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Meeting report

Genomics in the ecological arena

Luisa Orsini^{1,*}, Ellen Decaestecker^{1,2},
Luc De Meester¹, Michael E. Pfrender³
and John K. Colbourne⁴¹Laboratory of Aquatic Ecology and Evolutionary Biology, K.U. Leuven, Ch. Deberiotstraat 32, 3000 Leuven, Belgium²Aquatic Biology, Science and Technology, IRF-Life Sciences, K.U. Leuven-Campus Kortrijk, E. Sabbelaan 53, 8500 Kortrijk, Belgium³Department of Biological Sciences, University of Notre Dame, Notre Dame, IN 46556, USA⁴The Center for Genomics and Bioinformatics, Indiana University, 914 East Third Street, Bloomington, IN 47405, USA

*Author for correspondence (luisa.orsini@bio.kuleuven.be).

This meeting report presents the cutting-edge research that is developing around the waterflea *Daphnia*, an emerging model system in environmental genomics. *Daphnia* has been a model species in ecology, toxicology and evolution for many years and is supported by a large community of ecologists, evolutionary biologists and ecotoxicologists. Thanks to new advances in genomics and transcriptomics and to the sustained efforts of the *Daphnia* Genomics Consortium (DGC), *Daphnia* is also rapidly developing as a model system in environmental genomics. Advances in this emerging field were presented at the DGC 2010, held for the first time in a European University. During the meeting, a plethora of elegant studies were presented on the mechanisms of responses to environmental challenges using recently developed genomic tools. The DGC 2010 is a concrete example of the new trends in ecology and evolution. The times are mature for the application of innovative genomic and transcriptomic tools for studies of environmental genomics in non-model organisms.

Keywords: *Daphnia magna*; environmental genomics; transcriptomics

The 2010 *Daphnia* Genomics Consortium (DGC) meeting, the first held in Europe, in the city of Leuven (Belgium), was a pivotal point in the development of an emerging and powerful model system for environmental and ecological genomics. The waterflea *Daphnia* has been a key model organism in ecology, ecotoxicology and evolutionary biology for more than a century. Key assets of *Daphnia* are its ease of manipulation and culture, the possibility to work with clonal lineages and its sensitivity to environmental contaminants. Quantifying phenotypic trait variation and its link to fitness is relatively straightforward [1]. In addition, dormant egg banks in layered sediments allow historical reconstruction of evolutionary responses [2] and palaeogenetics. The extensive knowledge of the responses of *Daphnia* to environmental challenges

represents an important asset for the fast development of this organism as a model in environmental genomics and transcriptomics [3].

The meeting yielded a powerful picture of the development of genomics resources and their application in the model *Daphnia* to unravel the mechanisms of responses to environmental challenges. The meeting provided a unique overview of the progress achieved with the *Daphnia* genome sequence and key innovations that are emerging from this research. Key features of the *Daphnia* genome are the high number of genes (greater than 30 000) and the large fraction of genes lacking homology to other arthropod genomes. The number of genes without ontology is probably the result of *Daphnia*'s distant phylogenetic relationship to other arthropods with complete genome sequences, as well as its unique ecological context as the first fully aquatic arthropod sequenced. The recent assembly of the full transcriptome NimbleGen micro-array for *Daphnia pulex* will strongly boost gene function analysis. During the DGC meeting, a draft genome sequence of a second species, *Daphnia magna*, was presented, and strong momentum was generated for the development of full transcriptome micro-arrays for this species. *Daphnia magna* is the main *Daphnia* species used in European laboratories, and has been a pre-eminent model in studies of responses to a wide variety of stressors, including pollutants, predator risk, parasite exposure and climate change [4–6]. A recently developed single nucleotide polymorphism chip will guarantee fast progress in the study of adaptation to environmental stressors, natural or human-induced. This chip is able to capture polymorphisms in natural populations covering the entire genome of *D. magna*. It will be of key importance in identifying functional polymorphisms in the genome of *Daphnia* and its role in the adaptive processes.

Most inspiring, a plethora of elegant studies were presented on the mechanisms of responses to environmental challenges, which used recently developed genomic tools. These studies highlight the importance of a complete and well-annotated genome sequence in enabling evolutionary and ecologically relevant studies in natural populations. These included, among others, the genetic underpinning of inducible defences in *Daphnia* and changes in gene expression profiles associated with predator cues, quantitative trait locus analysis of parasite resistance, genomics of metal-induced stress responses, ecotoxicogenomics, methylome analysis and transcriptomics of responses to combined anthropogenic and natural stressors. The influence of environmental conditions on transcriptional responses was presented, along with an overview on recent insights in molecular and physiological responses to stress. These studies highlighted the great potential of *Daphnia* as model system in environmental genomics.

The growing interest in *Daphnia* as a model system in ecological genomics and the successful development of genomic infrastructure has gathered together a number of outstanding scientists ready to take advantage of the acquired tools and apply them in cutting-edge research. Some researchers of the DGC coordinated their efforts by joining a European network (EUROCORES funded project STRESS-FLEA, 09-EuroEEFG-FP 040, 2010–2013). The

DGC 2010 was the venue for announcing the starting of STRESSFLEA and to invite non-member groups to join the consortium as non-funded peripheral partners within the DGC. This will certainly enhance collaboration and communication within the consortium. The DGC 2010 was a concrete sign of the revolutionary development that is going on in biological and environmental science. In the last decade, new genomic resources from model organisms and advances in DNA-sequencing technologies have alleviated the limitations that researchers previously faced and opened new areas of research for studies of non-model organisms. Times are mature for the application of newly developed genomic resources for cutting-edge environmental genomic research on non-model organisms.

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- 1 Heckmann, L. H., Sibly, R. M., Connon, R., Hooper, H. L., Hutchinson, T. H., Maund, S. J., Hill, C. J., Bouetard, A. & Callaghan, A. 2008 Systems biology meets stress ecology: linking molecular and organismal stress responses in *Daphnia magna*. *Genome Biol.* **9**, R40. (doi:10.1186/gb-2008-9-2-r40)
- 2 Decaestecker, E., Gaba, S., Raeymaekers, J. A. M., Stoks, R., Van Kerckhoven, L., Ebert, D. & De Meester, L. 2007 Host–parasite Red Queen dynamics archived in pond sediment. *Nature* **450**, 870–874. (doi:10.1038/nature06291)
- 3 Shaw, J. R., Pfrender, M. E., Eads, B. D., Klaper, R., Callaghan, A., Colson, I., Jansen, B., Gilbert, D. & Colbourne, J. K. 2008 *Daphnia* as an emerging model for toxicological genomics. In *Advances in experimental biology on toxicogenomics* (eds C. Hogstrand & P. Kille), pp. 165–219. Amsterdam, The Netherlands: Elsevier Press.
- 4 Coors, A. & De Meester, L. 2008 Synergistic, antagonistic and additive effects of multiple stressors: predation threat, parasitism and pesticide exposure in *Daphnia magna*. *J. Appl. Ecol.* **45**, 1820–1828. (doi:10.1111/j.1365-2664.2008.01566.x)
- 5 Ebert, D. 2005 *Ecology, epidemiology, and evolution of parasitism in Daphnia*. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology.
- 6 Van Doorslaer, W., Stoks, R., Duvivier, C., Bednarska, A. & De Meester, L. 2009 Population dynamics determine genetic adaptation to temperature in *Daphnia*. *Evolution* **63**, 1867–1878. (doi:10.1111/j.1558-5646.2009.00679.x)