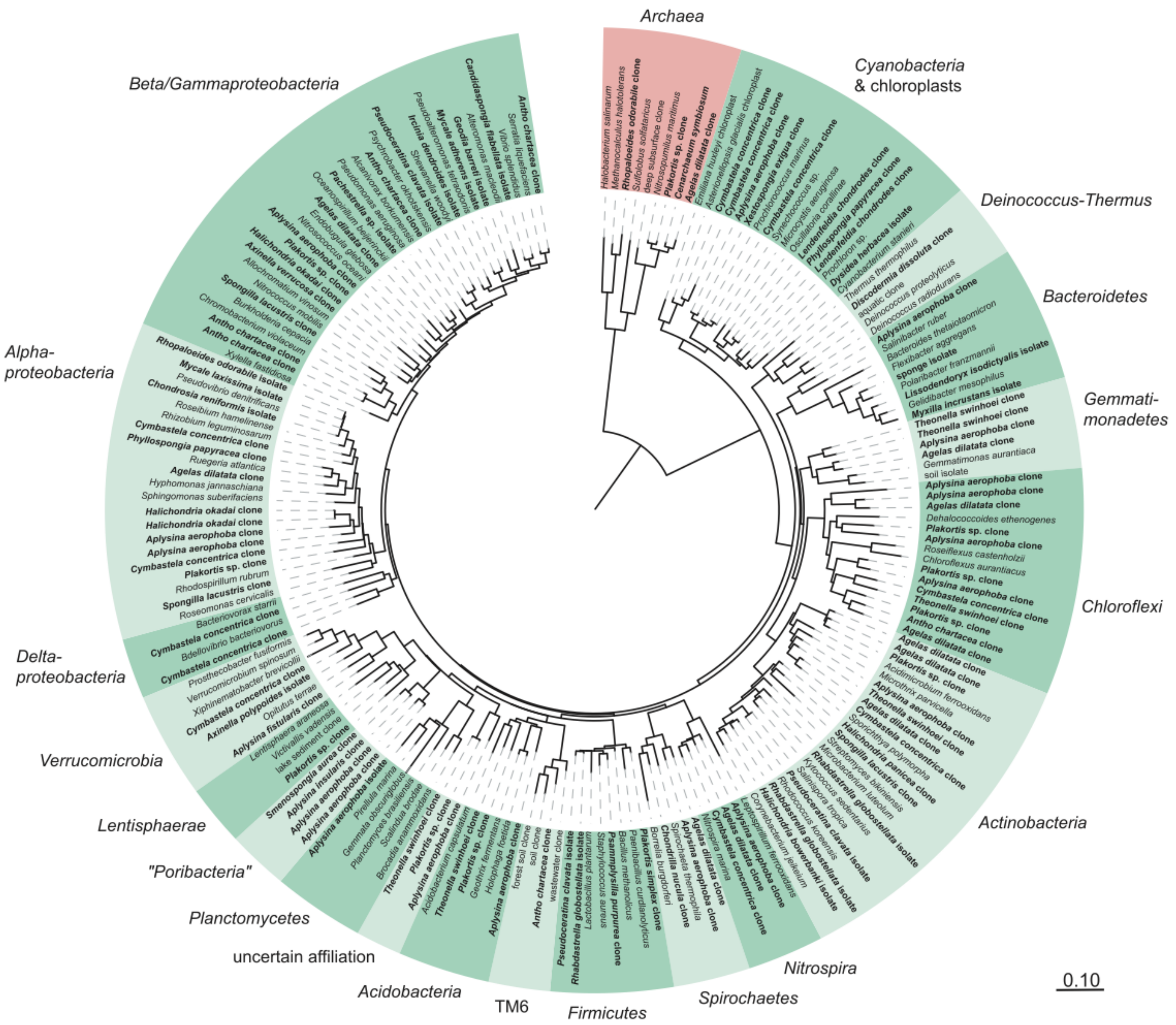
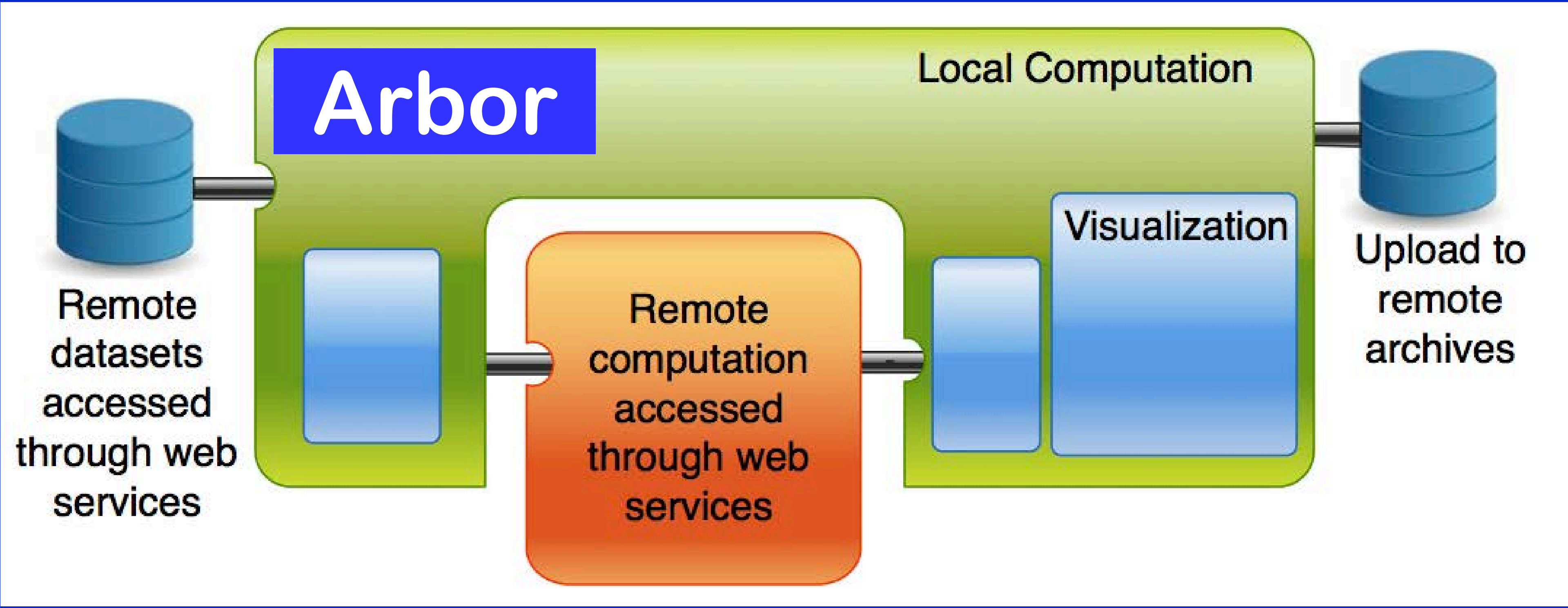


FIG. 4. 16S rRNA-based phylogeny showing representatives of all bacterial and archaeal phyla from which sponge-derived sequences have been obtained. Sponge-derived sequences are shown in bold, with additional reference sequences also included. The displayed tree is based on maximum likelihood analysis. Bar, 10% sequence divergence.

Representatives of 16 bacterial phyla and both major archaeal lineages are reported as sponge symbionts.

Comparative Analysis Workflows for the Tree of Life



- Shared workflows archived at Dryad
- Facilitate access to TeraGrid / XSEDE

NSF-Sponsored DRYAD
http://datadryad.org

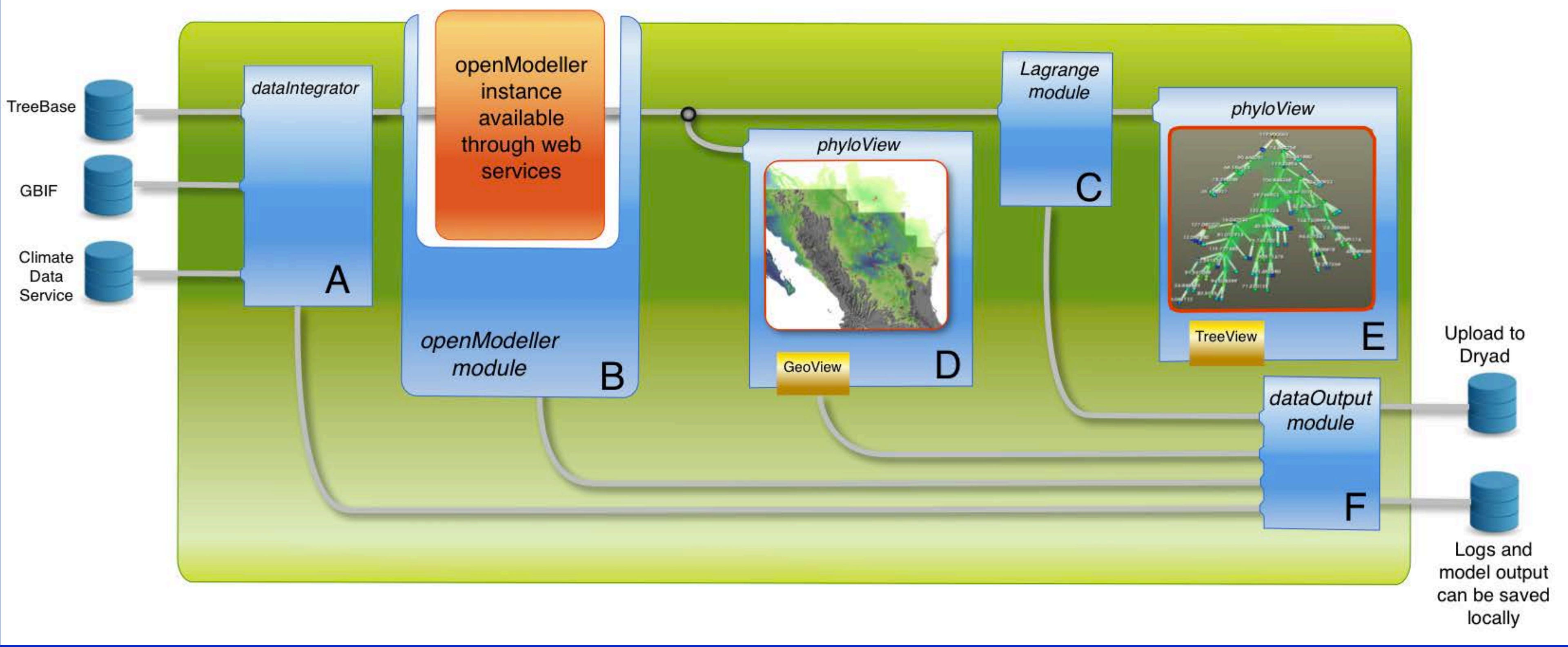
- Respository for phylogenetic data sets
- Currently expanding to accommodate any bioscience data
- Arbor workflows will be stored in DRYAD
- Reveal exactly how authors analyze data
- Retrieve methods and substitute your own data

Arbor: Case Studies

I. The Evolutionary Process of Spatial Diversification

II. The Evolution of Symbiotic Communities

III. The Evolution of Complex Interactions



How do species interactions shape long-term patterns of evolution?

Arbor Team

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