Ecological networks of microbial plankton influence the biological carbon pump processes in the oligotrophic ocean

Anne-Sophie Benoiston^{*1}, Damien Eveillard², Samuel Chaffron², Géraldine Jean², Erwan Delage², Sakina-Dorothée Ayata³, Chris Bowler⁴, Lionel Guidi³, and Lucie Bittner⁵

¹Sorbonne Université, CNRS, Institut de Biologie Paris-Seine (IBPS), Evolution Paris Seine, F-75005, Paris, France – Sorbonne Université – France

²LS2N UMR CNRS 6004, Université de Nantes, CN, IMT-A, France – Université de Nantes – France ³Sorbonne Université, CNRS, Laboratoire d'Océanographie de Villefanche, LOV, France – Sorbonne Université – France

⁴Ecole Normale Supérieure, PSL Research University, Institut de Biologie de l'Ecole Normale Supérieure (IBENS), CNRS UMR 8197, INSERM U1024, France – Ecole Normale Supérieure de Paris – ENS Paris – France

⁵Sorbonne Université, CNRS, Institut de Biologie Paris-Seine (IBPS), Evolution Paris Seine, F-75005, Paris, France – Sorbonne Unversité – France

Abstract

The biological pump corresponds to the combination of biologically driven processes encompassing the production of organic matter via photosynthesis, its export to the deep and its remineralization. Phytoplanktonic composition in surface influences the strength of carbon export. Besides, key players involved in the biological pump have been identified, such as diatoms because of their large size and fast sinking rates and copepods by the production of fecal pellets while migrating in the water column. However, the functions handled by micro-organisms in the biological pump are yet poorly characterized, and results suggest that the biological carbon pump is the result of their interactions rather than their independent actions. Here we defined three different states of the water column corresponding to situations where primary production, carbon export or flux attenuation is dominant over the two other processes. We used environmental and genomics data from the Tara Oceans project to disentangle planktonic interactions and functions involved in the variability of the biological carbon pump. Using ecological network inference methods, each of the states were analyzed to determine their underlying system organization at the level of prokaryotic species and functions. The states were then compared to check how their structure may differ or whether transitions between them can be detected. As the results suggest that the taxonomic and functional composition of prokaryotic plankton in the euphotic zone correlates with those states, we anticipate our results to be a starting point for monitoring the biological carbon pump over time and space and improve global carbon cycle models.

*Speaker