The *Daphnia* Genomics Consortium Meeting: The Genome Biology of the Model Crustacean *Daphnia*

July 7–9, 2007, Indiana University, Bloomington, IN, USA

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Expert Rev. Proteomics 4(5), 601–602 (2007)

The fourth *Daphnia* Genomics Consortium Meeting was held from July 7th through July 9th, 2007 at Indiana University (Bloomington, IN, USA). This year's meeting was entitled *The Genome Biology of the Model Crustacean* Daphnia and was highlighted by the initial public release of the draft version of the *Daphnia pulex* genome. In collaboration with the US Department of Energy Joint Genome Institute (JGI; CA, USA), the *Daphnia* Genomics Consortium (DGC) successfully sequenced the *D. pulex* genome, representing the first crustacean genome to be analyzed.

Daphnia are freshwater crustaceans found in most lakes and ponds throughout the globe, and have been ecologically investigated since the 1600s. They are arguably one of the best understood organisms. *Daphnia* are internationally recognized as an indicator of environmental health and, consequently, as a bioassay of aquatic toxicity, to define regulatory limits and to monitor effluents released into fresh water. *Daphnia* are primary grazers of algae and primary forage for fish; as such, they are considered keystone species in aquatic ecosystems.

The DGC is an international network of investigators committed to establishing *Daphnia* as a premiere model system, surpassing traditional model systems in investigations of environmental interactions, by incorporating *Daphnia*'s well-established ecological knowledge base. In a community-wide effort, the DGC is:

- Coordinating efforts towards developing the *Daphnia* genomic toolbox, which will then be available for use by the general community;
- Facilitating collaborative cross-disciplinary investigations;
- Developing bioinformatic strategies for organizing the rapidly growing genome database;
- Exploring emerging technologies to improve high-throughput analyses of molecular and ecological samples.

As an example of *Daphnia*'s utility across a variety of disciplines, this year's DGC meeting featured presentations covering topics in *Genome Structure and Evolution*; *Ecological Genomics*; *Predicting Gene Function using Comparative Phylogenetics*; *Gene Diversity and Function in Biological Processes*; and *Toxicological Genomics*.

The first day of the meeting was highlighted by a keynote address by Igor Grigoriev of the JGI, providing an overview of the quality of the genome sequence, assembly and computed annotation. Over 1.8 billion bases were sequenced and assembled, with half of the approximately 200 million base-pair genome represented in 103 scaffolds. Additionally, over 150,000 expressed sequence tags (ESTs) were characterized as part of this project, while functional genomic experiments that give condition-dependent expression information on a gene set comprising 50% unknowns are in full swing. Keynotes were also delivered by Don Gilbert of Indiana University, providing an overview of the genome annotation project; Hugh Robertson of the University of Illinois at Urbana-Campaign (IL, USA), discussing an expansion of the *opsin* genes in *Daphnia*; and by Francis Poulin of the University of California at Berkeley (CA, USA), discussing the evolution of developmental pathways in crustaceans and insects, specifically the *Daphnia Wnt* genes. A common revelation from a variety of researchers is that the number of genes (25,000–35,000) in *Daphnia* may be much greater than previously believed for a genome size comparable to that of flies (200 million bases) and that several gene families, revealing of the animal's unique biology and ecological settings, are expanded in *Daphnia* compared with other invertebrate genomes.

With the completion of the genome sequence, the next challenge for *Daphnia* researchers is to better connect genes to function. As such, this year's DGC meeting featured some of the first presentations on the *Daphnia* transcriptome, using genome tiling path microarrays designed and produced by NimbleGen Systems (WI, USA), and on the *Daphnia* proteome. Ralph Pirow of the University of Münster (Germany), presented the response of the *D. pulex* proteome to changes in oxygen concentration and temperature. Using 2D gel electrophoreses, he observed noticeable changes in protein shifts between *Daphnia* acclimated to different temperatures, as well as differential expression of hemoglobin subunits between *Daphnia* acclimated to varying oxygen concentrations.

A presentation by Gary Smejkal of Pressure BioSciences, Inc., (MA USA) kicked-off the poster session. Smejkal's presentation highlighted advances in sample preparation for genomics and proteomics using pressure cycling technology (PCT). Smejkal also presented a poster demonstrating the ability of pressure cycling technology to extract

  ISSN 1478-9450

proteins from a single *Daphnia*. Following PCT, 2D gel electrophoresis was able to resolve differences from single *D. magna* exhibiting the asexual and sexual phenotypes. In addition, approximately 1000 spots can be resolved from a single *D. pulex*.

This year's DGC meeting was highly successful and the public release of the *Daphnia* genome represented the accomplishment of a major goal of the DGC in its endeavor to establish *Daphnia* as a premiere model system.

Financial & competing interests disclosure

The author has no relevant affiliations or financial involvement with any organization or entity with a financial interest in or financial conflict with the subject matter or materials discussed in the manuscript. This includes employment, consultancies, honoraria, stock ownership or options, expert testimony, grants or patents received or pending, or royalties.

No writing assistance was utilized in the production of this manuscript.

Information resources

- *Daphnia* Genomics Consortium http://daphnia.cgb.indiana.edu
- Pressure BioSciences, Inc.: pressure cycling technology www.pressurebiosciences.com

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