Single Cell Ecogenomics of Mamiellophyceae picoplanktonic algae

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1 - Introduction:

Planktonic photosynthetic organisms of the Mamiellophyceae class include the smallest eukaryotes and form the basis of coastal marine ecosystems. Despite their ecological importance, their life cycle and organismal interactions in the marine environment remain enigmatic. Single amplified genomes (SAGs) of non-cultivated samples could allow the identification of novel biological associations, from predation to parasitism. Since SAG assemblies contain foreign DNA, they preserve a portion of the ecological context of the cell and may be viewed conceptually as metagenomes. Haploid SAGs may also indicate the prevalence of different mating types in natural populations. Here we investigated 12 Mamiellales SAGs sampled in the Indian Ocean during the Tara Oceans expedition (Alberti et al. 2017) to explore the biological insights this data provides within an ecogenomics framework.

2 - Pipeline:





3 - SAG identification:



4 - SAG taxonomic profiles:



SAGs were assigned through 18S rRNA analysis to *Bathycoccus* sp. (SAG1-3), *Micromonas bravo* (SAG5 and 8) and *Ostreococcus* sp. (SAG9-12). Mamiellophyceae reference genomes are denoted by red star, and SAGs are marked with orange star. Rapid bootstrap support is denoted by colored circles.

5 - Novel virus discovery:

0.02



Analysis of non-target contigs indicate possible biological interactions, mainly with Bacteria, oomycetes and viruses, including novel ssDNA viral genomes in SAG8 and SAG12. Percentages correspond to the sum of reads mapping contigs assigned to higher taxonomic levels of the total non-target fraction, ranging from 0.011 % in *Ostreococcus* (SAG10) to 6.09% in *Micromonas* (SAG8).

6 - SAG mating type profiles:

In *Ostreococcus* spp., core gene families (GF) on sex chromosome-like regions, the mating type locus (*MT*), cluster phylogenetically by mating type, not by species (Blanc-Mathieu et al. 2017, Benites et al. in prep.), because the origin of mating types predates speciation in this genus.



Genome structure, biogeography and phylogeny of Mamiellales associated circular virus. (a) Genome assembly of 1,586 bp virus encoding two open reading frames ; ORF1 is a replicase and ORF2 a putative capsid protein. (b) Biogeographic distribution of putative homologous sequences encoding to ORF2 (putative capsid) in the Ocean Gene Atlas (OGA) database per TARA station (b). (c) Maximum Likelihood Phylogeny of ORF2 (putative capsid) and (d) ORF1 (replicase) with homologous sequences retrieved from Genbank and OGA database.

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Contigs were compared with mating type GFs of reference genomes. In *Ostreococcus* SAGs we found a low fraction of these genes (ranging from 2 to 6 out of 23 gene families) Nevertheless, gene profiles indicate that SAGs have the same mating type (*MT+*) as the reference genome of *Ostreococcus* sp. RCC809. (a) Expected taxonomic affiliation for MT- and MT+ strains. Each square represents a gene family (GF) and colours represent mating type (MT) specificity. (b) Presence/absence matrix of hits to GFs in each SAG (c) phylogeny of the SAG sequences corresponding to GF16 with orthologous genes from Ostreococcus species.

7 - Conclusions:

Here we showed that even in the smallest eukaryotic cells of Mamiellophyceae algae, single cell genomics can be used to identify novel associations and interactions by retrieving *in-situ* ecological information that may be lost in conventional isolation and culture processes.