Goldschmidt 2021 Abstract
https://doi.org/10.7185/gold2021.8224

Integrated meta-omic analysis links chemical signaling to diatom bloom decline and viral infection

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Here we investigate phytoplankton bloom dynamics along the California Coast using an integrated meta-omics to explore links between the dissolved and particulate meta-lipidomes, cell-associated virome, and >1.3 um size fraction meta-transcriptome. This holistic approach revealed that bloom decline due to viral infection was associated with enhanced chemical signaling in the surface ocean. Specifically, the abundance of oxylipins in the dissolved lipidome was associated with senescence biomarkers in the particulate lipidome and high ratios of free-living viral metaT reads:cell-associated viral metaT reads. Oxylipins are bioactive on multiple tiers of the oceanic trophic structure and production has been linked to bloom decline in the Mediterranean [1, 2], inhibited growth of phytoplankton competitors [3], decreased copepod reproductive success [4], deterred grazing and inhibited growth of microzooplankton grazers[5, 6], and differential responses in bacterioplankton taxa [7]. Higher oxylipin concentrations at sites with recent viral lysis is consistent with laboratory studies showing oxylipin production during viral lysis of diatoms [8]. Deck-board incubations showed that the oxylipins produced during viral infection of diatoms have the potential to enhance nutrient recycling by stimulating particle associated bacteria and deterring grazing by microzooplankton communities. We predict that oxylipin chemical signaling by diatoms in response to viral infection would enhance the viral shunt whereby carbon is transferred from the particulate pool to the dissolved pool. This is in contrast to the observed biogeochemical impact of coccolithophore viruses which enhance the viral shuttle by which dying phytoplankton aggregate together and contribute to export [9]. This study is one example of how meta-omic approaches can illuminate nuanced details of the microbial interactions controlling large scale processes like oceanic carbon flux.

[1] Ribalet et al. 2014. *PloS one* 9 (1):e85947-e85947.
[2] Russo et al. 2020. *The ISME Journal* 14 (1):164-177.
[3] Ribalet et al. 2007. *Aquat Toxicol* 85 (3):219-27.
[4] Lauritano et al. 2016 *Harmful Algae*, *55*, 221-229
[5] Lavrentyev et al. 2015. *Marine drugs* 13 (5):2834-2856.
[6] Johnson et al. 2020. *Environmental Microbiology* 22 (2):629-645.
[7] Ribalet et al. 2008. *Aquat Toxicol* 86 (2):249-55.
[8] Edwards et al. in prep for Environmental Micro.
[9] Laber et al, 2019 *Nature Microbiology* 3 (5):537-547.