

# Study rearranges some branches on animal tree of life

March 5 2008

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A study led by Brown University biologist Casey Dunn uses new genomics tools to answer old questions about animal evolution. The study is the most comprehensive animal phylogenomic research project to date, involving 40 million base pairs of new DNA data taken from 29 animal species.

The study, which appears in *Nature*, settles some long-standing debates about the relationships between major groups of animals and offers up a few surprises.

The big shocker: Comb jellyfish – common and extremely fragile jellies with well-developed tissues – appear to have diverged from other animals even before the lowly sponge, which has no tissue to speak of. This finding calls into question the very root of the animal tree of life, which traditionally placed sponges at the base.

“This finding suggests either that comb jellies evolved their complexity independently from other animals, or that sponges have become greatly simplified through the course of evolution. If corroborated by other types of evidence, this would significantly change the way we think about the earliest multicellular animals,” said Dunn, assistant professor of ecology and evolutionary biology at Brown. “Coming up with these surprises, and trying to better understand the relationships between living things, made this project so fascinating.”

Charles Darwin introduced the idea of a “tree of life” in his seminal

book *Origin of Species*. A sketch of the tree was the book's only illustration. Nearly 150 years after its publication, many relationships between animal groups are still unclear. While enormous strides have been made in genomics, offering up a species' entire genome for comparison, there are millions of animal species on the planet. There simply isn't the time to sequence all these genomes.

To get a better grasp of the tree of life – without sequencing the entire genomes of scores of species – Dunn and his team collected data, called expressed sequence tags, from the active genes of 29 poorly understood animals that perch on far-flung branches of the tree of life, including comb jellies, centipedes and mollusks. The scientists analyzed this data in combination with existing genomic data from 48 other animals, such as humans and fruit flies, looking for the most common genes being activated, or expressed.

The aim of this new approach is to analyze a large number of genes from a large number of animals – an improvement over comparative genomics methods which allow for a limited analysis of genes or animals. The new process is not only more comprehensive, it is also more computationally intensive. Dunn's project demanded the power of more than 120 processors housed in computer clusters located in laboratories around the globe.

Dunn and his team:

- unambiguously confirmed certain animal relationships, including the existence of a group that includes invertebrates that shed their skin, such as arthropods and nematodes;
- convincingly resolved conflicting evidence surrounding other relationships, such as the close relationship of millipedes and centipedes to spiders rather than insects;
- established new animal relationships, such as the close ties between

nemertean, or ribbon worms, and brachiopods, or two-shelled invertebrates.

“What is exciting is that this new information changes our basic understanding about the natural world – information found in basic biology books and natural history posters,” Dunn said. “While the picture of the tree of life is far from complete after this study, it is clearer. And these new results show that these new genomic approaches will be able to resolve at least some problems that have been previously intractable.”

Source: Brown University

Citation: Study rearranges some branches on animal tree of life (2008, March 5) retrieved 20 April 2024 from <https://phys.org/news/2008-03-rearranges-animal-tree-life.html>

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