

RV Wecoma 2002, Chief Scientist: Ev Sherr
Data from discrete samples, Oregon upwelling system
Additional notes: December 30, 2005

Section 4. Scientific content of dataset

Water samples were collected from General Oceanics 5 L Niskin bottles mounted on a rosette.

Name of parameter	Units
Station latitude	°N
Station longitude	°W
depth	meters
nitrate	micromoles per liter
nitrite	micromoles per liter
phosphate	micromoles per liter
silicate	micromoles per liter
chlorophyll a	micrograms per liter
bacterial leucine incorporation	picomoles leucine per hour
heterotrophic bacterial abundance	cells per ml
abundance of high nucleic acid cells	cells per ml
abundance of low nucleic acid cells	cells per ml
abundance of <i>Synechococcus</i>	cells per ml
abundance of diatoms	cells per ml
abundance of picoeukaryotes	cells per ml
abundance of CTC-positive cells	cells per ml

The analyses for phosphate, nitrate plus nitrite (N+N), nitrite, and silicic acid (silicate) were performed using a hybrid Technicon AutoAnalyzerII™ and Alpkem RFA300™ system following protocols modified from Gordon et al. (1994). Chlorophyll *a* concentrations were determined using a Turner Designs 10-AU fluorometer (Strickland and Parsons 1972). Incorporation rates of ³H-leucine by bacterioplankton present in whole seawater samples were assayed following the protocol of Smith and Azam (1992). A Becton-Dickinson FACSCalibur flow cytometer was used for all cell enumeration (heterotrophic bacterial abundance, phytoplankton abundance, and abundance of CTC-positive cells). The details on the methods, sampling locations, and data are given in Longnecker et al. (2005)

References cited:

Gordon, L.I., J. J. C. Jennings, A.A. Ross and J.M. Krest (1994). A suggested protocol for continuous flow automated analysis of seawater nutrients (phosphate, nitrate, nitrite and silicic acid) in the WOCE Hydrographic Program and the Joint Global Ocean Fluxes Study. *WOCE Operations Manual, WOCE Report No 68/91 Revision 1, 1994.*

- Longnecker, K., B.F. Sherr and E.B. Sherr (2005). Activity and phylogenetic diversity of high and low nucleic acid content, and ETS-active, bacterial cells in an upwelling ecosystem. *Appl Environ Microbiol* 65: 7737-7749.
- Smith, D.C. and F. Azam (1992). A simple, economical method for measuring bacterial protein synthesis rates in sea water using ^3H -leucine. *Mar Microbial Food Webs* 6: 107-114.
- Strickland, J.D.H. and T.R. Parsons (1972). *A Practical Handbook of Seawater Analysis*. Fisheries Research Board of Canada. Ottawa.

References using these data:

- Longnecker, K. (2004). Bacterioplankton in the Oregon upwelling system: distribution, cell-specific leucine incorporation, and diversity. Ph.D. thesis, Oregon State University.
- Longnecker, K., D.S. Homen, E.B. Sherr and B.F. Sherr (accepted). Similar community structure of biosynthetically active prokaryotes across a range of ecosystem trophic states. *Aquatic Microbial Ecology*.
- Longnecker, K., B.F. Sherr and E.B. Sherr (2005). Activity and phylogenetic diversity of high and low nucleic acid content, and ETS-active, bacterial cells in an upwelling ecosystem. *Applied and Environmental Microbiology* 65: 7737-7749.
- Morris, R.M., K. Longnecker and S.J. Giovannoni (submitted to *Environmental Microbiology*). *Pirellula* and OM43 are among the dominant lineages identified in an Oregon coast phytoplankton bloom.
- Sherr, E.B., B.F. Sherr and K. Longnecker (in revision for *Deep-Sea Research I*). Distribution of bacterial abundance and cell-specific nucleic acid content in the northeast Pacific Ocean.

Section 5. Data format of dataset

Data are in ASCII format (comma-separated), with 356 rows and 16 columns (listed in order in the table for Section 4).

Contact people for the data are as follows:

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