

## Evolutionary Genomics of *Chlamydomonas*

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### Project background

In the proposed project, the student will study evolutionary genomics in *Chlamydomonas reinhardtii* and several related species. These species are members of a diverse group of single-celled plants, the chlorophytes, that are intensively studied as model organisms in plant physiology and genetics. Understanding the evolutionary biology of chlorophytes is important, because the group is of critical ecological importance: up to one-half of global photosynthesis occurs in the oceans, much of it carried out by microalgae. Moreover, *Chlamydomonas* is receiving increasing attention for its potential in generating biofuels. In spite of their key role in ecology and plant genetics, very little is known about the population genetics of chlorophytes. In the proposed project, the student will address a number of fundamental questions concerning the evolutionary genomics of the group, taking advantage of genomic resources that have only recently become available. The student will become part of a well-funded research group co-led by Colegrave and Keightley, working on experimental evolution and the impact of new mutations on quantitative variation in *Chlamydomonas*. The student will analyse genome sequences generated by our own lab and by collaborators. Annotated genome sequences of multiple natural isolates of *C. reinhardtii*, its close relative *C. incerta*, and the more distantly related *Volvox carteri* and *Coccomyxa subellipsoidea* (<http://www.phytozome.net/>) are available (Merchant et al. 2007; Prochnik et al. 2010; Blanc et al. 2012).

### Key research questions

1. Genomic diversity of *C. reinhardtii*. How much genetic diversity is present within *C. reinhardtii* populations and how is this diversity distributed across the geographic range of the species? What is the extent of population structure within the species? To what extent does diversity within *C. reinhardtii* and divergence between *C. reinhardtii* and its close relative *C. incerta* vary across the genome (e.g., between protein-coding exons, introns, intergenic DNA), and what does this tell us about the nature of the selective forces operating in these regions?
2. The evolutionary significance of noncoding DNA in chlorophytes. Annotated proteomes for several chlorophytes have been produced, but little work has been done on the evolutionary significance of noncoding DNA sequences in this group of organisms (Ding et al. 2012). Using comparative genomics and population genetics, we propose to investigate the nature of selection on noncoding DNA in chlorophyte genomes. We will address the following questions. First, are signatures of selection detectable in noncoding DNA sequences in chlorophytes? For example, do we see reduced nucleotide divergence or nucleotide diversity relative to that found in putatively neutrally evolving sites? What fraction of the noncoding genome is functional? Are the longer noncoding elements (e.g., introns, intergenic regions) more conserved between-species, as has been found in other taxa that have compact genomes, such as invertebrates (Halligan and Keightley 2006)? Are there identifiable ultra-conserved noncoding elements in the chlorophyte genome? Are these elements conserved across the plant kingdom or across the tree of life in general? Is there evidence of positive and negative selection around conserved coding and noncoding elements, and what does this tell us about the frequency of recombination and the nature of the selective forces operating in these regions?

## Methodology

The key approaches to address the research questions are as follows:

1. Analysis of next generation sequence data from *C. reinhardtii* and related species using widely used software packages (e.g., GATK) and annotation of the genome according to site class.
2. Alignment of the *C. reinhardtii* genome where possible to related species, or compilation of orthologous gene sets.
3. Identification of conserved noncoding elements across species, initially using Blast, with *C. reinhardtii* as the reference genome, and if genome alignments can be made, using Phastcons (Siepel et al. 2005).
4. Application of population genetics methodology to assess nucleotide diversity within *C. reinhardtii* and divergence from related species in protein-coding exons, conserved noncoding elements and their flanking regions, and to estimate the distribution of fitness effects of deleterious mutations, and to estimate the extent of population structure.

## Training

The project will provide training and experience in evolutionary genomics research, the analysis of next-generation sequence data and computational biology. The student will be expected to attend modules run in the Institute of Evolutionary Biology that are part of the MSc in Quantitative Genetics and Genome Analysis, including population genetics and statistics.

## Requirements

The student will have a strong background in population genetics and/or evolutionary genomics. Experience with computational science will be an advantage.

**See lab website:** <http://homepages.ed.ac.uk/eang33/>

## References

- Blanc G et al. 2012 The genome of the polar eukaryotic microalga *Coccomyxa subellipsoidea* reveals traits of cold adaptation. *Genome Biol.* 13:R39.
- Ding, J et al. 2012. systematic prediction of cis-regulatory elements in the *Chlamydomonas reinhardtii* genome using comparative genomics. *Plant Physiology* 160: 613-623.
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- Halligan, D. L. and Keightley, P. D. (2006). Ubiquitous selective constraints in the *Drosophila* genome revealed by a genome-wide interspecies comparison. *Genome Res.* 16: 875-884.
- Merchant, SS et al. 2007. The *Chlamydomonas* genome reveals the evolution of key animal and plant functions. *Science* 318: 245–251.
- Ness, RW et al. 2012. Estimate of the spontaneous mutation rate in *Chlamydomonas reinhardtii*. *Genetics* 192: 1447-1454.
- Prochnik, SE et al. 2010. Genomic analysis of organismal complexity in the multicellular green alga *Volvox carteri*. *Science* 329: 223-226.
- Siepel, A et al. (2005). Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. *Genome Res.* 15: 1034-1050.

## Project Summary

By the analysis of whole-genome sequences of *C. reinhardtii* and related species sampled from natural populations, we will investigate the nature of the selective forces operating in these species.