Discovery and identification of oxidative stress biomarkers in marine plankton using a new, open-source R package for lipidomics

Jamie Collins 1,2 *, Bethanie Edwards 1,2, Kevin Becker 1, Helen Fredricks 1, and Benjamin A.S. Van Mooy 1
1 Department of Marine Chemistry & Geochemistry, Woods Hole Oceanographic Institution
2 MIT/WHOI Joint Program in Oceanography; 3 School of Oceanography, University of Hawaii at Manoa

Introduction: ROS and the algal lipidome

Oxidative stress exerts a profound impact on the lives of marine microbes, including eukaryotic phytoplankton. Reactive oxygen species (ROS) can function as inter- or intracellular signals, alter various cellular metabolisms, and dramatically transform the individual molecules that make up the algal cell. As in terrestrial plants, the polar lipids of marine algae are a “front line” barrier in the battle against oxidative stress. Because these lipids are primary structural components of cell organelle membranes, they are particularly susceptible to chemical transformation by both inter- and extracellular ROS. The lipids transformed by ROS can be exploited as biomarkers for specific types of oxidative stress.

We use Lipidomics to analyze hundreds of these biomarkers simultaneously with their unoxidized counterparts. Patterns in their distribution, abundance, and chemical structure can be used to:

- Identify new biomarkers for various biological and abiotic stressors
- Localize the impact of oxidative stress within an ecosystem or single cell
- Examine the effect of ROS on biochemical pathways, microbial communities做梦的生态学 balance of biological systems

Results of pure culture: Oxidative stress in the model marine diatom Phaeodactylum

We applied LOBSTAHs to lipid data from an experiment in which hydrogen peroxide (H2O2) was used to induce oxidative stress in the model diatom Phaeodactylum tricornutum.

LOBSTAHs identifies 1039 unique oxidized and unoxidized lipids that serve as potential biomarkers

Results at Station ALOHA: Effect of UVB exposure on a microbial metalipidome

We applied different light screening treatments to large (~2 L) volumes of unfiltered seawater collected at Station ALOHA, in the North Pacific Ocean, during the SCOPE Marine NSO Legacy II cruise. LOBSTAHs was used to identify patterns & potential biomarkers of natural, daily-recurring UV radiation stress in HPLC-MS lipid data from three treatments. 1,747 different oxidized and unoxidized compounds were identified & quantified.

New oxidized lipids are observed, but increase in oxidation state driven primarily by fall in concentration of unoxidized molecules

Summary & significance

Shifts in the distribution, abundance, and chemical structure of lipids in (a) P. tricornutum and (b) the microbial community at Station ALOHA can tell us about the effects and targets of oxidative stress within the algal cell and within ecosystems.

- Extensive lipidome remodeling followed treatment with 150 µM H2O2 in Phaeodacty-

lum tricornutum. Additionally, oxidative stress promoted reallocation of biomass to triacylglycerols (TAG)

- At Station ALOHA, UVB radiation induced wholesale change in the oxidation state of the metalipidome