

# **Genomic basis of viral susceptibility in the Eukaryotic Phytoplankton *Ostreococcus tauri***

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Picoeukaryotic prasinophyte algae are abundant planktonic organisms throughout the oceanic euphotic zone, including the Mediterranean Sea<sup>1</sup>, 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*<sup>2</sup>, *Ostreococcus*<sup>3</sup> and *Micromonas*<sup>4,5</sup>. 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<sup>6</sup> and 48 independently isolated viruses<sup>7,8</sup>, and secondly by completely sequencing the genomes of these 13 host strains (unpublished data, collaboration JGI, USA) and assembling them using the annotated genome of *O. tauri*<sup>9</sup> 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 :**

1. Zhu, F., Massana, R., Not, F., Marie, D. & Vaultot, D. Mapping of picoeucaryotes in marine ecosystems with quantitative PCR of the 18S rRNA gene. *Fems Microbiology Ecology* **52**, 79-92 (2005).
2. Eikrem, W. & Throndsen, J. The ultrastructure of *Bathycoccus* Gen-Nov and *Bathycoccus prasinus*, a nonmotile planktonic alga (Chlorophyta, Prasinophyceae) from the Mediterranean and Atlantic. *Phycologia* **29**, 344-350 (1990).
3. Courties, C. et al. Smallest Eukaryotic Organism. *Nature* **370**, 255-255 (1994).
4. Marie, D., Zhu, F., Balague, V., Ras, J. & Vaultot, D. Eukaryotic picoplankton communities of the Mediterranean Sea in summer assessed by molecular approaches (DGGE, TTGE, QPCR). *Fems Microbiology Ecology* **55**, 403-415 (2006).
5. Viprey, M., Guillou, L., Ferreol, M. & Vaultot, D. Wide genetic diversity of picoplanktonic green algae (Chloroplastida) in the Mediterranean Sea uncovered by a phylum-biased PCR approach. *Environ Microbiol* **10**, 1804-22 (2008).
6. Grimsley, N., Pequin, B., Bachy, C., Moreau, H. & Piganeau, G. Cryptic Sex in the Smallest Eukaryotic Marine Green Alga. *Molecular Biology and Evolution* **27**, 47-54 (2010).
7. Bellec, L., Grimsley, N., Derelle, E., Moreau, H. & Desdevises, Y. Abundance, spatial distribution and genetic diversity of *Ostreococcus tauri* viruses in two different environments. *Environmental Microbiology Reports* **2**, 313-321 (2010).
8. Bellec, L., Grimsley, N. & Desdevises, Y. Isolation of Prasinoviruses of the Green Unicellular Algae *Ostreococcus* spp. on a Worldwide Geographical Scale. *Applied and Environmental Microbiology* **76**, 96-101 (2010).
9. Derelle, E. et al. Genome analysis of the smallest free-living eukaryote *Ostreococcus tauri* unveils many unique features. *Proceedings of the National Academy of Sciences of the United States of America* **103**, 11647-11652 (2006).

