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Exploring the Tree of Life

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Why Study the Tree of Life? — The Scientists Speak

Edited by Paula Mikkelsen

The U.S. National Science Foundation provides the largest and most prestigious chunk of federal funding to basic science in this country. Among its many initiatives, NSF funds research to study the evolutionary relationships — the Tree of Life — of a wide variety of organisms currently (and formerly) living on the Earth. Among the active and recently completed projects in the "Assembling the Tree of Life" (AToL) Program are large teams of investigators studying butterflies, fish, beetles, clams, algae, bacteria, sponges, crustaceans, flagellate protozoans, liverworts, seed plants, fungi, dinoflagellates, mammals, cnidarians, flowering plants, reptiles, birds, and bees. Each of these projects has assembled an authoritative team of scientists, students, and technicians to examine the anatomy and molecular sequences of their organisms and to run sophistocated *phylogenetic analyses* (or cladistics, which result in a cladogram or "tree") that will ultimately yield the best hypotheses of the evolution of these taxa. One day, all of these pieces and parts will fit together, providing us with a complete picture of how life evolved, and continues to evolve, on Earth.

But why are we doing this? Of what use is such information to everyday citizens? Each funded project is responsible not only for their science, but for what NSF calls "broader impacts," which usually includes teaching at various levels and, importantly, interpretation of their science to the public. As *American Paleontologist's* contribution to those efforts, and to the United Nations' International Year of Biodiversity, we asked AToL scientists to answer the question "Why do we need to assemble the [xxx] Tree of Life?" Here are their answers.

PorToL — The Sponge Tree of Life

https://www.portol.org

Assembling the Sponge Tree of Life is important for a number of reasons. The appearance of sponges occurred at a critical point in the history of animal life, and sponges provide clues about the events that happened as single-celled ancestors gave rise to multicellular animals. Establishing a strong Tree of Life for sponges will allow us to explore ideas about the evolution of complex body forms.

Sponges are also a common component of many benthic habitats, from the deep sea to coral reefs, and from mangrove swamps to freshwater lakes and streams. Given the growing concern over accelerating rates of biodiversity loss, we need a fuller appreciation of unique taxa for conservation purposes. Finally, described sponges number approximately 8,122 valid species, with half again as many — an estimated 4,000 species — awaiting discovery or description. Recent molecular research indicates that the current classification system (with 3 classes, 25 orders, 127 families, and 680 genera) is not a particularly accurate reflection of the group's evolutionary history. Thus, a well-supported Porifera Tree of Life will shed light on new lineages, new relationships among lineages, and new ways to view one of the earliest experiments in the evolution of multicellularity among the animals.

- Malcolm Hill, University of Richmond, mhill2@richmond.edu

RedToL — The Red Algal Tree of Life

http://dblab.rutgers.edu/redtol/home.php

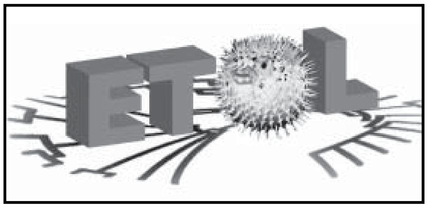
The Rhodophyta (red algae) is one of the most ancient groups, with fossil evidence stretching back 1.2 billion years. When anyone is exploring the rocky intertidal zone, these seaweeds are readily visible, with their bright red to purple hues. Red algae contribute significantly to the ecology of rocky shores, providing food and shelter for many marine fisheries. These plants are not only key members of aquatic environments, they are sources of important human foods such as dulse and sushi wraps. They also have a multitude of pharmaceutical and industrial uses, such as agarose and carrageenans. Perhaps most important is the role that red algae have played in the evolution of our planet through secondary endosymbiosis. More than one billion years ago, a red alga was the donor of the chloroplast in chlorophyll-*c* containing algae. These secondarily-derived algae rose to prominence in marine ecosystems after the end of the Permian Period (250 million years ago). Today, groups such as diatoms provide approximately 20% of the global supply of fixed carbon.

Research by the RedToL team could potentially revolutionize algal biology by providing new hypotheses and clarifying existing theories about the evolution of red algae and their place in the Tree of Life. One goal is to provide a red algal phylogeny based on multiple genes from the plastid, nucleus, and mitochondrion genomes. This framework is critical for supporting other types of research in such diverse fields as functional genomics, developmental biology, and ecology. A second goal is to learn about the evolution of red algae by sequencing the entire genomes of a number of key species. This part of the research will bring red algae into the "genomic age" alongside better-studied groups like vascular plants.

- Morgan L. Vis, Ohio University, vis-chia@ohio.edu
- Hwan Su Yoon, Bigelow Laboratory for Ocean Sciences
- Debashish Bhattacharya, Rutgers University
- Juan M. Lopez-Bautista, University of Alabama

EToL — The Euteleost Fish Tree of Life

http://www.fishtree.org



Euteleosts represent more than two thirds of all fish and a third of all vertebrate species, including virtually all fish of economic importance and those used as model systems in scientific research. Despite their importance in medical research, and their vast potential for exploring a wide range of evolutionary trends and issues, the higher-level relationships among fish taxa remain unclear — and for many, their status as natural groups has not been established. The Euteleost Tree of Life project (EToL) seeks to understand the diversity of euteleost fish by reconstructing a well-supported "backbone" for the group using morphological and molecular data from 1,500 carefully chosen species. Project members are collecting DNA sequences and compiling a comprehensive database of anatomical evidence. These materials and the euteleost tree that results will help future researchers to better understand fish relationships, to test hypotheses and make informed predictions for a wide range of evolutionary issues such as character evolution, ecology, biogeography, and fish diversity, and to expand the evolutionary context for key model organisms (*e.g.,* zebrafish and pufferfish) and for upcoming genomic projects.

EToL research will become part of an online educational product targeted at high school students in the form of an interactive tree exploring the evolution of a few fish characters, and an online module about molecular and morphological trees with activities that highlight the work of EToL scientists. These resources will be disseminated through Understanding Evolution (http://evolution.berkeley.edu), a major evolution education website that serves teachers, students, informal educators, and the general public.

EToL is part of the Tree of Life Web Project (http://tolweb.org/trees), an international endeavor to reconstruct the evolutionary history of all known organisms. Phylogenetic thinking is fundamental to understanding the diversity of life, and mapping the Tree of Life has enormous practical potential to assist in ecological management decisions, understanding the evolution of genomes and functional roles of genes, and discovering new biological compounds.

- Guillermo Orti, University of Nebraska Lincoln, gorti1@unl.edu
- Richard Broughton, University of Oklahoma
- Teresa MacDonald, University of Kansas

AToL Decapoda — The Decapod Crustacean Tree of Life

http://decapoda.arthroinfo.org

Estimated to contain more than 15,000 species, the decapods are the most species-rich and economically important group of Crustacea, including shrimp, crabs, crayfish, and lobsters. Furthermore, many living families have well-documented fossil records. Accordingly, the decapods have been the subject of more published papers than have all other crustacean groups combined. Given the prevalence of decapods in the public and scientific mind, understanding the evolutionary history of this significant crustacean group is crucial.

Our project brings together a team of international experts from a variety of disciplines, including comparative morphology (of both adult and larval decapods), paleontology, molecular biology, bioinformatics, evolutionary biology, taxonomy, systematics, and field biology, to collect samples, identify morphological characters and useful genes, sequence DNA, and analyze the resulting data to develop a robust view of the phylogeny of the Decapoda. This will allow us to adjust taxonomy to better reflect evolutionary relationships, to test hypotheses of the timing of diversification events and of morphological change over evolutionary time, and to study past and present trends in biodiversity and variables such as time, morphology, and climate change. Thus, the Decapod Tree of Life is the foundation for a wide variety of future studies in evolutionary and comparative biology.

- Keith A. Crandall, Brigham Young University, keith_crandall@byu.edu
- Rodney M. Feldmann, Kent State University

Early Bird — The Bird Tree of Life

http://www.biology.ufl.edu/earlybird

Birds are among the most visible organisms in the environment. Observing birds has delighted birdwatchers and provided information to scientists for hundreds of years. Studies of these beautiful animals have shaped biological thought. For example, Charles Darwin's theory of natural selection was influenced by observing closely related species that differ markedly in the shape of their beaks. Since then, birds have shaped our knowledge of topics such as speciation, behavior, ecology, development, and neurobiology. Given the level

of attention from the public and scientific communities, it might be surprising that the evolutionary relationships among birds — the Avian Tree of Life — have been declared intractable many times over the past century. Indeed, Erwin Stresemann wrote in 1959:

> *…so many distinguished investigators have labored in this field in vain, that little hope is left for spectacular break-throughs. Only lucky discoveries of fossils can help us, but the chances of making such finds are very small.*

The lack of an Avian Tree of Life prevents us from putting all of our knowledge about birds into context. Did the ability to learn songs – shared only by perching birds, hummingbirds, and parrots – arise three times, or more, or less? Do hawks and falcons hunt in similar ways because their abilities evolved once or separately in each bird? Did ostriches and emus lose the ability to fly separately or through a common ancestor?

By collecting large amounts of genetic data to compile the Avian Tree of Life, we now know to the answers to these questions. We now know that perching birds and parrots are related, and likely gained the ability to learn song from their ancestor, whereas hummingbirds learned independently. We also know that hawks and falcons are not closely related, so their similar hunting methods are not derived from a common stock. The large flightless birds of Southern continents — ostriches and emus — each lost the ability to fly independently. Continued efforts to improve our understanding of the Avian Tree of Life will allow even more connections between our extensive knowledge of bird biology to their evolutionary history, and will teach us more broadly about these processes as well.

- Edward L. Braun & Rebecca T. Kimball, University of Florida,
ebraun68@ufl.edu

Gymnosperm ToL — The Seed Plant Tree of Life

http://www.huh.harvard.edu/research/mathews-lab/atolHtmlSite

The evolution of the seed is one of the most important events in the history of land plants, leading to enhanced survival and dispersal capabilities and to greater mating control. Seed plants dominate the landscape and today, forests and grasslands are among our most important resources. Seed plants set the stage for the origin of agriculture, based on the cultivation of grain, which provides the majority of calories consumed by humans and the animals that feed them.

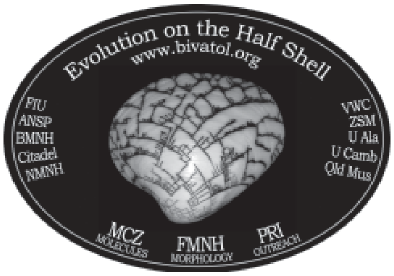
Despite the predominance of flowering plants (angiosperms) in most ecosystems and their inordinate contribution to land plant diversity, they are just one of many lineages that comprise the seed plant clade, all others being gymnosperms. Several gymnosperm lines are ancient, originating in the Paleozoic and reaching the height of their diversity in the Triassic and Jurassic Periods. Unlike the dinosaurs with which they coexisted, a few gymnosperms have persisted to the present: the conifers, cycads, *Ginkgo biloba*, and the strange and enigmatic gnetophytes (*Welwitschia, Gnetum, Ephedra*). However, their diversity has decreased dramatically; fossils show evidence of at least 18 extinct groups. Angiosperms have figured heavily in attempts to understand the evolution of seed plants, but this is like trying to understand the solar system without knowing the positions and composition of most of the planets. The Gymnosperm Tree of Life Project is focused on extensive sampling in both living and extinct clades of gymnosperms. Living gymnosperms comprise approximately 1,000 species, all of which are targets for DNA sampling for our molecular phylogeny. So that evidence from extinct and living plants can be integrated, we are also focusing on the morphology of fossils and a subset of living species (approximately 20% of species), broadly representing living diversity. Together these data will establish the context for understanding the evolution of seed plants.

The living collections found in botanic gardens and arboreta provide incomparable resources for teaching K-12 students about biology and evolution. We have capitalized on these resources by working together with the educational staff of several such institutions to offer workshops to middle and high school teachers that demonstrate how gymnosperms in nearby living collections can be used to teach key biological and evolutionary concepts. The workshops have been received very enthusiastically.

- Sarah Mathews, Arnold Arboretum of Harvard University,
smathews@oeb.harvard.edu

BivAToL — The Bivalve Tree of Life

http://bivatol.org



Bivalves (clams, oysters, mussels, scallops, etc.) are a diverse and familiar group of mollusks with an old and well-preserved fossil record, important ecological roles in marine and freshwater ecosystems, and economic roles including fisheries, the ornament industry, and health sciences. Diversity-wise, bivalves – with

20,000-30,000 living species – are the second largest class of living mollusks, which in turn constitute the second largest animal phylum and the largest in the marine realm.

Despite the ubiquitousness of bivalves, past efforts to study and understand their evolution have been uncoordinated and little consensus has been reached. The BivAToL team is taking a fresh look at bivalve anatomy (with special focus on gill and stomach anatomy, shell ultrastructure, and sperm morphology) and selected molecular markers (genes) for the same species investigated morphologically to be able to understand bivalve evolution in an integrated fashion.

While national and international BivAToL teams assemble morphological and molecular data in levels of detail never before attempted, other BivAToL participants are generating outreach products that will engage various audiences in the project's results and in evolutionary science in general. Most unusually, BivAToL is pleased to present, beginning in September 2010, the traveling exhibition "Science on the Half-Shell: How and Why We Study Evolution," extolling the beauty and scientific value of bivalves as model organisms for evolutionary studies in the laboratory and the classroom. Perhaps most important in this context, bivalves give us a unique opportunity to teach a complex subject in a unique way, which we hope will resonate with museum visitors, web surfers, teachers, and students of all ages.

- Paula M. Mikkelsen, Paleontological Research Institution,
pmm37@cornell.edu

References and Further Reading

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Tree of Life Web Project. http://tolweb.org/trees.

Understanding Evolution, http://evolution.berkeley.edu.

U. S. National Science Foundation, Assembling the Tree of Life Initiative, http://www.phylo.org/atol.

Paula Mikkelsen is Associate Director for Science at Paleontological Research Institution, and a Principal Investigator on BivAToL (Assembling the Bivalve Tree of Life). Email pmm37@cornell.edu.

Did You Know? The Tree of Life!

- The coconut palm is called the "Tree of Life" because it is one of the most useful trees in the world. In addition to its food value, the tree and its fruit are used for soap, cosmetics, rope, fertilizer, charcoal filters, and a host of domestic products woven from the leaves. Other "Trees of Life" are the acacia in ancient Egypt, Yggdrasil (an ash or yew) in Norse mythology, the fig tree in India, and the Cebia tree in Mayan culture.
- Elephants evolved from a pig-sized creature that lived in northern Africa 55-60 million years ago. Today, their closest living relatives are hyraxes and manatees.
- Seahorses are more closely related to zebras than to starfish, lobsters, or scallops. Seahorses and zebras are both vertebrates, whereas starfish, lobsters, and scallops (although marine creatures like the seahorse) are all invertebrates (without a backbone).

- Compiled by Sara Auer Perry, PRI Education Staff

Discovering Mississippi's Petrified Forest

In the heart of the south, just northwest of Jackson, lies Mississippi Petrified Forest, the only petrified forest in the eastern United States. Located in the small town of Flora, Mississippi Petrified Forest is a registered National Natural Landmark, and offers a campground, an Earth Science Museum, and a peaceful and well-maintained Nature Trail along which are strewn the leftovers of an ancient log jam deposited by a river 36 million years ago. Only a short drive off the beaten path between New Orleans, Memphis, and points north, it's well worth a visit! -The Editor