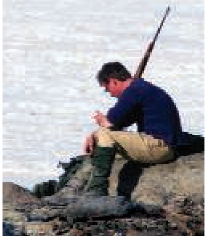

GENOMICS

Sea Anemone Provides a New View of Animal Evolution

Genome sequencers have just jumped down to a lower branch on the tree of life, and the view has given them a new perspective on animal evolution. The newly decoded DNA of a few-centimeter-tall sea anemone looks surprisingly similar to our own, a team led by Nicholas Putnam and Daniel Rokhsar from the U.S. Department of Energy Joint Genome Institute in Walnut Creek, California, reports on page 86. This implies that even very ancient genomes were quite complex and contained most of the genes necessary to build today's most sophisticated multicellular creatures.

"The work is truly stunning for its deep evolutionary implications," says Billie Swalla, an evolutionary developmental biologist at the University of Washington, Seattle. Until now, researchers have relied heavily on the sequenced genomes of the fruit fly, nematode, and that of a few other invertebrates to understand genome evolution leading up to the vertebrates. But the new work drives home how streamlined these invertebrate genomes have become. In contrast, the sea anemone's genome "has not changed much and retains many of the features present in our last common ancestor," says Jacek Majewski, a geneticist at McGill University in Montreal, Canada. It "seems to fill the niche essential to answer many evolutionary questions."

Animals divide into two groups, sponges and eumetazoans. The eumetazoans consist of comb jellies, cnidarians such as anemones, and bilaterians, which include everything else: limpets, lions, lobsters, and us. Comb jellies and cnidarians branched off before bilaterians diversified into the variety of animal groups known today, and they are considered relatively "simple" organisms. Cnidarians, for example, have a mouth but no anus; two tissue layers, not three; a nerve net, but no central nervous system per se.

Biologists have had plenty of bilaterian genomes to work with. But to look back in time, they needed a nonbilaterian genome for comparison—genes and genome features common to both bilaterians and nonbilaterians likely existed in their common ancestor 750 million years ago. In late 2004, Putnam, Rokhsar, and their colleagues began deciphering the 450-million-base genome of the cnidarian of choice, the starlet sea anemone, *Nematostella vectensis*.

The draft genome is already producing many surprises. Among the anemone's 18,000 or so protein-coding genes, the researchers have identified 7766 that are also present in bilaterians. Those shared genes represent the knowable part of the ancestral gene set. Three-quarters of the genes turn up in all three major animal groups examined, humans among them, but 1292 have been lost in the fruit fly and the nematode.

More than one way to do it. In addition to shedding light on evolution, the newly sequenced genome will help clarify how this sea anemone reproduces sexually, releasing eggs (*right*), and asexually, developing a second head, then cleaving across the middle of the body (*left*).

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One of the big surprises of the anemone genome, says Swalla, is the discovery of blocks of DNA that have the same complement of genes as in the human genome. Individual genes may have swapped places, but often they have remained linked together despite hundreds of millions of years of evolution along separate paths, Putnam, Rokhsar, and their colleagues report. Researchers see little conservation of gene linkages in nematodes and fruit flies.

Moreover, the anemone genes look vertebratelike. They often are full of noncoding regions called introns, which are much less common in nematodes and fruit flies than in vertebrates. And more than 80% of the anemone introns are in the same places in humans, suggesting that they probably existed in the common ancestor. "The work presents a missing piece of the puzzle, which people studying intron evolution have been searching for in the past few years," says Majewski. "They present a strong validation for an intron-rich ancestor," he says.

When they compared the anemone genome with those of fungi, plants, and protists, which include slime molds and ciliates, the researchers determined that 1500—20%—of the ancestral genes originated after animals diverged from plants and fungi. Some genes appear to be completely new. Others, including ones for cell-adhesion proteins and signaling molecules, are combinations of new sequences and much more ancient DNA or combinations of parts of ancient genes. These novel genes set the stage for the evolution of highly organized tissues, notably nerves and muscles, subsequently seen in bilaterians, says co-author John Finnerty of Boston University.

Finnerty and his graduate student James Sullivan also looked in the anemone genome for 283 human genes involved in a wide range of diseases. They will report in the July issue of *Genome* that they found 226. Moreover, in a few cases, such as the breast cancer gene *BRCA2*, the anemone's version is more similar to the human's than to the fruit fly's or to the nematode's.

All these results go to show, says Finnerty, that "*Nematostella*'s genome may provide more insights into the functional evolution of human genes than many far more closely related animals."

–ELIZABETH PENNISI

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