

Angiosperm AToL: Resolving the trunk of the angiosperm tree and 12 of its thorniest branches



Flowering Plants - Angiosperms

One of the greatest terrestrial radiations

At least 250,000 extant species

Major lineages originated 130-90 million years ago

Dramatic rise to ecological dominance 100-70 million years ago

Sources of our food plants

AToL Publications

Over 50 publications to date

Moore, M. M., C. D. Bell, P. S. Soltis, and D. E. Soltis. 2007. Using plastid genomic-scale data to resolve enigmatic relationships among basal angiosperms. *Proc. Nat. Acad. Sci. USA* 104: 19363-19368.

Davis, C. C., M. Latvis, D. L. Nickrent, K. J. Wurdack, and D. A. Baum. 2007. Floral gigantism in Rafflesiaceae. *Science* 315: 1812.

Cantino, P., J. Doyle, S. Graham, W. Judd, R. Olmstead, D. E. Soltis, P. S. Soltis, and M. Donoghue. 2006. Towards a phylogenetic nomenclature of Tracheophyta. *Taxon* 56: 822-846.

Howarth, D. G. and M. J. Donoghue. 2006. Phylogenetic analyses of the "ECE" (CYC/TB1) clade reveal duplications that predate the core eudicots. *Proc. Nat. Acad. Sci. USA* 103: 9101-9106.

Moore, M. J., A. Dhirga, P. S. Soltis, R. Shaw, W. G. Farmerie, K. M. Folta, and D. E. Soltis. 2006. Rapid and accurate pyrosequencing of angiosperm plastid genomes. *BMC Plant Biology* 6: 17.

Davis, C. C., and K. J. Wurdack. 2004. Host-to-parasite gene transfer in flowering plants: phylogenetic evidence from Malpighiales. *Science* 305: 676-678.

Press coverage

Miller, R. 2008. Peabody Museum exhibit explores the relationships that link all living creatures. *The News-Times, Danbury, CT*.

Ruvinsky, J. 2008. Tiny origin of the world's largest flower. *Discover: 100 top science stories of 2007*.

Bryner, J. 2007. Floral 'Big Bang' led to stunning diversity. *MSNBC Fountain*.

H. 2007. A smelly puzzle, solved. *The New York Times*.

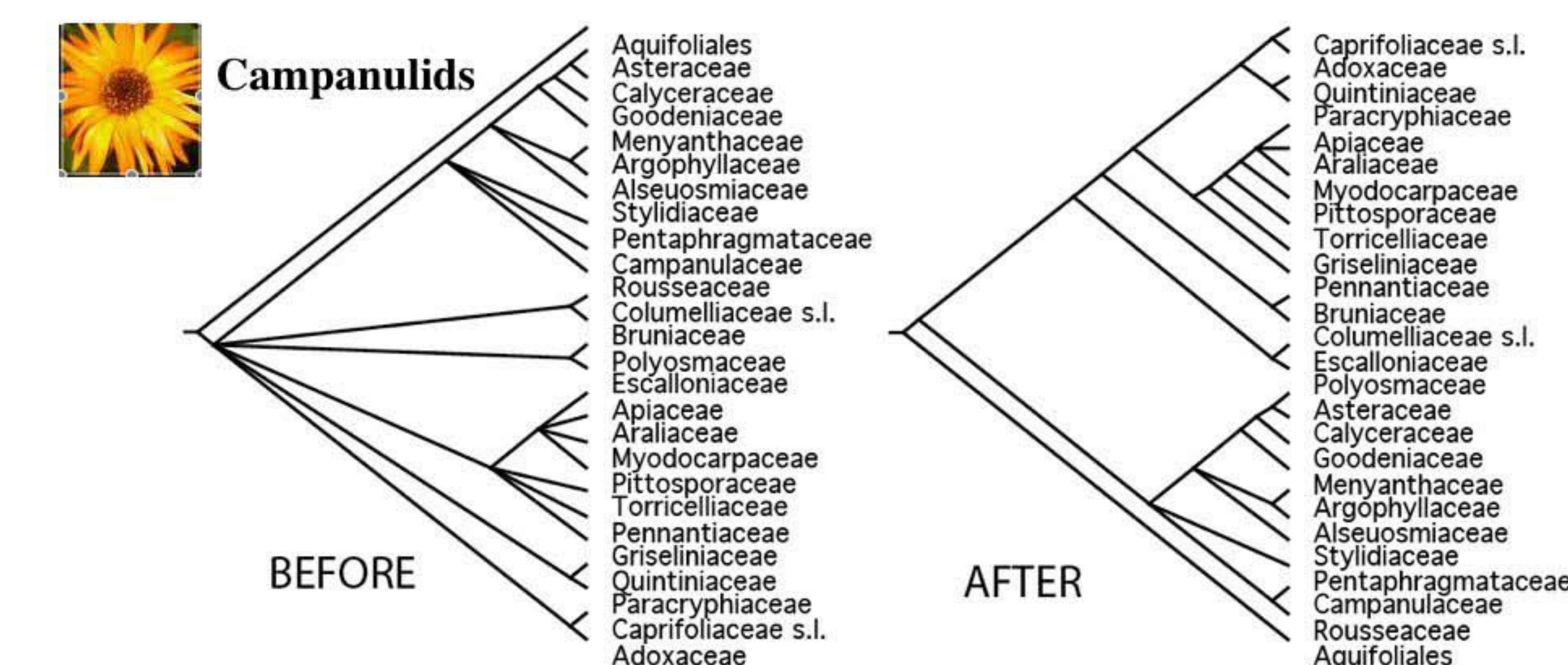
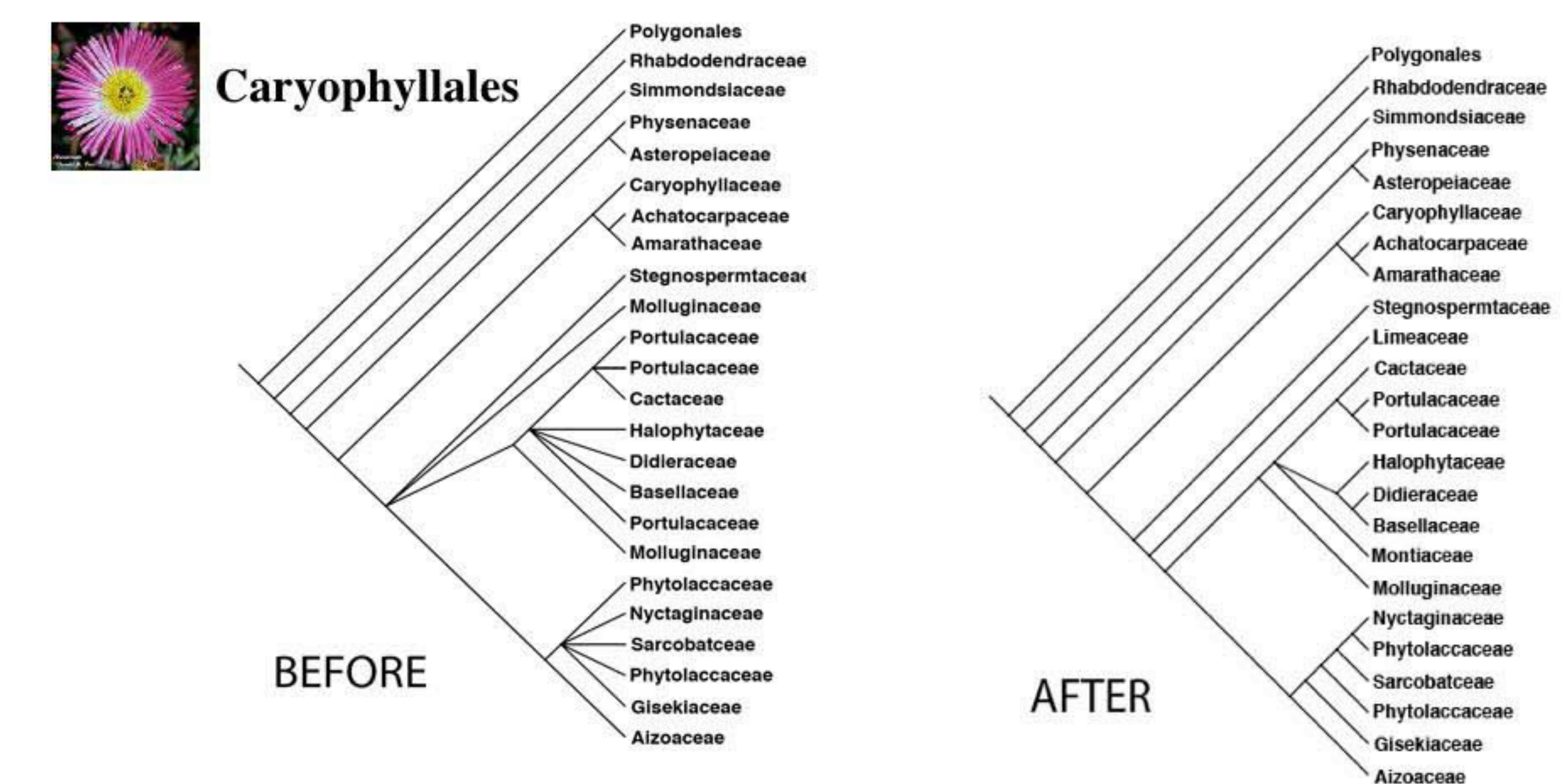
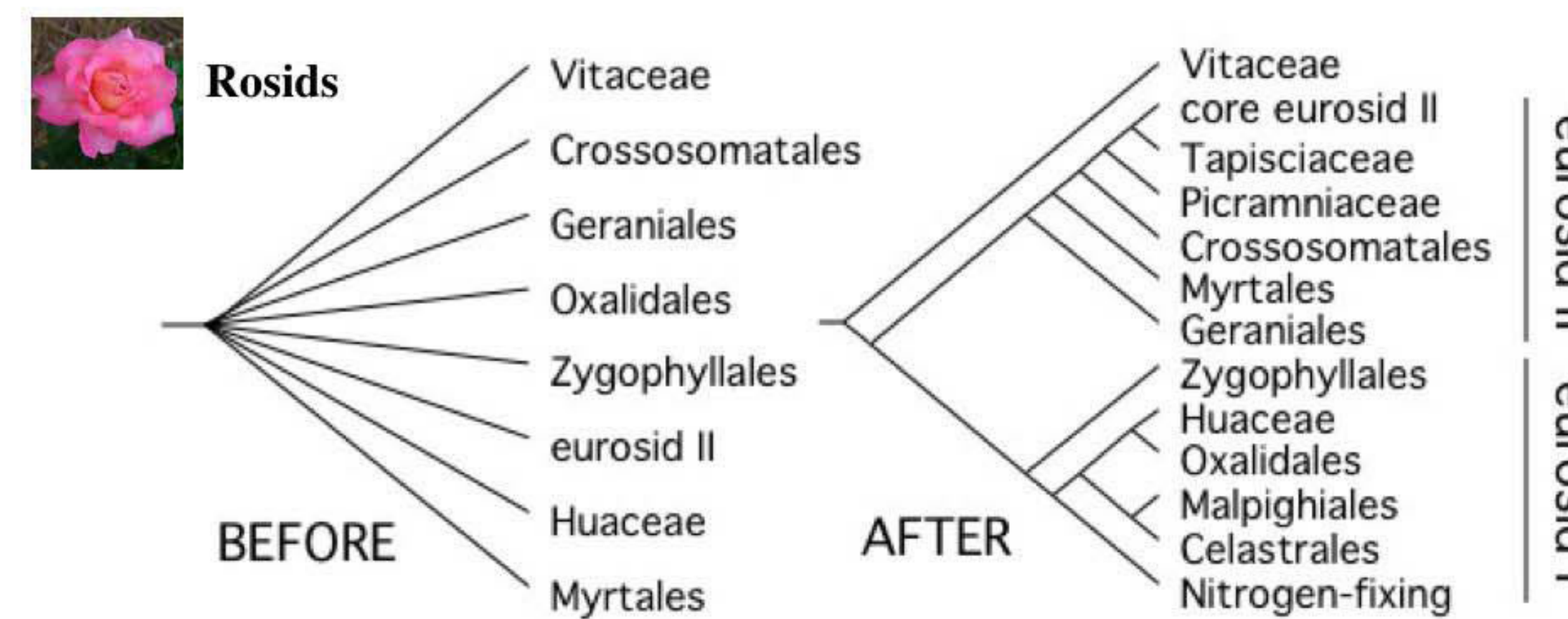
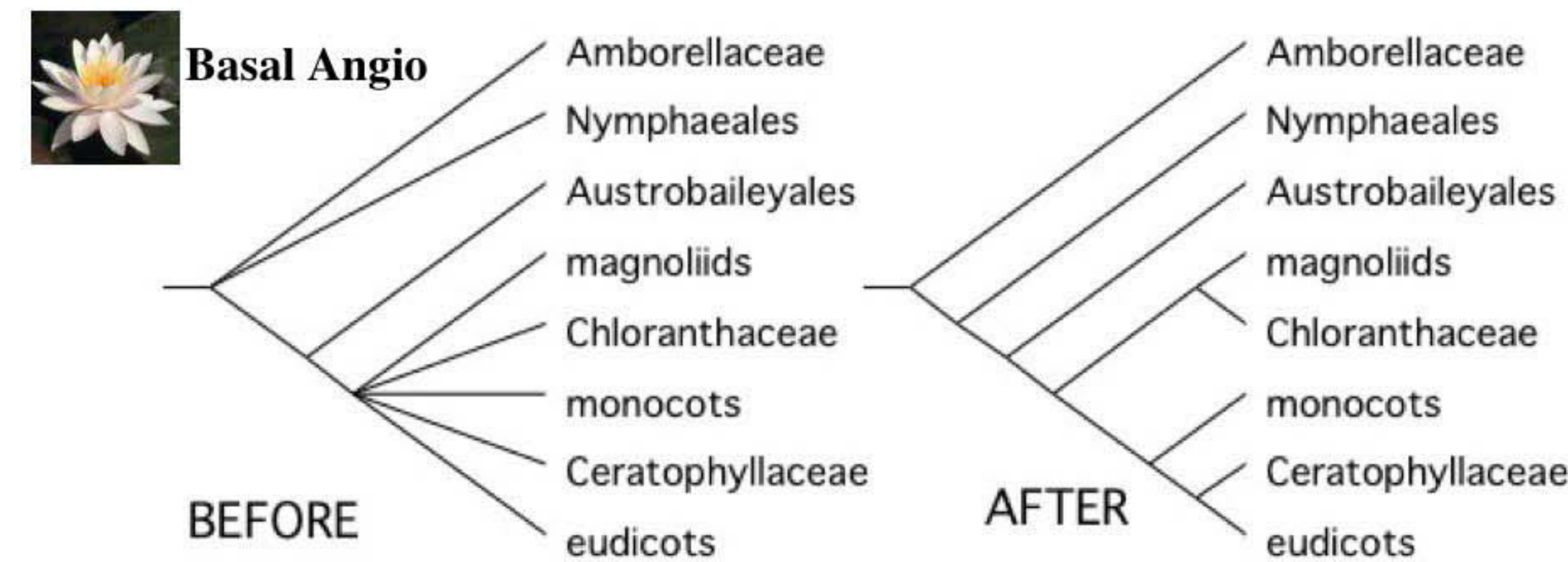
Angiosperm AToL Morphology

Assessment of over 100 morphological characters has been completed for the members of Malpighiales, Ericales, Saxifragales, Caryophyllales, and Lamiales included in the proposed phylogenetic analyses (a total of 140 taxa). All characters are documented by images (SEM or photos). We are now assessing the pattern of variation in these characters within these clades; currently, we have developed 93 morphological characters for Malpighiales. These characters will be mapped onto various molecular topologies. This group, as well as the Ericales, Saxifragales, and Caryophyllales, will provide a test of the methodology on integrating morphological data into the eventual 370-taxon cladogram of angiosperms. We are currently assessing variation within the campanulid clade. About 170 taxa remain to be databased and imaged.

Angiosperm AToL Team

- University of Florida: D. Soltis, P. Soltis, W. Judd, S. Manchester, R. Beaman, N. Cellinese
- University of Arizona: M. Sanderson
- Harvard University: C. Davis
- University of Michigan: Y. Qiu
- Smithsonian Institution: K. Wurdack
- University of Washington: R. Olmstead
- University of Wisconsin: K. Sytsma
- Virginia Tech University: K. Hilu
- Yale University: M. Donoghue, L. Hickey

The 12 Thorniest Branches: Now Untangled



454 Sequencing

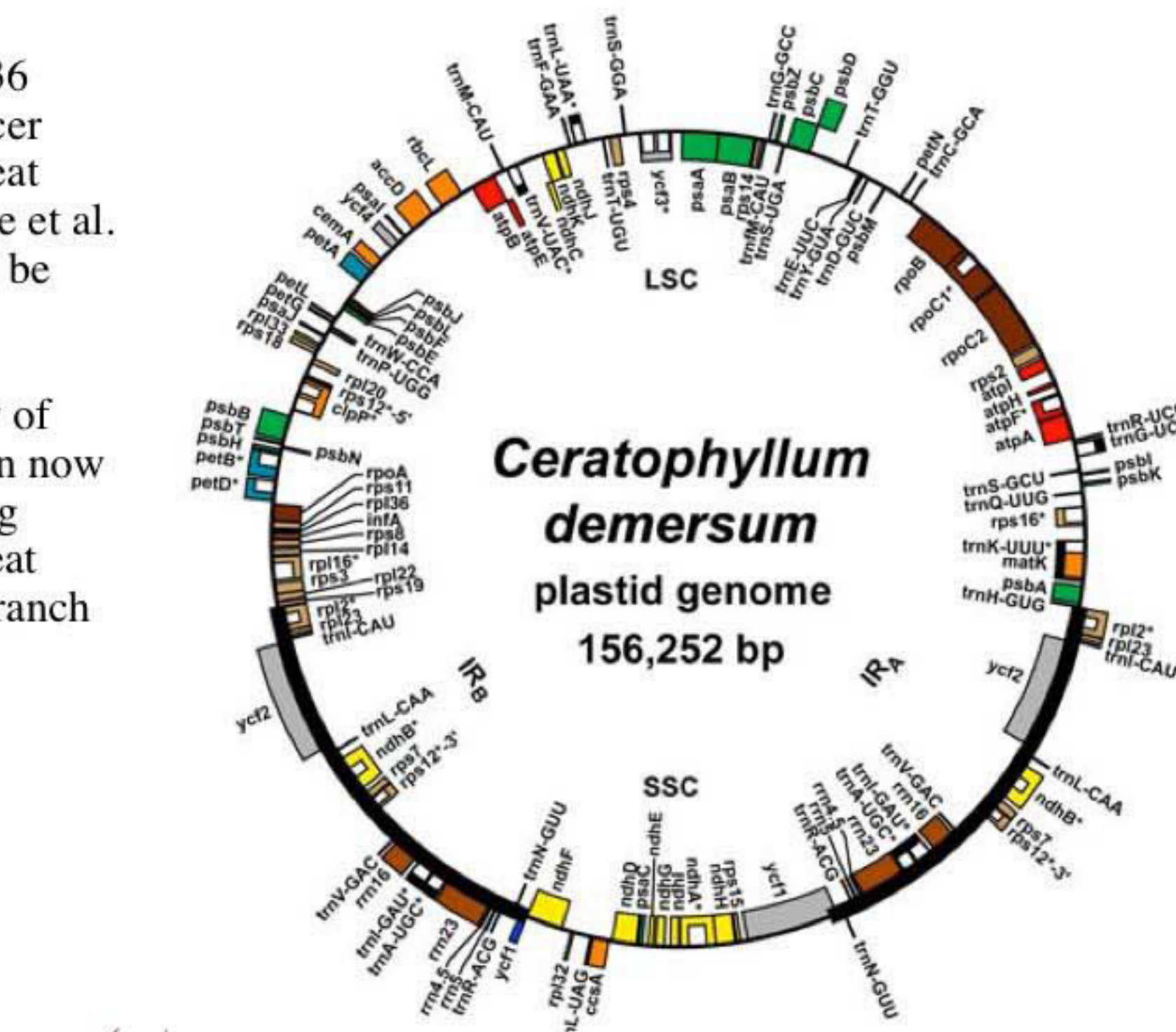
The Angiosperm AToL has employed the first of the "next generation sequencers," the 454 Life Sciences GS20/FLX platform, to sequence 36 flowering plant plastid genomes (Moore et al. 2007). The 454 sequencer produces highly accurate and complete plastid genome sequence at great savings of time and money over traditional shotgun sequencing (Moore et al. 2006). Recent advances in technology will allow up to 48 genomes to be sequenced simultaneously, at a cost of ~\$200/genome.

This revolution in plastid genomics has resulted in the current availability of over 100 complete plastid genome sequences for angiosperms. We can now address, with genome-scale data, the most difficult relationships among major groups of angiosperms. This new plastid genomics era holds great promise for resolving the remaining thorny nodes in the angiosperm branch of the Tree of Life.

Informatics: TOLKIN

TOLKIN is an information management and analytical web application for phylodiversity and biodiversity research. TOLKIN supports the Angiosperm AToL, as well as Gymnosperm and Liverwort AToLs, and the Euphorbia PBI. As a web-based application, collaborators in different locations can access shared data on voucher specimens, taxonomy, bibliography, morphology, DNA samples and sequences.

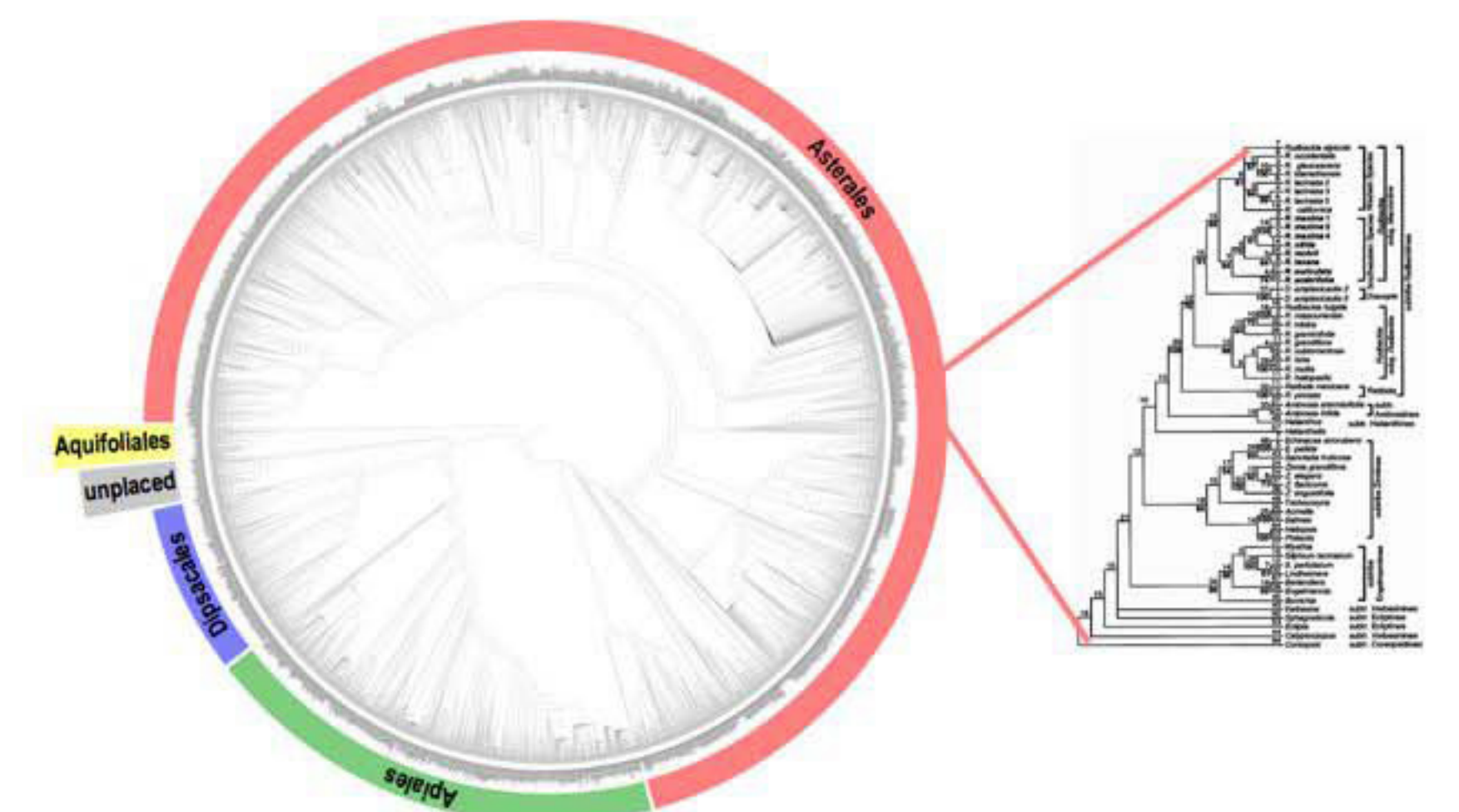
Users are able to see a summary of sequencing activities through a color-coded matrix. Automated links are generated to external data resources such as International Plant Names Index, Global Biodiversity Information Facility, Tropicos, GenBank, Index Nominum Genicorum, TreeBASE, and BioGeomancer. A developing analytical component of TOLKIN will provide workbench functionality for analysis of sequence data by automating the assemblage of Fasta files, BLASTing capability, multiple sequence alignments, and output of Nexus files, and automating deposit of digital data to repositories such as GenBank.



Supertree Construction

Few studies have compared supertree and supermatrix approaches for building comprehensive phylogenetic trees. The angiosperms provide an ideal system in which to explore such questions, and we are currently exploring supertree construction.

We created a Campanulid supertree of over 4,000 taxa using trees that were gathered and grafted together from more than 200 primary literature sources. To ensure a scientific standard, a set of construction rules was established *a priori*.



Angiosperm AToL Outreach

Training for postdocs, graduate, and undergraduate students (especially underrepresented groups).

Emphasis on interdisciplinary training, combining phylogenetic, genomic, and evolutionary biology.

PIs use information garnered in this study for their courses, and to update the widely used Judd *et al.* textbook, *Plant Systematics: A Phylogenetic Approach*

Public education through the new family-friendly exhibit, *Travels in the Great Tree of Life* (Peabody Museum of Natural History, Yale University), and through *First Flower*, part of the PBS television series NOVA (April 2007).

