Multi-omics insight into marine plankton diversity : Tara Oceans

Eric Pelletier $^{*\dagger 1},$ Quentin Carradec , Patrick Wincker , and Tara Oceans Consortium

¹Genoscope - Centre national de séquençage [Evry] (GENOSCOPE) – CEA, Genoscope – 2, rue Gaston Crémieux CP5706 91057 EVRY Cedex, France

Abstract

During a 3 years journey across the globe, the Tara schooner have sampled more than 200 open ocean stations to study a yet poorly describe important component of the global ecosystem : the plankton from the sunlit ocean. These micro-organisms, ranging from 0.2 to 2000 μ m, comprises main actors of several major biogeochemical cycles (carbon, oxygen and nitrogen). The shape and fluctuation of their population is largely undescribed, and their resilience to anthropic changes affecting the ocean are unknown. Using high-throuput sequencing approaches, both metagenomic and metatranscriptomic component of the bacterial and eukaryotic fractions of the sampled organisms were studied, and general analysis of both diversity and activity were undergone, allowing to draw the first set of global pictures of connexion between environmental parameters and marine planktonic communities. Highlights of bioinformatics approaches and main biological results will be adressed.

Keywords: Tara expedition, plankton, metagenomic, metatranscriptomic

^{*}Speaker

[†]Corresponding author: eric.pelletier@genoscope.cns.fr