

Füßy, Z., Lampe, R. H., Phaeocystis Sequencing Consortium; Allen, A. E. GENOME-RESOLVED BIOGEOGRAPHY OF PHAEOCYSTALES, COSMOPOLITAN BLOOM-FORMING ALGAE. Joint Meeting at the University of Washington, Seattle, WA - 29 July-1 August, 2024

Phaeocystis is a genus of nanoplanktonic haptophytes, prevalent in all of the world's oceans. At least three Phaeocystis species form large mucilaginous colonies that contribute to high-biomass blooms, making them major players in biogeochemical cycles, especially of carbon and sulfur. To investigate the ecological success of these primary producers, we assembled genomic data for thirteen Phaeocystis strains and annotated three with the highest contiguity. Using these data and additional metagenome-assembled genomes, we present a robust phylogeny for Phaeocystis and their sister clade, identifying several undescribed but abundant lineages. We distinguish two major ecological distribution patterns, cosmopolitan and polar, with fine-tuned preferences for nutrients, temperature, and motility. The gene repertoires of three annotated Phaeocystis reference genomes reflect a unique strategy of gene expansion among algae: repetitive elements, horizontal gene transfer, and full-length endogenous virus insertions. Phaeocystales thus emerge as an ecologically versatile group with diverse adaptations to biotic and abiotic stressors.

George, E. E., Wood, S. M., Li, H. T., Schreier, J. E., Lampe, R. H., Zheng, H., J. McCarthy, J. K., Moran, M. A., Allen, A. E. A CROWDED PHYCOSPHERE: MICROBIAL INTERACTIONS BETWEEN DIATOMS, BACTERIA AND NANOFLAGELLATES

The nutrient-rich phycosphere surrounding phytoplankton cells attracts bacteria and bacterivores like nanoflagellates, but the impact of nanoflagellate grazing on bacterial communities within the phycosphere and its subsequent effect on phytoplankton growth remains unknown. To explore these interactions, we established seven marine nanoflagellate cultures from diatom blooms in southern California, including an epiphytic nanoflagellate attached to diatom colonies. Co-culture experiments demonstrated that the presence of nanoflagellates and bacteria increased diatom growth compared to diatom cultures with bacteria alone. We hypothesized that nanoflagellate grazing on bacteria releases organic nitrogen (e.g. nitrate), thereby increasing nitrogen availability for phytoplankton. However, we found reduced diatom growth in nitrate-limited treatments when bacteria and nanoflagellates were present, suggesting that resource competition between phytoplankton and bacteria increases in nutrient-limited systems. Additionally, prey preference experiments using fluorescent bacterial strains revealed that nanoflagellates selectively graze on bacteria which influences the bacterial community structure and nutrient dynamics in the phycosphere. Overall, these diatom-nanoflagellate-bacteria experimental systems provide a tool to study top-down control on phytoplankton-associated bacteria and its impact on phytoplankton growth.

Wood, S. M, Rabines, A., Zheng, H., Fusy, Z., Thukral, M., Lampe, R. H. Schulberg, A., Moore, B. S., Allen, A.E., ENVIRONMENTAL DETECTION OF PSEUDO-NITZSCHIA SPP. AND DOMOIC ACID BIOSYNTHESIS IN THE SANTA BARBARA CHANNEL, 2019-2023. 2024 PSA-ISOP-ISEP. Joint Meeting at the University of Washington, Seattle, WA - 29 July-1 August, 2024

Domoic acid (DA), a type of neurotoxins, is known for causing amnesic shellfish poisoning. DA enters the food web through bioaccumulation, affecting various marine organisms including shellfish, fish, marine mammals, and humans. Pseudo-nitzschia, a type of diatom, is responsible for DA production. From May 17th to June 12th, 2022, in the Santa Barbara Channel, two underwater autonomous vehicles (LAUVS) with Environmental Sample Processors (ESP) documented transition from the end of an algal bloom, with relatively low but present DA signals, to the beginning of an upwelling event. This upwelling plume later fueled a large Pseudo-nitzschia bloom with high DA level in July. This transition provided an opportunity to study the dynamics and triggers of DA productions. The LAUVS and ESPs tracked changes in physical properties and phytoplankton communities within high chlorophyll water masses. Analysis of amplicons data revealed transitions in the diatom communities- from a bloom dominated by Eucampia, supported by real-time image data, to an increase abundance of Minutocellus. ITS2 amplicons results identified *P. multiseriata* as the dominant toxigenic Pseudo-nitzschia species during this period, which contrasted with the typical presence of *P. australis* species in the region. Metatranscriptomics analysis showed intriguing correlations between biotic and abiotic factors during this transition period. Notably, there was a higher expression of *dabA* genes compared to other *dab* genes (B,C,D), which are responsible for the DA signals.

Lampe, R. H., Rabines, A. J., Schulberg, A., Goericke, R., Venrick, E. L., Zheng, H.,; Zeigler, L. A., Goodwin, K. D., Allen A. E. DIATOM ABUNDANCE, DIVERSITY, AND GENE EXPRESSION PATTERNS IN A COASTAL UPWELLING BIOME. 2024 PSA-ISOP-ISEP. Joint Meeting at the University of Washington, Seattle, WA - 29 July-1 August, 2024

Coastal upwelling regions are among the most biologically productive regions in the ocean: a phenomenon attributed to the frequent delivery of cold, nutrient-rich water that fuels diatom-dominated phytoplankton blooms. Consequently, diatoms drive biogeochemical cycling and support highly productive fisheries in upwelling ecosystems. Here we comprehensively examine pelagic diatom abundances and diversity in the California Current Ecosystem, a coastal upwelling biome, via standardized surveys that comprise over 1,500 18S DNA samples supported with metatranscriptomics, microscopic cell counts, taxon-specific pigments, and a suite of environmental measurements. Surveys spanned dynamic nearshore environments to offshore oligotrophic waters with seasonal resolution over seven years capturing a high degree of biogeochemical and temporal variability. In contrast to other major phytoplankton groups, seasonal-driven upwelling conditions were distinctly associated with patterns in diatom abundances, diversity, and gene expression with upwelling resulting in increased diversity. Overall, diatom communities are dominated by large chain-forming

genera *Chaetoceros*, *Thalassiosira*, and *Pseudo-nitzschia*, but these taxa exhibit signs of regional dispersal limitation that is linked to export from the euphotic zone. By leveraging comparable sequencing data from global datasets, we provide updated estimates of both regional and global pelagic diatom diversity

Schulberg, A., Stief, P., McCarthy, J., Lampe, R., Li, H-T., Füssy, Z., Allen, A.E.
DISSIMILATORY NITRITE REDUCTASE ENZYME SUPPORTS DIATOM SURVIVAL UNDER ANOXIA AND IRON LIMITATION

Diatoms thrive throughout the world's oceans, and this ecological dominance can be partially attributed to a novel nitrogen metabolic strategy; uniquely to diatoms, two distinct nitrite reductase (NiR) enzymes within the nitrate assimilation pathway are functional. Previous transcriptional studies suggest a partitioning of duties, where ferredoxin (Fd) dependent NiR is upregulated in ideal light conditions, and NAD(P)H dependent NiR is upregulated in darkness. This study demonstrates that NAD(P)H-NiR also enables diatom survival in oxygen deficient and iron limited marine environments. Marine eukaryotic dissimilatory nitrite reduction to ammonium (DNRA) was recently first observed in diatoms under anoxic conditions, but the enzymatic pathway of this process is unknown. CRISPR-Cas9 mediated Fd-NiR and NAD(P)H-NiR knockout cell lines in *Phaeodactylum tricornutum* were probed for DNRA activity via stable isotope experiments, quantifying ¹⁵N labeled ammonium ejected from the diatoms under dark, anoxic conditions; the NAD(P)H-NiR-only cell line expelled labeled ammonium, indicating that NAD(P)H-NiR enables DNRA in diatoms. Comparative growth rates of NiR knockout strains under varying degrees of iron stress suggests NAD(P)H-NiR contributes to diatom survival in iron depleted conditions, likely due to its lower iron requirement for nitrite reduction compared to Fd-NiR. This work is supported ecologically through environmental metatranscriptomics generated from global oxygen minimum zones, where differential diatom NiR expression is correlated with nutrient and oxygen availability.

Hou, L., Preston, C., Ryan, J., Scholin, C., Ussler, B., Allen, A. E.,
AN ECOLOGICAL STUDY OF A TRANSIENT BLOOM OF TOXIGENIC PSEUDO-NITZSCHIA MULTISERIES IN SANTA BARBARA CHANNEL IN 2022. 2024 PSA-ISOP-ISEP Joint Meeting at the University of Washington, Seattle, WA - 29 July-1 August, 2024

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phytoplankton communities within high chlorophyll water masses. Analysis of amplicons data revealed transitions in the diatom communities- from a bloom dominated by *Eucampia*, supported by real-time image data, to an increase abundance of *Minutocellus*. ITS2 amplicons results identified *P. multiseries* as the dominant toxigenic *Pseudo-nitzschia* species during this period, which contrasted with the typical presence of *P. australis* species in the region. Metatranscriptomics analysis showed intriguing correlations between biotic and abiotic factors during this transition period. Notably, there was a higher expression of *dabA* genes compared to other *dab* genes (B,C,D), which are responsible for the DA signals.