

The volvocales genomes project

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Abstract:

The transition from unicellular to multicellular organisms is a major step in the evolution of life on earth. This transition is known to have happened independently in different organismal groups. However, the molecular basis of this transition has remained largely elusive. The volvocine algae consist of several species representing increasing multicellular complexity and thus provide an excellent model for the study of the evolution of multicellularity. We are studying the genomic basis of multicellular evolution by sequencing the genomes of volvocine species representing progressively increasing complexity, in evolutionary terms. The genomes of *Chlamydomonas reinhardtii* (unicellular), *Gonium pectorale* (undifferentiated multicellular) and *Volvox carteri* (differentiated multicellular) have been sequenced. Previously, by sequencing the genome of *Gonium pectorale*, we showed that the co-option of cell cycle regulatory genes plays a key role in the evolution of multicellularity. Subsequently, we have sequenced the genomes and transcriptomes of *Yamagishiella unicocca*, *Eudorina elegans*, *Pandorina morum*, *Pleodorina starii*, and *Volvox ferissi*. To understand how multicellularity and cell type specification evolve within the Volvocales, we are comparing the evolutionary history of these genome sequences. In particular, we are focusing on how the cell cycle regulated gene expression has evolved for organismal developmental plans. An update on our progress on assembly and annotation of the Volvocales genomes will be presented along with analysis of the cell cycle transcriptomes of several key species.