University of Birmingham

Professor John Kenneth Colbourne PhD

Professor, Chair of Environmental Genomics

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About

John Colbourne's investigations encompass the fields of evolutionary ecology, high-throughput biology, environmental and functional genomics. From this blend of disciplines emerges a research program that centers on connecting gene expression and genome structure with individual fitness and population-level responses to environmental challenges.

Qualifications

BSc. University of Toronto
PhD. University of Guelph

Biography

John Kenneth Colbourne joined the faculty of the University of Birmingham in 2012 and holds its inaugural Chair of Environmental Genomics. He is also Adjunct Professor at the Mount Desert Island Biological Laboratory, a founding member of the *Daphnia* Genomics Consortium (DGC) and of the Shanghai Consortium for Environmental Genomics and Toxicology, Section-Editor for BMC Genomics, and founding Editor of the journal Ecological and Environmental Genomics (due in 2013).

Professor Colbourne obtained his PhD in evolutionary biology from the University of Guelph in 1999. He was subsequently awarded a NSERC Postdoctoral Fellowship to begin genomics research at the University of Oregon, then at the University of Indiana where he served as Genomics Director of the Centre for Genomics and Bioinformatics from 2005 until 2012. During this time, he helped pioneer the application of genomics for the study of evolutionary ecology and toxicology, primarily using the freshwater crustacean *Daphnia* as model system to study how genes and the environment interact. This work, in conjunction with the global efforts of the DGC, resulted in *Daphnia*'s designation as a model species for biomedical research by the US National Institutes of Health.

Professor Colbourne regularly works with industry and advises government agencies and professional societies, aiming to transform practices at monitoring and protecting the environment, by utilizing high-throughput molecular biology methods applied to model systems. In 2012-13, he co-chairs the Gordon Research Conference on Ecological and Evolutionary Genomics - celebrating 10 years of community building - and was granted the Royal Society Wolfson Research Merit Award for his contributions to the field.

Postgraduate supervision

The Environmental Genomics group is recruiting postgraduate students to pursue PhD studies in the following research areas:

- Molecular mechanisms of developmental plasticity & acclimation
- Pioneering the use of genomic signatures for environmental health protection
- Forecasting environmental health threats on populations using *Daphnia* egg bank genomics
- Biostatistical and computational methods of analyzing high dimensional data and gene networks
- Population genomics
- Heritable basis of condition-associated molecular responses and adaptive tolerance to stress by QTL analysis and 'omics

Research

The long term research goal of my group is to develop *Daphnia* into a super-model organism to advance Environmental Genomics.

Environmental Genomics is a young and quickly changing field that uses interdisciplinary approaches to understand the genetic mechanisms underlying physiological and adaptive responses of organisms to their environment. The increasing availability of higher throughput methods for analyzing genetic variation is revolutionizing biology, and its innovative tools for general high-throughput biology, statistical analysis and informatics is enabling scientist to link gene-environment interactions to the fitness of individuals and the resulting population-level consequences.

Work by my group includes investigations on (i) the functional mechanisms of phenotypic plasticity, including environmental sex determination and cyclomorphosis, (ii) the genetic basis of evolutionary adaptation within natural populations, and (iii) the potential of aquatic organisms to counter chemical threats (pollution) in the environment. The freshwater crustacean *Daphnia* has been a focus of ecological studies for over 200 years. As a result, its ecology and evolutionary history are superbly understood. Most recently, *Daphnia* emerges as one of the best characterized genomic systems, primarily because of work that we do in conjunction with the Daphnia Genomics Consortium (DGC)

Other activities

Section-Editor for the journal BMC Genomics

Founding Editor for the journal Ecological and Environmental Genomics (due in 2013)

Associate Editor (Comparative Genomics) for the Journal of Experimental Zoology, Part A: Ecological Genetics and Physiology

Coordinator for BioMed Central publication series: “The Genome Biology of the Model Crustacean *Daphnia*”

Founding and lead member of the *Daphnia* Genomics Consortium (DGC)

Founding and lead member of the Shanghai Consortium for Environmental Genomics and Toxicology

Founding member of the *Fundulus* Genome Consortium

Founding member of the *Nasonia* Genome Working Group

Founding member of the Black Fly Genome Sequencing Initiative

Co-Director of the Mount Desert Island Biological Lab (MDIBL) Summer Course in Environmental Genomics

Publications

Selected publications:

Latta IV, L.C., L.J. Weider, J.K. Colbourne and M.E. Pfrender. 2012. The evolution of salinity tolerance in Daphnia: a functional genomics approach. Ecology Letters 15(8):794-802. DOI: 10.1111/j.1461-0248.2012.01799.x (Rated “Recommended” by Faculty of 1000; **http://f1000.com/716347800 (http://f1000.com/716347800)**)

Colbourne, J.K., M.E. Pfrender, D. Gilbert, W.K. Thomas, A. Tucker, T.H. Oakley, S. Tokishita, A. Aerts, G.J. Arnold, M. Kumar Basu, D.J. Bauer, C.E. Cáceres, L. Carmel, C. Casola, J.-H. Choi, C. Detter, Q. Dong, S. Dusheyko, B.D. Eads, T. Fröhlich, K.A. Geiler-Samerotte, D. Gerlach, P. Hatcher, S. Jogdeo, J. Krijgsveld, E.V. Kriventseva, D. Kültz, C. Laforsch, E. Lindquist, J. Lopez, J.R. Manak, J. Muller, J. Pangilinan, R.P. Patwardhan, S. Pitluck, E.J. Pritham, A. Rechtsteiner, M. Rho, I.B. Rogozin, O. Sakarya, A. Salamov, S. Schaack, H. Shapiro, Y. Shiga, C. Skalitzky, Z. Smith, A. Souvorov, W. Sung, Z. Tang, D. Tsuchiya, H. Tu, H. Vos, M. Wang, Y.I. Wolf, H. Yamagata, T. Yamada, Y. Ye, J.R. Shaw, J. Andrews, T.J. Crease, H. Tang, S.M. Lucas, H.M. Robertson, P. Bork, E.V. Koonin, E.M. Zdobnov, I. Grigoriev, M. Lynch and J.L. Boore. 2011. The ecoresponsive genome of Daphnia pulex. Science 331: 555-561. (Rated “Must Read” by Faculty of 1000; **http://f1000.com/8383958 (http://f1000.com/8383958)**)

Alföldi, J., F. Di Palma, M. Grabherr, C. Williams, L. Kong, E. Mauceli, P. Russell, C.B. Lowe, R. Glor, J.D. Jaffe, D.A. Ray, S. Boissinot, C. Botka, T.A. Castoe, J.K. Colbourne, M.K. Fujita, R. Godinez Moreno, B.F. ten Hallers, D. Haussler, A. Heger, D. Heiman, D.E. Janes, J. Johnson, P.J. de Jong, M.Y. Koriabine, P. Novick, C.L. Organ, S.E. Peach, S. Poe, D.D. Pollock, K. de Queiroz, T. Sanger, S. Searle, A.M. Shedlock, J.D. Smith, Z. Smith, R. Swofford, J. Turner-Maier, J. Wade, S. Young, A. Zadissa, Genome Sequencing Platform and Whole Genome Assembly Team, S.V. Edwards, T.C. Glenn, C.J. Schneider, J.B. Losos, E.S. Lander, M. Breen, C.P. Ponting and K. Lindblad-Toh. 2011. The genome of Anolis carolinensis, the green anole lizard, and a comparative analysis with birds and mammals. Nature 477:587–591 (29 September 2011).

Lee, E.-J., L. Pei, G. Srivastava, J. Trupti, G. Kushwaha, J.-H. Choi, X. Wang, K. Mockaitis, J.K. Colbourne, L. Zhang, G. Schroth, D. Xu, K Zhang and H. Shi. 2011. Targeted bisulfite sequencing by solution hybrid selection and massively parallel sequencing. Nucleic Acids Research (July 23, 2011) doi: 10.1093/nar/gkr598.

Jeyasingh, P.D., A. Ragavendran, S. Paland, J.A. Lopez, R.W. Sterner and J.K. Colbourne. 2011. How do consumers deal with stoichiometric constraints? Lessons from functional genomics using Daphnia pulex. Molecular Ecology (20)11:2341-52. (Rated “Must Read” by Faculty of 1000; http://f1000.com/10743958)

Simon, J.-C., D. Tagu, M. Pfrender, R. Tollrian and J.K. Colbourne. 2011. Genomics of environmentally-induced phenotypes in two extremely plastic arthropods. Journal of Heredity 102 (5):512-525. (invited paper).

Werren, J.H., S. Richards, C.A. Desjardins, O. Niehuis, J. Gadau, J.K. Colbourne, and the Nasonia Genome Working Group. 2010. Functional and evolutionary insights from the genomes of three parasitoid Nasonia species. Science 327:343-348.

Shaw, J.R., M. Pfrender, B.D. Eads, R. Klaper, A. Callaghan, I. Colson, B. Jansen, D. Gilbert and J.K. Colbourne. 2007. Daphnia as an emerging model for toxicological genomics. In: Advances in experimental biology on toxicogenomics. eds. C. Hogstrand and P. Kille. Elsevier Press. Volume 2:165-219 (invited paper).

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