Seminar

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Professor of Evolutionary Quantitative Genetics,
The University of Queensland, St Lucia

A Genomic View of Sexual Antagonism and Its Evolutionary Consequences

Tuesday, 27 November, 11:15 a.m.

In the Thunberg Lecture Hall
SCAS, Linneanum, Thunbergsvägen 2, Uppsala
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ABOUT STEVE CHENOWETH

Stephen Chenoweth holds a PhD in Population Genetics from Griffith University (1999). After a two-year period working in industry, he trained in evolutionary quantitative genetics at the University of Queensland in 2002 as an ARC Australian Postdoctoral Fellow. He was subsequently appointed to the faculty at the School of Integrative Biology in 2006 and was then awarded two consecutive five-year research fellowships from the Australian Research Council. He is currently Professor of Evolutionary Quantitative Genetics at the School of Biological Sciences at the University of Queensland.

Chenoweth is known for his work in quantitative genetics, specifically in the areas of evolutionary constraints, sexual dimorphism, sexual selection, and genomic conflicts. To these areas he has contributed key empirical results, new analytical approaches, and several major reviews. Chenoweth has published over seventy papers in international journals, including high-profile studies in *Science, PNAS, Current Biology, PLoS Biology,* and *Nature Reviews Genetics*, as well as made regular contributions to field-leading journals, such as *Genetics, Evolution, The American Naturalist, Molecular Ecology, Genome Biology & Evolution,* and *Molecular Biology & Evolution*. He currently serves on the editorial boards of *Genetics* and *The American Naturalist* and is a council member of the European Society for Evolutionary Biology.

At SCAS, Chenoweth will be developing analytical approaches to integrate large-scale genomic data sets with classic theory for predicting evolutionary responses. He will also work with SCAS Fellows Locke Rowe and Troy Day to understand how pleiotropy shapes sex differences in gene expression.

ABSTRACT

Males and females maximise fitness in very different ways and because of this experience contrasting forms of Darwinian selection that favors the evolution of sex differences. However, because males and females share almost all of their genes, constraints arise that can hamper sex-specific adaptation and generate genomic conflicts between the two sexes. While sexual antagonism has been detected in a broad range of species, we know far less about how it how manifests at the genomic level. In this seminar, I will present our recent studies that combine classic quantitative genetic tools with genomic methods to study sexual antagonism in the fruit fly *Drosophila serrata*. These include analyses of male and female gene expression evolvability, genome-wide association studies of male and female fitness, and fine-scale mapping of sexually antagonistic genes.