Genomic basis of viral susceptibility in the Eukaryotic Phytoplankton Ostreococcus tauri

Supervisors: G. Piganeau, N. Grimsley.

Lab.: Biologie Intégrative des Organismes Marins CNRS/UPMC, station marine de Banyuls/mer, FRANCE
Center for the Study of Evolution, School of Life Sciences, Sussex University, UNITED-KINGDOM

Picoeukaryotic prasinophyte algae are abundant planktonic organisms throughout the oceanic euphotic zone, including the Mediterranean Sea\(^1\), and play a significant role in the global Carbon cycle as they are key-players in the biological pump. The most abundant and widespread representatives of the *Prasinophyceae* are the *Mamiellales*, especially the three genera *Bathycoccus*\(^2\), *Ostreococcus*\(^3\) and *Micromonas*\(^4,5\). The populations of these species are regulated to a large extent by DNA viruses and it is therefore crucial to understand the role of viruses in plankton evolution.

To identify host genes responsible for resistance/susceptibility of *O. tauri* to viruses, detailed genetic analyses have already been done, firstly by pairwise analyses of specificities between 13 *O. tauri* wild-type clonal host lines\(^6\) and 48 independently isolated viruses\(^7,8\), and secondly by completely sequencing the genomes of these 13 host strains (unpublished data, collaboration JGI, USA) and assembling them using the annotated genome of *O. tauri*\(^9\) as a template. Haplotype analyses reveal about 4.10\(^4\) single nucleotide polymorphisms (SNP) between strains. The main objective of this project is to investigate the association between these haplotypes and the host/virus specificity dataset, to establish which genomic regions may be involved in the determination of host specificity to viral attack.

This project requires a strong interest in bioinformatic tools and sequence analysis.

References:
