

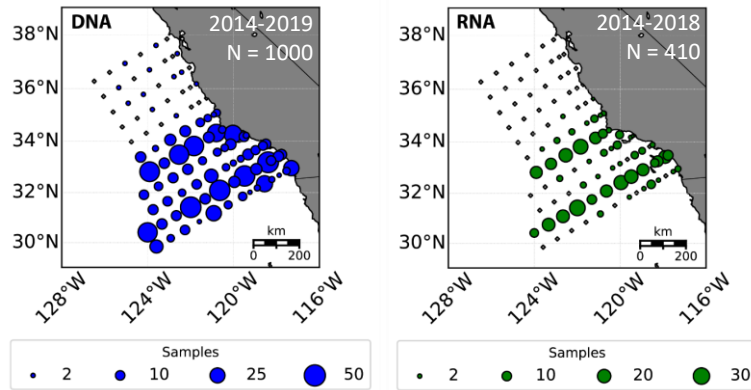
NOAA-CalCOFI Ocean Genomics (NCOG): Six years and counting

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Introduction

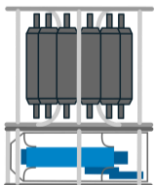
The NOAA-CalCOFI Ocean Genomics (NCOG) project has been collecting DNA and RNA on all CalCOFI cruises since 2014.



NCOG enables molecular-based assessments of diversity and functional activity to be examined in the context of traditional CalCOFI and CCE-LTER measurements.

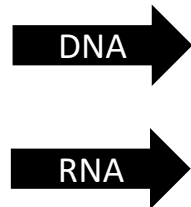
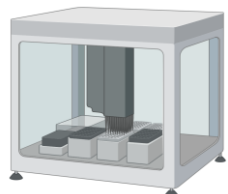
Methods

Seawater collection at 4 depths:



- 10m (DNA+RNA)
- Chl max (DNA+RNA)
- 170m (RNA)
- 515m (RNA)

Semi-automated nucleic acid extraction and library preparation



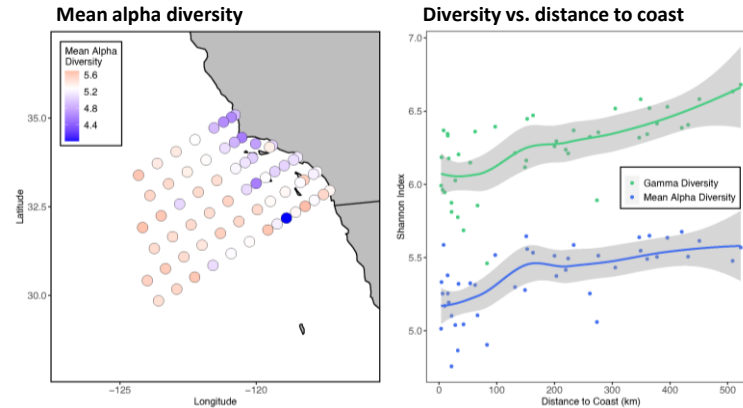
Amplicon Sequencing: 16S-V4/V5, 18S-V4, 18S-V9. *Future*: 12S, *Pseudo-nitzschia* ITS2



Prokaryotic + Eukaryotic metatranscriptomics

Science Highlight

James et al. (in prep) Ecological response of the pelagic ocean microbiome to cross shelf variation in physical forcing in a coastal upwelling biome

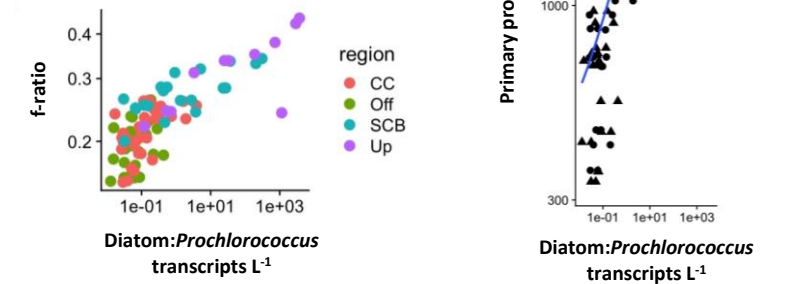


For different microbial taxonomic groups, cross-shore gradients in community structure and diversity are most common. In nearly all examined groups, nitracline depth and chlorophyll *a* are the strongest predictors of community structure and diversity.

Science Highlight

Zeigler Allen et al. (in prep) Regional structuring of the pelagic ocean microbiome in the Southern California Current Ecosystem

Total diatom:*Prochlorococcus* mRNA is strongly correlated with net primary productivity (NPP) and the predicted f-ratio. Therefore, this mRNA ratio correlates with expected patterns of nutrient utilization with *Prochlorococcus* and diatoms dominating at stations more favorable for regenerated or new production, respectively.



Interested in using genomics data? Get in touch.

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Open protocols!

protocols.io/workspaces/ae-allen-lab

github.com/allenlab