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Massive Daphnia Genome Leads to Understanding Gene-Environment Interactions

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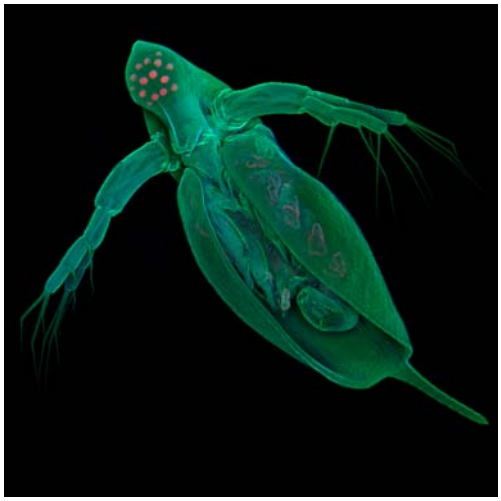

Daphnia pulex (commonly called waterflea)
Credit: Dr. Jan Michels (Christian-Albrechts-Universität zu Kiel), michels@zoologie.uni-kiel.de

DURHAM, N.H. – From an environmental perspective, *Daphnia pulex* -- the waterflea – is the best-studied organism on the planet. Scientists know how this species responds to pollution, predators, day and night, making it an important model for ecological and evolutionary research. Its genome, however, remained elusive, limiting understanding of how the environment and genes interact.

Until now. An international team of researchers comprising the *Daphnia* Genomics Consortium, including four from the University of New Hampshire's Hubbard Center for Genome Studies, has described the complete genome of *Daphnia*, opening the door to enhanced knowledge of this species and its response to its environment. And, despite the *Daphnia's* near-microscopic size, it contains more than 31,000 genes, more than any other animal with a complete gene sequence, including humans. The findings are detailed in an article in the journal Science this week.

"It's personally a major achievement," says W. Kelley Thomas, Hubbard Professor in Genomics and director of the HCGS, adding that the *Daphnia* sequence was among the center's original goals at its founding in 2001. "This genome gives biologists and ecologists the tools they need to do genomic analysis on this organism from an ecological perspective."

The end product is a better understanding of what genes matter for organisms to cope with environmental stresses like pollutants and global warming and of the technologies necessary to understand how these genes function within an animal that is easily studied in water reservoirs around the globe.

The study, "The Ecoresponsive Genome of *Daphnia pulex*," was led by researchers at Indiana University's Center for Genomics and Bioinformatics (CGB), Utah State University, the U.S. Department of Energy's Joint Genome Institute, and UNH's Hubbard Center. It found that the microscopic freshwater crustacean contains at least 30,907 genes, compared to approximately 25,000 in humans.

Scientists have studied *Daphnia* for centuries because of its importance in aquatic food webs and for its transformational responses to environmental stress. Predators signal some of the animals to produce exaggerated spines, neck-teeth or helmets in self-defense. And like the virgin nymph of Greek mythology that shares its name, *Daphnia* thrives in the absence of males -- by clonal reproduction, until harsh environmental conditions favor the benefits of sex.

Arguably, more is known about the ecology and stress biology of the water flea than any other animal. The genome project was conceived with an expectation that many new gene functions would be uncovered when studied in light of the animal's natural environment -- not necessarily expecting to discover many more genes.

Yet, *Daphnia*'s genome is no ordinary genome.

"*Daphnia*'s high gene number is largely because its genes are multiplying, by creating copies at a higher

rate than other species," said project leader and CGB genomics director John Colbourne. "We estimate a rate that is three times greater than those of other invertebrates and 30 percent greater than that of human."

"One theory is that Daphnia is so good at adapting to so many environments because it has this huge catalog of genes to call upon," says Thomas. The researchers note that more than one-third of *Daphnia's* genes are undocumented in any other organism – they are completely new to science.

At UNH, where the relatively new field of environmental genomics is at the core of the HCGS mission, the *Daphnia* project resulted in productive collaborations around the university. "It was a significant part of starting many science careers," says Thomas, noting that many undergraduate, graduate and visiting students participated.

Jim Haney, professor of freshwater biology, helped with cultures of *Daphnia*, which are common in New Hampshire lakes and ponds. In addition, as the science of genome sequencing evolved in the past decade to use "fewer pipettes and more computers," says Thomas, the Hubbard Center forged strong bonds with UNH's computer science department, in particular professors Dan Bergeron and Phil Hatcher.

International collaboration has been essential to this project. Over the course of the project, the *Daphnia* Genomics Consortium has grown from a handful of founding members to over 450 investigators distributed around the globe. Nearly 200 scientists have contributed published work resulting from the genome study, many in open-source journals published as a thematic series by BioMedCentral. A list of these publications can be found at http://www.biomedcentral.com/series/Daphnia. *Daphnia* Genomics Consortium projects are featured at http://daphnia.cgb.indiana.edu. More information on this article is available at http://newsinfo.iu.edu/news/page/normal/17183.html.

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The University of New Hampshire, founded in 1866, is a world-class public research university with the feel of a New England liberal arts college. A land, sea, and space-grant university, UNH is the state's flagship public institution, enrolling 12,200 undergraduate and 2,300 graduate students.

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Photographs available to download:

http://www.unh.edu/news/cj_nr/2011/feb/Daphnia_Hebert.jpg
Daphnia minnehaha (commonly called waterflea) with mild defensive neckteeth against predators
Credit: Dr. Paul D.N. Hebert (University of Guelph), phebert@uoguelph.ca

http://www.unh.edu/news/cj_nr/2011/feb/Daphnia_Laforsch.jpg
Defensive neckteeth in juvenile *Daphnia pulex* (commonly called waterflea) in response to phantom midge predators
Credit: Dr. Christian Laforsch (Ludwig-Maximilians-Universität München), laforsch@zi.biologie.uni-muenchen.de

http://www.unh.edu/news/cj_nr/2011/feb/Daphnia_Michels.jpg
Daphnia pulex (commonly called waterflea)
Credit: Dr. Jan Michels (Christian-Albrechts-Universität zu Kiel), michels@zoologie.uni-kiel.de

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