Data Inventory

Type of data collection

The raw data collected in this study include a large amount of genomic sequences from epibiotic and planktonic bacterial community, algal growth measurements as indicated by fluorescent assay under different biotic and abiotic conditions, domoic acid (DA) production by different species of *Pseudo-nitzschia* and the DA concentration under different conditions, measurements of bacteria and viruses growth and decline during co-incubation with algal culture, and bacterial extracellular enzymes and activities.

The physical, chemical, and biological parameters will be obtained at the field sampling-sites through harmful algal bloom (HAB) monitoring program, including water temperature, salinity, rainfall, chlorophyll and phytoplankton species and abundance.

Plans for sharing and eventually archiving the data

1) The genomic data after validation and trimming will be deposited in NCBI data bases for public access.
2) More "unusual" data such as species identification and counts, growth and decay experiments, toxin production under specific conditions will be provided as meta data on PI web site and finalized data supplied to BCO-DMO data management facility.
3) The environmental parameters at the field sites will be the property of the HAB mapping program owned by other researchers. We are using their metadata to interpret the relationship between environmental conditions and microscale bacterial-algal interactions. These metadata has already been archived by other researchers.