

What's Shaped Like a Pear and Has Two Genomes? Check The Pond

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If you could peer microscopically into the closest freshwater pond, you'd hesitate before dipping a toe. Amid the murky water, you'd probably notice an oddly furry, pear-shaped organism gliding along—and gobbling up everything in its path. This tiny predator has a big name--*Tetrahymena thermophila*--and a big fan club among scientists, as a star organism for research into how cells work.

Scientists have now sequenced, assembled, and analyzed *T. thermophila*'s macronuclear genome. Their work, reported in today's issue of Public Library of Science (PLoS) Biology, explains the organism's impressive versatility. Rather than dividing labor into several types of cells, as humans and other multicellular organisms do, *T. thermophila* divides its activities, either into different places inside a cell or by changing the cell over time. It is a master multi-tasker.

“This organism is a true generalist,” says evolutionary biologist Jonathan A. Eisen, who led the *Tetrahymena* project while at The Institute for Genomic Research (TIGR) and is now at the University of California, Davis. “Whatever this unicell touches with its hairlike projections, it will try to eat. If it does not bump into anything, the organism will seek out food with diverse sensory systems. It can protect itself from radiation and other threats and also can fight back against competitors and predators. In short, versatility is its strength. Now, we can understand how this versatility works.”

It takes plenty of genes. In fact, *T. thermophila* has roughly 25,000

genes—nearly as many as humans do. Although the organism is single-celled, it contains a genetic repertoire of seemingly more complex organisms. It shares, with humans and other animals, many genes and processes typically absent in single-celled organisms. That means *Tetrahymena* may be an ideal model organism for studies of the processes these genes encode.

In the new study, genome analysis showed that one way that *Tetrahymena* adapts to diverse environments via gene duplication, a process that allows organisms to diversify pre-existing genes and adapt them for new functions. In the case of *Tetrahymena*, duplications appear to be concentrated in genes involved in sensing and responding to environment. From a small number of proteases (enzymes that degrade proteins), for instance, *Tetrahymena* has built an eating machine that allows it to digest nearly any protein it encounters.

Among its most quirky features, *Tetrahymena* has, inside each of its cells, two distinct nuclei, each with a different genome. Inside one nucleus, the “micronuclear” genome is reserved for sex and reproduction, remaining genetically silent during growth. Inside the second, working nucleus is the “macronuclear” genome, which expresses genes that govern behavior. The current study sequenced the macronuclear genome, an impressively packaged bunch of coding genes, free of so-called junk DNA (noncoding sequences and other extraneous genetic elements) that litter the genomes of many organisms.

"Publication of the *Tetrahymena* genome marks the culmination of a remarkable collaboration within the research community," said Anthony Carter, Ph.D., of the National Institute of General Medical Sciences (NIGMS), which co-funded the project with the National Science Foundation (NSF). "*Tetrahymena* has a long and eminent history in the world of cell biology, and publication of its genome is likely to lead to further fundamental insights into how cells work."

Throughout the project, Eisen says, collaboration between researchers has been critical, including work by co-author Eduardo Orias of the University of California-Santa Barbara. The team emphasized open access to data, providing the genome sequence data to outside researchers, without restriction, since the project began in 2003. As a result, Tetrahymena researchers have already published dozens of studies making use of the genomic data.

In addition to releasing the sequence data early on TIGR's website (www.tigr.org/tdb/e2k1/ttg/index.shtml) and via Genbank, the project also underwrote the creation of a major free community resource: The Tetrahymena Genome Database (TGD; ciliate.org/), headed by Mike Cherry at Stanford University. The publication in the open access journal PLoS Biology represents a commitment to free and open access to scientific literature as well. Now anyone, anywhere in the world, can read about the genome of this fascinating organism before taking a dip in the local pond.

Source: The Institute for Genomic Research

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