The SOLAS BERGEN Mesocosm Experiment: sea surface microlayer dynamics during a phytoplankton bloom.

Introduction:
In May 2008 a SOLAS-NERC funded multidisciplinary project took place at the Marine Biological Station in Bergen, Norway. The diverse research team of micro-biologists, ecologists, oceanographers and biogeochemists studied the dynamics of an induced phytoplankton bloom in a mesocosm system. The high resolution and comprehensive data collected will be used to examine the following hypotheses:

The core hypothesis. The sea surface microlayer (SML) and subsurface water is linked. Biogenic compounds produced by phytoplankton, particularly surfactant compounds in the sub-surface water column, migrate up to the SML. This is particular so during a phytoplankton bloom.

Hypothesis 1. The phytoplankton bloom will cause elevated production of surface active compounds and this will affect the physio-chemical structure of the SML. The presence of a biogenic film, the SML, effects air-sea gas transfer. During a phytoplankton bloom the SML is altered.

Hypothesis 2. The changes caused by the phytoplankton bloom on the SML will alter air-sea gas transfer.

Hypothesis 3. The physio-chemical structure of the SML determines the microbial populations. Particularly, during the plankton bloom labile substrates will be produced causing changes in microbial population structural dynamics in the SML.

Hypothesis 4. As a result of microbial population structural changes (hypothesis 3) bacterial populations can have influence on air-sea gas transfer.

Experimental Design:
- 12 mesocosms were filled with approx. 2,500 L of water collected from the Raunefjord at the end of a natural bloom. The water was pre-filtered (300µm) to remove a large copepod bloom present.
- 6 mesocosms were maintained as controls and 6 had an artificial bloom induced using the Redfield Ratio (N:P 16:1): nitrate 16µmol L⁻¹ and phosphate 1 µmol L⁻¹.
- The temperature of the mesocosms was maintained by circulating pumped fjord water around the outside of the system.
- The mesocosms were sampled daily at 09.00 hrs for 12 days.

Sampling the surface microlayer:
- The SML was sampled with both polycarbonate membranes and a mesh screen (Garrett Screen).
- Membranes sample an approximate depth of 40 µm.
- The mesh screen used in this study sampled an approximate depth of 400 µm.

Preliminary Data: Phytoplankton bloom succession
- The phytoplankton bloom was monitored using standard protocols.
- Both nitrate and phosphate depleted in bloom mesocosms (below).
- The development of the phytoplankton bloom was monitored using chlorophyll a quantification (data not presented) and cell counting using a FACS cell sorter (below).

Parameters measured
- A broad range of parameters were measured during the experiment, including:
  - Surfactant production.
  - Biogenic trace gas and volatile organic compound production (e.g. dimethylsulfide).
  - Bacterioplankton cell counts.
  - Dissolved organic nitrogen and carbon production.
  - Microbial RNA/DNA extraction and community diversity analysis.

Bacterioneuston versus the bacterioplankton:
- Bacteria cell counts made using a FACS cell sorter from subsurface and SML samples collected using the mesh screen showed no differences in cell numbers between the SML and subsurface (see below).
- Bacteria diversity in SML and subsurface samples were compared by extracting DNA, PCR of bacteria 16S RNA genes and denaturing gradient gel electrophoresis (see below).
- Samples collected using membranes show distinct communities in the SML. Furthermore there appears to be little effect of the phytoplankton bloom on bacterial diversity (see below).

Initial findings:
- Bacterial biomass (determined by cell counts) is not different in the SML compared to subsurface water.
- Bacterial diversity (determined by community analysis using DGGE) is different in the SML compared to the subsurface.

Ongoing and future work:
- Bacterial diversity will be studied in more detail to determine the specific populations present in the SML and subsurface water during the course of the bloom.
- Biogeochemical process data will be analysed alongside molecular analysis of key bacterial functional genes hypothesised to drive these specific processes.

References:

Acknowledgments:
- We thank Agnes Aadnesen, Mikal Heldal and Jorun Egge at the University of Bergen for invaluable advice and technical support.
- This research was financially supported by the Natural Environment Research Council, UK.