California Current microbiomes: baselines and drivers

Nastassia V. Patin[1,2], Kelly D. Goodwin[1]

1. Ocean Chemistry and Ecosystems Division, NOAA Atlantic Oceanographic and Meteorological Laboratory
2. Cooperative Institute for Marine and Atmospheric Studies, Rosenstiel School of Marine, Atmospheric, and Earth Science, University of Miami

Importance

The California Current System (CCS) is environmentally, economically, and culturally valuable. It houses major fisheries and is impacted by oceanographic processes like marine heat waves and upwelling, which are predicted to be impacted by climate change. Understanding baseline microbial and plankton communities will help predict broader ecosystem change.

Approach

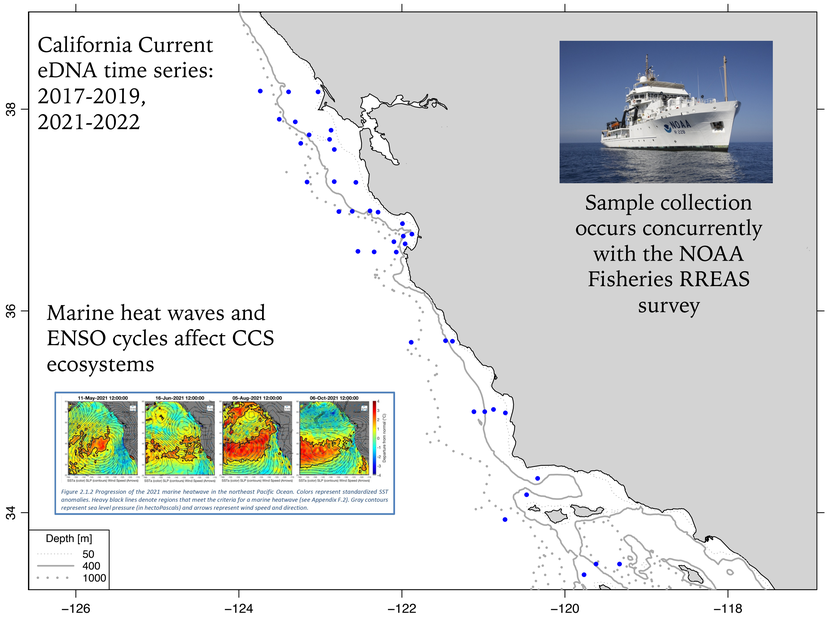
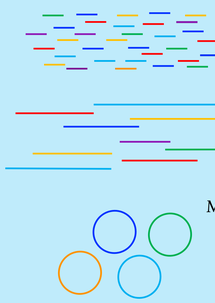


Figure 2.1.2 Progression of the 2021 marine heatwave in the northeast Pacific Ocean. Colors represent standardized SST anomalies. Heavy black lines denote regions that meet the criteria for a marine heatwave (see Appendix F.2). Gray contours represent sea level pressure (in hectoPascals) and arrows represent wind speed and direction.

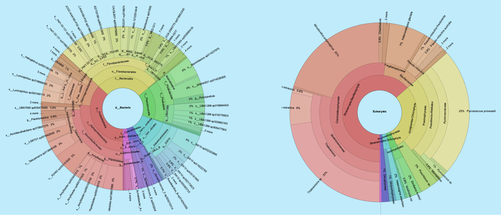
Sequencing and bioinformatics



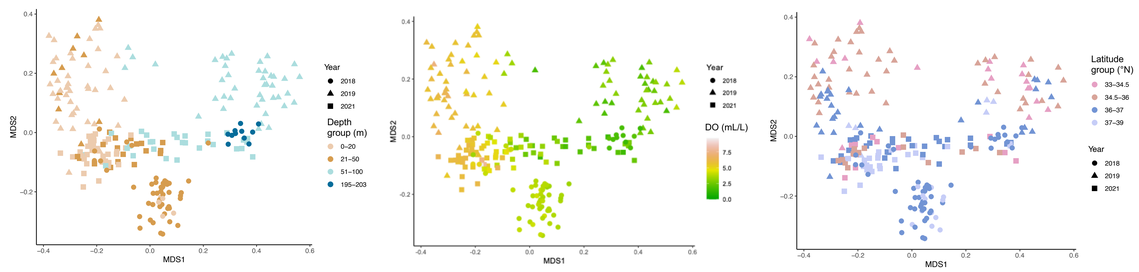
Shotgun metagenomes provide taxonomy, biochemical function, and whole genome sequences

Short reads are mapped back to contigs and MAGs for relative abundances of genes and taxa

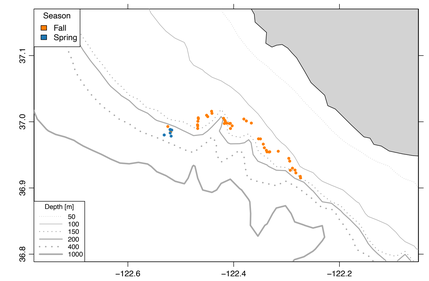
Taxonomy encompasses both prokaryotic and eukaryotic taxa

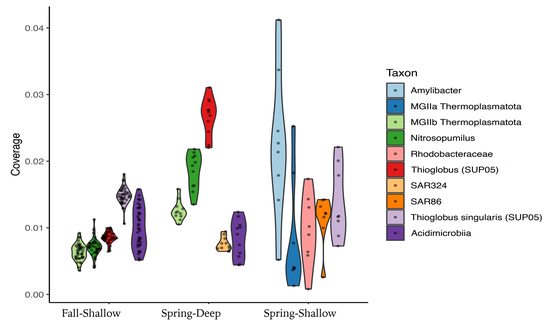


CCS microbiomes are shaped by depth, oxygen, latitude



MAGs show biochemical functions of water masses (2018)

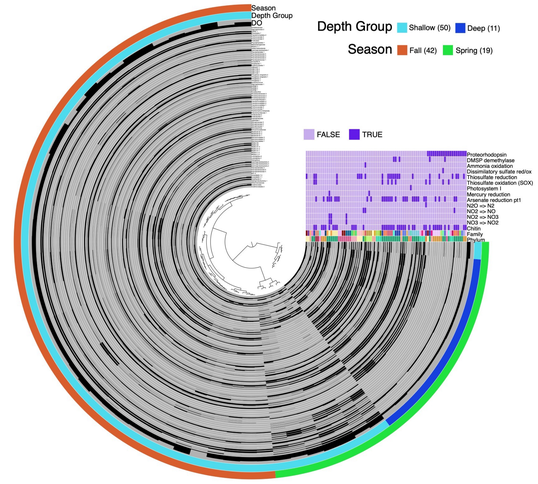




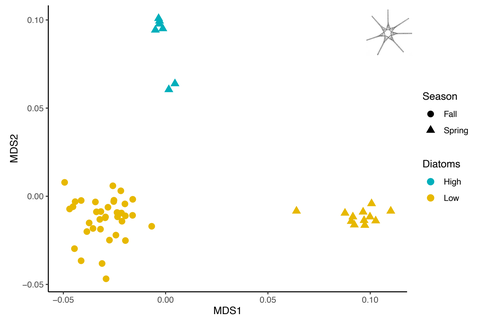
Top five most prevalent taxa in each season-depth group

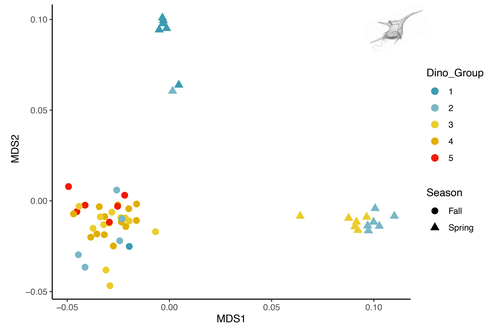
Functional differences include genes involved in nitrogen, sulfur, and arsenic cycling

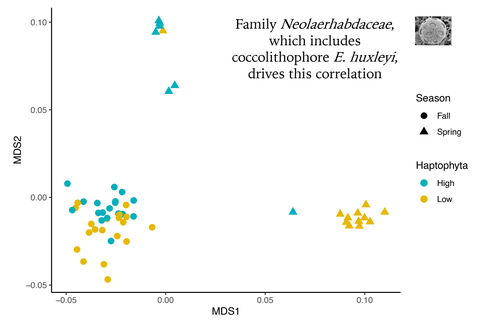
Biochemical processes are largely aerobic but include functions linked to low oxygen levels



Diatom, dinoflagellate, and haptophyte levels correlate with microbiomes (2018)

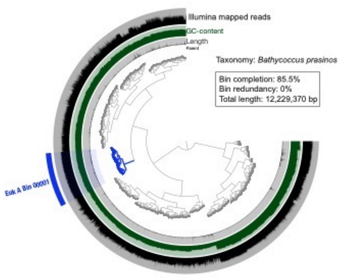


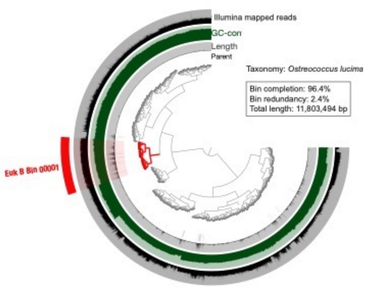




Family *Neolaerhabdaceae*, which includes coccolithophore *E. huxleyi*, drives this correlation

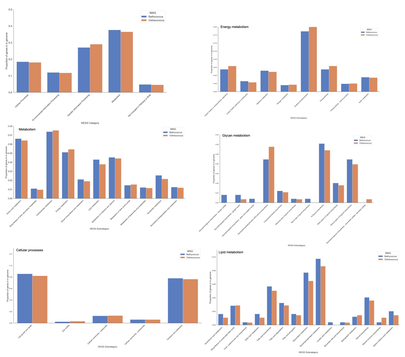
Beyond microbes: Long read sequencing reveals eukaryotic population distributions

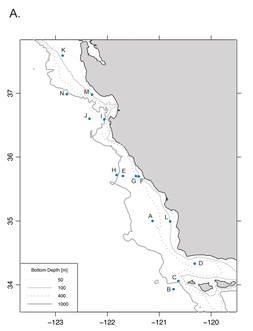




MAGs of ecologically important photosynthetic eukaryotes improve our understanding of baseline phytoplankton communities

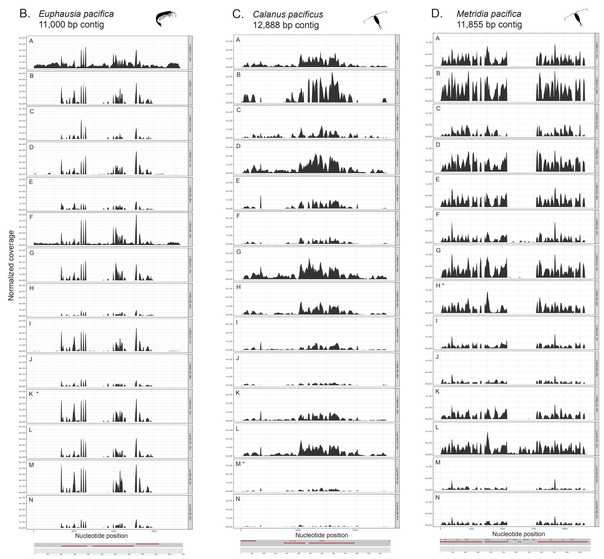
Bathycoccus and *Ostreococcus* are two of the three globally dominant picoprasinophyte lineages





Site	Sample depth (m)	Bottom depth (m)
A	10	560
B	50	1863
C	23	907
D	11	337
E	28	892
F	10	92
G	15	350
H	45	1091
I	7	680
J	26	2746
K	13	80
L	10	88
M	5	86
N	27	1178

* source sample of reference contig
location of rRNA genes on contig



Zooplankton marker gene coverages show population microdiversity and biogeography