

ENVIRONMENTAL MICROBIOLOGY

Pumping carbon to the deep ocean

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Marine plankton communities are known to mediate the transformation of atmospheric CO₂ into organic carbon, which is then exported as sinking particles to the deep ocean, where it is finally sequestered; this process is termed the biological carbon pump. However, it is unclear how the structure and functions of microbial communities regulate the carbon pump. Now, a new study shows that the abundance of specific microbial taxa, such as *Synechococcus* and their phages, is associated with carbon export in the oceans.

To elucidate the links between plankton community composition and carbon export, Guidi, Chaffron, Bittner, Eveillard, *et al.* used data collected as part of the *Tara* Oceans global circumnavigation expedition. As a correlate of carbon flux, the authors measured the concentration and size distribution of particles at a depth of 150 m in oligotrophic waters, which were used to estimate carbon export; this data was then correlated with the relative sequence abundance of eukaryotic, prokaryotic and viral lineages present in metagenomic samples

collected at the same sites. This analysis revealed several unicellular eukaryotic microorganisms, the abundance of which correlated with the variability in carbon export at 150 m, including three Rhizaria lineages and three dinoflagellate lineages, none of which had been previously shown to have major roles in the carbon cycle. Furthermore, several bacterial genera, particularly *Synechococcus*, correlated with increased carbon export. Notably, the abundance of two *Synechococcus* phages also correlated with increased carbon export, leading the authors to propose that phage-induced cell lysis may induce aggregate formation and potentiate particle sinking, thereby promoting carbon export to the deep ocean.

To investigate how community functions regulate the carbon pump, the authors then applied a similar analysis to identify bacterial genetic functions associated with carbon export. The main bacterial functions associated with carbon export were photosynthesis and growth, including the abundance of several groups of genes associated with membrane proteins, ABC-type transporters, carbohydrate breakdown and

chitinase, which suggests that these bacterial functions may be important for the formation and degradation of marine particles, thereby regulating the carbon pump.

In summary, this study identified several new components of plankton communities that contribute to the biological carbon pump in the ocean, highlighting the central role of microorganisms in mediating this process. However, the authors caution against extrapolating these findings, which are based on carbon export at 150 m, to predict carbon sequestration, which occurs deeper in the ocean and over a much longer timescale. Nonetheless, this study revealed community interactions and bacterial functions that may regulate carbon export in the ocean, which should be investigated in future functional studies.

Cláudio Nunes-Alves

ORIGINAL ARTICLE Guidi, L., Chaffron, S., Bittner, L., Eveillard, D. *et al.* Plankton networks driving carbon export in the oligotrophic ocean. *Nature* <http://dx.doi.org/10.1038/nature16942> (2016)

FURTHER READING Brum, J. R. & Sullivan, M. B. Rising to the challenge: accelerated pace of discovery transforms marine virology. *Nat. Rev. Microbiol.* **13**, 147–159 (2015)

