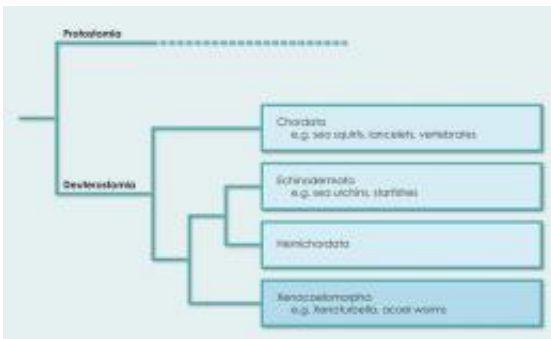


Xenacoelomorpha -- a new phylum in the animal kingdom

February 16 2011



Modified phylogeny: The Xenacoelomorpha represent the fourth phylum of the deuterostomia. Credit: Art for Science

An international team of scientists including Albert Poustka from the Max Planck Institute for Molecular Genetics in Berlin has discovered that Xenoturbellida and the acoelomorph worms, both simple marine worms, are more closely related to complex organisms like humans and sea urchins than was previously assumed. As a result they have made a major revision to the phylogenetic history of animals. Up to now, the acoelomate worms were viewed as the crucial link between simple animals like sponges and jellyfish and more complex organisms. It has now emerged that these animals did not always have as simple a structure as they do today.

The genus *Xenoturbella* lives off the coast of Scandinavia, Scotland and

Iceland. It shares a simple body structure with the acoelomorph [worms](#): these organisms, which reach a maximum size of just a few millimetres, have no through gut, no gill slits and no body cavity (Greek: *coelom* = cavity). Many members of both groups live on the [ocean floor](#) and feed on organic particles in the sediment. Some species live parasitic, e.g. in the intestines of sea cucumbers.



Worms of the genus *Xenoturbella* belong to another deuterostome branch.
Credit: University of Tsukuba, Japan/Hiroaki Nakano

The animal kingdom is divided into different evolutionary lines. These include, among others, the protostomes (“mouth first”) and deuterostomes (“second mouth”). In the protostomes, the mouth that develops at the beginning of embryonic development becomes the organism’s actual mouth, whereas, in the deuterostomes, it becomes the anus and the mouth develops at a later stage. Three deuterostome phyla were known up to now: the Chordates (e.g. vertebrates), the Echinoderms ([sea urchins](#), starfish, sea cucumbers) and the Hemichordates (e.g. acorn worm). “Our research shows that *Xenoturbellida* and *Acoelomorpha* together form the fourth phylum which we have called ‘*Xenacoelomorpha*’,” explains Albert Poustka from

the Planck Institute for [Molecular Genetics](#) in Berlin.

According to the scientists, Xenoturbellida and Acoelomorpha have a shared ancestor, from which the complex group of deuterostomes descend. “Therefore, contrary to what was previously assumed xenacoelomorph worms did not always have a simple structure but lost the characteristics typical for many deuterostomes over the course of evolution. The worms simplified their construction plan in reality because that was clearly as advantageous – or even more advantageous – than a complicated body structure,” says Poustka.



Hofstenia miamia also belongs to the deuterostomes. Credit: Uppsala University/Andreas Wallberg

With the help of extremely processor-intensive mathematical models, the scientists examined new “mini” genes (microRNAs) and amino acids from the fully sequenced mitochondrial genomes of Acoelomorpha and Xenoturbellida, and a large set of several hundred genes. The analysis of the *Xenoturbella* microRNAs and the acoelomate worm *Hofstenia miamia* showed that the previously analysed acoelomate worm *Symsagittifera roscoffensis* had lost many of these “mini” genes. The gene repertoire of the analyzed animals points instead to the kinship between these animals and the deuterostomes. For example, they have a

microRNA that was previously only known to exist in echinoderms and acorn worms. Moreover, all of the animals analysed up to now from the new Xenacoelomorpha phylum have the gene RSB66, which could previously only be demonstrated in deuterostomes.

The complex organisms of the protostomes and deuterostomes do not originate both from acoelomorph like worms as was previously assumed. Earlier studies were clearly subject to a systematic error that scientists refer to as the “long branch artefact”. This error often arises in the comparison of the genotypes of organisms that have long developed independently of each other. Even if the DNA sequences of some organisms mutated more quickly than the average, this effect can arise. “This was precisely the case with the acoelomorph worms,” says Poustka. As a next step the researchers are now decoding the entire genome of the different species of Xenacoelomorpha in order to reach a better understanding of the evolution of the deuterostomes.

More information: Hervé Philippe, et al. Acoelomorph flatworms are deuterostomes related to Xenoturbella published in online in *Nature*, February 10th 2011.

Provided by Max-Planck-Gesellschaft

Citation: Xenacoelomorpha -- a new phylum in the animal kingdom (2011, February 16) retrieved 15 July 2024 from <https://phys.org/news/2011-02-xenacoelomorpha-phylum-animal-kingdom.html>

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