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Molecular Biologists Prune Branches from the Animal Family Tree

Earthworms are kin to lobsters and flatworms are cousins of roundworms. These kinds of relationships have been drawn over the years by zoologists who painstakingly constructed evolutionary trees using animal morphology, or comparisons of form and structure. Morphology was, until recently, the best information available for such classifications. But new molecular evidence gleaned directly from DNA, the master blueprint of life is pruning the old evolutionary tree.

"Basically, we're redrawing the tree," says Jennifer Grenier, a Howard Hughes Medical Institute (HHMI) associate at the University of Wisconsin-Madison.

Grenier and HHMI investigator Sean Carroll, also at Wisconsin, were part of an international research team that performed the latest tree trimming. Their work substantiates earlier genetic investigations suggesting that the vast majority of animals, from oysters to humans, belong to one of three primary evolutionary lines, rather than the multiple branches suggested by morphological studies. The researchers reported their findings in the June 24, 1999, issue of the journal *Nature*.

Grenier and Carroll had been exploring the genetic regulation of animal development when they realized that the genes they were studying could shed light on animal evolution. Members of the *Hox* gene family ensure that organs and other systems form properly and in the appropriate places in the developing animal. For example, a *Hox* gene called *Ubx* allows only one pair of wings to arise in a fruit fly instead of the two pairs found in a dragonfly. Mutations in *Hox* genes cause severe abnormalities.

Because *Hox* genes are ubiquitous and well conserved having changed very slowly throughout animal evolution they provide powerful clues about the evolutionary history of an organism. Closely related animals share a similar assortment of *Hox* genes, while more distant relations have fewer in common. By decoding the *Hox* gene sequences of ancient groups of animals, Grenier and Carroll hoped to infer not only who was related to whom, but also which developmental genes were present in the shared ancestor.

The project quickly became an international collaboration. "Three labs independently started wondering about these questions," says Grenier. She

and Carroll decoded the *Hox* genes of a priapulid, a little-known marine worm of enigmatic evolutionary heritage, which looks like a small, squishy feather duster. Researchers at the University of Paris studied the *Hox* genes of a brachiopod, an ancient marine animal that looks like a clam. Scientists at Cambridge University worked on a polychaete, a marine relative of earthworms and leeches.

By comparing the assortments of *Hox* genes found in these three species to those found in previously studied animals including mice, fruit flies, leeches, and sea urchins the collaborating researchers confirmed the division of the animal kingdom into three primary evolutionary lines.

On the new, gene-based tree, animals with backbones are on the same branch as starfish and their relatives—a longstanding classification based on similarities in development. But the new tree reorganizes almost all of the remaining groups of animals. Animals that molt, such as crustaceans, insects, roundworms, and priapulids, now sit together on a second branch. A third branch holds brachiopods, earthworms, polychaetes, mollusks, and flatworms, each of which either has a feathery feeding structure or a special larval stage.

So far, the gene-based tree includes only animals with bilateral symmetry, or mirror-image left and right sides. The data on jellyfish and sponges—organisms which are radially symmetric, like a tire—are incomplete and therefore difficult to interpret, Grenier says.

The new work not only supports the idea of a three-limbed animal tree, explains Carroll, "but it also addresses the question of how sophisticated life was some 600 million years ago." The findings indicate that ancestors of these groups had more *Hox* genes than previously believed. "This potential to control development implies that the common ancestor may well have been a fairly sophisticated animal," Carroll says.

The reconstruction of the evolutionary tree has far-reaching implications, the researchers observe. For example, investigators may need to reexamine their choices of model species for basic research. "Understanding animal relationships is at the foundation of the assumptions we make when we do experiments on any animal," says Carroll.

The new understanding should also prompt changes in the way students are taught, Grenier says. "We're hoping this will have an impact on undergraduate classes," she says, "if only to emphasize that understanding evolutionary relationships is a continuing process."