

Sea anemone genome provides new view of our multi-celled ancestors

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view into the mouth of the starlet sea anemone, *Nematostella vectensis*. The anemone, only a few inches long and endowed with between 16 and 20 tentacles, lives in the mud of brackish estuaries and marshes. It is becoming a popular laboratory subject for studies of development, evolution, genomics, reproductive biology and ecology. (Nicholas Putnam/UC Berkeley photo)

The first analysis of the genome of the sea anemone shows it to be nearly as complex as the human genome, providing major insights into the common ancestor of not only humans and sea anemones, but of nearly all multi-celled animals.

"We are looking close to the base of the animal tree of life," said Daniel

Rokhsar, faculty member in the University of California, Berkeley's Center for Integrative Genomics and head of a team reporting the analysis in the July 6 issue of *Science*. "What was the common ancestor of all animals like" "What did it eat" "Did it have muscles" "a brain" Comparing genomes is a way of looking back in time to infer features of the ancestral genetic blueprint for animals."

According to Rokhsar, program head for computational genomics at the Department of Energy's Joint Genome Institute (JGI) in Walnut Creek, Calif., and UC Berkeley professor of genetics, the analysis of the genome allowed the team "to compare the sea anemone with other animals and see what the genome of their last common ancestor looked like, even though such creatures have been extinct for 600 or 700 million years."

The genome of the starlet sea anemone - *Nematostella vectensis*, a delicate, few-inch-long animal in the form of a transparent, multi-tentacled tube - was sequenced at JGI as part of its Community Sequencing Program. The raw sequence has been available to scientists on the Internet for the past year. The anemone burrows in the mud in brackish water along the east and west coasts of the United States and in the British Isles, and is becoming an increasingly important model system for the study of development, evolution, genomics, reproductive biology and ecology, thanks in large part to the urging of late marine biologist and UC Berkeley zoology professor Cadet Hand Jr.

All animals comprised of more than one cell are lumped together as "metazoan." But scientists usually distinguish between the sponges - strange animals unlike any other - and all the rest, which are dubbed eumetazoans (literally "true animals") and are characterized by defined tissues and distinct embryonic layers.

"Anything the sea anemone has that also is found in humans, flies, snails

or any other eumetazoans must already have been present in the common ancestor of eumetazoans," Rokhsar said.

Simply by comparing living animals, scientists have inferred that the early eumetazoans had many of the features we associate with animals today: a nervous system, muscles, senses, a gut and even sperm with little tails. By comparing genomes, it is now possible to infer which genes were present in this ancient progenitor and how their chromosomes were structured, Rokhsar said.

Surprisingly, the team found that the genome of the starlet sea anemone, which is lumped with jellyfish and corals into the earliest diverging eumetazoan phylum, Cnidaria, resembles the human and other vertebrate genomes more than it resembles the genomes of such well-studied "lab rats" as fruit flies and nematode worms. According to Nicholas Putnam, postdoctoral fellow at the JGI and lead author of the study, this is because both the anemone and vertebrate genomes have retained many ancestral genes that flies and nematode worms apparently lost over time. The genes of flies and worms also have been jumbled up among the chromosomes, making it hard to track genes through evolution.

The anemone genome, on the other hand, has apparently changed less through time and makes a good reference for comparison with human and other vertebrate genomes in order to discover the genes of our common ancestor and how they were organized on chromosomes.

The sea anemone, for example, has about 18,000 genes, while humans have about 20,000. According to the researchers, this implies that the common ancestor had about the same number of genes, between 18,000 and 20,000. Many of the anemone's genes lie on its 30 chromosomes in patterns similar to the patterns of related genes on the 46 chromosomes of humans.

"Many genes close together in the sea anemone are still close together in humans, even after six or seven hundred million years," said Putnam.

"We think we can identify where roughly half of the genes were located on the ancestor's chromosomes."

This similarity is present in the sea anemone and human genomes, despite the obvious differences between the two species.

"Complexity in the genome is not connected in any simple way to complexity of the organism," Putnam noted. Much of an organism's complexity can be ascribed to regulation of existing genes rather than to novel genes, he said, and the genome analysis will allow further study of such regulation.

The ancestral eumetazoan already had the genetic "toolkit" to conduct basic animal biochemistry, development and nerve and muscular function, according to the team's analysis. These functions were conferred by combining ancient genes that are found outside animals with about 1,500 new genes not seen before in earlier forms of life.

"We can trace the evolutionary history of roughly 80 percent of eumetazoan genes even further back in time to before the origin of animals, since related genes are found in fungi, plants, slime molds and other non-animals," said Rokhsar. "Only 20 percent of the ancestral eumetazoan genes seem to be unique to animals. Fifteen percent of these seem to be completely novel - we can't identify any related gene in non-animals. The other five percent were formed through substantial modifications to very ancient genes."

The novel genes of the eumetazoa are involved, to a large degree, with conversation among cells. "In the early animals, cells figured out how to talk to each other and coordinate their activities," Putnam said.

"The genes common to all complex cells are involved with critical signaling pathways inside the cell, while the new animal-specific genes seem to confer new modes of interaction between cells," Rokhsar said, noting that new genes appear in eumetazoa that let cells stick to one another, signal one another and transmit nerve impulses at a new structure called the synapse.

This makes sense, he added, because eumetazoans are characterized by tissues and organs in which cells must cluster and communicate, whereas single cells generally need to interact only with the outside environment and only loosely with their fellow cells.

"Basically, the sea anemone has all the basic mechanisms of interacting with the outside world seen in more morphologically complex creatures," Putnam said.

Rokhsar looks forward to comparing the sea anemone genome with the genomes of other animals and their relatives - sponges, placozoans and choanoflagellates - to learn more about the earliest eumetazoans and other early animals.

"Our goal is to learn how genes and genomes evolved throughout of the history of animals," he said. "This will help us to better understand not only animal origins, but also how biodiversity is created and shaped by genomic change."

Source: University of California - Berkeley

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