---TITLE: Lomas_Phytoplankton_subm_Dec_2011.xls

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---FUNDING SOURCE AND GRANT NUMBER:
NSF, Arctic Natural Sciences, Grant No. 0732359
---DATA SET OVERVIEW:
-These data were collected from process stations and other stations where my group collected bulk chlorophyll (Chl) measurements on the following BEST cruises: HLY08-02, HLY08-03, HLY09-02, KN195-10, TN249 and TN250. Data presented are direct pico- and nano-phytoplankton counts by flow cytometry and direct counts of microphytoplankton by inverted microscopy. For each phytoplankton group we derived an estimate of carbon per population (ie., carbon per cell times cell abundance). Carbon per cell for pico- and nano-phytoplankton were determined from the relationship between carbon per cell and forward angle light scatter per cell (e.g., DuRand *et al.*, 2001) but calibrated for our flow cytometer and analysis settings. Carbon per cell for microphytoplankton was determined by determining major and minor axes, and applying the appropriate geometric shape (e.g., Hillebrand *et al.*, 1999; Vadrucci *et al.*, 2007) to calculate biovolume. Biovolume was then converted to carbon using the equations of Menden-Deuer and Lessard (Menden-Deuer and Lessard, 2000). All samples were collected on the eastern Bering Sea shelf from 55-63^{o}N and 164-180^{o}Wduring spring and summer. At process stations, seven (7) depths were sampled representing roughly the 100%, 55%, 30%, 17%, 9%, 5% and 1.5% light depths. At other stations, generally four (4) depths were sampled and were chosen as surface, deep chlorophyll maximum, and two other depths selected based upon equal distributions throughout the water column or profile features (e.g., elevated concentrations near the bottom).

This data file reflects samples analyzed to date. As additional analyses are done, this file will be updated and resubmitted.

---INSTRUMENT DESCRIPTION:
- Samples for flow cytometric analysis were analyzed on a Becton Dickenson (formerly Cytopeia, Inc.) Influx cytometer. *Synechococcus*-like and Cryptophyte-like cells were separated from other phytoplankton by the presence of phycoerythrin fluorescence, with *Synechococcus*-like cells determined as the population between 1-2 µm (based upon forward scatter signals calibrated to standard beads), and Cryptophyte-like cells determined as those larger than 3 µm. Two other populations (presumed eukaryotes) were determined and are called Eukaryote-1

(<2.88 μm beads) and Eukaryote-2 (>2.88 μm beads) and are distinct from the other populations due to the lack of phycoerythrin fluorescence. Samples for microphytoplankton were analyzed on a Zeiss Axiovert inverted microscope at 200-400x and identified to the lowest taxonomic level possible. Measurements were made using a stage micrometer to calibrate the measuring tool in the AxioVision imaging software.

---DATA COLLECTION and PROCESSING:
-All samples were directly collected from the Niskin bottles. Pico- and nano-phytoplankton samples were fixed with 0.5% (final concentration) paraformaldehyde for two hours then stored at -80^{o}C until analysis. Microplankton samples were fixed with buffered formaldehyde (2% final concentration) and alkaline Lugol's solution (5% final concentration) and stored in amber glass bottles at room temperature until analysis. Pico- and nano-phytoplankton samples were thawed in the dark prior to analysis and then analyzed for 6min. Populations (defined above) were enumerating using FCS Express 4.0 and converted to cell abundances using the total volume analyzed method (Sieracki *et al.*, 1993). Microplankton samples, 100ml subsamples, were settled in a Utermohl chamber for 24hours and then two perpendicular transects were examined with all cells counted and sized. The abundances were then scaled to the total chamber volume and show very tight agreement with duplicate samples where the entire volume had been counted (Whole = 1.01 x transect + 0.5; R^2 = 0.95; N=12).

-Description of quality control procedures. Duplicate analyses were run (roughly 5% of the total number of samples) with the average difference found to always be <10%, and often better depending upon the abundance of organisms.

---DATA FORMAT:
-Data are reported as a comma delimited ASCII text file. Reported data are the averages where replicate analyses were made. File naming convention is by PI's last name, parameters reported (ie., Phytoplankton) and date submitted.

-Colum header information for dataset.

Cruise	Cruise name
Station_No.	Station Number within each cruise
Station_Name	Station Name for each Station Number
Cast _#	Consecutive CTD cast number within each cruise
Date/Time (UTC)	YYYYMMDDhhmmss; all times are time in the water
DecLat (oN)	Decmial degree latitude
DecLong (oW)	Decimal degree longitude
Nominal_Depth (m)	nominal depth
Niskin	niskin number sample collected from
Synechococcus abundance (x10^3 cells L^{-1})	cell abundance analyzed by flow cytometry
Cryptophyte abundance (x10^3 cells L^{-1})	cell abundance analyzed by flow cytometry
Eukaryote-1 (x10^3 cells L^{-1})	cell abundance analyzed by flow cytometry
Eukaryote-2 (x10^3 cells L^{-1})	cell abundance analyzed by flow cytometry

Synechococcus carbon (ugC L^{-1})	Population carbon calculated as the product of cell abundance and carbon per cell. Carbon per cell estimated from forward angle light scatter
Cryptophyte carbon (ugC L^{-1})	Population carbon calculated as the product of cell abundance and carbon per cell. Carbon per cell estimated from forward angle light scatter
Eukaryote-1 carbon (ugC L^{-1})	Population carbon calculated as the product of cell abundance and carbon per cell. Carbon per cell estimated from forward angle light scatter
Eukaryote-2 carbon (ugC L^{-1})	Population carbon calculated as the product of cell abundance and carbon per cell. Carbon per cell estimated from forward angle light scatter
Diatom abundance (cells L^{-1})	Cell abundance by inverted microscopy
Dinoflagellate abundance (cells L^{-1})	Cell abundance by inverted microscopy
Flagellate abundance (cells L^{-1})	Cell abundance by inverted microscopy
Diatom carbon (ugC L^{-1})	Population carbon calculated as the produce of cell abundance and carbon per cell. Carbon per cell determined by biovolume calculation and conversion using published carbon to biovolume calculations
Dinoflagellate carbon (ugC L^{-1})	Population carbon calculated as the produce of cell abundance and carbon per cell. Carbon per cell determined by biovolume calculation and conversion using published carbon to biovolume calculations
Flagellate carbon (ugC L^{-1})	Population carbon calculated as the produce of cell abundance and carbon per cell. Carbon per cell determined by biovolume calculation and conversion using published carbon to biovolume calculations
Large Autotroph Carbon (ugC L^{-1})	Sum of diatom, dinoflagellate and flagellate carbon values
Chla >5um (ugChla L^{-1})	Chla data from other Lomas datasets submitted. Included here for ease of reference
C_Chla (ugC ugChla^{-1})	Carbon to chla ratio for large autotrophs calculated as the quotient of the previous two columns

-All missing data are reported as "-9.99", however cells are formatted to report only integers as decimal cell abundances have little value. NOTE: as this more analyses are done this dataset will be updated and recorded below.

-Data version 2.0, December 2011

---DATA REMARKS:

-All data reported are free of known errors, whether in sample collection or sample analysis. Any data where there is a question that would compromise the data quality have been omitted and listed as missing data.

---REFERENCES:

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