

New research robustly resolves one of evolutionary biology's most heated disputes

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This research challenges earlier evidence that Ctenophore is the earliest branching animal lineage first and puts sponges in that position. Credit: Monterey Bay Aquarium

New research led by the University of Bristol has resolved evolutionary biology's most-heated debate, revealing it is the morphologically simple sponges, rather than the anatomically complex comb jellies, which represent the oldest lineage of living animals.

Recent genomic analyses have "flip-flopped" between whether sponges or [comb jellies](#) are our deepest ancestors, leading experts to suggest available data might not have the power to resolve this specific problem.

However, new research led by the University of Bristol has identified the cause of this "flip-flop" effect, and in doing so, has revealed sponges are the most ancient lineage.

Professor Davide Pisani of Bristol's Schools of Biological and Earth Sciences led the study, published today in *Current Biology*, with colleagues from the California Institute of Technology (Caltech - USA), Ludwig-Maximilians-Universität (LMU), Munich (Germany), and other institutes around the world, which analysed all key genomic datasets released between 2015 and 2017.

Commenting on the breakthrough research, Professor Pisani said: "The fact is, hypotheses about whether sponges or comb jellies came first suggest entirely different evolutionary histories for key animal organ systems like the nervous and the digestive systems. Therefore, knowing the correct branching order at the root of the animal tree is fundamental

to understanding our own evolution, and the origin of key features of the animal anatomy."

In the new study, Professor Pisani and colleagues used cutting edge statistical techniques (Posterior Predictive Analyses) to test whether the evolutionary models routinely used in phylogenetics can adequately describe the genomic datasets used to study early animal evolution. They found that, for the same dataset, models that can better describe the data favour sponges at the root of the animal tree, while models that drastically fail to describe the data favour the comb jellies.

Dr Feuda from Caltech continued: "Our results offer a simple explanation to the 'flip-flop effect' cogently discussed by Professor David Hillis in a recent interview in Nature."

Dr Dohrmann from LMU added: "Our results rationalise this effect and illustrate how you can draw robust conclusions from flip-flopping datasets."

Professor Gert Wörheide of LMU said: "Indeed, a flip-flopping dataset is a dataset that supports different evolutionary histories or phylogenetic trees, when analysed using different evolutionary models.

Discriminating between alternative hypotheses in the face of a flip-flopping [dataset](#) requires clarifying how good the models are that support alternative phylogenetic trees. Posterior Predictive Analyses allow us to do exactly that. We found that models which describe the data poorly invariably identify the comb jellies at the root of the tree. Models that better describe the data invariably find the [sponges](#) in that position."

Professor Pisani concluded: "Phylogenomics, the use of genomic data in phylogenetics, is a relatively new science. Evidence for comb jellies as the earliest branching animal lineage first emerged in 2008, a decade

ago, in the first, large-scale, phylogenomic analysis of the animal phyla. We have now better analytical tools and data and this study seriously challenges the accepted status quo."

More information: Improved Modeling of Compositional Heterogeneity Supports Sponges as Sister to All Other Animals. Roberto Feuda, Martin Dohrmann, Walker Pett, Herve Philippe, Omar Rota-Stabelli, Nicolas Lartillot, Gert Worheide, and Davide Pisani. *Current Biology*. [DOI: 10.1016/j.cub.2017.11.008](https://doi.org/10.1016/j.cub.2017.11.008)

Provided by University of Bristol

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