

Sorting Out Eukaryotic Pico/Nanoplankton Community Structure: the Single Cell Genomics Approach

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Marine eukaryotes smaller than 20µm are highly diverse and dominate bacterivory in the ocean, as well as the primary and secondary productivity, in many ocean regions. Mixotrophy is common. They take up and recycle major and minor inorganic nutrients and can harbor prokaryotic symbionts. Diversity surveys based on bulk DNA methods are distorted by the over-representation by types with multiple gene copies. Single cell sorting and amplification, followed by PCR screening may yield a more accurate picture of the diversity of the dominant types in a sample. I will present here our preliminary results of single cell genomics samples collected from the surface of the Adriatic Sea and Indian Ocean, as part of the Tara Oceans Expedition, a circum-global oceanographic survey of planktonic diversity. Phototrophs, as identified and sorted by autofluorescence, are less diverse than heterotrophs, and dominated by Prasinophytes and Chrysophytes. The heterotrophic cells are dominated by marine stramenopiles of the MAST groups. Single amplified genomes (SAGs) from these cells are a valuable resource for further sequencing and study of these important, but as yet uncultured, microorganisms. SAGs can serve as references for metagenomic assembly and recruitment analysis, and for finer analysis of phylo genetic and population genetic studies.

