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Genome of Water Flea Discovered to Contain Largest Number of Genes Recorded; UCSB Scientists Contributed to International Team Effort

The water flea –– Daphnia pulex –– has the largest inventory of genes ever recorded for a sequenced animal, according to a new study in the journal Science by 69 co-authors. An international team effort to sequence the genome of the water flea included work by UC Santa Barbara biologists.

Daphnia is the first crustacean to have its genome sequenced. The study found that it contains more than 31,000 genes. By comparison, humans have only about 23,000 genes.

"We were surprised to find the incredibly high level of complexity of the set of Daphnia vision genes," said co-author Todd Oakley, associate professor in UCSB's Department of Ecology, Evolution and Marine Biology.

Oakley is one of hundreds of scientists involved in the research project known as Daphnia Genomics Consortium. Oakley's team included nine UCSB scientists. They focused on vision genes in the tiny creature.

"While humans have four light-sensing proteins (opsins), the Daphnia genome has 46 opsins," said Oakley. "A possible explanation for this complexity is that Daphnia use these genes to understand the complex light regime of their aquatic environment."

In addition to studying the evolutionary history of vision genes, Oakley's team conducted statistical analyses to quantify the rate of gene duplications in Daphnia.

"Daphnia's high gene number is largely because its genes are multiplying, by creating copies at a higher rate than other species," said John Colbourne, project leader and director of the Center for Genomics and Bioinformatics at Indiana University Bloomington. "We estimate a rate that is three times greater than those of other invertebrates and 30 percent greater than that of humans."

Don Gilbert, co-author and scientist at IU Bloomington, added: "More than one-third of Daphnia's genes are undocumented in any other organism."

In other words, these genes are completely new to science.

In light of the findings in the paper, Daphnia has emerged as a model organism for the new field of Environmental Genomics, which aims to better understand how the environment and genes interact. This includes building research tools for investigating the molecular underpinnings of key ecological and evolutionary problems.

The support of a large research community is required for an organism to reach model status. Over the course of the project, the Daphnia Genomics Consortium has grown from a handful of founding members to over 450 investigators around the globe. Nearly 200 of these scientists have published work resulting from the genome study.

Onur Sakarya, former UCSB graduate student, and Kerry Samerotte, former UCSB research assistant, were part of Oakley's team at the time of the study and are co-authors of the paper.

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† Bottom photo: Pictured is the head of Daphnia pulex (commonly called water flea).

As part of a consortium to sequence and study the water flea's complete genome, UCSB scientists investigated the evolution of genes involved in vision and eye development.

The compound eye is the large black structure in the photo.

Credit: Christian Laforsch

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