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

W. Kumler[1], H. Fredricks[2], J. Ossolinski[2], A. Allen[3], K. Thamatrakoln[4], K. Bidle[4], B. Van Mooy[2], and B. R. Edwards[1]

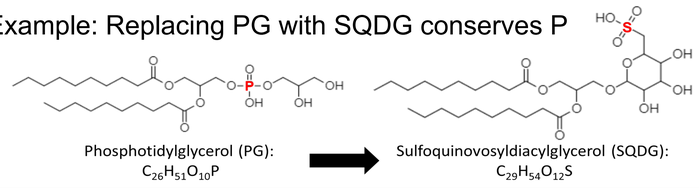
[1]Earth and Planetary Science, UC Berkeley; [2]Marine Chemistry and Geochemistry, WHOI; [3]Biological Oceanography, SIO; [4]Marine and Coastal Sciences, Rutgers

Background

- Phytoplankton blooms are impactful, large-scale events in the ocean that periodically cycle between growth and decay
- Causes of bloom collapse include grazing pressure, viral infection and lysis, and nutrient limitation
- As phytoplankton decay, lipids such as chlorophyll degrade into biomarkers such as pheophytin

Chlorophyll ➡ Pheophytin

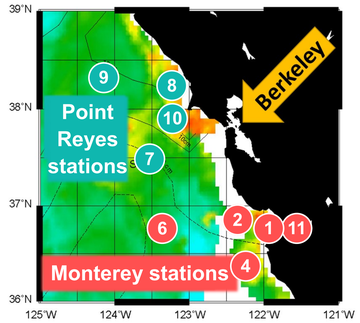
- Traditionally, studies have emphasized nutrient limitation as the major factor in bloom collapse
- Lipids are excellent biomarkers for environmental stressors and marine community composition
- In oligotrophic environments, lipid swapping has been used as a biomarker for nutrient stress
  - P-containing lipids are replaced with betaine lipids[1]
  - N-containing lipids are replaced with glycolipids[2]
- Example: Replacing PG with SQDG conserves P



Research question: Can we use lipids to assess bloom dynamics in eutrophic systems?
Approach: Pair lipidomics with biogeochemical measurements and metatranscriptomic data

Methods

Sampling locations:



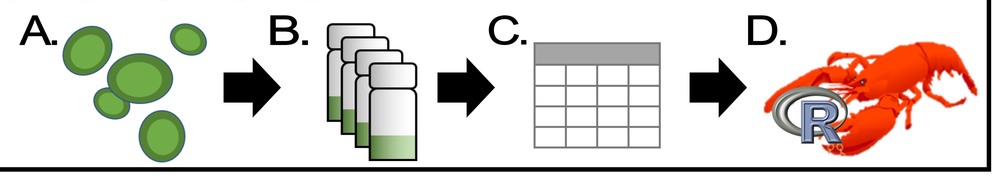
Samples were processed via lipidomics pipeline. Environmental samples were collected from 9 stations in the California Current Ecosystem then

A. filtered onto 0.2 µm Durapore filters and

B. extracted via a modified Bligh & Dyer.[3] These extracts were then

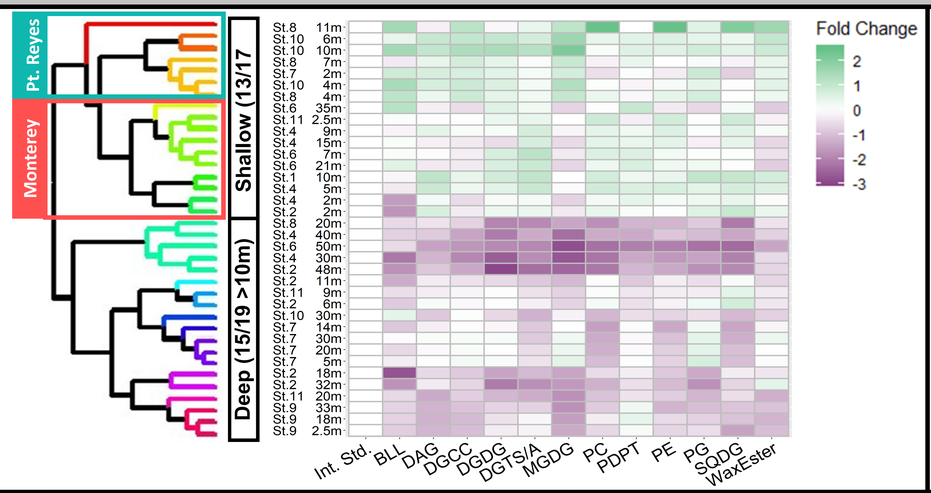
C. analyzed via HPLC-MS[4] and

D. annotated via the R packages xcms, CAMERA, and LOBSTAHS.[5]



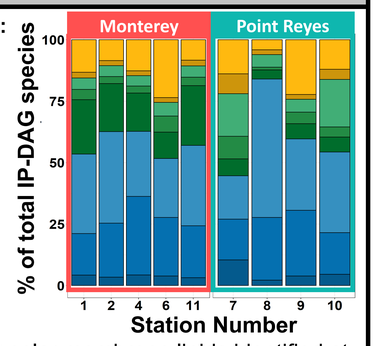
Results

- Heatmap data shows the fold-change of each major intact polar 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 (>10 meters) show a significant decrease in intensity, consistent with particulate organic matter produced in the surface and degraded at depth
- Among the shallow samples, all Point Reyes samples are significantly different from all Monterey samples

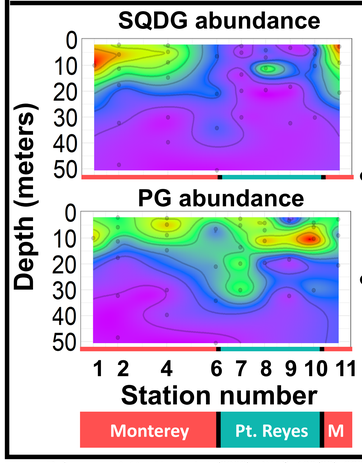


Common IP-DAGs:

- DGTS/DGTA
- DGCC
- MGDG
- DGDG
- SQDG
- PC
- PE
- PG

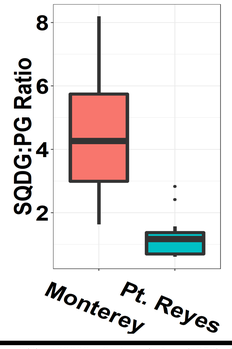


- Common intact polar membrane lipids identified at every station
- Variation in relative abundances imply either nutrient stress induced lipid swapping or shifts in community structure



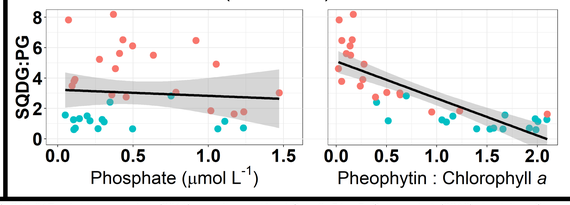
- PG is a ubiquitous lipid found in all domains of life
- SQDG is less common, and produced by cyanobacteria & photosynthetic eukaryotes

- Monterey stations have SQDG:PG ratios statistically different from Point Reyes stations (Mann-Whitney U, p-value < 0.001, n = 36

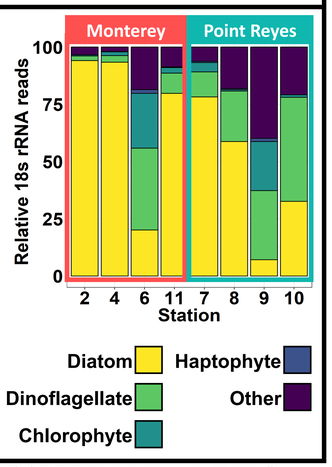


- Oligotrophic SQDG:PG values typically vary between 2 and 7[7]; identical to the Monterey metrics
- Is Monterey nutrient-limited, or is the SQDG:PG biomarker measuring something else?

- SQDG:PG and phosphorus concentration are very weakly correlated (R^2 < 0.01)
- More direct proxies for bloom health, such as chlorophyll: pheophytin ratios, show that SQDG:PG correlates strongly with bloom health (R^2 = 0.65)



- 18s rRNA sequences reveal that the SQDG:PG biomarker is instead a metric for community shift in eutrophic regions



Conclusions

- Lipidomics is a powerful technique for assaying environmental lipid diversity and abundance
- The lipid signature of phytoplankton communities varies dramatically, even over small spatial and temporal regions
- Traditional nutrient stress biomarkers such as SQDG:PG can become biomarkers for community shifts in eutrophic environments

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