New study finds our ancient relatives were not so simple after all

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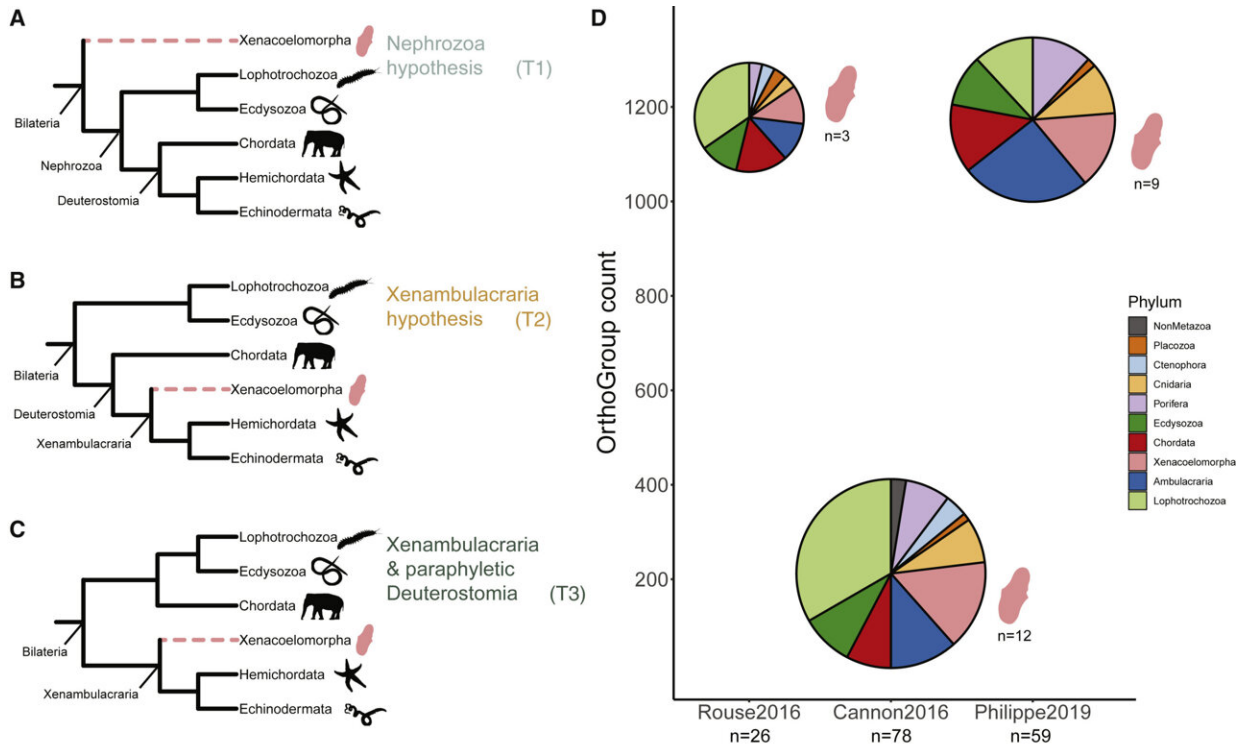

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Dataset	Orthology software	# transcriptomes/ genomes	Placement
Rouse 2016	Agalma[24]	12/14	Nephrozoa (T1)
Cannon 2016	HaMStR[25]	49/29	Nephrozoa (T1)
Philippe 2019	OMA[26]	4/55	Xenamb+paraDeut (T3)

Conflicting placements for Xenacoelomorpha and distribution of phylum sampling in three major datasets applied to resolve their position. (A) Nephrozoa hypothesis (T1) posits that Xenacoelomorpha are sister to the remaining bilaterian phyla. (B) Xenambulacraria hypothesis (T2) places Xenacoelomorpha

as sister to Ambulacraria, a clade consisting of Hemichordata and Echinodermata. (C) Xenambulacraria has also been suggested, along with non-monophyletic Deuterostomia, with Chordata placed sister to Protostomia. (D) Overview of previous phylogenomic studies addressing the placement of Xenacoelomorpha. Three studies are shown, with circle sizes based on the number of taxa sampled for the analysis. Each of the wedges in the circle are colored based on a given animal phylum (legend) and sized based on the number of species in that phylum that were used in the study. The y axis represents the number of orthogroups used in the phylogenomic analysis. (E) Summary table for the three datasets, Rouse et al., Cannon et al., and Philippe et al., included in this study, showing in each case the orthology detection software used, the proportion of the data from transcriptome or genome sequencing, and the placement resolved in the original publication. Note: Xenamb+paraDeut = Xenambulacraria and paraphyletic Deuterostomes. Credit: *Current Biology* (2022). DOI: 10.1016/j.cub.2022.10.036

Researchers at the University of Nottingham have solved an important piece of the animal evolution puzzle as their new study reveals that our ancient ancestors were more complex than originally thought.

Way back in our distant evolutionary history, animals underwent a major innovation. They evolved to have a left and right side, and two gut openings. This brought about a plethora of significant advantages in terms of propelling themselves directly forward at increased speed through the early seas, finding food, extracting nutrients, and/or avoiding being eaten.

It was such a successful strategy that, today, we share our planet with a huge diversity of other animals with bilateral symmetry and two gut openings just like us. They include animals as diverse as starfish, sea cucumbers, elephants, humans, crickets, and snails. They also include an enigmatic group of very simple marine worms called Xenacoelomorphs,

who lack many of the complex features of their fancier looking cousins.

For years, scientists have debated who is more closely related to who in this diverse collection of bilaterally symmetrical animals. Some experts argue that Xenacoelomorphs mark the first group to branch in that major jump in innovation from animals with circular body plans (e.g. jelly fish and corals) to bilateral symmetry. If this was the case, then the first bilaterian itself was also a very simple animal. Others argued for different placements of Xenacoelomorphs on the family tree.

However, a research team, led by Dr. Mary O'Connell at the University of Nottingham has found that Xenacoelomorphs branch much later in time, they are not the earliest branch on the bilaterian family tree, and their closest relatives are far more complex animals like star fish. This means that Xenacoelomorphs have lost many of the complex features of their closest relatives, challenging the idea that evolution leads to ever more complex and intricate forms. Instead, the new study shows that loss of features is an important factor in driving evolution.

"There are many fundamental questions about the evolution of animals that need to be answered... many parts of this family tree that are not known or not resolved. But what an exciting time to be an evolutionary biologist with the availability of exquisite genome data from the beautiful diversity of species we currently have on our planet, allowing us to unlock secrets of our most distant past," says Dr. Mary O'Connell, associate professor in life sciences.

The paper, titled "Filtering artifactual signal increases support for Xenacoelomorpha and Ambulacraria sister relationship in the animal tree of life" has been published in *Current Biology*. It details the application of a special phylogenetic technique to help in extracting signal from noise over deep time, showing increased support for Xenacoelomorphs being sister to ambulacraria (e.g. star fish) rather than

being the deepest diverging of the bilateria.

The research team at the University of Nottingham will now explore other challenging family trees and other connections between genome changes and phenotypic diversity.

More information: Peter O. Mulhair et al, Filtering artifactual signal increases support for Xenacoelomorpha and Ambulacraria sister relationship in the animal tree of life, *Current Biology* (2022). DOI: 10.1016/j.cub.2022.10.036

Provided by University of Nottingham