

DYNAMICS OF PHOTOSYNTHETIC PLANKTON IN THE OLIGOTROPHIC
NORTH PACIFIC SUBTROPICAL GYRE

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ABSTRACT

The North Pacific Subtropical Gyre (NPSG) is the largest marine ecosystem on Earth. However, the diversity and population dynamics of photosynthetic plankton in this ecosystem are not well understood, owing in part to undersampling of the habitat. In this dissertation, I utilized time-series observations at Station ALOHA (22°45' N, 158° W), the field site for the Hawaii Ocean Time-series (HOT) program, to examine temporal dynamics in size-dependant photophysiology, population structure of eukaryotic phytoplankton, and contributions of several eukaryotic phytoplankton taxa to particle flux. Photosynthesis-irradiance (P-E) relationships for two size-fractions ($> 2 \mu\text{m}$ and $0.2\text{-}2 \mu\text{m}$) of phytoplankton were used to evaluate variability in photophysiology over a 5 year period (2004-2009) in the NPSG. Our results indicate although larger phytoplankton appear to constitute a relatively small fraction of phytoplankton biomass and production, the photophysiological responses of these organisms demonstrate high variability. Despite persistently oligotrophic conditions, phytoplankton in this larger size class appear to undergo temporally dynamic variations in growth. Population dynamics of three major groups of eukaryotic phytoplankton in the larger size class were further investigated over a 2 year period (2007-2009). Quantitative polymerase chain reaction (QPCR) assays were developed based on form 1D *rbcL* genes for diatoms, prymnesiophytes and pelagophytes. Diatom *rbcL* genes were typically the most abundant among these groups, with elevated abundances often occurring in the upper euphotic zone (0-45 m) during the summer. Abundances of prymnesiophyte and pelagophyte *rbcL* genes often increased in the lower euphotic zone (75-125 m) during fall and winter months. Analyses of upper ocean (150 m) sediment trap samples revealed that export of prymnesiophytes and pelagophytes from

the euphotic zone tended to be greatest in the spring and fall. In contrast, diatom *rbcL* gene flux was often greatest in the summer when particulate carbon export was maximal. To gain insight into the role of diatoms in biogeochemical dynamics in this ecosystem, I examined temporal variability in upper ocean diatom population structure and their contributions to particle export at Station ALOHA. PCR amplification, cloning and sequencing of diatom *rbcL* genes provided insight into the phylogenetic structure of diatom populations in this ecosystem. QPCR amplification of *rbcL* genes from five major diatom genera (*Chaetoceros*, *Pseudonitzschia*, *Nitzschia*, *Rhizosolenia* and *Hemiaulus*) revealed that diatom population structure has high temporal variability. Diatoms belonging to the genera *Pseudonitzschia/Nitzschia* were typically the most abundant of the *rbcL* phylotypes examined, while *Hemiaulus* and *Rhizosolenia rbcL* gene abundances increased episodically in the upper euphotic zone in summer. Analyses of the upper ocean (150 m) sediment trap samples suggested that *Hemiaulus* group contributed the most to diatom *rbcL* gene fluxes. Sediment trap collections in the deep sea (4000 m) indicated a narrowly focused peak in the export of the *Hemiaulus*, *Chaetoceros* and *Rhizosolenia* groups in the mid-summer months. Our study suggests that temporally dynamic growth of the larger size phytoplankton, especially diatoms, contribute significantly to the new production in the upper ocean and carbon flux into the deep ocean.

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