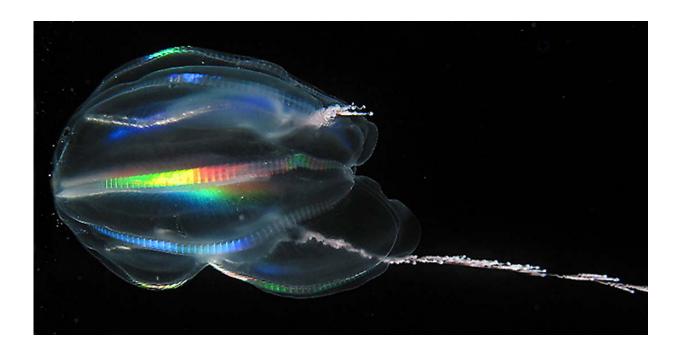


Forget sponges: The earliest animals were marine jellies

April 10 2017



Comb jellies, aka Ctenophores, similar to this may have been the earliest form of animal. Credit: Wikipedia Commons

When cartoonist and marine-biology teacher Steve Hillenburg created SpongeBob SquarePants in 1999, he may have backed the wrong side of one of the longest-running controversies in the field of evolutionary biology.

For the last decade, zoologists have been battling over the question,



"What was the oldest branch of the animal family tree?" Was it the sponges, as they had long thought, or was it a distinctly different set of creatures, the delicate marine predators called comb jellies? The answer to this question could have a major impact on scientists' thinking about how the nervous system, digestive tract and other basic organs in modern animals evolved.

Now, a team of evolutionary biologists from Vanderbilt University and the University of Wisconsin-Madison have devised a new approach designed specifically to settle contentious phylogenetic tree-of-life issues like this. The new approach comes down squarely on the side of comb jellies.

The method and its application to this and 17 other controversial phylogenetic relationships was published online on Apr. 10 by the journal *Nature Ecology & Evolution* in an article titled "Resolution of contentious relationships in phylogenomic studies can be driven by one or a handful of genes."

For nearly a century, scientists organized the animal family tree based in large part on their judgement of the relative complexity of various organisms. Because of their comparative simplicity, sponges were considered to be the earliest members of the animal lineage. This paradigm began to shift when the revolution in genomics began providing vast quantities of information about the DNA of an increasing number of species. Evolutionary biologists started to apply this wealth of information to refine and redefine evolutionary relationships, creating a new field called phylogenomics. In most cases, the DNA data helped clarify these relationships. In a number of instances, however, it gave rise to controversies that intensified as more and more data accumulated.

In 2008, one of the early phylogenomic studies fingered the comb jellies (aka ctenophores) as the earliest members of the animal kingdom, rather



than sponges. This triggered an ongoing controversy with the latest round being a <u>massive study</u> published last month that marshalled an unprecedented array of genetic data to support the sponges' position as the first animal offshoot.

"The current method that scientists use in phylogenomic studies is to collect large amounts of genetic data, analyze the data, build a set of relationships and then argue that their conclusions are correct because of various improvements they have made in their analysis," said Antonis Rokas, Cornelius Vanderbilt Professor of Biological Sciences, who devised the new approach with Vanderbilt postdoctoral scholar Xing-Xing Shen and Assistant Professor Chris Todd Hittinger from the University of Wisconsin-Madison. "This has worked extremely well in 95 percent of the cases, but it has led to apparently irreconcilable differences in the remaining 5 percent."

Rokas and his collaborators decided to focus on 18 of these controversial relationships (seven from animals, five from plants and six from fungi) in an attempt to figure out why the studies have produced such strongly contradictory results. To do so, they got down into the weeds, genetically speaking, and began comparing the individual genes of the leading contenders in each relationship.

"In these analyses, we only use genes that are shared across all organisms," Rokas said. "The trick is to examine the gene sequences from different organisms to figure out who they identify as their closest relatives. When you look at a particular gene in an organism, let's call it A, we ask if it is most closely related to its counterpart in organism B? Or to its counterpart in organism C? And by how much?"

These analyses typically involve hundreds to thousands of genes. The researchers determined how much support each gene provides to one hypothesis (comb-jellies first) over another (sponges first). They labeled



the resulting difference a "phylogenetic signal." The correct hypothesis is the one that the phylogenetic signals from the most genes consistently favor.

In this fashion, they determined that comb jellies have considerably more genes which support their "first to diverge" status in the animal lineage than do sponges.

Another contentious relationship the researchers addressed was whether crocodiles are more closely related to birds or turtles. They found that 74 percent of the shared genes favor the hypothesis that crocodiles and birds are sister lineages while turtles are close cousins.

In the course of their study, they also discovered that in a number of contentious cases one or two "strongly opinionated genes" among all the genes being analyzed appear to be causing the problem because the statistical methods that evolutionary biologists have been using are highly susceptible to their influence.

In some cases, such as the controversies over the origins of flowering plants and modern birds, they determined that the removal of even a single opinionated gene can flip the results of an analysis from one candidate to another. In cases like this, the researchers were forced to conclude that the available data is either inadequate to support a definitive conclusion or it indicates that the diversification occurred too rapidly to resolve.

"We believe that our approach can help resolve many of these longstanding controversies and raise the game of phylogenetic reconstruction to a new level," Rokas said.

More information: Contentious relationships in phylogenomic studies can be driven by a handful of genes, *Nature Ecology & Evolution* (2017).



nature.com/articles/doi:10.1038/s41559-017-0126

Provided by Vanderbilt University

Citation: Forget sponges: The earliest animals were marine jellies (2017, April 10) retrieved 24 April 2024 from <u>https://phys.org/news/2017-04-sponges-earliest-animals-marine-jellies.html</u>

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