

Sign of the times: the lipid signature of a collapsing phytoplankton bloom

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Atmospheric CO₂

Phytoplankton

Sinking particles

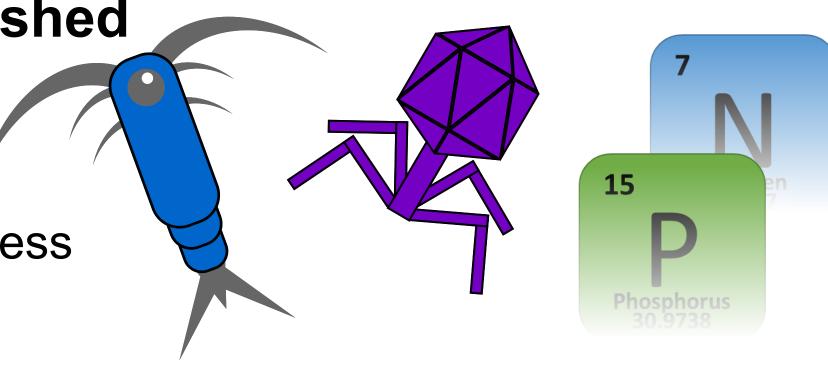
Deep sea sediments

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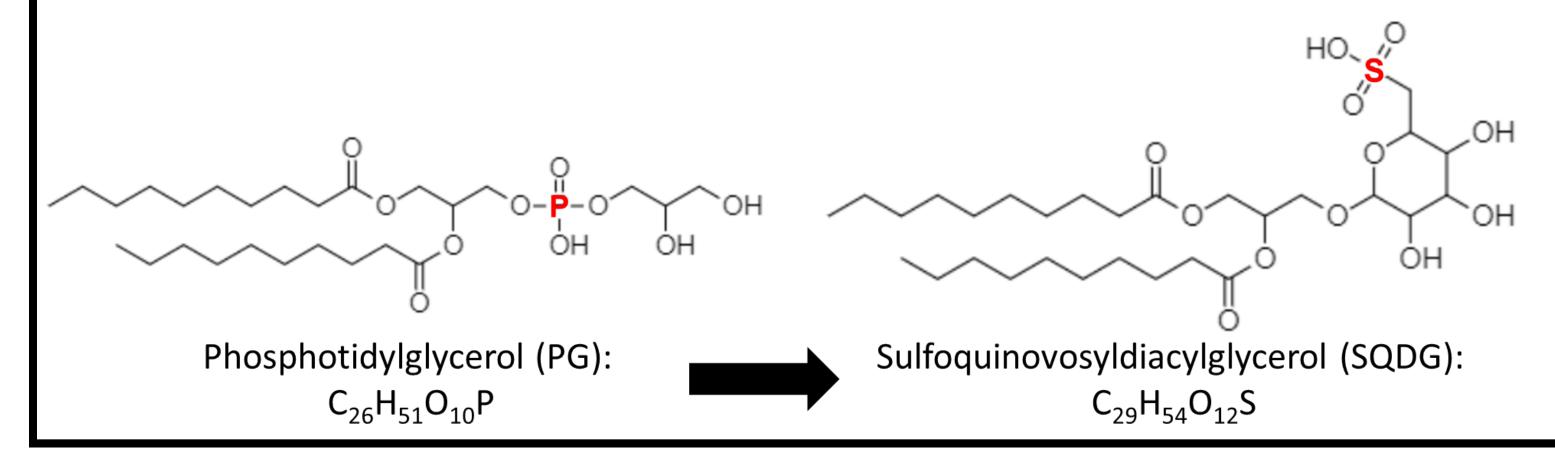


Background

- Phytoplankton are a vital part of marine ecosystems
 - Sequester carbon into sediments
 - o Serve as the foundation of the food web
- o Cycle nutrients through environment
- Phytoplankton "bloom" intensely when conditions are right...
 - o Triggered by the addition of nutrients to the environment
 - o Large scale events hundreds or thousands of km²
- ...then collapse abruptly when population controls are re-established
- o Grazing pressure
- Viral infection and lysis
- Nutrient depletion and stress



- Lipidomics can be used to elucidate proxies for bloom decline
- Membrane lipids (IP-DAGs) are excellent biomarkers for environmental conditions
- In oligotrophic environments, lipid swapping can be used as a biomarker for nutrient stress
 - o P-containing lipids are replaced with betaine lipids^[1]
 - o N-containing lipids are replaced with glycolipids [2]

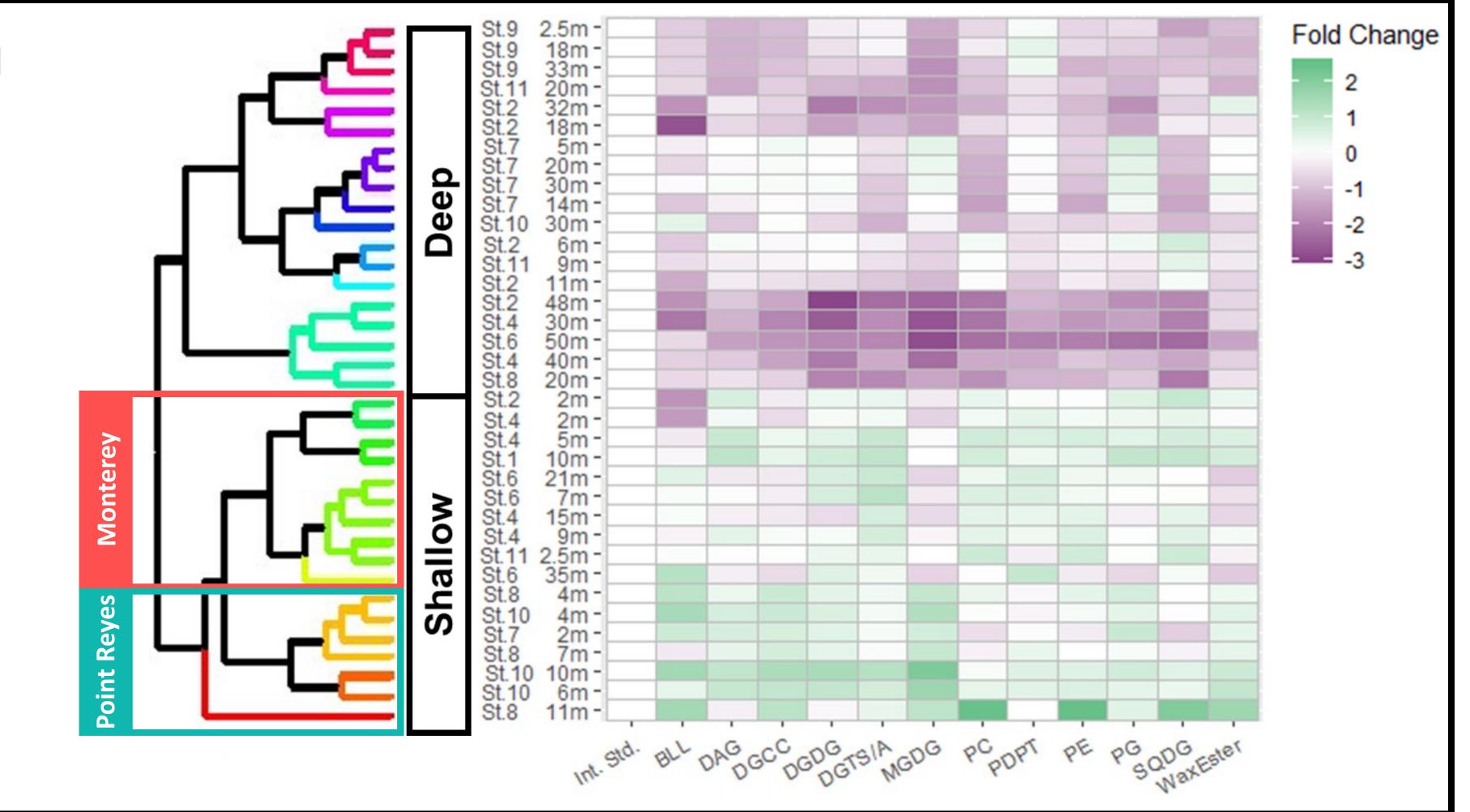


Questions addressed

- 1. Can we use lipidomics to describe membrane lipid distribution off the coast of California?
- 2. Can we use oligotrophic biomarkers in eutrophic ecosystems?

Results

- Heatmap data shows the fold-change of each lipid sub-class relative to the mean across stations
- Dendrogram group colors denote that the lipidome structure is significantly similar between those samples^[6]
- Deep samples have a different lipid signature from shallow samples
- Among the shallow samples,
 Point Reyes samples are significantly different from Monterey samples

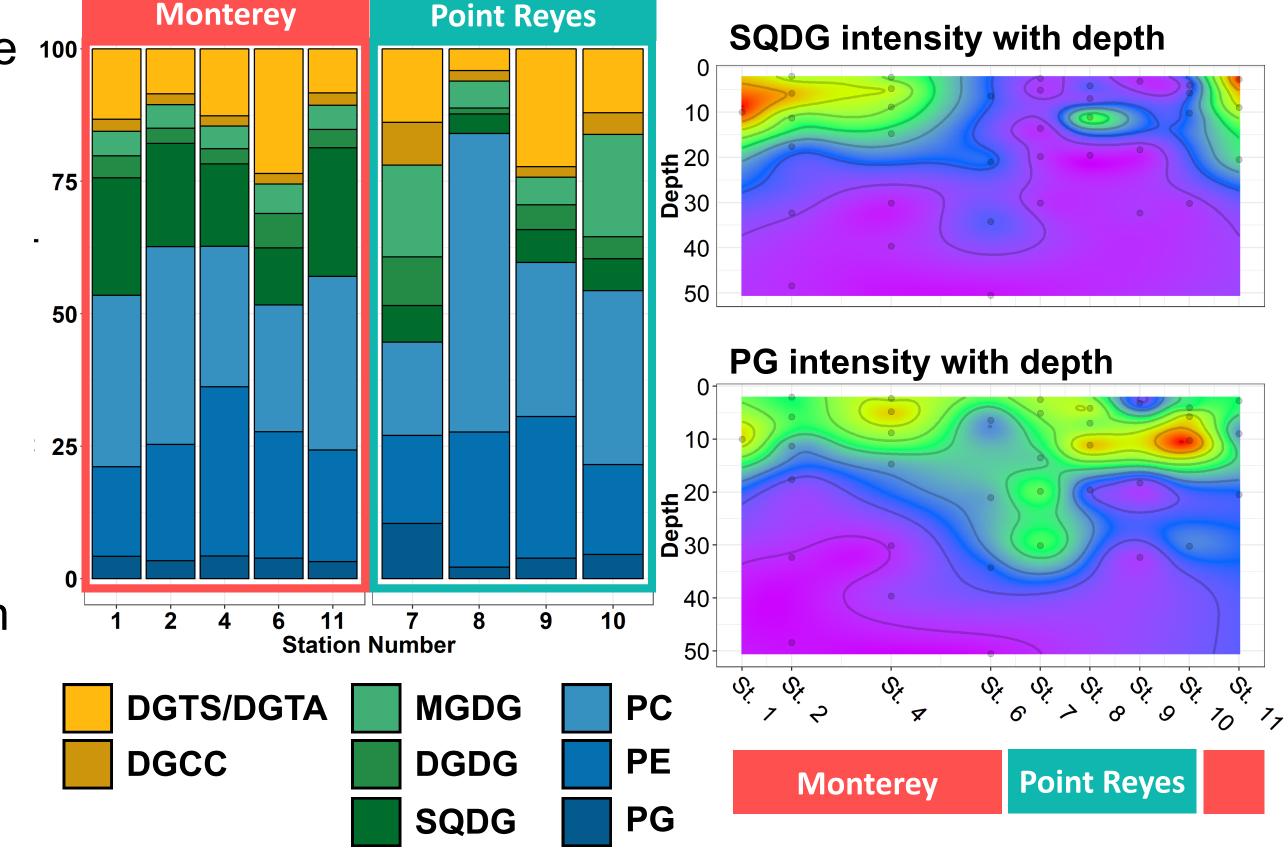


- Common intact membrane 100
 lipids (IP-DAGs) identified
 at every station 75
- Variation in relative
 abundance implies either
 nutrient stress lipid
 swapping or community
 composition shift
- Plots of intensity vs. depth highlight key locations of high lipid abundance

DGTS = diacylglyceryltrimethylhomoserine

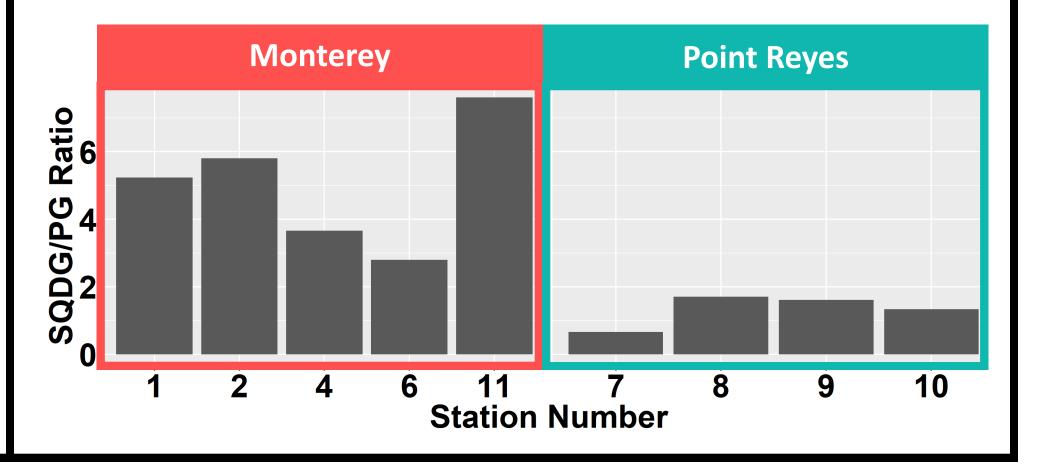
DGTA = diacylglyceryl hydroxymethyltrimethyl-β-alani

DGCC = diacylglyceryl carboxyhydroxymethylcholine

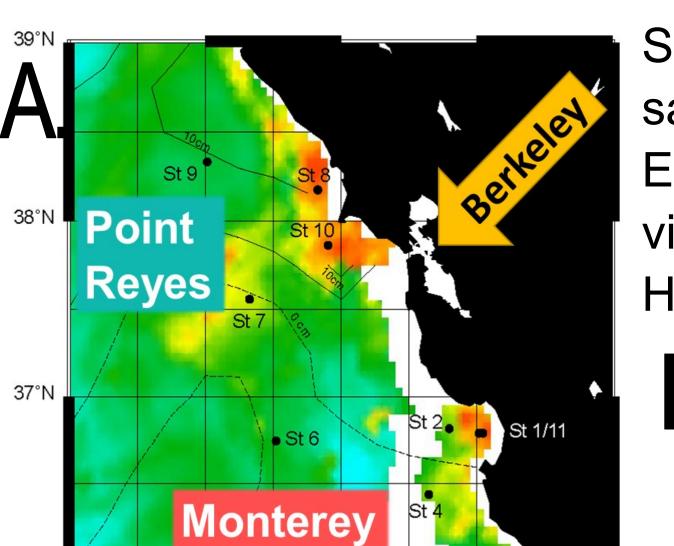


MGDG = monogalactosyldiacylglycerol PC = phosphatidylcholine
DGDG = digalactosyldiacylglycerol PE = phosphatidylethanolamine
SQDG = sulfoquinovosyldiacylglycerol PG = phosphatidylglycerol

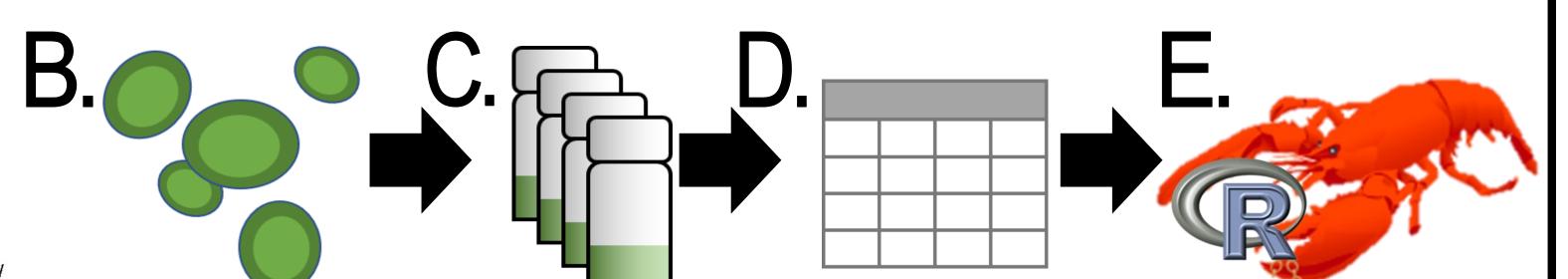
- Monterey stations have statistically significant SQDG:PG ratios from Point Reyes stations (Mann-Whitney U, p-value <0.001, n = 36)
- High SQDG:PG ratio in Monterey stations implies biomarker for healthy bloom biomass, not nutrient stress



Methods



Samples were processed via lipidomics pipeline. **A.** Environmental samples were collected from 9 stations in the California Current Ecosystem then **B.** filtered onto 0.2 µm Durapore filters and **C.** extracted via a modified Bligh & Dyer. These extracts were then **D.** analyzed via HPLC-MS^[4] and **E.** annotated via the R package LOBSTAHS. [5]



Credits

Enormous thanks to the entire Van Mooy lab for sample preparation and data collection

Thank you also to the captain and crew of the R/V Point Sur for enabling the research cruise

References: 1. Van Mooy et al. (2006). PNAS, 103(23): 8607-8612. 2. Martin et al. (2014). PLOS One, 9(8) e103389. 3. Bligh & Dyer (1959). Canadian Journal of Biochemistry and Physiology, 37(8): 911-917. 4. Hummel et al. (2011). Frontiers in Plant Sci., 2: 54. 5. Collins et al. (2016). Analytical Chemistry, 88