**Diatom Dynamics in the North Pacific Subtropical Gyre (NPSG)**

**Abstract**

Diatoms generally comprise minor components of plankton biomass in oligotrophic open ocean ecosystems. However various lines of evidence suggest diatoms are major contributors to annually recurring phytoplankton blooms in the NPSG. Moreover, these diatom-dominated blooms play central roles in the exchange of material between the upper ocean and the deep sea. Our understanding of diatom bloom dynamics has been hampered in part by lack of knowledge on temporal variability in diatom community structure. In this study, we investigated the temporal and spatial dynamics in diatom assemblages in the NPSG. Quantitative PCR primers targeting diatom rbcL genes were designed and employed to examine time and space dependent changes in the abundances of several major diatom genera. In addition, we evaluated the contributions of several groups of diatoms to particulate matter export at Station ALOHA (22°45’ N, 158°W).

**Introduction**

Satellite observations: Satellite remote sensing of surface ocean chlorophyll concentrations in the NPSG indicate recurring summertime phytoplankton blooms. Direct observations: In 12 of the past 20 years (1989-2008) shipboard measurements indicate diatoms comprise important components of these blooms.

**Objectives**

- Development of an rbcL gene based method for quantification of specific diatom groups
- Investigation of the temporal and spatial variability in diatom-community structure in the NPSG
- Examination of the contributions of the specific diatom groups to carbon export

**Approaches**

**Sample collection**

*Time-series:* Monthly cruises to Station ALOHA (2007-2009)
*Spatial variation:* Station ALOHA vs Subtropical Convergence Zone (32°N, STCZ)

**Identification and quantification of diatoms**

Molecular marker: rbcL gene – large subunit of RuBisCO

PCR – clone library and QPCR to study the diversity and abundances of diatoms from the NPSG

**Phylogenetic relationships among diatom rbcL sequences obtained from the NPSG**

**Conclusions**

- A molecular approach based on rbcL gene was developed to investigate diatom community structure in the NPSG.
- The population structure of the diatoms in the NPSG demonstrates high temporal and vertical variability.
- Specific groups of diatoms display different temporal patterns of vertical flux to the deep ocean.
- Abundances and fluxes of specific diatom groups were significantly higher in the STCZ comparing to St. ALOHA.
- The temporal and spatial dynamics of other diatom groups, such as Rhizosolenia, is going to examined in the near future.