



The First Meeting of SCOR WG134
Microbial Carbon Pump in the Ocean

Oct. 27-30, 2009

Xiamen, China



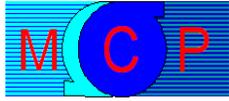
International Council for Science
Scientific Committee on Oceanic Research

The First Meeting of SCOR WG 134

Microbial Carbon Pump in the Ocean

**October 27-30, 2009
Xiamen, China**

Sponsored by
Xiamen University, China
National Science foundation, USA



Meeting catalogue

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► **Workshop Conveners**

Nianzhi Jiao State Key Lab of Marine Environmental Science,
Xiamen University

Farooq Azam Scripps Institution of Oceanography, USA

► **Venue**

Oct. 28 B-206 Zeng Cheng Kui Building, MEL, Xiamen
University

Oct. 29-30 Canghai Hall of Asia Gulf Hotel

► **Accommodation**

Asia Gulf Hotel from Oct. 27-30, on the Ring Road.

► **Secretariat**

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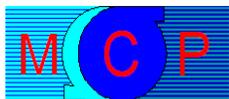
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SCOR WG134 Members

Co-Chairs: Nianzhi Jiao (China) and Farooq Azam (USA)

Other Full Members

Xosé Antón Álvarez-Salgado (Spain)
Chen-Tung Arthur Chen (China-Taipei)
Dennis Hansell (USA)
Gerhard Herndl (Netherlands)
Gerhard Kattner (Germany)
Michal Koblížek (Czech Republic)
Colin Stedmon (Denmark)
Markus Weinbauer (France)

Associate Members

Ronald Benner (USA)
Craig Carlson (USA)
Feng Chen (USA)
Sang-jin Kim (Korea)
David Kirchman (USA)
Ingrid Obernosterer (France)
Nagappa Ramaiah (India)
Carol Robinson (UK)
Richard Sempere (France)
Christian Tamburini (France)
Steven Wilhelm (USA)
Yongfu Xu (China)
Chuanlun Zhang (USA)
Meixun Zhao (China)
Jizhong Zhou (USA)
Susan Ziegler (Canada)



Background of SCOR WG134 on

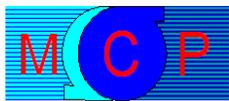
Microbial Carbon Pump in the Ocean

Scientific Committee on Oceanic Research (SCOR) is a leading non-profit organization promoting international cooperation in ocean science. Working Groups (WG) are one of the SCOR most effective activities which deliberate on focused topics and develop publications for the primary scientific literature. All WGs are expected to make significant contributions to advancing understanding of their topics.

Dissolved organic carbon (DOC) in the ocean is comparable in magnitude to the total inventory of atmospheric CO₂, its biogeochemical behavior is critically important in understanding global carbon cycling and climate change. Marine microbial processes can shape the chemical composition of organic carbon and thereby influence the residence time of carbon in the ocean. This process is coined “Microbial Carbon Pump (MCP)” which is analogous, in function, to the known biological pump, but different in mechanism from the biological pump.

The MCP is a conceptual framework intended to cover a broad multidisciplinary ground, and it seeks a synthesis for future research on the kinetic and mechanistic bases of DOC dynamics. To this end, microbiologists and biogeochemists need to work together to bridge the fields of microbial ecology and organic biogeochemistry. The WG134 on the MCP will document the state of the art in microbial processing of organic carbon and acquire new insights through analyzing the available data on microbial biomass, production and diversity along with DOC data from a variety of marine environments, and will identify priority scientific questions and the corresponding technical needs to advance the relevant researches under the umbrella of the MCP.

The SCOR WG134 on the MCP is co-chaired by Prof. Nianzhi Jiao from the State Key Lab of Marine Environmental Science, Xaimen University, China and Prof. Farooq Azam from Scripps Oceanography Institute, USA, and joined by 12 countries including China, USA, Germany, UK, France, Canada, Spain, The Netherlands, Denmark, Czech, India and Korea. The MCP WG will work for 4 years starting from 2009.



Meeting Program

| Tuesday, October 27, 2009 | | | |
|--|--|--|--------------|
| Time | Event | | |
| 14:00-21:00 | Registration——Asia Gulf Hotel | | |
| 18:00- | Reception——Asia Gulf Hotel | | |
| Wednesday, October 28, 2009 | | | |
| Session I Open Science Meeting | | | |
| B-206 Ocean Building,Mel (Zeng Cheng Kui Building) | | | |
| Xiamen University | | | |
| Time | Topic | Speaker | Conveners |
| | Opening and Welcome Remarks | | |
| 08:30-09:00 | Vice President of Xiamen University IGBP Vice Chair Director of MEL WG134 Co-Chair | Ying Zhang Chen-Tung Arthur Chen Minghan Dai Farooq Azam | Nianzhi Jiao |
| 09:00-09:20 | Microbial Carbon Pump in the ocean——from theory to practice: The known, unknown and what we need to know | Nianzhi Jiao | Farooq Azam |
| 09:20-09:40 | Microscale interactions of bacteria and the regulation of Microbial Carbon Pump | Farooq Azam | |
| 09:40-10:00 | Group photo and coffee break | | |

| | | | |
|-------------|--|----------------------------|-------------------------------------|
| 10:00-10:20 | Major players in DOM degradation in the sea: The SAR11 and Roseobacter clades | Meinhard Simon | Gerhard Herndl/ Markus Weinauerb |
| 10:20-10:40 | Auto-versus heterotrophic prokaryotic carbon cycling in the dark North Atlantic | Gerhard Herndl | |
| 10:40-11:00 | Viral ecology of organic aggregates: Impact on carbon cycling and export | Markus Weinauerb | |
| 11:00-11:20 | Viruses and the marine carbon cycles: moving beyond models | Steven Wilhelm | |
| 11:20-11:40 | Understanding microbial processes in the ocean in the omics age | Feng Chen | |
| 11:40-12:00 | Geo Chip 3.0: a high throughput metagenomic tool for analyzing microbial communities | Zhili He | |
| 12:00-14:00 | Lunch (On site, Lunch Box provided) (Individual visit to the Key lab of marine science, Xiamen University) | | |
| 14:00-14:20 | On the extreme complexity of dissolved organic matter: a major reason for its slow degradation? | Gerhard Kattner | Gerhard Kattner/ Colin Stedmon |
| 14:20-14:40 | Linking optical properties of marine dissolved organic matter to its biogeochemical cycling | Colin Stedmon | |
| 14:40-15:00 | Optical properties of marine high molecular weight dissolved organic matter and their transformation by heterotrophic activity in the oceans | Xosé Antón Álvarez-Salgado | |
| 15:00-15:20 | Effect of pressure on prokaryotic degradation of organic matter according its quality/composition | Christian Tamburini | |

| | | | |
|-------------|---|--------------------------|--|
| 15:20-15:40 | Use of specific biomarker molecules for measurements of bacterial growth rates. Implications for DOC cycling in the sea. | Michal Koblížek | |
| 15:40-16:00 | Tetraether archaeal lipid biomarkers for detecting the instability of marine gas hydrates: implications for paleo-climate change | Chuanlun Zhang | |
| 16:00-16:20 | Coffee break | | |
| 16:20-16:40 | Dissolved organic carbon in the global deep ocean: consideration of sources and sinks | Dennis Hansell | Dennis Hansell Chen-Tung Arthur Chen |
| 16:40-17:00 | Export of DOC from Marginal Seas | Chen-Tung Arthur Chen | |
| 17:00-17:20 | Input, production and export of DOC in the marginal seas—implications for global ocean carbon cycling | Minhan Dai | |
| 17:20-17:40 | An overview on the role of bacterial abundance and production in the carbon cycling in biogeochemically disparate regions of the Indian Ocean | Nagappa Ramaiah | |
| 17:40-18:00 | Phytoplankton growth in surface oceans: interactive effects of temperature, nutrients, size, and grazing | Hongbin Liu | |
| 18:00-18:20 | Numerical simulations of the carbon cycle in the world ocean | Yongfu Xu | |
| 18:30- | Welcome Banquet by the State Key Lab of Marine environmental Science, Xiamen University (Jiali Seafood Restaurant) | | |
| 20:00-21:30 | Meeting of the Discussion Leaders after dinner (Sea View Resort) | | |

Thursday, October 29, 2009

Asia Gulf Hotel

Session II Closed Workshop

Morning Session

| Time | Topics | Discussion Leaders |
|-------------|--|--|
| 08:30-12:00 | WG134 terms of reference, missions, desired outcomes, and future planning | Nianzhi Jiao Farooq Azam |
| | Characterization of key microbial groups related to C cycling in the ocean | Michal Koblížek Feng Chen |
| | Characterization of DOM (including DOC and CDOM measurements) | Gerhard Kattner, Collin Stedmon, |
| | Carbon metabolism of functional microbial groups and their contributions to carbon pools | Markus Weinbauer Gerhard Herndl |
| | DOC dynamics (distribution, sink/source, models) | Dennis Hansell Chen-Tung Arthur Chen |
| 12:00- | Lunch (Asia Gulf Hotel Cafeteria) | |

Afternoon Session

14:30-18:00

(Members share common interests discuss while enjoying the hotspring)

Trithorn Hotspring SPA

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|--------|-----------------------------------|
| 18:00- | Field Buffet (Trithorn Hotspring) |
|--------|-----------------------------------|

Friday, October 30, 2009

Asia Gulf Hotel

Session II Closed Workshop

| | |
|-------------|---|
| 08:30-12:00 | Group Discussions (continued) (Group leaders use this time to prepare the discussion summary) |
| 14:00-18:00 | Summary of the first WG meeting and assignments of WG missions, planning of the WG activities for the next 3 years, decision on the second WG meeting place |
| 18:30-20:30 | Banquet by the University (Yifu Restaurant) |

Saturday, October 31, 2009

Departure



Microbial Carbon pump in the ocean —from theory to practice: The known, unknown and what we need to know

Nianzhi Jiao¹ & Farooq Azam²
On behalf of the WG134

1 Xiamen University, China

2 Scripps Institution of Oceanography, USA

Comparable in magnitude to the total inventory of atmospheric CO₂, the dissolved organic carbon (DOC) in the ocean and its biogeochemical behavior is critically important in understanding global carbon cycling and climate change. DOC in seawater undergoes rapid cycling (hours to months) if it is labile or slow cycling (years to centuries) if it is recalcitrant. Microorganisms utilize labile dissolved organic carbon (LDOC) at very low concentrations and can generate recalcitrant DOC (RDOC) resulting in the accumulation of RDOC over time. At the same time, this process increases the C: N and C: P ratios of the preserved organic matter. Such process acts as a “microbial carbon pump (MCP)” that prolongs the residence time of carbon in the ocean. Compared with inorganic carbon storage, RDOC storage is less sensitive to environmental changes and has no chemical equilibrium consequences such as ocean acidification caused by CO₂ storage. The MCP is a conceptual framework intended to cover a broad multidisciplinary ground, and it seeks a synthesis for future research on the kinetic and mechanistic bases of DOC dynamics. We define this area of emphasis in terms of a set of new testable hypotheses related to DOC sources, sinks, spatial-temporal variability and underlying biogeochemical mechanisms and consequences for the future biogeochemical state of the ocean. The emphasis on the MCP should help better constrain the pools, fluxes and mechanisms in the oceanic carbon cycle. Microbes’ role in carbon biogeochemistry has extensively been studied but often in a piece-meal manner. With the advent of new techniques and concepts a concerted multidisciplinary focus on the problem promises to revolutionize the field, with important implications for models of carbon cycle and climate. The MCP is a promising framework to formulate hypotheses and develop the necessary methodology to rapidly advance the field.

Major players in DOM degradation in the sea: The SAR11 and Roseobacter clades

Meinhard Simon

University of Oldenburg, Germany

There is ample evidence today that the SAR11 and *Roseobacter* clades are prominent components of the bacterioplankton and play major roles in processing organic matter in marine surface waters. It is less clear how and under which environmental conditions and in which oceanic regions each of this group and subgroups contribute to this process in general and with respect to distinct pathways. On the basis of studies mainly in a neritic sea in the temperate zone (North Sea) and in the Southern Ocean it will be argued that distinct clusters of both clades are differently involved in organic matter processing seasonally and in the course of phytoplankton blooms, obviously as a result of different growth and substrate requirements. In order to better understand processing and degradation of labile and refractory marine organic matter we need a better insight into the growth and functional response of these subgroups to the given environmental situation but also into the complexity of the DOM.

Auto- versus heterotrophic prokaryotic carbon cycling in the dark North Atlantic

G.J. Herndl

University of Vienna, and NIOZ, Netherlands

The deep-water masses of the North Atlantic undergo substantial alterations from their formation in the northern regions to the equatorial regions in terms of inorganic nutrient concentrations and microbial community composition and activity. In the northern North Atlantic, ammonium concentrations are relatively high even in the bathypelagic waters due to their recent formation and coinciding with the presence of ammonia oxidizing Archaea in the northern bathypelagic waters. Towards the equator, the abundance of ammonia oxidizing prokaryotes in the mesopelagic realm decreases by orders of magnitude, while in the bathypelagic waters near the equator ammonia

oxidizing Archaea are below the detection limit of Q-PCR. As all nitrifiers are autotrophs using carbon dioxide as a carbon source, prokaryotic autotrophy might represent a significant source of newly fixed organic carbon in the dark ocean. It is estimated that the mesopelagic chemoautotrophic carbon fixation amounts to about 20% of the export phytoplankton production. This 'dark ocean's primary production', albeit hitherto largely ignored, might stimulate the heterotrophic food web in the meso- and bathypelagic global ocean. Overall, there is accumulating evidence now from actual rate measurements and molecular approaches that the dark ocean's prokaryotic community is, on a per cell level, more active than assumed hitherto. To reconcile the carbon budget for the deep waters of the North Atlantic remains a challenge, as the measured meso- and bathypelagic carbon demand exceeds the supply by about an order of magnitude. Potential pitfalls in our current understanding of the dark ocean's carbon flux will be discussed.

Viral ecology of organic aggregates: Impact on carbon cycling and export

M. G. Weinbauer

Laboratoire d'Océanographie de Villefranche
sur Mer (LOV), CNRS-UPMC, France

Viruses are the most abundant signs of life in the ocean and cause significant mortality of bacterio- and phytoplankton. Viruses play a dual role in the ocean. On the one hand, lysis of cells reduces carbon fixation and biological carbon oxidation by causing mortality. On the other hand lysis transfers cells into the dissolved fraction and fuels heterotrophic processes. The net outcome of these two roles remains largely unknown. There is also an ongoing debate, whether viruses 1) prime the biological pump by accelerating host export from the euphotic zone, 2) short-circuit the biological pump by releasing nutrients back into the dissolved phase or 3) drive aggregation and transfer of carbon into the deep-sea through the release of sticky colloidal cellular components during viral lysis. Here I summarize general problems and knowledge gaps on the role of viruses for carbon and nutrient cycling and provide avenues for further research particularly linked to global change.

Viruses and the marine carbon cycle: moving beyond models

Steven W Wilhelm

Department of Microbiology,
University of Tennessee, USA

Viruses are pervasive elements in marine surface waters and impart significant mortality on marine microbial communities. Viruses effectively redistribute nutrient elements and carbon from large biological particles (*i.e.*, bacteria, algae) to biologically inactive (*dead*) particulate and dissolved pools of organic compounds. Many of these compounds contain macro- and micronutrients (*e.g.* P, N, Fe) that can be rapidly recycled back into the food web and various studies have quantified this efficiency. Carbon has, however, been long overlooked in this arena: while various models suggest that virus activity may either prime or deprive the “biological pump”, we remain (at this point) without a sufficient body of research to include this process in biogeochemical carbon models or budgets. Currently there is a significant need to understand the fate of virally-remobilized carbon, including its partitioning into the spectrum of recalcitrant to labile, and the efficiency with which these pools of carbon are reincorporated back into biology. As part review, this presentation will outline the existing knowledge concerning the role of viruses in marine carbon cycles: as part scientific paper it will outline ongoing efforts and future directions needed to understand how viruses influence biological carbon cycling in marine surface waters.

Understanding microbial processes in the ocean in the omics age

Feng Chen

Center of Marine Biotechnology,
University of Maryland, USA

Advances in genomics and community genomics have uncovered potential novel microbial functions in various marine microbial consortia. Some of these new microbial processes are important to the function of global ecosystem because they are related to energy and carbon cycles. Post-genomic tools such as transcriptomics, proteomics, bolomics, etc. have been developed quickly to explore the actual

activities of these unknown functions. These molecular tools become even more powerful when combined with some other biological techniques such as cultivation methods or incorporation of traceable substrates. Scientists have begun to understand which groups of microbes are responsible for the breakdown or uptake of specific organic carbon in the natural environment. However, linking microbial diversity with specific activities is challenging due to the complexity of microbial communities in sea. Nevertheless, we are now entering into the omics age where the functions of microbial ecosystems can be inferred from bioinformatics and functional genomics. The omics technologies can be used to explore the key metabolic pathways associated with the microbial carbon pump.

Use of specific biomarker molecules for measurements of bacterial growth rates. Implications for DOC cycling in the sea.

Michal Koblížek¹, Ondřej Prášil¹ & Benjamin A.S. Van Mooy²

¹*Institute of Microbiology CAS, Opatovický mlýn, Czech Republic*

Current data based on radiolabelled Leucine or Thymidine incorporation suggest that marine bacterioplankton in the oligotrophic upper ocean grows at rates of one division per week. However, such low rates conflict with observations from laboratory cultures, genomics studies and the role of the microbial loop in the sea. We analyzed diel changes in bacteriochlorophyll to assess *in situ* turnover rates of aerobic anoxygenic phototrophs in the euphotic zone of major oceanic gyres in the Atlantic and Pacific Oceans. Using this approach we found that phototrophic bacteria in the Sargasso Sea, in the South Atlantic and in oligotrophic regions of the South Pacific grew at rates of about one division per day. In addition, bacterial phospholipid biosynthesis rates showed similar turnover rates for the broader bacterioplankton community. These results indicate that the bacterioplankton community in the upper oligotrophic oceans grows at rates of about one division per day, which is almost an order of magnitude faster than current estimates. This suggests that bacteria and microbial loop play much more important role in the marine carbon cycle than currently appreciated.

Tetraether archaeal lipid biomarkers for detecting the instability of marine gas hydrates: implications for paleo-climate change

Chuanlun Zhang¹ & Yige Zhang²

1 Department of Marine Sciences
University of Georgia, USA

2 Department of Geology and Geophysics
Yale University, USA

Gas hydrates are one of the largest pools of readily exchangeable carbon on Earth surface. Releases of the greenhouse gas methane from hydrates are responsible for a number of important climate changes in geological history. Many of the inferred events were based on the $\delta^{13}\text{C}$ values of carbonates, which have been challenged lately. Here we propose a molecular fossil proxy “Methane Index (MI)” to better document the destabilization of marine gas hydrates. MI is constructed by the relative distribution of glycerol dialkyl glycerol tetraethers (GDGTs), the core membrane lipids of *Archaea*. Our study in the Gulf of Mexico sediments clearly shows the correlation between gas venting, microbial community and lipid profile shifts and the MI, corroborating the idea that MI might be a robust indicator for hydrate dissociation. MI provides us a more precise and effective proxy for evaluating the gas hydrate instability in Earth’s geological history.

Phytoplankton growth in surface oceans: interactive effects of temperature, nutrients, size, and grazing

Hongbin Liu, Bingzhang Chen

Hong Kong University of Science and Technology, Hong Kong

We compile two datasets from ^{14}C uptake and dilution experiments conducted in surface waters of the global ocean to investigate the relationship between phytoplankton mass-specific growth rate and cell size. After temperature correction, both datasets suggest that this relationship might be described by a hump-shaped quadratic curve with the modal size (the size corresponding to the maximal value of the curve) being $2.8 \mu\text{m}$ and $5.4 \mu\text{m}$ in the ^{14}C and dilution datasets, respectively. Nutrient enrichment does not change the qualitative nature of the relationships and

we also conclude that it is due to composition differences, but not the nutrient effect, that lead to the positive relationship on the left part of the hump-shaped curves. Temperature corrected phytoplankton grazing mortality rate is positively correlated with phytoplankton average size, but the proportion of daily primary production consumed by microzooplankton is negatively correlated with size, suggesting a reduced grazing effect as size increases. We propose a hypothesis that this positive relationship existing in most areas of the oligotrophic open ocean might reflect an adaptive response of phytoplankton to strong top-down control in marine systems when compared with other ecosystems.

GeoChip 3.0: a high throughput metagenomic tool for analyzing microbial communities

Zhili He^{1,2}, Ye Deng^{1,2}, Meiyong Xu^{1,3}, Joy D. Van Nostrand^{1,2},
Liyou Wu^{1,2}, Christopher L. Hemme^{1,2}, Terry J. Gentry⁴, Jost Liebich⁵,
Qichao Tu¹, Adam P. Arkin^{6,2}, Terry C. Hazen^{6,2}, and Jizhong Zhou^{1,2}

¹University of Oklahoma, Norman, OK, USA

Functional gene arrays (FGAs), or GeoChips constructed with key genes involved in various biological and geochemical processes have been widely used to analyze microbial communities. Based on GeoChip 2.0, a new generation of GeoChip (GeoChip 3.0) has been developed. GeoChip 3.0 has several new features in terms of coverage, design, and data analysis. GeoChip 3.0 contains about 27,700 functional gene probes and covers approximately 52,000 gene sequences of 310 gene families, and especially functional genes involved in antibiotic resistance and energy processes, and phylogenetic marker GyrB have been added, which allows us to obtain more comprehensive information about microbial communities and analyze more diverse environmental samples. For probe design, sequence-specific, and group-specific probes were selected, and all those probes together greatly increase the gene coverage. For data analysis, two unique strategies have been implemented. First, a universal standard has been implemented so that data normalization and comparison of samples from different sites, experiments, time points, or laboratories can be conducted. Second, a software package (including databases) has been developed for sequence retrieval, probe design, information storage, and especially, data analysis and automatic update, which greatly facilitates the management and analysis of complicated GeoChip data sets. GeoChip 3.0 has been used for analyses of responses of microbial communities to elevated CO₂. Under elevated CO₂, the relative abundance of genes encoding key enzymes for CO₂ fixation, labile carbon degradation, nitrogen fixation, denitrification, and phosphorus utilization significantly increased, but the abundance of most genes encoding key enzymes for

recalcitrant carbon degradation, methane production and oxidation, and sulfur metabolism did not significantly change. Multivariate statistical analyses (e.g., DCA, CCA) revealed that the microbial community functional structure was significantly different between ambient CO₂ and elevated CO₂, and correlated with soil C and N dynamics and plant productivity. All results demonstrate that GeoChip 3.0 is a powerful tool to analyze microbial communities important to the global climate change, agriculture, bioenergy, ecosystem management, environmental cleanup and restoration, and human health as well. It is also particularly useful for linking microbial genes/populations to ecosystem processes and functions.

On the extreme complexity of dissolved organic matter: a major reason for its slow degradation?

Gerhard Kattner

Alfred Wegener Institute for Polar and Marine Research,
Ecological Chemistry, Germany

Dissolved organic carbon (DOC) in the ocean is estimated to be 700 Pg C, whereas the particulate marine organic carbon accounts only for about 30 Pg C. DOC is almost as much as the amount of carbon in atmospheric CO₂ (~800 Pg) or terrestrial biomass (~610 Pg). A small portion of dissolved organic matter (DOM) is labile, but the main portions is refractory or recalcitrant, thus, sequester carbon on very long time scales and is not remineralized back to CO₂ for thousands of years. However, the mechanisms of the generation of recalcitrant DOM are still unclear. Without knowledge on molecular structures it is impossible to discern why DOM is so resistant against biotic and abiotic decomposition. Tools for the chemical characterization of DOM in the ocean are limited, and thus, the molecular structure of marine DOM is largely unknown. The present molecular level determination of DOC in seawater is essentially restricted to carbohydrates, amino acids, lipids and aminosugars. Unfortunately, these compound classes usually represent less than 10% of the open ocean DOC. Size exclusion chromatography can provide bulk information on molecular size and polarity. Other data on molecular level characterization are obtained by the combination of analytical techniques with various methods of isolation and fractionation such as ultrafiltration and solid phase extraction. Recently, Fourier Transform Ion Cyclotron Resonance Mass Spectrometry (FT-ICR-MS) enabled to determine the molecular elemental composition of thousands of DOM molecules. The extremely complex compositions may be a major reason that recalcitrant DOM is not or only slowly utilized by microorganisms. It might be not profitable for bacteria to degrade these molecules because there is no energetic advantage. To understand global biogeochemical cycles, it is crucial to

identify sources and transformation processes as well as molecular structures of DOM as detailed as possible.

Linking optical properties of marine dissolved organic matter to its biogeochemical cycling.

Colin Stedmon

University of Aarhus, Denmark

The focus of this SCOR working group is to study the role than microbes play in producing refractory dissolved organic matter (DOM). This process increases the residence time of organic carbon in the world's oceans and is therefore an important link in the global carbon cycle. For this a combination of microbial and chemical techniques need to be applied. The study of DOM is hindered by the fact that it is a very complex mixture of compounds which is difficult to isolate or characterise completely. As a result a range of different approaches are applied one of which is absorption and fluorescence measurements, collectively known as UV-Visible spectroscopy. A fraction of DOM absorbs UV-visible light and can be quantified and characterised according to its optical properties. These measurements can then be used as a proxy for the dynamics of the DOM pool as a whole. These optical measurements offer high resolution information. They can be made in situ in conjunction with CTD profiles (high spatial resolution), or be made with high spectral resolution (qualitative and quantitative) on water samples in the laboratory. Recent work has revealed the potential that these techniques have for the study of DOM biogeochemistry. In this talk I will summarize them and present some of the perspectives for studying the oceanic microbial carbon pump.

Optical properties of marine high molecular weight dissolved organic matter and their transformation by heterotrophic activity in the oceans

X.A. Álvarez-Salgado*, C. Romera-Castillo,
C. Lønborg, M. Nieto-Cid, C. Marrasé

* CSIC Instituto de Investigaciones Marinas
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The transformation of labile LMW-DOM into refractory HMW-DOM by the marine microbial food web is a key component of the recently defined “microbial carbon pump” that occurs in ocean margins as well as in epi-, meso- and

bathypelagic open ocean waters. Recent methodological advances have enabled to trace this transformation on basis of the optical properties of DOM. The coloured fraction of DOM (CDOM) absorbs light at UV–visible wavelengths. The CDOM fraction that can emit blue fluorescence when irradiated with UV light is called fluorescent CDOM (FDOM).

The production of coloured HMW–DOM by the marine microbial food web can be followed either *in vitro* or *in situ*. In the *in vitro* methods, the time course of the CDOM absorption spectra and the FDOM excitation–emission matrices are monitored for time intervals that depend on the microbial activity of the incubated waters. The *in situ* methods require the separation of the physical (advection, mixing) from the biogeochemical sources of variability of the spatial and/or temporal distributions of CDOM and FDOM applying a water masses mixing model (W3M).

Finally, the HMW–DOM from different marine ecosystems can be isolated by flow–cross ultra filtration and their optical properties determined to trace their origin and biogeochemical transformations. Furthermore, these materials can be re–dissolved, inoculated with natural microbial assemblages, and incubated to study additional transformations.

Examples will be presented on the results obtained (i) following the optical properties of DOM in short and long term *in vitro* experiments; (ii) applying W3Ms to time–series and oceanic sections of CDOM and FDOM, and (iii) comparing the optical properties of ultra filtered DOM from contrasting marine environments.

Effect of pressure on prokaryotic degradation of organic matter according its quality/composition

Christian Tamburini^{1*}, Mehdi Boutrif¹, Marc Garel¹,
Badr Al Ali¹, Bruno Charrière¹, Philippe Cuny¹,
Madeleine Goutx¹, Gérald Grégori¹, Vincent Grossi²,
Catherine Guigue¹, David L. Kirchman³, Cindy Lee⁴,
Dominique Lefèvre¹, Stéphane Pepa⁵, Richard Sempéré¹

¹ Université de la Méditerranée, Centre d'Océanologie de Marseille, LMGEM,
UMR 6117 CNRS – INSU, Campus de Luminy, France

The effects of elevated hydrostatic pressure concern all organisms living in the world's largest (by volume) habitat: the deep sea. Historically underestimated in terms of its contribution to the Biosphere, the deep sea remains one of the least known and most poorly understood environments on our planet.

To understand how the effects of pressure on microorganisms are important to understand the role of microbes in the OM mineralization, we are studying both the

effect of pressure on deep-sea prokaryotes and prokaryotes originating from the surface of the ocean attached-to-particles sinking through the water column.

Using a pressurized vessel to obtain re-pressurized deep-sea samples, early studies found that pressures affect bacterial physiology and growth (ZoBell and Oppenheimer 1950). ZoBell define barophile (now called piezophile) bacteria, bacteria able to grow better under pressure than at atmospheric pressure. In contrast, using pressure-retaining samplers, Jannasch and Wirsen (1973) concluded that elevated pressure substantially decreases rates of growth and metabolism of microbes collected from deep waters. However, recent evidence challenges this view that deep-sea microbes in bathypelagic waters display minimum responses to the inputs of organic matter and play only a minor role in biogeochemical cycles.

Here, we first present our data set obtained in Mediterranean Sea and first results obtained in the North Atlantic Ocean, showing that the effects of hydrostatic pressure on microbial activities indicate that bathypelagic microbial activity is generally higher under in situ pressure conditions than at atmospheric pressures. In contrast, the capacity of attached-to-particles bacteria to degrade organic carbon and ballast material (e.g., opal) decreases with increasing pressure.

Finally, we will present new results obtained using high molecular weight compounds comparatively to low molecular weight compounds face to pressure.

Dissolved organic carbon in the global deep ocean: consideration of sources and sinks

Dennis A. Hansell¹ & Craig Carlson Craig²

1 University of Miami, USA

2 University of California Santa Barbara

Dissolved organic matter in seawater is the largest ocean reservoir of reduced carbon, holding >200 times the carbon inventory of marine biomass and serving as substrate to vast microbial populations. It is produced in the surface ocean, but overturn of the ocean water column exports DOM to depth, thus contributing to the biological pump whereby biogenic carbon is sequestered in the deep ocean. Until recently, our knowledge of dissolved organic carbon (DOC) biogeochemistry on the global scale had been limited to very few high quality measurements scattered widely across ocean basins. A new, vastly enlarged global ocean data set is employed here to produce unprecedented insights on the distribution and turnover of marine dissolved organic carbon. From the distribution, the deep ocean biotic and abiotic

sinks for this carbon are inferred. While the DOC data demonstrate net removal in the deep ocean, DOC is concomitantly being added by solubilization of sinking particles. Little is known of this addition process, but newly determined distributions of a biochemical tracer of the process give novel insights on the deep accumulation of modern DOC and its transport with deep ocean currents. The totality of the data presented demonstrates that great challenges remain for understanding the dynamics of organic matter in the vast volumes of the deep ocean.

Export of DOC from Marginal Seas

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As early as 1999 Chen and Wang(Carbon, alkalinity and nutrient budgets on the East China Sea continental shelf, JGR, 104,20675-86) reported that the East China Sea exports $1.03 \pm 0.31 \times 10^{12}$ mol/yr of DOC to the open oceans. This export is mainly in the surface outflow. Here we show that the South China Sea also exports DOC to the Philippine Sea, but here the export in the intermediate layer (350-1350m) is important. Globally the marginal seas transport about 50×10^{12} moles of DOC to the open oceans each year, about twice the river outflow.

Input, production and export of DOC in the marginal seas-implications for global ocean carbon cycling

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Coastal and marginal seas play a key role in the global carbon cycle by linking the terrestrial, oceanic, and atmospheric carbon reservoirs. The marginal seas receive $0.36 \text{ Pg C yr}^{-1}$ riverine input of organic carbon. Moreover, the high biological activity in the marginal seas is stimulated by both the riverine nutrients and more importantly the upwelled nutrients. The net production of DOC in the ocean margins is estimated

for $0.38 \text{ Pg C yr}^{-1}$, which accounts for 20% of the new production. As a result of a short water residence time, the margin may serve as a net CO_2 sink by exporting a significant fraction of locally produced or river-discharged organic carbon to the open ocean interior. The export of such organic carbon, thereby less likely to return to the atmosphere may therefore contribute significantly to the carbon sequestration in the ocean. At the same time, this relatively freshly produced organic carbon, when exported into the adjacent open ocean interior might also contribute to the dark ocean respiration. This presentation sought to use the South China Sea and East China Sea as two unique and contrasting marginal systems to examine the input, production and export of DOC therein. The implications of DOC export from the marginal seas will also be discussed.

An overview on the role of bacterial abundance and production in the carbon cycling in biogeochemically disparate regions of the Indian Ocean

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Heterotrophic bacteria (Hbac) in the marine ecosystems enjoy more than one life-style, nutritionally versatile and, ecologically pivotal. As a consequence of their metabolic activities, they are central to mediating most biological and many geochemical processes in the marine realms. This presentation will describe the physical settings, chemical regimes and biological productivity processes in the highly productive northern Arabian Sea, moderately productive Bay of Bengal (BoB) and oligotrophic regions of the equatorial Indian Ocean (EIO). Hbac abundance and productivity data from several programs such as JGOFS, BoB Process Study and the explorations in the EIO will be described. Spatio-temporal variations in Hbac abundance and production in central and eastern Arabian Sea; central and western Bay of Bengal and, equatorial Indian Ocean will be described. In the overall, there are wide spatio-temporal differences in Hbac carbon biomass in the Arabian Sea. The Hbac abundance and production (BP) are the largest during the periods of low chlorophyll *a* concentrations and primary production (PP) and, *vice versa*. For instance, in the central Arabian Sea, the highest BP (2.86 to $22.93 \text{ mg Cm}^{-3}\text{d}^{-1}$) during spring intermonsoon (SpIM; March-May) is when the PP is the least. Via microbial loop, the Hbac help sustain the paradoxically larger biomasses of mesozooplankton in the Arabian Sea. This role is of great biogeochemical significance in the export flux of carbon to the deep. In BoB, where cold-core eddies appear to play a prominent role in governing the biological productivity, the Hbac abundance coincides with

higher primary production. Although the BP accounts for 43% and 56% of PP respectively in the western and central Bay, spatial and temporal variations are clearly evident. The BP is higher during southwest monsoon period (July –August: $0.18 - 6.75 \text{ mg C m}^{-3} \text{ d}^{-1}$) and winter time (Dec-Jan: $0.35 - 18.56 \text{ mg C m}^{-3} \text{ d}^{-1}$), moderate during fall intermonsoon (Sept-Oct: $0.01 - 4.19 \text{ mg C m}^{-3} \text{ d}^{-1}$) and the least during SpIM ($0.001 - 2.49 \text{ mg C m}^{-3} \text{ d}^{-1}$). In the oligotrophic regions of the EIO, both Hbac abundance and production are the lowest throughout the year. Intriguingly, the BP: PP ratios are invariably high signifying the importance of Hbac in the food web dynamics of the EIO. A summary of our understanding of Hbac role in the biological productivity processes as well as carbon fluxes will be presented.

Numerical Simulations of the Carbon Cycle in the World Ocean

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and Atmospheric Chemistry, Institute of Atmospheric Physics,
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A global ocean general circulation model (OGCM) with a resolution of $2^\circ \times 2^\circ \times 30$ is employed to study the carbon cycle in the global ocean, in which three different carbon models are used, including a perturbation approach, an inorganic carbon model and a biogeochemistry model. The OGCM (LICOM) used in this work was developed by the State Key Laboratory of Numerical Modeling for Atmospheric Sciences and Geophysical Fluid Dynamics (LASG) of IAP/CAS. The OGCM considers an explicit free surface, and is forced at the surface by monthly mean climatologies. A subgrid-scale mixing scheme for tracers called GM90 is used in the model. The model well reproduces the general features of the ocean circulation and water mass. Natural ^{14}C is used to further examine the performance of the model. After more than 3000 years of integration, the model generates the basic characteristics of distributions of observed natural ^{14}C although the model gives the oldest water at the bottom of the North Pacific. A perturbation approach estimates that the global ocean takes up about 105 GtC of anthropogenic CO_2 for the period 1800-1999, and that the air-sea exchange flux of anthropogenic CO_2 is about 2.0 GtC/yr in 1999. Furthermore, a carbon cycle model with and without biological processes is incorporated into the OGCM to estimate historical anthropogenic CO_2 that is estimated from the difference in the DIC storage relative to equilibrium abiotic carbon and biotic carbon. The steady state models for both inorganic carbon and biogeochemistry models are integrated for over 5000 years. Simulated results show that 111 and 112 GtC of anthropogenic CO_2 has been taken up in the inorganic carbon model and biogeochemistry model for the period of 1800-1999, respectively. The distributions of carbon related variables are also discussed in this work.

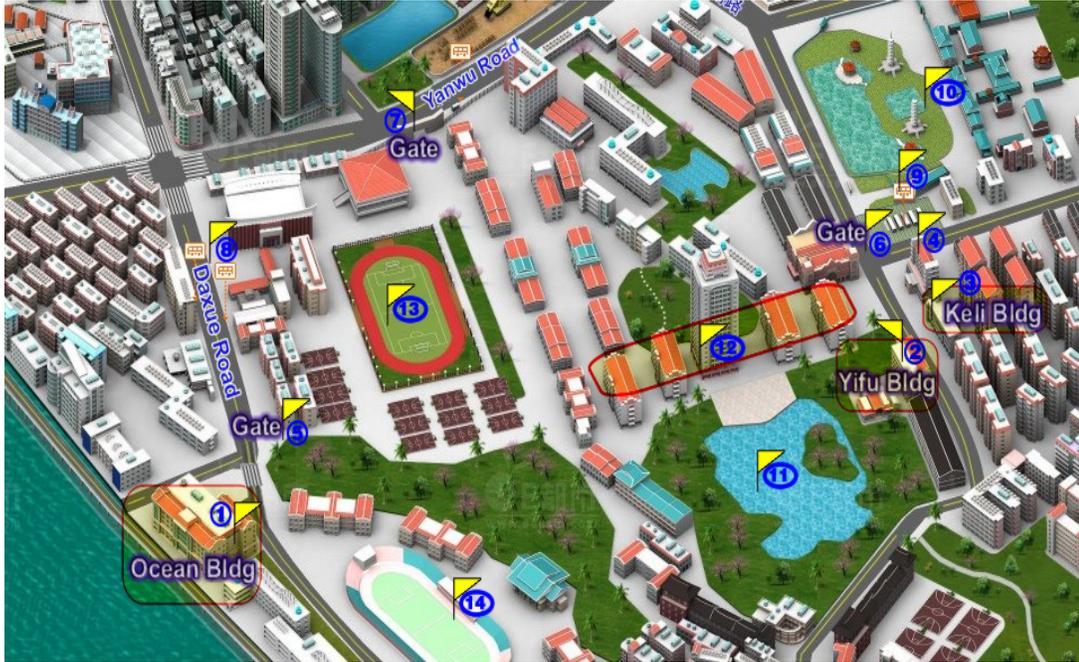


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Meeting Place and Directions

1) Ocean Building, Xiamen University



1. Ocean Building (Zeng Cheng Kui Building) – location of the State Key Lab for Marine Environmental Science
2. Yifu Building (University International Academic Exchange Center)
3. Keli Building
4. Jianwen Building
5. University Vehicle Exit Toll Gate
6. University Da'nan Gate
7. University Western Gate
8. Xia Da Yi Yuan Bus Stop (Xiamen University Hospital Bus Station)
9. Xiamen University Bus Terminal
10. Nanputuo Temple
11. Furong Lake
12. Jiageng Buildings

2) Asia Gulf Hotel Xiamen



Asia Gulf Hotel is a five-star hotel, it enjoys unique geographical situation, only 15kms from the airport. It's also the only villa-garden-style resort in Xiamen with full-seascape.

<http://www.gulf-hotel.com.cn/en/index.asp>

Tel: 86-592-219-8888

3) Trithorn Hotspring Resort Xiamen



Trithorn SPA Hotspring Park locates side of Tingxi Tong'an Reservoir. It has a comfortable environment, natural unpolluted hot spring. Trithorn SPA Hotspring Park covers 48 unique designed, styled unit outdoor pools, Minnan Hotspring Villa and Badekurort SPA. It is blended with the natural landscape. The hotspring will give you a total relaxation. Swimming suit and cap should be prepared by yourself. You can find more in: <http://www.trithorn-resort.com/index-1.htm>

Introduction to Xiamen University

Xiamen University Address: 422 South Siming Road, Xiamen
(17 kilometers from Xiamen Gaoqi International Airport)



Xiamen University is one of the top 20 universities in China and the premier university in Fujian Province. It was founded in 1921 by Tan Kah Kee, the well-known patriotic overseas Chinese leader. It was the first university in China founded by an overseas Chinese. Marine Science is one of its featured disciplines, in which the State Key Lab for Marine Environmental Science is harbored. The main campus of Xiamen University is located in a picturesque setting between the sea and a scenic mountain, spreading over 150 hectares, and is among the most beautiful campuses in China.

Travel and Local Info

•Travel Information:

Xiamen International Airport has direct flights to and from Hong Kong, Macao, Singapore, the Philippines, Malaysia, and Japan. However, the most convenient international transition are Shanghai, Hong Kong or Guangzhou (60-80 minute flight to Xiamen).



•**Electricity:** 220 Volts 50 Hz. The standard sockets:

•Water:

Tap water is not suitable for drinking. Visitors are advised to drink boiled water, bottled purified water or mineral water. Complimentary bottled water may be offered in some hotels.

•**Time zone:** GMT/UTC plus 8 hours

•Useful Numbers:

Telephone country code: +86

Telephone area code: 592

Police: 110

Fire Department: 119

Ambulance: 120

Local directory assistance: 114

•Currency and Bank Information:

The RMB (Renmin bi) is the official currency, also called Chinese Yuan.

Only RMB can be used when you are in China. Visa, Master, American Express, Diners Club and JCB are widely accepted in most malls, shopping centers, restaurants and hotels.

Current exchange rate (July 2009):

1 USD \approx 6.8 RMB

1 Euro \approx 9.5 RMB

The universal Currency Converter: <http://www.xe.com/ucc/>

The airport Office of the Bank of China is located on the Departure Level, at which currency exchange service is available. Bank of China, Industrial and Commercial Bank of China, Construction Bank of China, and Guangda Bank also provide ATM service in the terminal.

There are a few banks on the campus of Xiamen University. Banking hours and days

vary from bank to bank in Xiamen. However, most Chinese banks are open from 9 a.m. to 5 p.m. or 5:30 p.m., and have branches that are open on Saturdays and Sundays.

.Tipping

Tipping is not a part of Chinese custom. A 10 to 15% service charge may be added to your bill at some tourist hotels thus no tipping is expected unless you are provided with extra service. It is not necessary to tip a taxi driver unless he/she assists with luggage or provides extra service.

.Business hours

Typical business hours in China are 8:30 to 17:30, governmental offices are closed on Saturday and Sunday. Most shops are open from 9:30 to 21:30 or later, and open seven days a week.

.Weather

Xiamen is a subtropical coastal city. The average temperature in October is about 23.2°C, and the averaged precipitation in October is about 17.7 mm.

Yahoo's 5-day Xiamen weather report:

http://weather.yahoo.com/forecast/CHXX0140_f.html

