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WHAT'S HOT IN... BIOLOGY, May/June 2010

New Molecules Delineate an Ancient Tree of Life

by *Jeremy Chertas*



It isn't often that the Hot Papers in Biology allow one to focus on science for the pure joy of discovery. Even the most esoteric investigations of detailed molecular biology usually tend to be highly cited because of some anticipated medical value. Not so the paper newly arrived at #7.

Casey Dunn, of Brown University in Rhode Island, and his colleagues use a broad array of DNA sequencing and computational tools to confirm a new view of the animal tree of life that contains quite a few surprises for anyone who learned their zoology more than about 10 years ago. Older biologists, for example, will be familiar with the group known as coelomates, animals with a fluid-filled body cavity within the tissue known as mesoderm. The molecular trees admit of no such thing.

Inferring the "true" structure of the tree of life—assessing which species are more closely related to one another and which more distant—has been part of the great project of biology ever since *The Origin of Species*. The idea, essentially, is to use similarities among living species and fossils to deduce their evolutionary history.

The problems are many. Taxonomists can use shared characteristics, such as an opposable thumb, to say that chimpanzees, gorillas, and humans all share an ancestor that itself had an opposable thumb. Evolution, however, can throw a spanner in the works, as it does in the case of the panda's thumb, made famous in an essay of the same name by Stephen J. Gould.

The panda's "thumb" is not, in fact a true digit like yours and mine. It is, instead, a modified wrist bone that would never have fooled any anatomist into treating the giant panda as a great ape and is, in any case, only a single character. The business of phylogeny, however, is full of similar little traps that make building an evolutionary tree on which all can agree extraordinarily difficult.

One breakthrough was the realization that taxonomists could use molecules as well as gross anatomy to examine phylogenies. This is not a new idea—it goes back at least to the pioneering studies of G.H.F. Nuttall in the early 1900s—and it received a considerable boost from the work of Vincent Sarich and Allan Wilson in the 1960s.

What is relatively new is the sheer deluge of molecular data that taxonomists have to work with. Since the advent of high-speed sequencing there has been a steady stream of papers re-examining time-honored anatomically based family trees, especially those where taxonomists could not agree, and generally trumping anatomy with molecules. Nevertheless, disagreements remained, particularly over some of the very early branches of the tree and how some large groups were related.

Dunn and his colleagues systematically gathered molecular data from 29 different animal species belonging to 21 phyla, including 11 phyla that had not previously been included in studies of this kind. The sequence data were derived from expressed sequence tags (ESTs) that are associated with genuine working genes, rather than random stretches of DNA, and so can be assumed to be reasonably important. Software then uses the similarities and differences among sequences to build phylogenetic trees, which confirm many of the more important ideas about relationships.



A member of the ctenophores.

For example, in 1997, using evidence from a ribosomal subunit, a new clade (a clade groups together all taxa derived from a single ancestor; it is one branch of the tree) called the Ecdysozoa was proposed, grouping all animals that moult. This grouping, which joins arthropods, tardigrades, nematodes, and others, was hotly contested, but the new analysis confirms it is almost certainly a correct reflection of evolutionary history. Although seemingly very diverse, all those animals do in fact share a common ancestor.

The analysis also confirms another clade that at first glance seems very odd. The Lophotrochozoa groups the annelid worms and molluscs with bryozoans (moss animals) and phoronids (horseshoe worms, one of the smallest and least well-known animal phyla). It also offers a clear sub-division of the Lophotrochozoa into three distinct clades.

In addition to confirming some older new hypotheses with stronger data, the broad analysis by Dunn and his colleagues comes up with a couple of new hypotheses that will repay further study. Perhaps the most interesting is the identification of ctenophores, also known as comb-jellies, as "the earliest diverging extant multicellular animals." This gives the lie to a very common belief, that more recently diverged animals are generally more complex. Ctenophores are indeed morphologically much more complex than, say, sponges and jellyfish (which the ctenophores used to be lumped with).

Dunn *et al.* are careful to say that their conclusion is provisional, but that if confirmed "it would have major implications for early animal evolution, indicating either that sponges have been greatly simplified or that the complex morphology of ctenophores has arisen independently from that of other metazoans." In other words, molecular data have much to say, but to really understand evolutionary history it would be nice to have some fossils too. ■

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Biology Top 10 Papers

Rank	Paper	Citations This Period (Nov-Dec 09)	Rank Last Period (Sep-Oct 09)
1	K. Takahashi, <i>et al.</i> , "Induction of pluripotent stem cells from adult human fibroblasts by defined factors," <i>Cell</i> , 131(5): 861-72, 30 November 2007. [Kyoto U., Japan; CREST, Kawaguchi, Japan; Gladstone Inst. Cardio. Dis., San Francisco, CA] *243MG	114	1
2	J.C. Barrett, <i>et al.</i> , "Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease," <i>Nature Genetics</i> , 40(8): 955-62, August 2008. [31 institutions worldwide] *331QF	49	6
3	D. Baek, <i>et al.</i> , "The impact of microRNAs on protein output," 455(7209): 64-71, <i>Nature</i> , 4 September 2008. [Whitehead Inst., Cambridge, MA; Howard Hughes Med. Inst., MIT, Cambridge; Harvard Med. Sch., Boston, MA] *343XS	42	10
4	E. Zeggini, <i>et al.</i> , "Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes," <i>Nature Genetics</i> , 40(5): 638-45, May 2008. [5 U.S. and U.K. institutions] *293WS	38	7
5	M. Selbach, <i>et al.</i> , "Widespread changes in protein synthesis induced by microRNAs," <i>Nature</i> , 455(7209): 58-63, 4 September 2008. [Max Delbruck Ctr. Molec. Med., Berlin, Germany; U. Glasgow, U.K.] *343XS	38	9
6	S.A. Mani, <i>et al.</i> , "The epithelial-mesenchymal transition generates cells with properties of stem cells," <i>Cell</i> , 133(4): 704-15, 16 May 2008. [8 U.S. and Swiss institutions] *301NQ	38	†
7	C.W. Dunn, <i>et al.</i> , "Broad phylogenomic sampling improves resolution of the animal tree of life," <i>Nature</i> , 452(7188): 745-9, 10 April 2008. [13 institutions worldwide] *285QY	37	†
8	D.R. Bentley, <i>et al.</i> , "Accurate whole genome sequencing using reversible terminator chemistry," <i>Nature</i> , 456(7218): 53-9, 6 November 2008. [7 European and U.S. institutions] *369DH	34	2
9	M. Nakagawa, <i>et al.</i> , "Generation of induced pluripotent stem cells without Myc from mouse and human fibroblasts," <i>Nature Biotech.</i> , 26(1): 101-6, January 2008. [Kyoto U., Japan; CREST, Kawaguchi, Japan; Gladstone Inst., San Francisco, CA] *249IW	33	5
10	M.W. Karaman, <i>et al.</i> , "A quantitative analysis of kinase inhibitor selectivity," <i>Nature Biotech.</i> , 26(1): 127-32, January 2008. [Ambit Biosciences, San Diego, CA; Tufts U., Boston, MA] *249IW	33	†

SOURCE: Thomson Reuters Hot Papers Database. Read the Legend.

KEYWORDS: Taxonomy, animal tree of life, clades, ctenophores, Lophotrochozoa, metazoans, evolutionary tree.

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