

International Workshop on Marine Geomicrobiology – A Matter of Energy

Sandbjerg Manor, Denmark

August 28 to September 1, 2017

Program, Abstracts, and Information

Convened by

Bo Barker Jørgensen, Center for Geomicrobiology, Aarhus University, Denmark

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<http://conferences.au.dk/geomicrobiology2017/>

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**International Workshop on
Marine Geomicrobiology – A Matter of Energy**

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Background for the workshop

The redox ladder of electron donors and electron acceptors provides a systematic approach to explore the many possibilities of microbial energy metabolism. Calculations of Gibbs free energy by the reactions provide a means to predict their feasibility under in situ conditions. Yet, we are repeatedly confronted with new and surprising examples of how microorganisms harvest energy from their environment. Have we now discovered the most important strategies or are great and unexpected discoveries still waiting for us out there?

During this workshop we will climb up and down the redox ladder to explore how chemical potential is exploited by microbial life in the seabed. We will explore the possible combinations of electron donors and electron acceptors and search for new principles of microbial energy metabolism. We will discuss recent knowledge on microbial ecophysiology and how microbes evolve and interact to conserve energy from their dynamic environment.

In addition to the exciting science, there are two occasions that motivate this workshop.

Firstly, the Center for Geomicrobiology at Aarhus University, which was founded October 1, 2007 with a ten-year perspective, will end September 2017. The Center research has focused on microbial life in the deep sub-seafloor biosphere. This theme was the background for three international workshops organized through the Center on "Microbial life under extreme energy limitation" in 2007, 2012 and 2015.

Secondly, the head of the Center, Bo Barker Jørgensen, will officially retire after the Center terminates in September 2017. He will continue as emeritus professor at the Department of Bioscience, Aarhus University. The themes of the workshop and the invited speakers reflect the life-long research interests and international collaborations of Bo. Thus, this workshop will both provide a status of current and future research in marine geomicrobiology and will be an opportunity to bring together the scientific family of old colleagues and new young scientists in the field.

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Local organizers:

Inga Barker Jørgensen
Caitlin Petro, PhD Student
Lara Jochum, PhD Student

Program

Monday, Aug. 28:

- 15:00 – 18:00 **Registration and mounting of posters**
- 18:00 – 18:15 **Opening address**
- **Bo Barker Jørgensen** (Center for Geomicrobiology, Aarhus University)
- 18:15 – 19:00 **Opening Lecture**
- **Kenneth H. Nealson** (University of Southern California):
Bioelectricity –bacteria pumping electrons
- 19:00 – ? **Mixer with buffet dinner**

Tuesday, Aug. 29:

- 08:30 – 10:00 ***Oxygen***
- **Niels Peter Revsback** (Aarhus University): *Oxic respiration under low oxygen availability*
 - **Ronnie N. Glud** (University of Southern Denmark): *How the seabed consumes oxygen – from coastal waters to hadal trenches*
 - **Michael Kühl** (University of Copenhagen): *Light energy and oxygenic photosynthesis*
- 10:00 – 10:30 **Break**
- 10:30 – 12:00 ***Bioelectricity***
- **Lars Peter Nielsen** (Center for Geomicrobiology, Aarhus University): *Cable bacteria – a novel principle of energy conservation*
 - **Filip J. R. Meysman** (Aarhus Institute of Advanced Studies): *Biogeochemistry of sediments*
 - **Andreas Schramm** (Center for Geomicrobiology, Aarhus University): *Genomic insights into the function and evolution of cable bacteria*
- 12:00 – 13:30 **Lunch**
- 13:30 – 15:00 ***Nitrogen***
- **Michael Wagner** (University of Vienna): *A new perspective on microbes formerly known as ammonia- and nitrite-oxidizers*

- **Marcel Kuypers** (Max Planck Institute, Bremen): *Anammox and other discoveries in the nitrogen cycle*
- **Bo Thamdrup** (University of Southern Denmark): *The multiple roles of nitrate as an oxidant*

15:00 – 17:30 **Break and poster session**

17:30 – ? **Cultural evening and dinner at Sønderborg Castle**

Wednesday, Aug. 30:

08:30 – 10:00 ***Sulfur***

- **Don E. Canfield** (University of Southern Denmark): *Evolution of the sulfur cycle*
- **Tim Ferdelman** (Max Planck Institute, Bremen): *Cryptic cross-linkages among biogeochemical cycles*
- **Dirk de Beer** (Max Planck Institute, Bremen): *Light energy and anoxygenic photosynthesis*

10:00 – 10:30 **Break**

10:30 – 12:00 ***Sulfur***

- **Alex Loy** (University of Vienna) *Sulfate reducers – how great is the diversity?*
- **Kai Finster** (Aarhus University): *Energy conservation from disproportionation reactions*
- **Heide N. Schulz-Vogt** (Institute for Baltic Sea Research, Warnemünde): *Energy strategies of big sulfur bacteria*

12:00 – 13:30 **Lunch**

13:30 – 15:30 ***Methane and hydrocarbons***

- **Antje Boetius** (Alfred Wegener Institute and Max Planck Institute, Bremen): *Anaerobic oxidation of methane fueling benthic ecosystems*
- **Karen G. Lloyd** (University of Tennessee): *Different lives of archaea and bacteria*
- **Joel E. Kostka** (Georgia Institute of Technology): *Oil spill biodegradation*
- **Ian M. Head** (Newcastle University): *Biodegradation of hydrocarbons in sediments*

15:30 – 18:00 **Break and 1st breakout session / posters**

18:00 – 19:30 **Dinner**

- 19:30 – 21:00 **High energy**
- **Rudi Amann** (Max Planck Institute, Bremen): *Coupling identity and function of microbial communities*
 - **Markus Hüttel** (Florida State University): *Microbial processes in permeable sediments*
 - **Andreas Teske** (University of North Carolina): *Microbial communities at deep-sea hydrothermal vents*

Thursday, Aug. 31:

- 8:30 – 10:00 **Low energy**
- **Fumio Inagaki** (JAMSTEC, Japan): *Limits to deep sub-seaflor life and geosphere-biosphere interactions*
 - **Steve D'Hondt** (University of Rhode Island): *Subseafloor microbial communities and their energy sources*
 - **Hans Røy** (Center for Geomicrobiology, Aarhus University): *Sulfate reduction and the respiration rate of bacteria*
- 10:00 – 10:30 **Break**
- 10:30 – 12:00 **Low energy**
- **Mark A. Lever** (ETH Zürich): *Microbial life under extreme energy limitation*
 - **Kasper U. Kjeldsen** (Center for Geomicrobiology, Aarhus University): *Evolution and persistence during deep burial of microbial communities*
 - **Jan Amend** (University of Southern California): *The redox ladder of microbial energy metabolism – what are we missing?*
- 12:00 – 13:30 **Lunch**
- 13:30 – 15:00 **Before break-out session**
- **Boran Kartal** (Max Planck Institute, Bremen): *Multiple pathways of anaerobic oxidation of methane and ammonium*
 - **Victoria Orphan** (California Institute of Technology): *How energy is shared in consortia*
 - **Tori Hoehler** (NASA Ames Research Center): *Energy in a planetary context*
- 15:00 – 18:00 **2nd break-out session**
- 18:00 – 18:30 **Closing lecture**
- **Bo Barker Jørgensen** (Center for Geomicrobiology, Aarhus University): *Forty years of sediment geomicrobiology*

19:00 – ? **Workshop dinner**

Friday, Sept. 1:

06:15 – ? **Breakfast and departure**

Social events

Mixer, Magasinet, Sandbjerg Manor – Monday, August 28 at 19:00

The mixer will take place after the opening lecture by Ken H. Nealson. The mixer is with buffet dinner and beverages will be served. The mixer is included in the registration fee.

Cultural Evening: Sønderborg Castle – Tuesday, August 29 at 17:30

Sønderborg Castle will give an introduction to the castle and its history including a guided tour of the castle and its museum. Bus transportation will be arranged for all participants. After the tour participants will be served a Danish dinner in the Great Hall's eastern antechamber. The Cultural Evening Dinner is included in the registration fee.

Workshop dinner – Thursday, August 31 at 19:00

Magasinet, Sandbjerg Manor, will serve a three-course dinner, wines (ad libitum), and coffee. The workshop dinner is included in the registration fee.

Posters

- Jeanine L. Ash**, Matthias Egger, Issaku Kohl, Tina Treude, Caroline P. Slomp, Barry Cragg, R. John Parkes, Douglas Rumble and Edward D. Young
 $\Delta^{13}\text{CH}_3\text{D}$ and $\Delta^{12}\text{CH}_2\text{D}_2$ Signals of Methanogenesis and Methanotrophy
- Jacob P. Beam**, Jarrod J. Scott, Sean M. McAllister, Clara S. Chan, James McManus, Filip J.R. Meysman, and David Emerson
 Biological Iron Oxidation in Marine Sediments
- Felix Beulig**, Hans Røy, Bo B. Jørgensen
 Mineralization Rates Across the Sulfate-Methane-Transition of Holocene Marine Sediments are Continuous and Partially Mediated by Syntrophic Acetate Oxidation
- James A. Bradley**, Jan P. Amend, Douglas E. LaRowe
 Necromass as a Source of Energy for Microorganisms in Marine Sediments
- Volker Brüchert**, Lisa Bröder, Joanna Sawicka, Xiaole Sun, Christoph Humborg, Magnus Mörrth, Samantha Joye, Igor Semiletov, Vladimir Samarkin
 Degradation Rates of Refractory Terrestrial Organic Carbon on the East Siberian Shelf and Slope
- Matthias Egger**, Natascha Riedinger and Bo. B. Jørgensen
 Anaerobic Oxidation Of Methane In Marine Sediments: A Global Synthesis
- Philip Eickenbusch**, Clemens Glombitza, Bo B. Jørgensen and Mark A. Lever
 Microbial Control of Formate Concentrations in Batch Incubations of Sulfate-Reducing and Methanogenic Sediments
- Alyssa J. Findlay** and Alexey Kamyshny
 Turnover Rates of Sulfide Oxidation Intermediates (S_x^{2-} , S^0 , $\text{S}_2\text{O}_3^{2-}$, $\text{S}_4\text{O}_6^{2-}$, SO_3^{2-}) in Freshwater and Sediments
- Stefan Forster**, Martin Powilleit, Hanna Schade, Stefan Richter and Ulrich Floth
 Permeability and Bioirritation Affecting TOU in Coastal Baltic Sediments
- Bernhard M. Fuchs**, Ben Francis, Burak Avci, Karen Krüger, Meghan Chafee, Tanja Woyke, Hanno Teeling, Rudolf Amann
 Dissecting the Metabolic Potential of a Marine Prime Responder After the Spring Diatom Bloom at Helgoland Island
- Jeanine S. Geelhoed** and Filip J.R. Meysman
 Microbial Community Composition and Metabolic Sulfur Cycling Potential in a Sediment with Cable Bacteria
- Susann Henkel**, Verena B. Heuer, Fumio Inagaki, Yuki Morono, Kai-Uwe Hinrichs and Expedition 370 Scientists
 How Stable Iron Isotopes Can Help in Identifying the Limit of Life in Deep Marine Sediments of the Nankai Trough (Iodp Expedition 370)

Casey Hubert, Anirban Chakraborty, Carmen Li, Daniel Gittins, Emily Ellefson, Bernie Bernard, James Brooks

Marlene M. Jensen, C. Ma, G. Lavik, B. F. Smets, B. Thamdrup

Lara M. Jochum, Lars Schreiber, Ian P.G. Marshall, Bo Barker Jørgensen, Andreas Schramm, Kasper U. Kjeldsen

Alexey Kamyshny, Khoren Avetisyan, Werner Eckert and Alyssa Findlay

Sabine Kasten, Gerard Versteegh, Andrea Koschinsky, Heiner Villinger, Ingrid Dohrmann, Julia Fronzek, Jan Hartmann, Charlotte Kleint, Inken Preuss, Simon Ritter and Thomas Kuhn

Adam J. Kessler, Perran L. M. Cook, Michael F. Bourke, Sharlynn Koh, Chris Greening, Ronnie N. Glud, Harald Hasler-Sheetal

Richard Kevorkian, IODP Expedition 366 Science Party, Karen G. Lloyd

Katharina Kitzinger, Cory C. Padilla, Hannah K. Marchant, Maria Mooshammer, Craig W. Herbold, Frank J. Stewart, Michael Wagner, Marcel M. M. Kuypers, Laura A. Bristow

Beate Kraft, Kai Finster, Donald E. Canfield

Erik Kristensen, Hans Røy, Kristian Debrabant, Thomas Valdemarsen

Mei-Chin Lai, Sheng-Chung Chen, Hsin-Hsin Chien, Mei-Fei Chen, Chieh-Yin Weng

Katja Laufer, Alexander B. Michaud, Hans Røy, Bo B. Jørgensen

Distributions of Thermophilic, Endospore-Forming Bacteria in Hydrocarbon Seep Prospective Sediments in the Eastern Gulf of Mexico

Dynamics of N₂O Production Pathways Analysed by ¹⁵N/¹⁸O Dual Isotope Labelling – Data from a Full-Scale Wastewater Treatment Plant

Single Cell Genomics Reveals a Diverse Metabolic Potential of Uncultured *Desulfarculaceae* Widely Distributed in Marine Sediment

Detailed Study of Sulfur Cycling in Chemocline of Monomictic Lake Kinneret (Israel)

Widespread Diffusion of Oxygen from Oceanic Crust into Overlying Sediments in the NE Pacific Ocean – Early Diagenetic Consequences and Significance for Biogeochemical Cycles (RV Sonne Cruise SO 240)

How Do Sands Breathe? Reimagining the Redox Cascade in Permeable Sediments

Microbial Ecology at Serpentinite Seamounts Associated With the Mariana Convergent Margin

Cyanate and Urea as Substrates for Marine Thaumarchaeota

Transition Between Aerobic Respiration and Denitrification at Low Oxygen Concentrations

Organic Carbon Oxidation and Bioirrigation in Sediments Along a Skagerrak-Kattegat Belt Sea Depth Transect

Methanoarchaea From Marine Mud Volcano and Gas Hydrate Habitats

Controls on Iron And Sulfate Reduction in Arctic Fjord Sediments

Yang Liu, Zhichao Zhou, Jie Pan, Brett J. Baker, Ji-Dong Gu , Meng Li	Genomic Resolution of Metabolic Pathways of Thorachaeota
Angeliki Marietou , Clemens Glombitza, Gijs J Kuenen, and Bo B. Jørgensen	Through the Looking Glass: The Controls of Volatile Fatty Acid Oxidation by Sulfate Reducers in Marine Sediments
Ugo Marzocchi , Sebastiaan van de Velde, Stefano Bonaglia, Nils Risgaard-Petersen, Filip J.R. Meysman, and Per O.J. Hall	A Major Baltic Inflow Creates a Temporal Niche for Cable Bacteria in Eastern Gotland Basin Sediments
Harry.L.O. McClelland , David. A. Fike, Yuki. Morono, IODP Expedition 370 Science Party, & Alexander S. Bradley	An In Vivo Investigation into Temperature-Controlled Stratification of Sub-Seafloor Populations
Massimiliano Molari , Tobias Vonnahme, Felix Janssen	Assessing Microbial Biomass Production in Deep-Sea Sediments Via ¹⁴ C-Bicarbonate Uptake
Marc Mussmann , Stefan Dyksma and Petra Pjevac	Beyond the ‘Usual Suspects’: Overlooked but Abundant Sulfur Oxidizers in Marine Sediments
Claus Pelikan , Albert Müller, Clemens Glombitza, Julia R. de Rezende, Kenneth Wasmund, and Alexander Loy	Microbial Necromass Degradation in Arctic Marine Sediments: Physiological Interactions of Microorganisms Involved in Anoxic Degradation of Cellular Organic Matter
André Pellerin , Gilad Antler, Alyssa Findlay, Felix Beulig, Hans Røy, Alexandra Turchyn and Bo Barker Jørgensen	Revisiting the Cryptic Sulfur Cycle in Sulfate-Limited Sediments Of Kattegat
Caitlin Petro , Birthe Zäncker, Piotr Starnawski, Lara Jochum, Timothy G. Ferdeman, Bo Barker Jørgensen, Hans Røy, Kasper U. Kjeldsen, Andreas Schramm	Marine Deep Biosphere Microbial Communities Assemble in Near-Surface Sediments
Aude Picard , Amy Gartman, Julie Cosmidis, David R. Clarke, Peter R. Girguis	Revisiting Biogenic Iron Sulfide Minerals
Alex Enrich Prast	Global and Local Regulation of Microbial Activity in Coastal Subsurface Sediments
Alberto Robador , Jan P. Amend, and Steven E. Finkel	Determination of Generation Time and Growth Rate of The GASP Phenotype in Long-Term Stationary Phase <i>E. Coli</i> Cultures by Nanocalorimetry

Clemens Schaubberger , Bo Thamdrup, Ronnie Glud	Towards Artefact Free Studies on Deep Sea Sediments
Caroline Scholze , Bo Barker Jørgensen, Hans Røy	Only Long-Term Incubations Reveal Temperature Adaptation in Environmental Samples
Kirsten Oswald, Corinne Jegge, Jana Tischer, Jasmine Berg, Andreas Brand, Maria R. Miracle, Xavier Soria, Eduardo Vicente, Moritz F. Lehmann, Jakob Zopfi and Carsten J. Schubert	Methanotrophy Under Versatile Conditions in the Water Column of the Ferruginous Meromictic Lake La Cruz (Spain)
Alberto Scoma , Robert Heyer, Ridwan Rifai, Frederiek-Maarten Kerckhof, Christian Dandyk, Eric Boshker, Filip J. R. Meysman, Pieter Vermeir, Ian Marshall, Ibrahim Banat, Udo Reichl, Dirk Benndorf and Nico Boon	Hydrostatic Pressure Can Shape Microbial Oil-Degrading Communities and Their Metabolism
Orit Sivan , Itay Bar-Or, Hanni Vigderovich, Marcus Elvert, Werner Eckert	Microbial Iron Reduction in Lacustrine and Marine Methanogenic Sediments
Martijn Hermans, Nils Risgaard-Petersen, Filip J. R. Meysman, Caroline Slomp	The Impact of Electrogenic Sulphide Oxidation on the Biogeochemistry of Coastal Black Sea Sediment
Oona L.O. Snoeyenbos-West , Carolin R. Löscher and Amelia-Elena Rotaru	The Electromicrobiome of Oxygen Minimum Zones and its Biogeochemical Significance
Anja Spang , Courtney Stairs, Jonathan Lombard, Nina Dombrowski, Eva Fernández Cáceres, Steffen L. Jørgensen, Brett J. Baker and Thijs J.G. Ettema	Asgard Archaea – A Metabolically Diverse Superphylum that has Played a Key Role in the Origin of Eukaryotes
Casper A. Thorup , Ugo Marzocchi, Ann-Sofie Dam, Tobias Sandfeld, Lars P. Nielsen, Nils R.-Petersen, Andreas Schramm	Transcriptomics of the Cable Bacterium <i>Candidatus</i> Electronema Nielsenii
Stephanie Turner , Daria Frohloff, Marcus A. Horn and Axel Schippers	Microbial Nitrogen Cycling Potential in Deep Sediments of the Baltic Sea
Kenneth Wasmund , Claus Pelikan, Margarete Watzka, Andreas Richter, Amy Noel, Casey Hubert, Thilo Hoffman, Alexander Loy	Stable Isotope Probing and Metagenomics Identifies Diverse and Uncharacterised Bacteria that Degrade DNA in Anoxic Marine Sediments
Gunter Wegener , Rafael Laso-Pérez, Katrin Knittel, Antje Boetius, Friedrich Widdel, Dietmar Riedel and Florin Musat	Archaea Activate Short-Chain Hydrocarbons by the Formation of Alkyl-CoM in Highly Divergent Methyl-CoM Reductases

Laura M. Wehrmann, Sandra Arndt,
Benjamin Brunner, Patrick Meister, Charlotte
Ockert, Christian März, Nikolaus Gussone,
Barbara M.A. Teichert, Timothy G. Ferdelman

The Dynamic Deep Biosphere – Linking
Changing Paleo-Environmental Conditions,
Rates and Pathways of Microbial Processes, and
Diagenetic Signals in the Sedimentary Record

Ke-Qing Xiao, Felix Beulig, Hans Røy, Bo
Barker Jørgensen and Nils Risgaard-Petersen

Methylotrophic Methanogenesis Fuels Cryptic
Methane Cycling in Surface Sediment of Aarhus
Bay, Denmark

Tingting Yang, Zegao Wang, Mindong Dong,
Lars Peter Nielsen

Asymmetric, Synchronized Cell Division
Decides the Cell Size Differences in Cable
Bacteria

Abstracts

SCALE-BRIDGING STUDIES OF BACTERIOPLANKTON-PHYTOPLANKTON INTERACTIONS

Rudi Amann (*) et mult. al.

(*) *Max Planck Institute for Marine Microbiology*

Oceans and seas of the higher latitudes are characterized by recurrent phytoplankton blooms of dimensions that are best monitored by satellites. The huge Gt amounts of dissolved and particulate organic matter released by the breakdown of algal blooms convert such surface waters temporally to high energy environments where the competition among heterotrophic bacteria for polysaccharides and proteins is fierce. We have over the past years studied spring blooms in the North Sea with a polyphasic approach including FISH, tag sequencing, metagenomics and metaproteomics. Our data suggest a deterministic succession of distinct taxonomic clades of Bacteroidetes and Gammaproteobacteria which have evolved specific strategies for the utilization of complex polysaccharides. The genomes of marine Bacteroidetes contain often several polysaccharide utilization loci encoding ordered sets of glycoside hydrolases, sulfates and transporter proteins. By short-term incubations of surface water samples with fluorescently labelled polysaccharides a "selfish" uptake mechanism reminiscent of the starch utilization system of gut Bacteroidetes could be visualized by super resolution light microscopy. This rather complex mechanism is minimizing the loss of substrate by the uptake of oligosaccharides through TonB-dependent outer membrane transporters into the periplasmic space. The fact that the respective proteins are among the most abundant proteins in metaproteomes of the 0.2-3 μm size fraction further corroborates the central importance of the fight for energy.

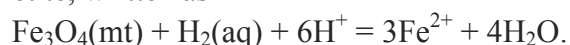
THE REDOX LADDER OF MICROBIAL CATABOLISM: WHAT ARE WE MISSING?

Jan Amend (*), Doug LaRowe

(*) *Department of Earth Sciences, University of Southern California, Los Angeles, USA*

“Thermodynamic tables are mines of information” (Kuehnen, 2008). This quote refers to the time-tested approach of evaluating the energetics of redox reactions to assess if they can serve as catabolic strategies for microorganisms. Perhaps the best-known example of using thermodynamics to predict a novel catabolism ‘missing in nature’ is anammox, the anaerobic oxidation of ammonia with nitrite (Broda, 1977). Curiously, in that prediction, Broda used the *standard state* Gibbs energy of reaction (DG_r^0) and not the Gibbs energy of reaction (DG_r) appropriate for the environmental condition of interest. Values of DG_r^0 are often, but incorrectly, used to infer the direction and magnitude of a reaction, but these values do not take into account the concentrations (and hence the activities) of all the products and reactants in that reaction. However, ‘all is well that ends well’, at least in the case of anammox, as van de Graaf et al. (1995) demonstrated experimentally that anammox is indeed a microbially mediated process.

For many reactions, however, relying on DG_r^0 will incorrectly predict whether the reaction is energy-yielding or not. This is a particularly common problem for reactions involving iron oxides, elemental sulfur, CO, or CO₂ as a reactant. As an example, let’s consider the lithotrophic reduction with H₂ of the mineral magnetite, written as



Over the biologically reasonable temperature range of 0-120°C, values of DG_r^0 vary from approximately -120 to -100 kJ/mol e⁻ transferred. If the sign and value of DG_r^0 were meaningful, this would suggest this process to be strongly exergonic. It isn’t. Evaluations of the appropriate DG_r at ‘high energy’ conditions (e.g., slightly acidic pH and high H₂ levels) show the reaction to be only moderately exergonic, yielding approximately 60-20 kJ/mol e⁻ over this temperature range. At ‘low energy’ conditions (e.g., slightly basic pH and low H₂ levels), this reaction is endergonic, with DG_r values of approximately +50 to +25 kJ/mol e⁻.

In this presentation, we take a close look at the energetics of redox reactions to evaluate microbially mediated reactions in nature. We provide examples of reactions where changes in temperature can change the sign of DG_r^0 (i.e., from negative to positive, or vice versa), and where values of DG_r^0 and DG_r have different signs at the same temperature. We then use thermodynamics to gain insight into poorly described catabolisms and perhaps to predict yet unknown energy strategies by microorganisms under certain geochemical conditions.

REFERENCES:

- Kuehnen, JG (2008) Anammox bacteria: from discovery to application. *Nature Reviews Microbiology*, **6**, 320-326.
Broda, E (1977) Two kinds of lithotrophs missing in nature. *Zeitschrift fuer Allgemeine Mikrobiologie*, **17**, 491-493.
van de Graaf, AA, Mulder, A, de Bruijn, P, Jetten, MSM, Robertson, LS, Kuehnen, JG (1995) Anaerobic oxidation of ammonium is a biologically mediated process. *Applied and Environmental Microbiology*, **61**, 1246-1251.

$\Delta^{13}\text{CH}_3\text{D}$ AND $\Delta^{12}\text{CH}_2\text{D}_2$ SIGNALS OF METHANOGENESIS AND METHANOTROPHY

Jeanine L. Ash (*), Matthias Egger, Issaku Kohl, Tina Treude, Caroline P. Slomp, Barry Cragg, R. John Parkes, Douglas Rumble and Edward D. Young

(*) *University of California, Los Angeles, USA*

Methanogens in marine sediments are estimated to produce between 85-300 Tg of methane (CH_4) annually, yet the net flux of CH_4 to the water column is strictly controlled by the anaerobic oxidation of methane (AOM). Hypotheses that abrupt imbalances in this delicate cycle can occur as a result of anthropogenic climate change drive our desire to better understand microbial CH_4 production and consumption in the deep biosphere. The ability to measure the relative abundances of two doubly-substituted rare isotopologues of gases with biogeochemical relevance provides new constraints on sources and sinks of these gases. Here, we report the first measurements of fully resolved $^{13}\text{CH}_3\text{D}$ and $^{12}\text{CH}_2\text{D}_2$ from samples of deep biosphere CH_4 gas collected during IODP Exp. 347 to the Baltic Sea. We measured sedimentary CH_4 samples from Bornholm Basin and Landsort Deep in the Baltic Sea for $\Delta^{13}\text{CH}_3\text{D}$, $\Delta^{12}\text{CH}_2\text{D}_2$, $\delta^{13}\text{C}$ and δD . Results are interpreted within the context of porewater geochemistry, activity measurements, and a multicomponent diagenetic model that estimates rates of CH_4 production, SO_4 -AOM and Fe-AOM. $\Delta^{13}\text{CH}_3\text{D}$ and $\Delta^{12}\text{CH}_2\text{D}_2$ vary with depth concurrent with changing rates of methanogenesis and methanotrophy. Samples associated with higher rates of methanogenesis exhibit disequilibrium of up to 2‰ in $\Delta^{13}\text{CH}_3\text{D}$ and 13‰ in $\Delta^{12}\text{CH}_2\text{D}_2$ while those with higher rates of methanotrophy approach intra-species thermodynamic equilibrium. We hypothesize that methanogenesis creates CH_4 in isotopic disequilibrium by combinatorial, reservoir and quantum tunneling effects, and enzymatic back reaction during AOM drives the residue towards equilibrium.

BIOLOGICAL IRON OXIDATION IN MARINE SEDIMENTS

Jacob P. Beam (*), Jarrod J. Scott, Sean M. McAllister, Clara S. Chan, James McManus, Filip J.R. Meysman, and David Emerson

(*) *Bigelow Laboratory for Ocean Sciences, East Boothbay, USA*

The biogeochemical cycle of iron is intricately linked to the carbon, sulfur, nitrogen, manganese, and phosphorous cycles. Although reductive biological processes that bridge the iron cycle to other element cycles is established, little is known about the importance of microbial oxidative processes on iron cycling in sedimentary environments. Nevertheless, biological iron oxidation results in the production of iron oxides that are important components of marine sediments. Here, we show that a major source of sedimentary iron oxides originates from the metabolic activity of iron-oxidizing bacteria from the class Zetaproteobacteria, stimulated by burrowing animals in coastal sediments. A lithoautotrophic, iron-oxidizing bacterium was isolated from the sedimentary environment and was representative of a dominant clade of Zetaproteobacteria that are globally distributed in sediments. Zetaproteobacteria were estimated to be a global total of 10^{26} cells in coastal, bioturbated sediments and their activity would equate to an annual production of approximately 7.9×10^{15} grams of sedimentary iron oxides—twenty-five times larger than the annual flux of iron oxides by rivers to coastal sediments. Bioturbation mesocosm incubations with the polychaete *Nereis diversicolor* under various simulated bottom water oxygen concentrations (10-280 μM) revealed that iron-oxidizing Zetaproteobacteria enhanced the production of iron oxides at low oxygen, and combined with bioirrigation activity of *N. diversicolor*, resulted in a net increase in the flux of dissolved iron from sediments. These data suggest that Zetaproteobacteria are keystone organisms in marine sedimentary environments given their low numerical abundance; yet exert a profound impact via the production of iron oxides. Biological iron oxidation by Zetaproteobacteria—stimulated by ecosystem engineering macrofauna— is an important biological control on the sedimentary iron cycle, linking reduced and oxidized phases.

LIGHT ENERGY AND ANOXYGENIC PHOTOSYNTHESIS

Dirk de Beer (*)

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Oxygenic phototrophs, Cyanobacteria, evolved at least 3.5 Ga ago from anoxygenic phototrophs predecessors. However, it took at least 1 Ga before oxygen developed in the oceans and atmosphere, in the Great Oxidation Event (GOE). Many strains of Cyanobacteria have retained the ability to also perform anoxygenic photosynthesis. We are interested in what controls the mode of phototrophy. Single-algal enrichment cultures showed a variety of responses to sulfide, but usually the presence of sulfide inhibited oxygenic photosynthesis. Anoxygenic photosynthesis is thus preferred, however, the ability to perform oxygenic photosynthesis must have been of selective advantage in the reduced world from before the GOE. We investigated mats from an anoxic and slightly sulfidic lake, which we considered an analog of aquatic systems from before the GOE. A 1-2 mm thick red mat dominated by filamentous Cyanobacteria covered a thick layer of Green Sulfur Bacteria. Oxygenic and anoxygenic photosynthesis were studied with O₂ and H₂S microsensors, as well as fiberoptic light sensors, *in situ* and in the lab. Within 3-4 mm inside the mats, the incident radiation was attenuated to undetectable levels. *In situ* microsensor data showed oxygenic photosynthesis in the red surface layer and light-induced sulfide dynamics to at least 1 cm depth. Anoxygenic photosynthesis occurred during all daylight hours, with complete sulfide depletion around midday. Oxygenic photosynthesis was limited to 4 hours per day, due to sulfide inhibition in the early morning and late afternoon. Oxygenic photosynthesis was reversibly inhibited by sulfide. In patches Fe(III) alleviated the inhibition of oxygenic photosynthesis by sulfide. We argue that the first evolution of oxygen could have occurred in a setting where Fe(III) does not sink and mass transfer resistance allows the development of microzones without sulfide. This emphasizes the importance of microbial mats in the evolution of aerobic life.

MINERALIZATION RATES ACROSS THE SULFATE-METHANE-TRANSITION OF HOLOCENE MARINE SEDIMENTS ARE CONTINUOUS AND PARTIALLY MEDIATED BY SYNTROPHIC ACETATE OXIDATION

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Knowledge about controls and rates of organic matter (OM) degradation in marine sediments is key to our understanding of carbon cycling in the deep biosphere. Although individual processes in the microbially mediated OM degradation chain are thought to be well constrained it remains highly uncertain how rates of OM mineralization progress through different geochemical zones. In order to study the transition from sulfate reduction– to methanogenesis–driven mineralization, we performed highly depth-resolved analyses of geochemistry and microbial activities in Holocene sediment cores (up to 8 m length) from 5 stations in the Baltic Sea. Sulfate reduction rates, as determined by ^{35}S - SO_4^{2-} tracer experiments, decreased along a similar depth-trend at all sampling sites. At the sulfate-methane transition the rate of sulfate reduction dropped abruptly, with a concomitant increase of ^{14}C -DIC methanogenesis rates. As a result, overall rates of mineralization progressed continuously with OM age and reactivity throughout the sediment, irrespective of the prevailing redox zonation and associated changes in the microbial degradation pathway. This suggests that the efficiency of OM mineralization in marine sediments is not attenuated under methanogenic conditions, and confirms the often predicted primary ‘donor’ control on the activity of the sediment microbiome. In all depths CO_2 reduction was the predominant pathway of methanogenesis, and ^{14}C -acetate was almost exclusively converted to ^{14}C - CO_2 , even in the methane zone where potential electron acceptors other than CO_2 are depleted. Challenging previous views of the microbial degradation chain in marine sediments, we attribute this observation to the only known alternative pathway for acetate consumption under methanogenic conditions – acetate oxidation (to CO_2 plus H_2 and/or electrons) that is syntrophically coupled with hydrogenotrophic methanogenesis.

ANAEROBIC OXIDATION OF METHANE FUELLING BENTHIC ECOSYSTEMS

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The biological sink for methane in aquatic systems comprises the aerobic and anaerobic oxidation of methane, which is mediated by communities of bacteria, archaea, and symbiotic or opportunistic animals that interact with microbes to tap into this energy source. This presentation will discuss current hypotheses as to the fate of methane and other hydrocarbons in the seabed, and the link between methanotrophs and benthic communities in different seafloor habitats. It aims at providing an overview on current knowledge as to the distribution and diversity of seabed archaea and their contribution to methane and carbon cycling, with a focus on recent studies tackling the question of methanotrophy and ecophysiological adaptations to the variety of hydrocarbon-fueled benthic ecosystems. Understanding spatial and temporal scales of methanotroph community turnover in relation to environmental dynamics has helped to assess the efficiency with which methane can be removed from the seabed. Global ocean studies show that a few cosmopolitan microbial taxa mediate the bulk of methane oxidation at the seafloor, and that these taxa have developed distinct interaction mechanisms to share the energy gain from hydrocarbon oxidation. While the principle biological mechanisms underlying this relevant biogeochemical function remain rather enigmatic, progress has been made with linking the observed archaeal diversity to different hydrocarbon substrates.

NECROMASS AS A SOURCE OF ENERGY FOR MICROORGANISMS IN MARINE SEDIMENTS

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It is no longer conjecture that microbial dead-matter (necromass) can fuel part of the subsurface biosphere. However, the production of necromass in marine sediments, the energy and power available to microorganisms from necromass oxidation, and its role in sustaining heterotrophic communities have not been quantified. Here, we have developed a physical, bio-energetic and geochemical model to quantify the total power demand of sediment microbial communities and the total power available from the oxidation of microbial necromass that is produced by dying cells. This model is then applied to sediments from the oligotrophic South Pacific Gyre, where organic carbon and biomass concentrations are extremely low, yet microorganisms persist for millions of years in some of the lowest energy states on Earth. We show that the rate of cell death (and thus necromass oxidation) is insufficient to match the power demands of the living community (<39%), assuming all counted cells are viable. Application of our model on a global scale shows that necromass produced and subsequently oxidized can provide sufficient energy to satisfy the maintenance power demands of the surviving microbial community for up to 60,000 years after burial. If not all counted cells are alive, the role of necromass as an electron donor in microbial metabolisms is even greater (e.g. up to 600,000 years if 10% of cells are viable). Insight from this study requires a reassessment of carbon fluxes in the deep biosphere. Further, we demonstrate a mechanism for microbial communities to persist over geological timescales and endure unfavorable, low-energy settings that might be analogous to conditions on early Earth and on other planetary bodies.

DEGRADATION RATES OF REFRACTORY TERRESTRIAL ORGANIC CARBON ON THE EAST SIBERIAN SHELF AND SLOPE

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The Siberian Arctic Sea shelf and slope is a key region for the mineralization of terrestrial organic material transported from the organic carbon-rich permafrost regions of Siberia to the sea. We report on sediment carbon mineralization rates and sediment porewater analyses from 20 shelf and slope stations in the Laptev, East Siberian, and Chukchi Sea. In the Laptev Sea these sediments are dominated by refractory terrestrial organic material with a small contribution of fresh marine organic material. The latter contribution increases substantially from west to east across the Siberian shelf. Degradation of the fresh marine organic material supports oxygen uptake rates comparable to other global shelf areas, but these rates are not indicative of the terrestrial organic matter degradation. Instead, the anaerobic degradation rates by manganese, iron, and sulfate reduction below the topmost cm provide direct evidence for the degradation rate kinetics of the buried terrestrial organic material. The data suggest substantial mobilization of refractory terrestrial organic carbon during anaerobic carbon mineralization. About 16 Tg total C per year are respired in the outer shelf sea floor sediment, to which terrestrially-derived organic matter contributes between 0.3 to 0.5 Tg per year. These data provide rare data on the magnitude of aerobic and anaerobic carbon mineralization rates and help to constrain biogeochemical interactions between the Siberian land mass and the Arctic Ocean under conditions of Arctic warming.

THE EVOLUTION OF THE SULFUR CYCLE

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My talk will focus on the evolution of the sulfur cycle, but probably not what you might expect.

ENERGY SOURCES AND TAXONOMIC SELECTION IN SUBSEAFLOOR SEDIMENTARY COMMUNITIES

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First-order distributions of net metabolic activity in subseafloor sediment are broadly resolved. Subseafloor activity is generally anaerobic in the fast-accumulating organic-rich sediment of continental margins and upwelling regions, and aerobic in the slowly accumulating abyssal sediment of the deep open ocean (D'Hondt et al., 2015). The principal electron donor in anoxic marine sediment and in relatively young oxic marine sediment appears to be buried organic matter. In oxic sediment older than a few million years, radiolytic H₂ may be the dominant fuel. Our experimental studies indicate that the entire seafloor is covered by sediment that catalyzes radiolytic H₂ production (Sauvage et al., in review). The highest H₂ yields occur in deep-sea clay, which amplifies radiolytic H₂ production by up to a factor of 27 compared to pure water. Our study of geographically diverse sites indicates that in regions of anoxic subseafloor sediment, bacterial richness decreases exponentially with increasing sediment age, in parallel with organic degradation rate (Walsh et al., 2016). This relationship suggests that (i) community catabolic rate and/or electron-donor diversity exerts a primary influence on bacterial richness in marine sediment. Richness consistently takes a few hundred thousand years to decline from near-seafloor values to much lower values in deep anoxic sediment, regardless of sedimentation rate, predominant terminal electron acceptor or oceanographic context. At these sites, the best predictor of taxonomic presence or absence in old sediment is relative abundance in near-seafloor sediment. This relationship suggests that taxonomic perseverance into deep, old sediment is primarily controlled by relative population size when the sediment was young and near the seafloor. Comparison of community composition to cell concentration at an example site indicates that the rise to dominance of the few dominant taxa in its deep subseafloor community does not require cell replication, but might simply result from lower mortality of those taxa relative to competing taxa on the long timescale of community burial (up to 1,300,000 years).

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ANAEROBIC OXIDATION OF METHANE IN MARINE SEDIMENTS: A GLOBAL SYNTHESIS

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Methane acts as a powerful greenhouse gas in the Earth's atmosphere and its emissions from marine sediments are substantially reduced by anaerobic oxidation coupled to sulfate reduction within a distinct sulfate/methane transition zone (SMTZ). Despite recent breakthroughs in our understanding of the biological mechanisms of anaerobic oxidation of methane (AOM), the global removal of methane in the seafloor remains poorly quantified.

In this study, we establish a comprehensive marine database of methane and sulfate fluxes, as well as related parameters from > 700 sediment cores. Our analyses reveal a linear correlation between the magnitudes of diffusive fluxes of methane and sulfate to the SMTZ and the corresponding depth of the SMTZ over several orders of magnitude. The depth of the SMTZ, in turn, shows a linear correlation with the associated sedimentation rates. Using these linear relationships in combination with gridded data sets of key environmental parameters we develop a spatially resolved AOM budget for marine sediments, covering different oceanic regions.

We also demonstrate that most flux ratios between methane and sulfate do not show a 1:1 relation, as would be expected from a simple AOM stoichiometry, but rather indicate a higher sulfate flux relative to the methane flux. Our findings thus further provide new insights into the biogeochemical coupling of the sulfur and carbon cycles in marine sediments.

MICROBIAL CONTROL OF FORMATE CONCENTRATIONS IN BATCH INCUBATIONS OF SULFATE-REDUCING AND METHANOGENIC SEDIMENTS

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In anoxic environments, short-chain organic acids are generated by microbial fermentation and respired by several different metabolic groups of microorganisms during energy production. Links between microbial phylogeny and metabolic function during the anaerobic mineralization of low-molecular-weight organic carbon compounds in anoxic sediments are poorly resolved. To elucidate some of these links we used batch incubations of sulfate-reducing and methanogenic marine sediments of Aarhus Bay (Denmark) and stimulated both sediment types with 50 μM pulses of ^{13}C -labeled formate, acetate, propionate, or butyrate. Despite previous studies indicating acetate as the quantitatively most important organic acid in anaerobic sediments, degradation of formate was remarkably faster than degradation of acetate, propionate, or butyrate. Formate appeared to be oxidized to molecular hydrogen (H_2) and dissolved inorganic carbon (DIC) via a bidirectional reaction, possibly carried out by the enzyme formate dehydrogenase, with most H_2 escaping to the headspace rather than being converted to methane. Despite the overall lower rates of microbial activity in the methanogenic compared to the sulfate-reducing sediments, formate oxidation was much faster in methanogenic sediment. To test whether the same trends could be observed in a different sedimentary setting, we incubated freshwater sediments of Lake Lucerne (Switzerland) using a similar experimental setup. In these lacustrine sediments, as in marine sediments, H_2 production occurred and was fastest in sediments dominated by methanogenesis, with again most H_2 escaping to the headspace rather than being converted to methane. Next generation amplicon sequencing of 16S rRNA genes, as well as genes and gene transcripts encoding the alpha subunit of formate dehydrogenase, were analyzed next to provide information on microbial key players controlling formate turnover in anoxic sediments.

CRYPTIC CROSS-LINKAGES AMONG BIOGEOCHEMICAL CYCLES: A KEY ROLE FOR ELEMENTAL SULFUR?

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Elemental sulfur appears to play a pivotal role in linking various biogeochemical processes, especially those of iron and carbon. For example, intermediate sulfur species are used in electron shuttling in bacterially driven Fe (III) mineral reduction by sulfur-reducing bacteria [1,2]. The deep, reduced, sulfidic zone of marine sediments is also often paradoxically characterized by the presence of elemental sulfur and polysulfides [3,4]. Fluxes of oxidized iron have been suggested as the source of oxidizing power as a driver of a cryptic sulfur cycle in these deep, anoxic and sulfidic sediment systems [3]. Alternatively, Milucka et al. [5] has shown that S(0) can also form during sulfate reduction (SR) coupled to the anaerobic oxidation of methane (AOM), and concluded that S(0) is a product of a novel pathway for sulfate reduction performed by the methane oxidizing Archaea (ANME). Thus, if coupled to AOM, SR might not necessarily proceed all the way to sulfide, and thus, can provide a source of sulfur intermediates (e.g. elemental S and polysulfides) at depth. This could also drive the deep “cryptic sulfur cycle” observed in and below the methane transition zone [3]. S(0) in the form of polysulfides, in particular hydrodisulfide, can serve as a substrate for disproportionation by the Deltaproteobacteria associated with the ANME [5]. Thus, the interplay between carbon respiration, methane oxidation, iron oxides and the deep cryptic sulfur cycle may be even more complex and challenging than previously imagined, and the unique biogeochemistry of elemental sulfur greases these processes.

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TURNOVER RATES OF SULFIDE OXIDATION INTERMEDIATES (S_x^{2-} , S^0 , $S_2O_3^{2-}$, $S_4O_6^{2-}$, SO_3^{2-}) IN FRESHWATER AND SEDIMENTS

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The microbial reduction of sulfate to sulfide coupled to organic matter oxidation followed by the transformation of sulfide back to sulfate drives a dynamic sulfur cycle in a variety of environments. The oxidative part of the sulfur cycle in particular is difficult to constrain because the eight electron oxidation of sulfide to sulfate occurs stepwise via a suite of biological and chemical pathways and produces a wide variety of intermediates (S_x^{2-} , S^0 , $S_2O_3^{2-}$, $S_4O_6^{2-}$, SO_3^{2-}), which may in turn be oxidized, reduced or disproportionated. Although the potential processes affecting these intermediates are well-known from microbial culture and geochemical studies, their significance and rates in the environment are not well constrained. In the study presented here, time-course concentration measurements of intermediate sulfur species were made in amended freshwater water column and sediment incubation experiments in order to constrain consumption rates and processes. In sediment incubations, consumption rates were $S_{0colloidal} > S_x^{2-} > SO_3^{2-} \approx S_4O_6^{2-} > S_2O_3^{2-}$, which is consistent with previous measurements of SO_3^{2-} , $S_4O_6^{2-}$ and $S_2O_3^{2-}$ consumption rates in marine sediments. In water column incubations, however, the relative reactivity was $S_{0colloidal} > SO_3^{2-} > S_x^{2-} > S_2O_3^{2-} > S_4O_6^{2-}$. Consumption of thiosulfate, tetrathionate and sulfite was primarily biological, whereas it was not possible to distinguish between abiotic and biological polysulfide consumption in either aqueous or sediment incubations. $S_{0colloidal}$ consumption in water column experiments was biologically mediated, however, rapid sedimentary consumption was likely due to reactions with iron minerals. These experiments provide important constraints on the biogeochemical reactivity of intermediate sulfur species and give further insight into the diversity of biological and geochemical processes that comprise (cryptic) environmental sulfur cycling.

DESULFURIVIBRIO ALKALIPHILUS PROVIDES INSIGHTS INTO SULFIDE OXIDATION COUPLED TO SULFUR DISPROPORTIONATION BY REVERSAL OF THE CANONICAL SULFATE REDUCTION PATHWAY.

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We demonstrated that the Deltaproteobacterium *Desulfurivibrio alkaliphilus* can grow chemolithotrophically by coupling sulfide oxidation to the dissimilatory reduction of nitrate and nitrite to ammonium. Key genes of known sulfide oxidation pathways are absent in the genome of *Desulfurivibrio alkaliphilus*. Instead, the genome contains all necessary genes for sulfate reduction including a reductive-type dissimilatory bisulfite reductase. Despite this, growth by sulfate reduction was not observed. Transcriptomic analysis revealed a very high expression of sulfate reduction genes during growth by sulfide oxidation and disproportionation of elemental sulfur, while inhibition experiments with molybdate pointed to elemental sulfur/polysulfides as intermediate. Consequently, we propose that *Desulfurivibrio alkaliphilus* initially oxidizes sulfide to elemental sulfur, which is then either disproportionated or oxidized by a reversal of the sulfate reduction pathway. This is the first study providing evidence that a reductive-type dissimilatory bisulfite reductase (DSR) is involved in both the sulfide oxidation and sulfur disproportionation pathway.

PERMEABILITY AND BIOIRRITATION AFFECTING TOU IN COASTAL BALTIC SEDIMENTS

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Typical coastal sea floors in the Southern Baltic are composed of sandy permeable and muddy impermeable sediments. Enhanced oxygen availability due to bioirrigation and advective pore water flows, as well as respiring macrofauna, increase total oxygen uptake (TOU). Here, we compile data to compare the partitioning of TOU into different processes for two coastal locations with different sediments: a sandy sediment and a mixed silty sand. The increase of oxygen utilization driven by seasonal temperature increase can theoretically ($Q_{10} \sim 3$) account for a 4-5-fold TOU in summer as compared to winter. This leaves roughly $15 \text{ mmol m}^{-2} \text{ d}^{-1}$ of oxygen consumption unaccounted for, when we compare the data to seasonal TOU measurements obtained from bimonthly core incubations ($n=3-5$ per date) at the two locations. In some cases, this difference may reach up to $30 \text{ mmol O}_2 \text{ m}^{-2} \text{ d}^{-1}$. This increase amounts to between 60% and 150% of the TOU levels explained by temperature variation. In impermeable sediments infauna (polychaetes and bivalves) with their respiration and bioirrigation effects contribute to this enhanced uptake. Variability in TOU, and thus the observed extreme TOU values, may well be related to spatial variability in the abundance of benthos. In permeable sands, too, *Mya arenaria* and *Arenicola marina* add a macrofauna component to TOU. Overall, both sediment types reach comparable yearly average TOU values and similar mean maximum TOU ($\sim 36 \text{ mmol O}_2 \text{ m}^{-2} \text{ d}^{-1}$). Our measurements do not include pore water advection, since our core incubations did not allow for this process to occur. Separate experiments indicate that advective O_2 -transport may stimulate TOU additionally in the sandy sediment; however, environmental conditions that trigger this effect may be relatively rare.

THE POTENTIAL FOR IRON REDUCTION BY OBLIGATE METHYLOTROPHIC METHANOGENS IN MARINE SEDIMENT

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Methanogenesis and iron reduction affect organic compounds degradation in marine subsurface sediments globally. Presently it is unclear, how iron reduction impacts methanogenesis in marine sediments. Here, we investigated the capability of iron reduction by methylotrophic methanogens in marine sediment of the Helgoland mud area. Iron reduction was found to correlate with methanol-dependent methanogenesis, but lower amounts of methane were produced in the presence of iron oxides. Methanogenic archaea including *Methanococcoides* and *Methanlobus* spp. were enriched with methanol as substrate with or without iron oxides. Amendment with lepidocrocite increased archaeal 16S rRNA and *mcrA* gene copies in qPCR analysis, whereas bacteria were suppressed. No facilitative effect of goethite and hematite on gene copies of methanogens and bacteria was detected. These results suggest that obligate methylotrophic methanogens have the potential to reduce iron(III) oxides in sediment incubations and possibly in methanic zones of marine subsurface sediments, where elevated concentrations of dissolved iron have been detected.

DISSECTING THE METABOLIC POTENTIAL OF A MARINE PRIME RESPONDER AFTER THE SPRING DIATOM BLOOM AT HELGOLAND ISLAND

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Recurrent clades of heterotrophic Bacteria process the bulk of the biomass produced by spring diatom blooms each year in the North Sea around the island of Helgoland. For some of the main bacterial responders it has been shown by cultivation and by metagenomic binning and annotation that they are specialised for polysaccharide degradation. For other key degraders these approaches failed to produce either a high quality metagenome bin or a cultured close relative. Fluorescence *in situ* hybridization (FISH) with specific oligonucleotide probes was used to identify those missing key degraders in their natural context, from which they were enriched in high purity by flow cytometric sorting. A new FISH-method, the so-called Hybridization-Chain-Reaction FISH, provided the high signal-to-noise ratios necessary for flow cytometric sorting. This allowed for sorting FISH-positive cells with high-speed and accuracy for subsequent whole genome amplification and sequencing. An in-depth genomic analysis of one of the main degraders of algal biomass will be presented – the novel flavobacterial genus *Prosiliobacter*. Unlike other flavobacterial genera, which specialise on polysaccharide degradation, the 95% complete metagenome bins showed a reduced genome size with little to no hints of polysaccharide degradation. In contrast, *Prosiliobacter* instead appears to make use of an as yet unidentified substrate, transported by a single pair of homologues of the SusC/D family. This substrate is predicted not to be polysaccharide, given the genomic context of these genes and the paucity of carbohydrate active enzymes that would be required for polysaccharide degradation in the *Prosiliobacter* pangenome. Obviously this genus fills a completely different niche than most of the polymer degrading Flavobacteria in favour of small substrates. With its small genome *Prosiliobacter* is well equipped to react as fast and early responder to decaying diatom blooms.

MICROBIAL COMMUNITY COMPOSITION AND METABOLIC SULFUR CYCLING POTENTIAL IN A SEDIMENT WITH CABLE BACTERIA

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Cable bacteria are long filamentous bacteria that couple sulfide oxidation in deeper sediment to oxygen reduction at the sediment surface via electron transport along the bacterial filament. This metabolic activity creates a suboxic zone devoid of both oxygen and free sulfide, in which intensive cryptic sulfur cycling takes place. Recently, it was hypothesized that other (autotrophic) bacteria use the electron transport capacity of cable bacteria as electron sink (Vasquez-Cardenas et al. 2015 ISMEJ 9, 1966-74). Our study investigates the microbial community of marine electro-active sediment using shotgun metagenome sequencing and provides a first exploration of the sulfur cycling metabolic potential.

Sediment was sampled at Station 130 in the southern North Sea (Belgium) where cable bacteria activity was present (Van de Velde et al. 2016 GCA 194, 211-232). We sampled the sediment surface, two depths in the suboxic zone, and at deeper depth without cable bacteria.

For all depths, Gamma- and Deltaproteobacteria were the most abundant, comprising approximately 20% of the microbial community. We identified several bins of Deltaproteobacteria representing sulfate-reducing bacteria and cable bacteria. Gammaproteobacteria bins were present either only at the sediment surface, or at all depths. The latter bins were large (> 1 genome) and encoded autotrophy, sulfur oxidation, and aerobic and nitrate-reducing metabolism. One bin was most closely affiliated to the Lambdaproteobacteria, and also contained potential for sulfur cycling. Overall, the metagenome indicates a metabolic potential for extensive sulfur cycling linked to the presence of long-distance electron transport. Much of the sulfur cycling potential is found in uncultured groups with currently limited physiological and genomic information. Among these are uncultured Gammaproteobacteria with sulfur-oxidizing and autotrophic potential which could be implicated in direct associations with cable bacteria.

HOW THE SEABED CONSUMES OXYGEN FROM COASTAL OCEANS TO HADAL TRENCHES

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Oxygen is the energetically most favorable electron acceptor in marine sediments and the first to be exhausted in the vertical redox ladder. However, it has been increasingly recognized that despite an overall vertical sequence in the diagenetic processes that largely reflect their energy yield, surface sediments are characterized by a large spatio-temporal heterogeneity. Macro- and meiofauna activity, plants, particulate deposition, resuspension, variations in light and flow all led to a highly dynamic distribution of processes and the microbial communities mediating them. This not only affects the rates of important diagenetic processes but also the coupling between them. The presentation will give examples and discuss the importance of micro and meso scale dynamics for the distribution and turn-over of oxygen in sediments.

On the oceanic scale, there is an overall decrease in benthic diagenetic activity with increasing water depths reflecting the reduced supply of organic material. But variations in surface production, seascapes and currents led to very heterogeneous supply of material to the benthic communities with focal areas acting as biological hot spots of intensified O₂ consumption and turn-over of organic material. The extreme end points of the seascape are the hadal trenches stretching down to 11 km of water depth. Recent explorations have documented that the trenches function as depocenters for relatively labile organic material and that they host intensified O₂ consumption and diagenesis presumably mediated by unexplored piezophiles microbes. The hadal trenches represent another unexplored and challenging microbial frontier to be targeted in the coming years.

RESERVOIRS, SEEPS AND SPILLS; UNDERSTANDING THE CONTROLS ON ANAEROBIC BIODEGRADATION OF CRUDE OIL

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Petroleum reservoirs harbor a diverse array of microorganisms which on production and geological timescales, influence the properties and quality of emplaced oil, affect its production and ultimately its value. Heavy oil formation over tens of millions of years, more rapid oil-driven sulfide formation leading to souring, microbially influenced corrosion and the potential to enhance oil recovery, all have a central microbiological component and in some cases there may be microbiological solutions to detrimental processes that occur during petroleum production. When petroleum enters surface environments from petroleum reservoirs, either through natural seepage or anthropogenic activity, the fate of the petroleum is also influenced significantly by the microbial communities present. Aerobic biodegradation of crude oil is generally considered to be the most important route for microbial removal of crude oil from the environment, however there is a range of situations where oil contamination of anoxic sediments occurs. The fate of contaminant hydrocarbons in anoxic environments, and the behaviour of the microbial communities responsible for their transformation sometimes defy conventional wisdom. The reasons for some of the unexpected behaviour of crude oil-degrading microbial communities in anoxic systems will be explored and factors controlling the rate and extent of crude oil biodegradation in anoxic environments will be discussed in the context of both subsurface petroleum reservoirs and oil-contaminated surface sediments.

HOW STABLE IRON ISOTOPES CAN HELP IN IDENTIFYING THE LIMIT OF LIFE IN DEEP MARINE SEDIMENTS OF THE NANKAI TROUGH (IODP EXPEDITION 370)

Susann Henkel (*), Verena B. Heuer, Fumio Inagaki, Yuki Morono, Kai-Uwe Hinrichs and Expedition 370 Scientists

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Iron reduction is one of the most ancient forms of microbial respiration. This and the observation that iron reducers can grow under high temperature and pressure conditions suggests that they may play an important role in the deep biosphere. We will use stable Fe isotopes to disentangle microbial and abiotic processes involved in deep Fe cycling at IODP Site C0023 in the Nankai Trough. This will help to reach the goal of Expedition 370: "T-Limit of the Deep Biosphere off Muroto" – the assessment of how microbial communities change with increasing sediment depth and temperature, by which factors changes are controlled, and where microbial life ceases. Dissolved iron was found at Site C0023 only within the methanic zone from 400 to 600 mbsf. The total drilling depth was 1180 mbsf. Is the Fe^{2+} release coupled to microbial activity? If yes, is it confined to the 200 m thick interval due to presence of reactive Fe minerals or because the microbes cannot cope with the temperatures prevailing in deeper sediments?

Microbial iron reduction is known to cause pronounced enrichments of ^{54}Fe in pore water, which should also be reflected by authigenic Fe minerals. The residual Fe pool, in contrast, becomes progressively enriched in ^{56}Fe . Kinetic reactions of iron with sulfide enrich ^{56}Fe in pore water, which allows a discrimination between microbial reduction and abiotic iron - sulfur interactions based on $\delta^{56}\text{Fe}$. As a result of different origins of incorporated Fe and different reactivities towards microbial reduction and sulfidation, Fe minerals in sediments possess different $\delta^{56}\text{Fe}$ signatures and may show geochemical indications for microbial life. By analyzing $\delta^{56}\text{Fe}$ of pore water and sequentially leached reactive and refractive Fe phases from Site C0023 sediments we will gain insight into the processes driving Fe^{2+} liberation at depth and hopefully assess links between the microbial activity and mineralogy (the presence of electron acceptors) as well as temperature.

ENERGY IN A PLANETARY CONTEXT

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The productivity of Earth's biosphere is dominated by the energy flux represented in sunlight, but the planet itself also provides energy, and the emergence and early history of life on Earth must be considered in this latter context. How different are the solar and planetary energy fluxes, and what consequences are implied for the biosphere? Of the 173,000 TW of solar radiation incident on our planet, about 780-2300 TW are captured into photosynthesis, and the organic matter and oxygen that result supply 63-105 TW to the chemosynthetic biosphere. Planetary chemical energy flux is ultimately traceable to radiogenic and accretionary heat flux, which serves to sustain a reservoir of fresh crustal rocks and circulate fluids through them. We estimated chemical energy fluxes for the major niches created by this process. Of the 40 TW of modern planet-wide heat flux, we estimate that approximately 0.006 TW becomes available to biology as chemical energy flux – 5-6 orders of magnitude lower than the photosynthetic energy flux. The efficiency with which heat flux drives bioavailable energy flux – about 0.015% for the modern Earth – may vary significantly with the style and partitioning of heat flux into different temperature regimes. These factors, and the implications for a pre-photosynthetic Earth, will be discussed.

DISTRIBUTIONS OF THERMOPHILIC, ENDOSPORE-FORMING BACTERIA IN HYDROCARBON SEEP PROSPECTIVE SEDIMENTS IN THE EASTERN GULF OF MEXICO

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Dormant endospores of thermophilic bacteria (thermospores) can be routinely detected in permanently cold marine sediments. These hardy and low-abundance endospores, belonging to the phylum *Firmicutes*, remain undetected in typical nucleic-acid-based community surveys, but proliferate when sediments are experimentally heated. Thermospores are close phylogenetic relatives of microorganisms indigenous to subseafloor petroleum reservoirs; if they originate from these deep habitats, hydrocarbon seepage from reservoir to seabed could explain their occurrence in the cold ocean. As such, thermospore distributions and physiological features around seabed hydrocarbon seeps might have utility in locating and characterising working petroleum systems. Marine sediments from 111 locations in the Eastern Gulf of Mexico (100 to 3300 m water depth; 6 to 600 km apart) were sampled during an industry-sponsored piston coring survey. Geochemical analyses of three segments per core allowed oil-positive and oil-negative classifications for each location. To test for thermospores, sediments were thawed and amended with 20 mM sulfate and a mixture of organic substrates, pasteurized at 80°C, and incubated at 50-55°C for 14 days. Thermophilic sulfate reduction occurred to a greater extent in oil-positive sediments (n=59/71) relative to the oil-negative (n=25/40) sediments. 16S rRNA gene amplicon libraries (V3-V4 region; Illumina MiSeq) before and after 14 days of high temperature incubation revealed enrichment of species-level thermospore OTUs in all 110 locations except one. Using abundance cut-offs, 115 significantly enriched thermospore OTUs were chosen to investigate thermospore biogeography in the study area. Most of these OTUs were considered to be endemic, with only 16 OTUs present in >20 locations. Among these, the most 'cosmopolitan' OTUs, detected in up to >70% of the 111 sediment locations, included those affiliated with thermophilic sulphate-reducing *Desulfotomaculum* spp. detected in similar sediment surveys elsewhere in the world's oceans. On the other hand, 26 OTUs appeared only in a single location, with 16 of these instances being oil-positive sediments. The site with the strongest geochemical signals for hydrocarbon seepage harbored 4 of these strictly endemic OTUs, including most prominently one identified as *Halanaerobium*, a genus frequently detected in subsurface oil reservoirs. The ability of thermospores to survive in cold sediments where they can be routinely detected in high temperature activity assays despite low in situ abundance points towards potential utility for these organisms as biosensors for hydrocarbon seep prospection in offshore oil and gas exploration. The biogeography of thermospores may therefore complement nucleic acid surveys of in situ sediment microbial communities better adapted to these cold environments, as well as seabed geochemistry, for mapping interesting areas of the sea floor.

COASTAL SAND BEDS: BIOGEOCHEMICAL HOT SPOTS IN THE INNER SHELF

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Only 15% of the organic matter released from land to the coastal zone and less than 5% of the shelf primary productions reach the deep ocean. The majority of this material is mineralized or buried in the continental margin. This presentation focuses on the role of sandy shelf sediments in the coastal carbon cycle and transport mechanisms that influence the microbial decomposition processes. Highly permeable sand beds cover approximately 50% of the global shelf area, and sandy beaches line about two thirds of the world's coastlines. The decreasing water depth near the coast leads to an amplification of physical, chemical, and biological processes affecting biogeochemistry and cycles of matter. The influence of currents, waves, turbulence and tidal movement on transport and exchange at the sea floor increases, affecting organic matter distribution and mineralization processes. Water chemistry, temperature and light climate change, and the role of the sediment as site for production and decomposition increases. Examples from the beach environment, intertidal zone and inner shelf are used to illustrate the tight links between organic matter cycling and transport processes. The Deepwater Horizon oil spill revealed the significance of the biocatalytical function of the coastal sands for the recovery process of the shore. The presentation concludes with estimates of the role of permeable shelf beds in the global cycles of matter and how anthropogenic activities may affect the functioning of these sediments.

LIMITS TO DEEP SUBSEAFLOOR LIFE AND GEOSPHERE-BIOSPHERE INTERACTIONS

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Over the past decades, scientific ocean drilling has explored subseafloor environments at various oceanographic and geological settings, which resulted in numerous discoveries on Earth's planetary sub-systems —the atmosphere, hydrosphere, geosphere, and biosphere. The dynamism fostering the co-evolution of life and the Earth system is principally constrained by extra- and intra-terrestrial energy sources. The lithosphere consisting of sediments, crusts and upper mantle plays a significant role as an interface between the Earth's asthenosphere and the overlying hydrosphere and atmosphere. Drilling deep into the Earth's lithosphere has significantly expanded our understanding of Earth's sub-systems and will continue to do so in the future. To date, only little is known about how Earth's various spheres interact, despite the awareness that such spheres connect and interact with each other. Building this knowledge will provide useful insights at various levels into the past, present and future of life and Earth, and illuminate the sustainable planetary habitability.

Accumulating evidence from ocean margin sites indicates that remarkable numbers of anaerobic microbial cells are present at least down to at least ~2.5 km below the ocean floor (Inagaki et al., 2015). In open ocean sites, the occurrence of microbial communities and oxygen was observed in the entire sediment column of the ultra-oligotrophic South Pacific Gyre, qualifying the deep biosphere as aerobic over up to ~37% of the global seafloor (D'Hondt et al., 2015). These recent findings through scientific ocean drilling have characterized the deep biosphere as one of the important Earth's sub-systems, where microbial life inhabiting the vast oceanic lithosphere influences whether several important elements are sequestered for millions of years or returned to the ocean as active agents with an impact on life and climate (Hinrichs & Inagaki, 2012).

Only a better understanding of the Earth's multi-sphere interactions through scientific ocean drilling will enable informed conclusions regarding the origins and evolution of life, oceans and Earth. The characterization and monitoring of multi-sphere boundaries, including the temperature limit of the deep biosphere (Hinrichs et al., 2016), will highlight the organization and interactions of Earth's sub-systems, providing critical information for adaptation and evolution of subseafloor life and the planetary habitability sustained through Earth's multi-sphere interactions.

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DYNAMICS OF N₂O PRODUCTION PATHWAYS ANALYSED BY ¹⁵N/¹⁸O DUAL ISOTOPE LABELLING – DATA FROM A FULL-SCALE WASTEWATER TREATMENT PLANT

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Nitrous oxide production associated with biological nitrogen transformations can contribute substantially to the CO₂ footprint of both man-made and natural systems, but the pathways and regulation of N₂O production are poorly understood. We developed a ¹⁵N/¹⁸O dual isotope labelling technique to distinguish and quantify these pathways in mixed communities. The use of ¹⁸O-O₂ permits differentiation of hydroxylamine oxidation and nitrifier-denitrification driven N₂O production by ammonium oxidizing bacteria. We analysed N₂O production pathways during biological nitrogen removal at Lynetten wastewater treatment plant. Under anoxia, N₂O accumulated due to denitrification, but N₂O accumulation was ~3 and 1.7 times higher at 30 and 100 μM O₂, respectively. Oxic N₂O production was dominated by nitrifier-denitrification, reaching 73% of the total with the remainder due to hydroxylamine oxidation. Our results demonstrate three active pathways of N₂O production, each with different environmental controls. The dual ¹⁵N/¹⁸O isotope labelling approach can contribute to the development of strategies to minimise N₂O emissions from man-made and natural systems.

SINGLE CELL GENOMICS REVEALS A DIVERSE A METABOLIC POTENTIAL OF UNCULTURED *DESULFARCULACEAE* WIDELY DISTRIBUTED IN MARINE SEDIMENT

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Sulfate-reducing microorganisms are key players in the marine carbon and sulfur cycles, especially in coastal sediments. Here, they occur throughout the sediment column, despite increasing sulfate and organic carbon limitation with depth. The family *Desulfarculaceae* comprises one of the most abundant groups of sulfate-reducers in Aarhus Bay sediments. Characterized *Desulfarculaceae* isolates are able to degrade aromatic hydrocarbons. We therefore hypothesized that aromatic compounds are an important energy source for *Desulfarculaceae* in marine sediments. To test this hypothesis and to infer the ecophysiology of marine *Desulfarculaceae* we sequenced and analyzed the genomes of 7 *Desulfarculaceae* single cells from Aarhus Bay sediments. The average assembly length was 1.3 mio bp and completeness estimates ranged between 20% -50%.

Marker genes for benzoyl-CoA degradation were present in 3 single cells, while the remaining 4 single cells did not encode genes diagnostic for aromatic hydrocarbon degradation. This suggests that utilization of aromatics may be an opportunistic trait in uncultured marine sediment *Desulfarculaceae*. From the genome sequences we predicted heterotrophic growth by fatty acid and alcohol degradation and growth by acetogenesis. Interestingly, we found genes encoding a reductive dehalogenase (rdhA) in 2 single cells, pointing to a so far unrecognized role of organohalide respiration in the energy metabolism of marine *Desulfarculaceae*. Five single cells encoded a complete pathway for dissimilatory sulfate reduction, while sulfate reduction genes were absent in the two others. All single cells encoded sulfatases, which are not present in cultured *Desulfarculaceae*, and allow them to access sulfate esters as source of sulfate and organic carbon. We conclude that marine *Desulfarculaceae* constitute a metabolically diverse group of bacteria. This versatility likely reflects different strategies for coping with the energy limitation in the subsurface seabed.

DETAILED STUDY OF SULFUR CYCLING IN CHEMOCLINE OF MONOMICTIC LAKE KINNERET (ISRAEL)

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Sulfur cycling in chemocline of monomictic Lake Kinneret was studied with high spatial resolution. Hydrogen sulfide concentrations increased linearly with depth below the chemocline. The highest concentrations of sulfur oxoanions were detected 2.5 m below the chemocline. Concentrations of elemental sulfur increase with depth below the chemocline and depend on the time of day. During the day, concentrations of elemental sulfur are approximately seven times higher than during the night. The observed trends in concentrations of sulfur species may be explained by a combination of light-independent processes (microbial sulfate reduction and oxidation of hydrogen sulfide to sulfur oxoanions) and light-dependent oxidation of hydrogen sulfide to elemental sulfur (phototrophic sulfide oxidation).

NEW INSIGHTS INTO NITRATE- AND IRON-DEPENDENT ANAEROBIC OXIDATION OF METHANE

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Anaerobic oxidation of methane (AOM) is crucial for controlling the emission of this potent greenhouse gas to the atmosphere. Nitrite-, nitrate-, and sulfate-dependent methane oxidation is well-documented, but AOM coupled to the reduction of oxidized metals has so far been demonstrated only in environmental samples. Using a freshwater enrichment culture, we showed that archaea of the order Methanosarcinales, related to “*Candidatus Methanoperedens nitroreducens*,” couple the reduction of environmentally relevant forms of Fe^{3+} and Mn^{4+} to the oxidation of methane. We obtained an enrichment culture of these archaea under anaerobic, nitrate-reducing conditions with a continuous supply of methane. Via batch incubations using [^{13}C]methane, we demonstrated that soluble ferric iron (Fe^{3+} , as Fe-citrate) and nanoparticulate forms of Fe^{3+} and Mn^{4+} supported methane-oxidizing activity. CO_2 and ferrous iron (Fe^{2+}) were produced in stoichiometric amounts. Our study connects the previous finding of iron-dependent AOM to microorganisms detected in numerous habitats worldwide. Consequently, it enables a better understanding of the interaction between the biogeochemical cycles of iron and methane.

WIDESPREAD DIFFUSION OF OXYGEN FROM OCEANIC CRUST INTO OVERLYING SEDIMENTS IN THE NE PACIFIC OCEAN – EARLY DIAGENETIC CONSEQUENCES AND SIGNIFICANCE FOR BIOGEOCHEMICAL CYCLES (RV SONNE CRUISE SO 240)

Sabine Kasten (*), Gerard Versteegh, Andrea Koschinsky, Heiner Villinger, Ingrid Dohrmann, Julia Fronzek, Jan Hartmann, Charlotte Kleint, Inken Preuss, Simon Ritter and Thomas Kuhn

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The classical view of early diagenetic processes in the seabed is based on exchange of oxygen (O₂) and other compounds between bottom waters and surface sediments. As a result, sediments generally show a downward succession of redox zones with decreasing energy yield of the particular redox reaction. Recently, it has been observed that the circulation of O₂-rich seawater in oceanic basaltic basement driven by temperature and pressure gradients generates an upward diffusive flux of oxygen into the overlying sediment. Work on long sediment cores taken from the NE Pacific Ocean demonstrates that upward diffusion of O₂ is a widespread phenomenon in these deep-sea sediments (Kuhn et al., 2017). Close to seamounts, where sediment cover is thin, and larger faults, sediments are oxic throughout, with O₂ decreasing downward from the sediment surface and upward from the underlying crust. These sediments provide an exemplary insight into the processes occurring close to the sediment/basement interface. The low sedimentation rates (<0.5 cm/kyrs) and abundant supply of O₂ from above and below lead to an almost complete organic carbon (OC) mineralisation resulting in OC-lean sediments (<0.2 wt%). Ventilation of the basement may be considered omnipresent due to the pressure gradients present between spreading-zones/hot spots and old oceanic crust. As such upward O₂ transfer into overlying sediments and exchange of elements across the crust/sediment interface should be omnipresent processes as well – calling for the need to assess element redistribution in the basal sediments and crust, as well as to recalibrate the biogeochemical cycles and fluxes of carbon and other elements.

HOW DO SANDS BREATHE? REIMAGINING THE REDOX CASCADE IN PERMEABLE SEDIMENTS

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Permeable sediments - once treated as the deserts of sediments - have been shown in recent years to be a significant research area for biogeochemists. With every new study, however, sands prove to be more difficult to fit into existing paradigms. Recently, we showed that under anoxia, metabolic mineralisation in coastal sands is relatively constant, but that established redox cascade of nitrogen, iron, sulfur and methane cycling does not dominate [Evrard et al. BGS 2013, Kessler et al. L&O 2012].

Instead, the predominant carbon mineralisation process is a fermentation pathway, with H₂ gas being excreted and other metabolites being stored intracellularly for later reoxidation [Bourke et al. NatGeo 2017]. Adding to the intrigue, this fermentation is performed by diatoms, which are well-distributed in the surface 20-30 cm of the sediment. Here we present an overview of fermentation in permeable sediments and propose a wider, more complex redox cascade for these environments.

MICROBIAL ECOLOGY AT SERPENTINITE SEAMOUNTS ASSOCIATED WITH THE MARIANA CONVERGENT MARGIN

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Serpentinizing sediments are an analog to an early Earth environment, as well as being relevant to astrobiology, since they represent a unique environment for chemolithoautotrophic life. Sediments at the summit of three seamounts associated with the Mariana Convergent Margin were sampled down to 250 mbsf during IODP expedition 366. Samples were enriched with molecular hydrogen, methane, and elevated pH approaching 12.5. It is not clearly understood how microbes tolerate these conditions or how the process of serpentinization might facilitate their abundance. Preliminary data suggest that the methane is not biogenically produced and similar sites are dominated by archaea associated with methanotrophy. We attempted to determine metabolic strategies and stress responses of individual taxa by utilizing Single cell Amplified Genomes (SAGs) with microbial cells from these sediments. By investigating the interactions of serpentinization-derived fluids using single cell genomics we will be able to describe deeply branching, uncultured, and short chain hydrocarbon utilizing archaea and bacteria.

CYANATE AND UREA AS SUBSTRATES FOR MARINE THAUMARCHAEOTA

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In marine systems the first step of nitrification, ammonia oxidation, is mainly performed by ammonia oxidizing archaea (AOA) of the phylum Thaumarchaeota. AOA are thought to be metabolically restricted organisms that use only ammonia as an energy source. However, some AOA can also use urea and recently, an AOA isolate was found to use cyanate (Palatinszky et al. 2015), another simple organic nitrogen compound, as a sole energy source. Cyanate and urea are ubiquitous in the ocean and we hypothesize that they can serve as substrates for marine AOA.

We assessed the use of urea and cyanate by marine AOA in the Gulf of Mexico hypoxic zone by combining complementary methods – biogeochemical rate measurements, molecular, and single cell analyses. In-situ cyanate and ammonium concentrations were highest in bottom waters, while urea concentrations did not show a clear depth distribution. We compared oxidation rates of ammonia, cyanate and urea at in-situ oxygen concentrations. Ammonia oxidation rates reached up to $2.5 \mu\text{M d}^{-1}$, whereas urea- and cyanate-derived oxidation rates ranged between 0.5 to 10% of the measured ammonia oxidation rates. Thaumarchaeota were the only detectable ammonia oxidizers and showed a distinct depth distribution, peaking in abundance below the oxycline. The AOA community comprised 15 operational taxonomic units (97% sequence similarity clusters) based on 16S rRNA gene sequencing. We further found a broad diversity of transcribed cyanases and ureases, suggesting that cyanate and urea are used as energy or nitrogen sources by a number of microorganisms in this system. Furthermore, we could observe and compare uptake of ammonium, urea and cyanate by AOA on a single cell level using NanoSIMS.

We could show use of all of the investigated substrates by AOA, implying that use of simple organic nitrogen compounds may be an overlooked, yet important factor in shaping AOA abundance and diversity.

EVOLUTION AND PERSISTENCE DURING DEEP BURIAL OF MICROBIAL COMMUNITIES

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Cut off from fresh inputs of primary produced organic matter marine subsurface sediments are highly energy-limited environments. Still an immense number of bacterial and archaeal cells populate these sediments yet metabolizing at rates, which are orders of magnitude lower than those of laboratory-grown cultures. It is not understood how microbial life adapts to and evolves under such extreme starvation conditions.

We have used a combination of PCR amplicon sequencing, metagenomics and single cell genomics to explore how microbial communities assemble and evolve during burial from the surface to the subsurface of marine sediments.

We find that generally a limited number of species-level populations dominate the subsurface sediment and are present throughout the sediment column. At one location we followed the genome evolution and diversification of four such populations from surface to 2 m sediment depth by mapping metagenomic sequence reads onto single cell genomes. Genomic sequence diversity was low within the individual persisting populations and did not change with sediment depth. The strength of purifying selection (ratio of nonsynonymous to synonymous substitutions) remained constant across depth, both overall and when considering individual functional gene categories. Mutation rates, inferred from measured genetic diversity and population size, and from estimated numbers of generations that cells underwent in the sediment, were low and either decreased or remained constant with sediment depth.

Our results suggest that genetic change and diversification is diminished in subsurface sediment likely as a result of long generation times and strong environmental filtering, and that subsurface sediments are colonized from the surface by selective survival of taxa able to persist in this environment.

A MOVEABLE FEAST: THE RESPONSE OF BENTHIC MICROBES TO THE DEEPWATER HORIZON OIL WELL BLOWOUT IN THE GULF OF MEXICO

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The blowout of the Deepwater Horizon (DWH) drilling rig resulted in the world's largest accidental release of oil into the ocean in recorded history. The equivalent volume of approximately 4.9 million barrels of light crude oil were discharged into the Gulf of Mexico from April to July 2010. Approximately one-half of the discharged oil reached the ocean surface, and coastal sediments represent a major repository of DWH oil contamination as surfaced oil was either redeposited onto the seafloor of the coastal zone through the formation of marine snow or washed ashore. Similar to the breakdown of natural organic matter, biodegradation mediated by indigenous microbial communities is the ultimate fate of the majority of hydrocarbons that enter the marine environment. Facilitated by next generation sequencing approaches, much progress was made to determine the response of microbial communities to the DWH disaster. However, the response of microbial communities to hydrocarbon exposure is complex and variable, driven to a large extent by hydrocarbon chemistry, ambient oceanographic processes, and factors that regulate microbial physiology (e.g. substrate and nutrient availability). Thus despite progress, the impacts of oiling on the specific functions of indigenous microbial communities and implications for ecosystem services provided by these communities remain unclear. Moreover, understanding of baseline sedimentary microbial communities remains insufficient to assess the impacts of major environmental perturbations such as oil spills. This lack of fundamental knowledge acts as a critical obstacle to the effective parameterization of oil plume models. The risk of another oil well blowout in the Gulf of Mexico remains high, given the petroleum industry trend of increasing oil and gas production from ultradeep (>1500 m) wells and the lack of technologies to fix problems in the deepsea. It is not a question of "whether" another major spill will happen but rather "when" it will occur. This presentation will report on research that characterizes the response of sedimentary microbial communities from Pensacola Beach, Florida, to the DWH oil spill, as an in-situ experiment of the effects of disturbance on functional and taxonomic diversity. Oil was rapidly and completely degraded after DWH reached the shoreline at Pensacola Beach. Results from a metagenomic time series show profound impacts of oil deposition to sedimentary microbial communities. For example, oiling leads to large impacts on the microbial nitrogen cycle. After one year, the beach sand microbial communities had largely recovered and reestablished.

TRANSITION BETWEEN AEROBIC RESPIRATION AND DENITRIFICATION AT LOW OXYGEN CONCENTRATIONS

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Oxygen levels constitute an important control on the on-going nitrogen cycle dynamics: Low oxygen aquatic environments are major sites of nitrogen loss to the atmosphere. For example, marine oxygen minimum zones account for at least one third of marine nitrogen loss.

Denitrifiers are capable of switching between oxygen respiration and denitrification. However, relationship between rates of N_2 production and oxygen concentration are not well understood, particularly not at low oxygen concentrations as we encounter them in marine low oxygen environments.

Here, we investigated the regulation of dinitrogen production as a function of oxygen availability and the transition between aerobic and anaerobic metabolism. We performed physiological experiments of denitrifying isolates from marine oxygen minimum zones that are well-adapted to a low oxygen environment. The results presented will provide helpful insights in order to understand how increasing ocean deoxygenation in response of global climate change may influence the ocean's nitrogen budget.

ORGANIC CARBON OXIDATION AND BIOIRRIGATION IN SEDIMENTS ALONG A SKAGERRAK-KATTEGAT BELD SEA DEPTH TRANSECT

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Four stations in the Skagerrak-Kattegat-Belt Sea area were visited during a cruise in late August 2014 on board the R/V Aurora to examine carbon oxidation and bioirrigation in the upper 20 cm of the sediments. The stations were SKA 2 (586 m) and SKA 1 (318 m) in the Skagerrak, SKA 4 (45 m) in the northern Kattegat and SKA 5 (38 m) in Lillebælt. Biogeochemical reactions involving carbon dioxide, ammonium, iron and sulfur were measured from anoxic incubations and porewater profiles. The emphasis was particularly on the determination of bioirrigation based the reaction rate and vertical distribution of major solutes using a diagenetic modeling approach. This was compared with the standard on-deck bromide incubation for the determination of bioirrigation. The results showed that the overall rate of benthic carbon oxidation decreased with water depth and distance from land. Sulfate reduction was the dominating process, except at the deepest station where most carbon oxidation occurred through iron reduction. Bioirrigation estimated from the modeling approach also decreased with water depth, and the associated downward translocation of oxygen provided sufficient oxidized iron to maintain high iron reduction, particularly at the deepest station. No bioirrigation was evident at the azoic SKA 5. The bromide bioirrigation results deviated considerably from those obtained by diagenetic modeling. The former approach revealed negligible bioirrigation at the deep SKA 2 and SKA 1, and excessive bioirrigation at SKA 4, which is densely populated by the brittle star *Amphiura filiformis*. The discrepancies are probably caused by erroneously low bioirrigation at the deep station due to damage of infaunal burrows and tubes by coring; and too high brittle star bioirrigation at SKA 4 due to stress caused by vibrations from the ship. It must therefore be concluded that the most reliable in situ bioirrigation estimates are obtained using diagenetic modelling.

LIGHT ENERGY AND OXYGENIC PHOTOSYNTHESIS: LINKING OPTICAL PROPERTIES AND STRUCTURAL HETEROGENEITY TO PHOTOSYNTHETIC EFFICIENCY IN BIOFILMS AND CORALS

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Surface-associated assemblages of oxygenic microbial phototrophs (microalgae and cyanobacteria) in biofilms and photosymbioses are characterized by a high optical density and (sub-)mm-thick photic zones, wherein steep and dynamic gradients of light, temperature, pH, O₂ and other chemical species modulate photosynthetic performance. While application of various microscale methods has given detailed insight to photosynthesis in such gradient environments, links between the optical properties and structural complexity of such assemblages remain largely unstudied. My group has employed microsensors and novel imaging techniques to explore structure-function relationships and photosynthetic quantum efficiency in biofilms, sediments and corals. I present a new conceptual view of how light harvesting is balanced against light protection in biofilms and corals, enabling optimization of the photosynthetic performance of microbes under a wide range of optical niches. Based on recent studies of the coral microenvironment, I argue that high photosynthetic efficiency in corals is largely modulated by the microscale optical properties and three-dimensional structure of coral tissue distribution over the underlying skeleton. Such links between coral function and morphology can be understood in the framework of canopy effects, in analogy to the function of plant canopies (albeit at much larger scales), enabling efficient and flexible light harvesting. I review the current evidence for how corals modulate their light microenvironment. This includes recent findings about scattering and light propagation in coral tissue and skeleton that together with tissue plasticity (expansion/contraction) can explain the high efficiency of coral photosynthesis. I also argue and provide first evidence that similar microscale canopy effects modulate light harvesting and photosynthesis in sediments and biofilms.

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ANAMMOX AND OTHER DISCOVERIES IN THE NITROGEN CYCLE

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Until a century ago, microbial nitrogen (N) cycling, the interconversion of inorganic N-compounds by microorganisms, determined the availability of this essential element for life. Since the industrial revolution however, the need to feed a growing human population has required extensive use of synthetic fertilizer, leading to an unprecedented N-input into the environment. The pressing need to reduce this N-input has primarily driven the discovery of many novel microbial processes and players in the last two decades. The subsequent hunt for these processes in the marine environment has revealed a highly complex network of N-cycling processes catalyzed by a dazzling variety of microorganisms interacting with each other. Here I will focus on novel discoveries in the marine N-cycle, including new processes, the involved microorganisms, their interactions and impact on biogeochemical cycles.

METHANOARCHAEA FROM MARINE MUD VOLCANO AND GAS HYDRATE HABITATS

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The topography offshore southwestern Taiwan were complex with mud volcanos, ridges, seeps and canyons. Geophysical surveys also indicated the existence of gas hydrate. The marine sediment core samples were collected by ORI cruise, and the cultivated and uncultivated survey indicated *Methanoculleus* clades are dominant in mud volcano and gas hydrate habitats. The hydrogenotrophic *Methanoculleus sediminis* S3FaT and new genus *Methanovulcanius yangii* CYW5 were isolated from the mud volcanoes. The cannulae like structure as *Pyrodictum abyssi* growing as networks of cells was observed in strain CYW5. The range of temperature growth for strain S3FaT and CYW5 was 20-50°C and 20-42°C, respectively. *Methanoculleus taiwanensis* CYW4T along with lytic DNA virus were isolated from gas hydrate habitat. Trehalose synthetase gene cluster are similar among known gas hydrate *Methanoculleus*, but not the one from sewage. Trehalose storage and lytic virus may relate with carbon conservation and nutrient recycling in these unique habitats.

CONTROLS ON IRON AND SULFATE REDUCTION IN ARCTIC FJORD SEDIMENTS

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Anaerobic organic matter mineralization in marine sediments is a multi-step process, including hydrolysis, fermentation, and terminal oxidation to carbon dioxide. Usually, the initial hydrolysis and fermentation steps are rate-limiting and microorganisms which perform terminal-oxidization compete for the fermentation products. Iron reduction (FeR) and sulfate reduction (SR) are quantitatively the most important terminal oxidation processes in marine sediment. The energy yield of FeR is typically higher than that of SR, meaning that FeR should predominate if iron is available. Yet, FeR and SR often occur simultaneously. We wanted to understand which factors impact the balance between FeR and SR. Therefore, we investigated the partitioning of organic matter mineralization between the different terminal oxidation processes in sediments of different fjords along the west coast of Svalbard. These fjords are an ideal natural laboratory to study the competition between FeR and SR, due to the natural variability of glacial delivery of iron. We find sediments with a predominance of either FeR or SR, as well as intermediate sites where both processes occur. The results show that the predominance of FeR is not only dependent on the presence of iron, but also on its reactivity. In a hematite-dominated sediment FeR could only out-compete SR after the addition of poorly crystalline iron. Furthermore, amending the different sediments with organic carbon or molybdate influenced the tight coupling of the initial and terminal organic matter oxidation steps, indicated by the accumulation of fermentation products. In summary, we show that the competition between FeR and SR is not only controlled by the amount but also by the reactivity of the iron.

MICROBIAL LIFE UNDER EXTREME ENERGY LIMITATION

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In recent decades, studies on microorganisms have shown that energy limitation is the main variable controlling the growth and survival of microorganisms across many ecosystems on Earth. In certain environments, such as deep subsurface habitats, microorganisms appear to live under permanent energy limitation, at energy turnover rates that are many orders of magnitude below those found in surface habitats. The mechanisms and adaptations that allow microorganisms to live and even grow under such extreme and long-term energy limitation are not understood, however, recent evidence based on laboratory-based starvation experiments and studies of natural microbial populations are revealing key variables that regulate microbial population size in these long-term energy limited environments. This presentation will provide an overview of the factors that may determine the minimum energy turnover per cell, also known as the basal power requirement (BPR), and address how environmental controls on this BPR, in particular in situ temperature, exert a key influence on the microbial population size in any given setting. Genetic analyses on microbial community structure from surface to subsurface environments combined with recent analyses on microbial metagenomes will provide insights into the community structures of low-energy adapted microorganisms and the metabolic pathways and strategies that provide advantages during long-term energy limitation. Evidence that subsurface microorganisms are not mere survivors from surface environments, but instead grow and thrive in certain parts of the subsurface, will be presented along with recent phylogenetic data showing that the transition from surface to subsurface microbial communities follows predictable environmental trends.

GENOMIC RESOLUTION OF METABOLIC PATHWAYS OF THORACHAEOTA

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Thorarchaeota are new archaeal phylum within the Asgard superphylum, whose ancestors have been proposed to play important roles in cellular evolution. However, only three high quality genomic bins of Thorarchaeota are available, thus little is known about the lifestyles of these uncultured archaea. To provide a better resolution of the ecological roles and metabolic capacity of Thorarchaeota, we obtained three high quality Thorarchaeota genomes from mangrove wetlands by metagenomic approaches. Comparative genomic analysis reveals updates in their complex metabolic capacities for CO₂ reduction, such as Thorarchaeota contain both the archaeal and bacterial types of Wood-Ljungdahl (WL) pathways, i.e. tetrahydromethanopterin- and tetrahydrofolate-WL pathways respectively. These archaea encode ribulose biphosphate carboxylase like protein and a near complete Calvin-Benson-Bassham cycle, inferring their previously undiscovered potentials to fix carbon. Thorarchaeota also encode genes for nitrogen fixation and a full arsenic efflux detoxification pathway, which renew our understanding of their roles in biogeochemical cycles. In addition, we not only confirmed the discovery of eukaryote-specific proteins, but also identified eukaryotic selenocysteine insertion sequences along with a selenoprotein biogenesis system encoded in Thorarchaeal genomes.

GEOCHEMICAL EVIDENCE FOR GENOMIC PREDICTIONS IN UNCULTURED ARCHAEA AND BACTERIA

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Despite extreme energy-limitation, microbes in deep marine sediment communities are active, persisting in maintenance states at near-zero growth. However, little is known about the specific mechanisms used to overcome low-energy stress because most clades in marine sediments are uncultured. In up to 85 meters below seafloor from IODP Expedition 347: Baltic Sea Paleoenvironment, single cell genomics, transcriptomics, and metabolomics revealed survival strategies during long-term energy stress. Microbes from abundant uncultured phyla such as Atribacteria, Aminicenantes, and Actinobacteria-OPB41 focused their resources on producing chemical protectants and growth inhibitors, maintaining cell NAD⁺ pools, and catabolizing organic matter substrates. Coupling these predicted functions to direct enzymatic assays of whole sediment showed that some survival strategies were universal and others were used only by a few clades. This suggests that the often-observed high microbial diversity in deep subsurface sediments may be supported by different metabolic niches for survival in the face of extreme energy limitation.

SULFATE REDUCERS – HOW GREAT IS THE DIVERSITY?

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Whether in the mammalian intestinal tract, freshwater wetlands or marine sediments, sulfate-reducing microorganisms (SRM) play vital roles in organic carbon degradation and nutrient cycling in almost every anoxic ecosystem on Earth. But how to identify SRM and study their diversity and ecological functions? Individual strains can be isolated from the environment and tested in the lab to provide unambiguous proof of their capability for dissimilatory sulfate reduction and other physiological features. Longstanding efforts of many cultivation experts from all over the world have contributed to our current understanding that the guild of SRM encompasses physiologically versatile members from multiple bacterial and archaeal taxa. However, comprehensive ecological studies of SRM in the environment are very much dependent on the use of molecular methods. In my talk, I will discuss the opportunities of gene- and genome-centric approaches in identifying SRM and monitoring their environmental diversity, biogeography and dynamics. Our perception of the usefulness of individual molecular approaches and marker molecules has evolved along with new insights into the genomic and metabolic properties of SRM and microorganisms that metabolize other sulfur compounds. Unambiguous identification of a SRM without a pure culture remains a challenge, but well-thought-out experiments combining isotope-labeling with biogeochemical and molecular analytics provide opportunities for identifying new SRM that have thus far not been isolated.

THROUGH THE LOOKING GLASS: THE CONTROLS OF VOLATILE FATTY ACID OXIDATION BY SULFATE REDUCERS IN MARINE SEDIMENTS

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Sulfate reducers use sulfate as terminal electron acceptor for the oxidation of organic matter such as volatile fatty acids (VFA). VFAs are key intermediates in the anaerobic microbial food chain, however we have a limited understanding of what controls their concentration in situ.

We used a laboratory based approach in order to examine the microbial controls on VFA concentration in marine sediments. Axenic cultures of environmentally relevant sulfate reducing bacteria were grown in batch or continuous reactors, while we monitored sulfate and VFA utilization.

The residual acetate concentration ranged from 44 μM to below the detection limit (0.19 μM) depending on the growth conditions, while the energy yield of the metabolic reaction (ΔG) was estimated to be equal to or fall below -30.3 kJ per mole of acetate. The residual propionate concentration ranged from 8 to 3 μM . We also report a half saturation constant (K_m) for propionate of 22 μM , this value is lower than the reported K_m values for acetate (600-70 μM) and matches the lower in situ propionate concentrations in marine sediments [1, 2]. Finally, we measured an extremely high affinity for lactate ($K_m = 1.6 \mu\text{M}$) which reflects the very low lactate concentrations reported previously [3].

We will discuss the role of the in situ microbial activity in controlling substrate concentrations in the environment, and address the physiological and energetic constraints involved.

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A MAJOR BALTIC INFLOW CREATES A TEMPORAL NICHE FOR CABLE BACTERIA IN EASTERN GOTLAND BASIN SEDIMENTS

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Cable bacteria are filamentous Desulfobulbaceae able to perform electrogenic sulfide oxidation (e-SOx), i.e. the electric coupling between anodic H₂S oxidation and cathodic O₂ reduction over centimeter distances in the seafloor. Cable bacteria have been reported in sediments from a wide range of sites, but their physiological limits as well as the environmental factors that regulate their growth in natural settings are not well constrained. In this study, we investigated if a natural bottom-water oxygenation event, namely a Major Baltic Inflow (MBI), stimulates the growth of cable bacteria in the long-term (~10 y) anoxic sediment of the Eastern Gotland Basin, Baltic Sea. In April 2016 intact sediment cores were collected at 4 sites across a depth transect including a permanently oxic site (60 m depth), a permanently anoxic site (130 m), and two sites that experienced a transient oxygenation due to the inflow (170 and 210 m). Cable bacteria were identified at the oxic and transiently oxic sites, but not at the anoxic site, suggesting that transient O₂ availability allowed cable bacteria growth. The highest filament density (42 m cm⁻²) was found at the 170 m site, where a 6.3 mm zone depleted in both O₂ and free H₂S, in absence of bioturbation, indicated a substantial impact of cable bacteria metabolism on sediment biogeochemistry. In 2017, pH and electric field anomalies compatible with ongoing e-SOx indicate that cable bacteria were still active, likely supported by the persisting hypoxic conditions. Our data demonstrate that cable bacteria can exploit transient hypoxic niches as induced by a MBI. The bottom water O₂ levels (< 15 µM) are the lowest reported for cable bacteria growth, and this expands our understanding on their potential environmental distribution.

AN IN VIVO INVESTIGATION INTO TEMPERATURE-CONTROLLED STRATIFICATION OF SUB-SEAFLOOR POPULATIONS

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The deep subsurface is characterized by a paucity of carbon substrates and biologically exploitable chemical potential energy. These metabolic challenges can be exacerbated by high temperatures, due to increased costs of cellular maintenance. Though sparse, microbial life persists in such environments, however, the degree to which temperature gradients result in the stratification extremophilic sub-seafloor populations is poorly understood.

During Expedition 370, we established a matrix of incubation experiments with sediment samples taken from 8 depths corresponding to in situ temperatures of approximately 37, 50, 60, 70, 80, 90, 100 and 110°C, which were incubated in oxygen-free, acetate- and sulfate- supplemented, artificial seawater at temperatures of 37, 50, 60, 70 and 80°C. Substrates include large isotopic labels, which, once cells are separated from the sediment, and analyzed using SIMS, will allow estimates of biomass synthesis rates.

We are interested in discussing potential future experiments and collaborations using this unique resource.

MICROBIAL ELECTRON TRANSPORT OVER CENTIMETER-SCALE DISTANCES IN AQUATIC SEDIMENTS

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Long-distance electron transport enables a novel type of microbial metabolism, whereby long, multicellular bacteria are capable of transporting electrons from cell to cell along their centimeter-long filamentous bodies. By establishing such electrical circuitry, these so-called cable bacteria are able to exploit spatially segregated pools of electron acceptors and donors, equipping them with a competitive advantage for survival in natural redox gradients.

The electron transport induced by cable bacteria exceeds the known length scale of biological electron transport by orders of magnitude. So somehow, cable bacteria must have evolved a proficient mechanism for long distance electron transmission, but presently, neither the mechanism of charge transfer nor the identity of the charge localizing sites have been identified.

Here, we present a model of long-distance electron transport, where cells acts as cathodes/anodes and periplasmic fibers in the cell envelope function as conductive structures. The model is based on newly collected microscopy and spectroscopy data. Resonance Raman spectroscopy of cytochromes confirms that electrical currents run through individual living cable filaments. Electron microscopy reveals the three-dimensional architecture of the fiber network that is the prime candidate for the conductor. When we combine this new information with existing electrochemical and microbiological data, we find that fiber currents are remarkably similar across different experiments and field observations. When simulating the electron transport in the fiber network using the standard description for electron transmission in biological redox chains, the model closely reproduces the observed geochemical signatures in electro-active sediments. Overall, the model provides a plausible mechanism how biological electron transfer can occur across centimeter-scale distances and how this can be combined with a low dissipative loss.

ASSESSING MICROBIAL BIOMASS PRODUCTION IN DEEP-SEA SEDIMENTS VIA ^{14}C -BICARBONATE UPTAKE

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Bacteria play a crucial role in carbon transformation in deep-sea sediments, however only few studies were addressed to accurately measure the biomass production. One of the most widely used approaches is radiotracer-labelled leucine based method, which is however affected by methodological biases (e.g. leucine dilution factor, uncertainties in conversion factors). Recent investigation showed that dark CO_2 fixation (DCF) rates are closely related to microbial abundances in deep-sea sediments, even better than leucine up-take, suggesting that this is an important process for deep-sea microbes. For elucidating the relationship between DCF and microbial biomass production, changes in bacterial abundance, community structure and ^{14}C -bicarbonate and ^3H -leucine uptake were investigated in deep-sea sediments collected in central Arctic Ocean (4000 m depth). After 10 days the microbial doubling time was of about 15 days and the bacterial community resembled that at natural sediments. ^{14}C -bicarbonate and ^3H -leucine uptakes followed the microbial biomass production, increasing in exponential phase and decreasing in stationary phase. Unexpectedly the ^{14}C -bicarbonate incorporated in DOC was up to 5-fold what was fixed in cells biomass and it was positively correlated with ^3H -leucine uptake. ^3H -leucine also increased during microbial growing phase but it remained constant during stationary phase. Analysis of relationship between change in cells number and incorporation rates yielded empirical conversion factors for calculating accurate bacterial production rates from ^{14}C -bicarbonate and ^3H -leucine incorporation rates. These findings support that DCF is not an invasive method that can be applied for better assessing biomass production in deep-sea sediments.

BEYOND THE ‘USUAL SUSPECTS’: OVERLOOKED BUT ABUNDANT SULFUR OXIDIZERS IN MARINE SEDIMENTS

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The current perception of sulfur oxidation in marine sediments is focused on chemical processes and few, morphologically conspicuous bacteria with a rather patchy distribution. The general role of microbial sulfur oxidation in vast areas of the seafloor remains unknown. In cultivation-independent studies we previously detected novel, potentially sulfur-oxidizing bacteria (SoB) that appear to be highly abundant in marine sediments worldwide. In particular, gammaproteobacterial SoB related to symbionts of marine invertebrates and the gammaproteobacterial family Woeseiaceae occur in virtually all types of marine sediment. Here, I present a synopsis of my recent research on the genomic repertoire, gene expression and carbon fixation by uncultured SoB from a marine tidal sediment. Metatranscriptomes and radiotracer incubations indicated highest carbon-fixing/sulfur-oxidizing activity in the oxidized surface layer (0-1 cmbsf during low tide). Sulfur oxidation is likely coupled to denitrification, O₂ respiration and perhaps iron respiration. Surprisingly, also sulfate-reducing bacteria (SRB) displayed highest activity in the surface layer. These SRB may supply SoB with sulfide, which is instantly oxidized and thereby escapes chemical oxidation and detection by microsensors. This still hypothetical scenario raises the exciting possibility of substantial cryptic sulfur cycling in oxidized sediment layers that has not been accounted for in previous studies. Given that biological likely outcompetes chemical sulfur oxidation in most environments, these widespread and abundant SoB are possibly important, yet-overlooked drivers of sulfur oxidation in organic-rich marine sediments.

ECOPHYSIOLOGY OF THE HALO-ALKALIPHILE *DESULFONATRONOSPIRA THIODISMUTANS* ASO3-1^T

Emily Melton, Lex Overmars, Cherele Balkema, Dimitry Sorokin and **Gerard Muyzer (*)**

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Biogeochemical element cycling is essential to the maintenance of ecosystems. Microbes contribute to these cycles by catalyzing non-spontaneous redox reactions, thereby cycling energy and substrate through the system. Soda lakes are extreme environments that have been named Mars analogs, because of their high salt content and high pH values. Although many halo-alkaliphilic microorganisms have been isolated from soda lakes, little information exists on their microbial ecophysiology. Here, we investigated litho-autotrophic and heterotrophic S-metabolism of *Desulfonatronospira thiodismutans* ASO3-1^T, a strictly anaerobic halo-alkaliphilic sulfidogen, in continuous culture chemostats. Four different growth conditions were implemented: heterotrophic sulfate-reduction, heterotrophic sulfite-reduction, heterotrophic sulfite-disproportionation and autotrophic sulfite-disproportionation. RNA was extracted from the reactor biomass at steady state and sequenced using RNA-Seq. From the transcriptomics data, we identified differentially expressed genes in those 4 different growth conditions. This enabled us to identify genes expressed specifically during autotrophic sulfite-disproportionation, a so far elusive pathway of the dissimilatory microbial sulfur cycle. The transcriptomes of the autotrophic and heterotrophic sulfite disproportionation bioreactors were relatively similar. The transcriptomes of the heterotrophic S-reduction bioreactors were significantly different from the litho-autotrophic S-disproportionation bioreactors. However, these differences were not accountable to known sulfite oxidation and reduction genes, but were mainly due to genes that have not before been linked to S-metabolism. This is the first large scale transcriptomics study on the ecophysiology of a halo-alkaliphilic sulfur and carbon cycling microbe in continuous culture and provides important leads to which genes could be instrumental to sulfite-disproportionation.

EXTRACELLULAR ELECTRON TRANSFER (EET): NEW METABOLIC WINDOWS AND NEW LIFESTYLES

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Since its discovery nearly 30 years ago, extracellular electron transfer (EET) has moved from “it can’t be true” to “maybe so” to “I knew it all the time”, and finally to “actually, it was my idea” signaling a rise to at least respectability. The problem with the idea was that in order for EET to occur, a prokaryotic cell must do what it was designed to avoid: i.e., the delivery of electrons from the cell interior to the exterior without gaining the maximum energy. It is appropriate for this conference that the ability of bacteria to interact electrochemically with insoluble electron donors and/or electron acceptors was discovered because of a geochemical anomaly. Thus, the discovery of microbes capable of using solid manganese oxide (*Shewanella*) or solid iron oxide (*Geobacter*) as respiratory electron acceptors (30 years ago) will be briefly noted. While the process has been studied for decades, it is only in the past 10 years that the actual mechanism for the movement of electrons through the periplasm and across the outer membrane has been defined as an electron “hopping” mechanism involving several multi-heme c-type cytochromes. Both *Shewanella* and *Geobacter* employ this mechanism to accomplish the “impossible” task of delivering electrons to the extracellular environment. Once to the outside, the electrons can be used for: 1) direct reduction of insoluble EAs; 2) indirect reduction via soluble electron shuttles or insoluble conductive minerals; or 3) long-distance reduction via conductive appendages, which, in the shewanellae, are synthesized in response to energy stress (either electron donor or electron acceptor limitation). Of particular interest to this conference are some of the new findings dealing with: 1) the importance of surface charge for attachment and growth of microbes; 2) the ability of bacteria to sense and respond to changes in surface charge at the transcriptional level; 3) the ability of bacteria to take up and utilize electrochemical energy for growth and metabolism; and, 4) the use of electrodes to isolate many new and different microbes capable of EET. These findings lead us to the exciting conclusions that first, EET-capable microbes are far more diverse than first imagine; second, that many of our well known microbial groups are capable of EET; and third, that many of the EET-capable microbes are using as yet unknown mechanisms to accomplish their EET activity

GENOMIC AND ECOPHYSIOLOGICAL INSIGHTS INTO METABOLIC COOPERATION BETWEEN METHANOTROPHIC ARCHAEA AND SULFATE-REDUCING BACTERIA IN METHANE SEEPS

Victoria Orphan (*), Grayson Chadwick, Connor Skennerton, Hank Yu, Shawn McGlynn, Roland Hatzenpichler, Rex Malmstrom, Tanja Woeke, Danielle Goudeau², Ariel O'Neill, Chris Kempes, and Christof Meile.

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Microbially mediated sulfate-coupled methane oxidation in anoxic environments is a globally important sink for methane in the oceans. This process is believed to be mediated through a symbiosis between multiple methanotrophic archaeal lineages (ANME-1, 2 and 3) and sulfate-reducing bacteria (SRB), which form highly structured, multi-celled consortia in anoxic methane seep sediments. The spatial arrangement of partners and specific membership among individual sediment-hosted consortia in the environment is highly diverse. This inherent environmental complexity, combined with slow rates of growth, and associated challenges with culturing ANME and their SRB partners, has slowed progress in understanding fundamental aspects of energy conservation, metabolic interactions, and ecology. Through the use of single-cell / single consortia sequencing, high resolution electron microscopy imaging, and FISH-nanoSIMS coupled with stable isotope probing, we are developing new insights into ANME-SRB physiology, interactions, and specific syntrophic associations that appear to be linked through direct extracellular transfer of electrons from methanotrophic archaea to their sulfate-reducing bacterial partners.

MICROBIAL NECROMASS DEGRADATION IN ARCTIC MARINE SEDIMENTS: PHYSIOLOGICAL INTERACTIONS OF MICROORGANISMS INVOLVED IN ANOXIC DEGRADATION OF CELLULAR ORGANIC MATTER

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Seafloor microorganisms remineralize vast quantities of organic matter from marine primary production and decomposition of dead cells, and thus are key players of the global carbon cycle. The Arctic is strongly impacted by rising temperatures and burial of organic matter from primary production will increase. Nonetheless, the identities and roles of microorganisms in organic matter degradation remain understudied. We supplemented individual anoxic incubations of arctic marine sediment with diverse ^{13}C labeled substrates: (I) *Spirulina* biomass, to mimic bulk organic matter input, (II) proteins and lipids representing individual cellular macro-molecules, and (III) acetate, a major degradation intermediate. Sulfate reduction rates and concentrations of volatile fatty acids during substrate degradation were monitored and the specific incorporation of ^{13}C into microbial biomass or DNA was analyzed by catalyzed reporter deposition fluorescence in situ hybridization combined with Raman spectroscopy and DNA stable-isotope probing, respectively. We identified members of the genera *Psychrilyobacter*, *Psychromonas*, *Marinifilum*, and *Fusibacter* as primary degraders of cyanobacterial biomass and revealed substrate preferences of *Psychrilyobacter* and *Psychromonas* species for proteins and lipids, respectively. The concentrations of volatile fatty acids that were produced during substrate degradation were tightly controlled by sulfate-reducing Deltaproteobacteria, but none of the ^{13}C -acetate was incorporated into cellular biomass. Our findings provide an essential step in understanding the identities and metabolic interactions of key microbes in complex organic matter degradation in arctic marine sediments and revealed several primary hydrolyzing microorganisms not previously linked to these ecological processes.

OXIC RESPIRATION UNDER LOW OXYGEN AVAILABILITY

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Oxygen is the energetically most favorable electron acceptor for respiration, even when the concentrations are vanishingly low. At sub-micromolar O₂ concentrations there may, however, be limitation of the rate of respiration by the half-saturation (K_m) values of the terminal oxidases, ranging from a few nanomolar and up to 0.2 μM. Large cells respiring at high rates may furthermore be limited by the diffusional O₂ supply, which shows up as apparent K_m values that are higher than the K_m values for the enzymes.

During the last decade we have explored how new analytical approaches can be used to quantify O₂ respiration and oxygenic photosynthesis at nanomolar O₂ concentrations. The new techniques include electrochemical and optical sensors that can quantify O₂ in the 1-1000 nM range, all-glass incubation systems, and efficient methods to remove relatively high levels of O₂ originating from unavoidable contamination during sampling and transfer.

The primary study area for studies of microbial metabolism at low O₂ concentrations has been the Oxygen Minimum Zones of the Eastern Pacific Ocean, which after we started our work have been renamed “Anoxic Marine Zones”. Our work has served to characterize the real oxygen status of these areas, and it has also resulted in quantification of O₂ respiration rates throughout the oxic part of the water column. Special attention has been given to the photosynthetic activity in the deep chlorophyll peak that is often found at about 100 m depth in predominantly anoxic water layers. Photosynthesis and respiration rates in the deep chlorophyll peak were a few nM per hour. The work has also served to characterize the relationship between O₂ concentration and the oxic processes of ammonia and nitrite oxidation and the predominantly anoxic processes of denitrification and anammox.

REVISITING THE CRYPTIC SULFUR CYCLE IN SULFATE-LIMITED SEDIMENTS OF KATTEGAT

André Pellerin(*), Gilad Antler, Alyssa Findlay, Felix Beulig, Hans Røy, Alexandra Turchyn and Bo Barker Jørgensen

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Sulfate concentrations below the sulfate-methane transition (SMT) of marine sediments are a deterministic factor in assessing microbial energetic limits and sulfur cycling activity. We therefore carefully studied sulfate concentrations at three sites in Aarhus Bay (Denmark). Sulfate penetration into the sediment varied from 60 to 400 cm. We found sulfate concentrations below the SMT are constant with depth and lower than previous studies have observed in marine sediments of a similar nature. Our concentrations were on average near 10 μM but at some points falling below our detection limit of 5 μM . Thermodynamic assessment suggests the concentrations measured are still above thermodynamic limits imposed on microbial communities operating on extremely low energy yields. Tracer insertions and sulfur and oxygen isotopic measurements suggest sulfate concentrations measured are likely true or overestimated. We believe our reported sulfate concentrations below the SMT can be generalized to most sulfidic marine sediments. Depth of the SMT did not seem to exert a control on the background concentration but sulfate reduction rates dropped in a phase manner at the transition to sulfate limitation but were still detectable, indicating the sulfate supply is clearly limiting rates but that a steady supply of sulfate is generated in-situ. In some instances, sulfate reduction rates were as low as ≈ 0.01 picomole/cm³/day. Sulfate reduction rates below SMT had an inverse correlation with age of sediment but not with depth of SMT, offering a quantitative insight into the hidden sulfur cycle in marine sediments as well as a mechanistic understanding of its driver. Turnover times of the sulfate pool below the SMT ranged between 10 to 3000 years depending on the site which indicates drastic differences in sulfur cycling depending on age of the sediment. Importantly, these are not correlated with sulfate concentration. Measurements of iron monosulfides and disulfides as well as elemental sulfur concentrations in porewater and solid phase hint at a constant recycling of sulfide below the SMT at least to intermediate oxidation states and suggest the sulfur cycle below the SMT is active, variable, but predictable by an age relationship. Potentially, a portion of the S cycle may bypass sulfate altogether.

MARINE DEEP BIOSPHERE MICROBIAL COMMUNITIES ASSEMBLE IN NEAR-SURFACE SEDIMENTS

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Deep marine sediments are densely populated by diverse microbial communities that subsist under strikingly low energy fluxes. Population surveys of these unique environments have identified a small subset of ‘persister’ microorganisms, which comprise a significant portion of deep biosphere communities at geographically distinct locations. Despite their prevalence, little is known about how these specialized communities are formed. We hypothesize that assembly of these deep biosphere communities occurs near the surface, where bioturbative mixing ceases and energy fluxes sharply decline. To explore this hypothesis, we performed a fine-scale analysis of the distribution and activity of microbial populations present within the upper 50 cm of a sediment core from Aarhus Bay (Denmark). The core was approached as a vertical time series, with the aim of examining population dynamics occurring with burial of resident microbial communities. Sequencing and qPCR were combined to determine the distributions of bacterial and archaeal taxa (16S rRNA genes) and sulfate-reducing microorganisms (*dsrB* gene), as well as their relative abundances at each depth. Sulfate reduction rates were measured to estimate average generation times of the community, which were used to interpret any observed population dynamics in relation to growth and diversification potential. Changes in community composition were most striking at the bottom of the bioturbation zone, as marked by a shift from dominant surface populations (Proteobacteria) to common deep biosphere taxa (Chloroflexi, Atribacteria, Archaea). The population stability and energetic limitations encountered below this region suggest that subsurface communities are shaped by selection of specialized populations from the surface environment.

GLOBAL AND LOCAL REGULATION OF MICROBIAL ACTIVITY IN COASTAL SUBSURFACE SEDIMENTS

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A sediment core from Guanabara Bay, Rio de Janeiro - Brazil, covering a timescale of ca. 6.000 years, was used to estimate subsurface microbial activity. Diagenetic processes had a strong influence on the quality of sedimentary organic matter and the origin of presented molecules and, as expected, organic matter (OM) was progressively degraded with depth. The overall microbial activity was low, decreasing its activity from 1 to 4 m depth. Microbial biomass production is sustained by organic carbon deposited from sediment surface in a short period of time, but microbial necromass is recycled over timescales of hundreds of years. Turnover times of total organic carbon pool increased with depth, indicating that it became progressively more refractory and unavailable to microorganisms with the increase in depth. Buried organic carbon was sufficient to fuel microbial activities over timescales of hundreds of years, due to very slow mineralization rates. A comparison between microbial activity in tropical Guanabara Bay and temperate Aarhus bay showed an interestingly result. Total carbon oxidation rates in Guanabara Bay were higher than in Aarhus Bay. Biomass turnover times were in the range of 0.7 and 2.9 years at Guanabara Bay, a lower value than previously reported for Aarhus Bay. Degradation index were in the same range in both bays, however, Guanabara Bay presented a unexpected result, with a significant increase in this index from 1 to 4 m. One explanation would be the OM production via chemosynthesis. These differences could be attributed to different ages of buried sediment, quality of buried OM or due to higher microbial metabolism as a result of higher temperatures in lower latitudes. However, results are inconclusive and we intend to fill this gap by evaluating the regulating factors on microbial activity in subsurface sediments from deep sea, bays and lakes of tropical and amazonian environments, mainly linking it to organic matter quality and quantity.

DETERMINATION OF GENERATION TIME AND GROWTH RATE OF THE GASP PHENOTYPE IN LONG-TERM STATIONARY PHASE *E. COLI* CULTURES BY NANOCALORIMETRY

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The study of long-term stationary phase cultures of bacterial populations has provided insight into the physiological adaptation to low-energy conditions in nature. Though apparently static, these communities are, in fact, highly dynamic and are characterized by the rapid emergence and succession of distinct mutants expressing the GASP phenotype, which can include an improved ability to withstand energy limitation relative to the original parental strain. Although the expression of this phenotype in laboratory culture becomes evident only during long-term stationary phase, recent studies suggest that nascent GASP mutants might be present within the bulk wild-type population as early as in an overnight-grown batch culture. Here we investigate the generation time and growth rate of these GASP mutants within an evolving population. We aged *E. coli* in anaerobic batch cultures by incubating them over 30 days inside an isothermal calorimeter. The decaying metabolic heat following the decline in viable cell counts was monitored through the extended stationary phase. Distinct heat effects marked the emergence of three mutant populations expressing the GASP phenotype after 1½, 5, and 7 days, respectively. The corresponding specific growth rates were estimated from the heat flow data to be 0.1, 0.01, and 0.001 h⁻¹, respectively. The number of mutants at the onset of the stationary phase was then calculated by dividing the heat flow by the cell-specific heat production rate as determined in parallel competition experiments of aged against wild-type cells. The abundance of GASP mutants coexisting with the initial population was estimated at 8.8 x 10⁵, 4.8 x 10⁴, and 2.4 x 10⁴ cells per culture, respectively. This indicates that mutants capable of expressing the GASP phenotype can initially be acquired during the exponential growth phase and subsequently expressed at different times following the increasing selection pressure of lower energy availability in the culture.

SULFATE REDUCTION AND THE RESPIRATION RATE OF BACTERIA

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Microorganisms in old sediments are living from recalcitrant organic matter that was deposited tens, thousands or millions of years ago. We found a remarkably tight correlation between the age of the deposited organic material and the rate at which it was degraded. The number of microorganisms was distinctly related to the rate of degradation of organic matter. However, as the number of microbes decreased faster than the rate of organic matter degradation, the mean metabolic rate of the organisms decreased continuously for at least 3.7 million years. We distinguished the liberation of energy from degradation of organic matter in an initial step linked to fermentation to acetate, and a second step of acetate-oxidation to CO₂ linked to sulfate reduction. Our results show that the sulfate reducers in deeply buried sediments dissipate power at a rate of near 5×10^{-18} W cell⁻¹, regardless of depth, and that this was in the same range as the slowest growing laboratory cultures. The relatively high activity per cell was caused by the proportion of sulfate reducers being low, so that the low rates of sulfate reduction was shared among a relatively small number of cells. The rate of power dissipation per sulfate reducing cells was constant regardless of sediment age, and we propose that the rate represents the minimum power required to maintain a sulfate reducing cell. In contrast, the fermenting cells had ever decreasing average dissipation of power per cell as the sediment age increased. The lowest values reached was 5×10^{-22} W cell⁻¹, which is only barely enough to cover even a conservative estimate of the minimum power needed to counter razzimation of aspartic acid in cell-proteins. The vast difference in power consumption between fermenters and sulfate reducers cause the microbial community in deep and old sediments to consist of a minute fraction of sulfate reducers and a vast majority of fermenting microbes.

TOWARDS ARTEFACT FREE STUDIES ON DEEP SEA SEDIMENTS

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Hadal sediments are, due to their remoteness and extreme pressures, one of the most scantily explored marine environments. Despite the energetic dependence upon organic material, supplied from the distant euphotic zone, recent studies indicate these sediments to be hotspots of deposition and mineralization relative to surrounding abyssal plains. However, the microbes that regulate and perform these processes remain virtually unknown. With this project we aim to bridge this knowledge gap and provide the first comprehensive insight into benthic diagenesis and microbial ecology of hadal trenches exposed to different sedimentation rates.

One of the major challenges hampering accurate investigations on such deep sea sediments are artefacts, associated with sample recovery. These artefacts are already well documented for biogeochemical parameters, and analogous effects on the microbial community composition and gene expression profiles appear likely, but remain unknown.

To minimize sampling artefacts on biogeochemical and microbial ecological parameters, we developed autonomous sampling instruments, which are able to inject, e.g., isotope tracers or preservation solutions for DNA and RNA via needles into sediment cores in situ. As a first step, we are currently evaluating novel fixation solutions that are resistant to cold temperatures, high pressures and potent enough to be applied in low volumes - requirements not met by current commercial fixatives. We are also investigating the stability of ribosomal RNA to the changes imposed during sediment recovery.

A novel fixation solution in combination with in situ incubations should be an important step towards artefact free studies on deep sea sediments and ultimately enable us to explore and characterize the uniqueness in both structure and function of benthic microbial communities across hadal trenches in low, intermediate, and high productivity regions of the ocean.

REVISITING BIOGENIC IRON SULFIDE MINERALS

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Throughout Earth's history, the burial of iron sulfide minerals and organic carbon has governed the oxygen concentration in the Earth's atmosphere. On modern Earth, sulfate-reducing microorganisms (SRM) are the major source of dissolved sulfide in low-temperature sedimentary environments, though their role in iron sulfide mineral formation is currently assumed to be limited to providing dissolved sulfide to the Fe-S system. Here we present experimental data that challenge this assumption, and posit that SRM also play a role in the nucleation and growth of iron sulfide minerals by providing both organic templates for nucleation and growth of iron sulfide minerals and organic material which informs mineralization. Using the deep-sea sulfate-reducing bacterium *Desulfovibrio hydrothermalis* AM13, and a combination of microscopy and spectroscopy, we demonstrate that iron sulfide minerals precipitated in the presence of SRM bear unexpected physical characteristics that will potentially affect their reactivity and transformation. Moreover, upon forming, "biogenic" iron sulfide minerals become associated with organic carbon, potentially protecting labile organic material from degradation. We propose that the physical and chemical characteristics conferred to biogenic iron sulfide minerals could play a role in preserving organic carbon in sedimentary environments and potentially affect further transformations of solid phases, controlling pyrite formation pathways.

ONLY LONG-TERM INCUBATIONS REVEAL TEMPERATURE ADAPTATION IN ENVIRONMENTAL SAMPLES

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The temperature adaptation of dissimilatory sulfate reduction in marine sediments can be characterized by the optimum temperature and the apparent activation energy of respiration rates determined during short-term incubations with $^{35}\text{SO}_4^{2-}$ radiotracer in a temperature gradient. But the optimum temperatures derived from such experiments are much above the environmentally relevant temperature range, and the measured activation energies appears not to be related to temperature regimes at the sampling sites. Thus, the relevance of the optimum temperature and apparent activation energy as proxies for temperature adaptation in marine sediments is not clear. We performed similar experiments, but followed sulfate reduction rate as a function of temperature over 11 days. This revealed that the optimum temperature shifted downwards from 28°C to 15°C. An optimum temperature of 15°C is similar to that of psychrophilic sulfate reducers in pure cultures that have been isolated from permanently cold environments. During the 11 day long experiment the rate of sulfate reduction increased due to growth. The maximum growth occurred at 15°C, i.e at the same temperature as the maximum rate of respiration. Above 25°C rates decreased dramatically relative to the initial observation. Thus, previous investigations of temperature adaptation using only short-term incubations may have been masked by unsustainably high rates of sulfate reduction at detrimentally high temperatures. We plan to revisit sites with permanent temperatures from -1.5°C to 40°C to investigate if the apparent lack of latitudinal gradient in activation energy and optimum temperatures above the optimum for growth seen in the literature is caused by this artefact.

GENOMIC INSIGHTS INTO THE FUNCTION AND EVOLUTION OF CABLE BACTERIA

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Cable bacteria are centimeter-long, filamentous bacteria that occur globally in the oxic-anoxic transition zone of marine and freshwater sediments. They couple sulfide oxidation in deeper sediment layers with oxygen respiration at the sediment surface via long distance electron transfer, generating suboxic zones devoid of oxygen and sulfide. Phylogenetically, cable bacteria are members of a narrow, as yet uncultured lineage of the Desulfobulbaceae, and to date two candidate genera, *Ca. Electrothrix* and *Ca. Electronema*, have been described. Here we used genome reconstruction from single filaments combined with genome and proteome analysis of a clonal enrichment of *Ca. Electronema* to gain insights into the genome content and metabolism of cable bacteria. Evolutionary analysis revealed few gene losses compared to the conserved core genome of all Desulfobulbaceae but a large proportion of unique genes, and pointed to horizontal gene transfer and gene diversification as important drivers of cable bacteria evolution. Metabolic reconstruction suggests that cable bacteria oxidize sulfide by reversing the canonical sulfate reduction pathway, have a limited potential to utilize organic carbon but the ability to fix CO₂ and nitrogen; oxygen, nitrate and nitrite are potential electron acceptors. The genomes are rich in diverse cytochromes, including multi-heme cytochromes, and also contain so-called e-pili, implied in electron conductance in *Geobacter*. Their potential role for the still enigmatic long distance electron transfer in cable bacteria will be discussed.

METHANOTROPHY UNDER VERSATILE CONDITIONS IN THE WATER COLUMN OF THE FERRUGINOUS MEROMICTIC LAKE LA CRUZ (SPAIN)

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Lakes represent a considerable natural source of methane to the atmosphere compared to their small global surface area. Methanotrophs in sediments and in the water column largely control methane fluxes from these systems, yet the diversity, electron accepting capacity and nutrient requirements of these microorganisms have only been partially identified. Here we investigated the role of electron acceptors alternative to oxygen and sulfate in microbial methane oxidation at the oxycline and in anoxic waters of the ferruginous meromictic Lake La Cruz, Spain. Active methane turnover in a zone extending well below the oxycline was evidenced by stable carbon isotope-based rate measurements. We observed a strong methane oxidation potential throughout the anoxic water column, which did not vary substantially from that at the oxic/anoxic interface. Both in the redox-transition and anoxic zones, only aerobic methane-oxidizing bacteria were detected by fluorescence in situ hybridization and sequencing techniques, suggesting a close coupling of cryptic photosynthetic oxygen production and aerobic methane turnover. Additions of nitrate, nitrite and to a lesser degree iron and manganese oxides also stimulated bacterial methane consumption. We could not confirm a direct link between the reduction of these compounds and methane oxidation and we cannot exclude the contribution of unknown anaerobic methanotrophs. Nevertheless, our findings from Lake La Cruz support recent laboratory evidence that aerobic methanotrophs may be able to utilize alternative terminal electron acceptors under oxygen limitation.

ENERGY STRATEGIES OF BIG SULFUR BACTERIA

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Over the last decades many new aspects on how large sulfur bacteria adapted to use sulphide as their main electron donor have been revealed. This includes, for example, the accumulation of nitrate, the storage of polyphosphate and a directed movement in gradients. Nevertheless, the role of polyphosphate in the metabolism of sulphide oxidizing bacteria is not completely clear yet. Laboratory and field studies on *Beggiatoaceae* have shown the degradation of polyphosphate as a specific response to higher sulphide concentrations. Nevertheless, the reason for this reaction is unclear. Polyphosphate storage is also obviously not essential for large sulphur bacteria, because it is notably absent in some genera, for example in *Marithioploca* spp. off the coast of Chile and *Parabeggiatoa* spp. at the edge of the Gotland Basin. In this presentation, we are going to report on a so far overlooked larger pelagic bacterium, which oxidizes sulphide. Seemingly, this bacterium relies on polyphosphate storage in a similar way as the large sulphur bacterium *Thiomargarita namibiensis* and combines this with a directed vertical movement, as well known from *Marithioploca araucae*.

HYDROSTATIC PRESSURE CAN SHAPE MICROBIAL OIL-DEGRADING COMMUNITIES AND THEIR METABOLISM

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Hydrocarbons can be used as a carbon source by bacteria in the deep sea following natural seeps or accidental spills. Although hydrostatic pressure represents a distinctive feature of deep-sea environments its impact on the physiology of hydrocarbons degradation remains unclear. In this study, we used a cultivation-based approach to investigate the potential impact of hydrostatic pressure. Hydrocarbon-free samples from 1 km below sea level (bsl) (about 10 MPa) were supplied with either eicosane (C20) or triacontane (C30) as sole carbon source. Cultures were enriched, isolated and further tested in synthetic communities in a pressure range between 0.1 to 30 MPa. HP shaped microbial communities, their capacity to grow on hydrocarbons and their metabolism. HP inhibited hydrocarbonoclastic bacteria (i.e., *Alcanivorax*, *Thalassolituus*) and favored secondary oil degraders (e.g., *Halomonas*, *Thalassospira*, *Pseudoalteromonas*, *Vibrio*). In enrichments, hydrostatic pressure reduced the expression level of proteins related to Lipid and Fatty Acid degradation and increased house-keeping biological functions. In hydrostatic-pressure-adapted synthetic communities, expression level of these catabolic pathways was not impacted by hydrostatic pressure. However, microbial oil degradation capacity was comprehensively decreased in both set ups already at 10 MPa. As observed for temperature, electron acceptor and hydrocarbons' chemical nature, this data indicates that HP has the capacity to impact microbial oil degradation.

MICROBIAL IRON REDUCTION IN LACUSTRINE AND MARINE METHANOGENIC SEDIMENTS

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In many aquatic sediments significant microbial iron reduction has been observed not only in its expected traditional depth but also in the deep methanogenic zone, sometimes accompanied by methane decrease. Using geochemical isotopic approach, we have investigated the coupling of this microbial reduction to methane in sediment diffusive profiles of Lake Kinneret (Israel) and the Eastern Mediterranean continental shelf. The results show that in Lake Kinneret iron is linked to the methane cycle mainly by its reduction via anaerobic oxidation of methane (AOM). Surprisingly, the less reactive iron minerals such as magnetite and hematite are more accessible to this process. The iron coupled AOM process involves complex community that is able to sustain life under highly-reducing low energy conditions using novel strategies. Sediments collected from the Eastern Mediterranean continental shelf show also active microbial iron reduction in the methanogenic zone and reactivation of iron minerals as magnetite, however, it seems that AOM does not have a significant role there.

THE IMPACT OF ELECTROGENIC SULPHIDE OXIDATION ON THE BIOGEOCHEMISTRY OF COASTAL BLACK SEA SEDIMENT

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Electrogenic sulphide oxidation (e-SOx), performed by cable bacteria, has been shown to greatly impact biogeochemical cycling in sediments. Here, we assess the impact of e-SOx on the cycling of iron, sulphur and phosphorus in laboratory incubations with coastal Black Sea sediment. Our results show a rapid establishment of cable bacteria (<5 days), as deduced from high resolution depth profiles of oxygen, sulphide, pH and electric potential, followed by a long period of activity (> 200 days). Strikingly, porewater sulfide concentrations remained extremely low (<4 μM), despite high sulphate reduction rates. The free sulphide thus was effectively oxidised by e-SOx or precipitated as iron monosulfides at depth. Microscopic observations of the cable bacteria indicate that, throughout the experiment, the cable bacteria remained extremely small in size. Nevertheless, the activity of the cable bacteria had a significant impact on the mobilization of iron and sulfur and sequestration of phosphorus in the sediment.

THE ELECTROMICROBIOME OF OXYGEN MINIMUM ZONES AND ITS BIOGEOCHEMICAL SIGNIFICANCE

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The electromicrobiome may play a crucial role in the production of methane (CH₄) via direct interspecies electron transfer (DIET) and in the biogeochemical cycling of iron (Fe) in marine Oxygen Minimum Zones (OMZs). Electroactive *Geobacter* species and Methanosarcinales methanogens can form syntrophic associations where direct exchange of electrons via electrically conductive pili (e-pili), rather than hydrogen transfer promotes CH₄ generation. In natural settings, *Geobacter* are arguably the most important dissimilatory Fe(III) reducers in anoxic terrestrial and freshwater sediments but to date have been regarded as absent and unimportant in fully marine environs. New -omics data from the Peruvian OMZ show for the first time that *Geobacter* are, in fact, abundant in fully marine anoxic sediments as well as in the water column, where they co-occur with methanogens that are known to participate in DIET. Molecular signatures of DIET including the PilA pilin monomer of e- pili and C type cytochrome oxidase genes from *Geobacter* are also present. This is a significant and novel discovery that suggests electron flow from oxidation of organic carbon is being directed towards methanogenesis via DIET as an electron sink, or alternatively to extracellular iron oxides with the concomitant release of Fe(II) and trace elements. Release of Fe(II) is crucial to N-cycling and primary production in surface waters but if enough electron flow is directed into methanogenesis via DIET, it could have profound effects on Carbon cycling and other biogeochemical cycles. Discerning the role of DIET in methanogenesis and Fe-cycling is key to understanding the expansion of OMZs as the world's oceans become deoxygenated due to changes in oceanic temperature, chemistry and circulation and will facilitate our understanding of how anthropogenic climate change will respond.

ASGARD ARCHAEA – A METABOLICALLY DIVERSE SUPERPHYLUM THAT HAS PLAYED A KEY ROLE IN THE ORIGIN OF EUKARYOTES

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The origin of eukaryotes represents an unresolved puzzle in evolutionary biology. For a long time, it was assumed that Archaea have played a central role in hypotheses on eukaryogenesis, and recent findings support the view that eukaryotes evolved from a symbiosis between an archaeal host and an alphaproteobacterial endosymbiont. The recent discovery of the Asgard superphylum, including Lokiarchaeum, has shed additional light on this enigmatic event. Asgard archaea, whose genomes were obtained by metagenomics from various sediment samples across the world, represent the closest prokaryotic relatives of eukaryotes identified so far. Furthermore, their genomes harbor a plethora of eukaryotic signature proteins that may have been key in the evolution of complex eukaryotic cells. So far however, little is known about their metabolic potential and the evolution of their functional characteristics.

To unveil the metabolism of the elusive archaeal ancestor of eukaryotes, we have reconstructed the carbon metabolism of Asgard archaea in a comparative genomics framework. Initial analyses suggest, that the four different Asgard phyla, i.e. Odin-, Thor-, Loki- and Heimdallarchaeota are metabolically diverse and characterized by different metabolic lifestyles. While Thor- and Lokiarchaeota seem to be able to fix carbon via the Wood-Ljungdahl pathway and may be able to obtain energy from, amongst others, acetate and short chain fatty acids, Heimdallarchaeota seemingly encode terminal oxidases suggesting the ability to reduce nitrate or even oxygen. Altogether, our current analyses of these metabolic features and the reconstruction of the evolution of metabolic traits in the diversification of this superphylum will help to resolve the nature of the elusive archaeal ancestor of eukaryotes.

MICROBIAL COMMUNITIES AT DEEP-SEA HYDROTHERMAL VENTS: NEW RESULTS ON FILAMENTOUS SULFUR-OXIDIZING MAT-FORMING BACTERIA AT GUAYMAS BASIN

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Large, vacuolated mat-forming filamentous bacteria of the family *Beggiatoaceae* represent visually conspicuous microbial community on hydrothermally active sediments of Guaymas Basin. The center of a hydrothermal hot spot, where the chemical and thermal gradients in the underlying sediment are steepest, is commonly dominated by orange *Beggiatoaceae* of ca. 35 to 40 μm diameter; these orange areas are surrounded by an extensive fringe of colorless (white) *Beggiatoaceae* of more than 100 μm diameter; cooler sediments surrounding these fried-egg structures may still harbor large sulfur-oxidizing bacteria, but not in the form of conspicuous mats.

By analogy with other large, vacuolated members of the *Beggiatoaceae*, the Guaymas representatives were assumed to be nitrate-reducing sulfur oxidizers. We examined nitrate- and nitrite-reducing pathways in Guaymas *Beggiatoaceae* by [meta]genome sequence analysis of orange and white Guaymas *Beggiatoaceae*, by cloning and expression of candidate nitrite reductases from orange *Beggiatoaceae*, and by assaying the nitrate reduction pathways of live Guaymas *Beggiatoaceae* with ^{15}N -labeled substrates in combination with microsensor studies.

Three candidate nitrite reductase genes from the orange *Beggiatoaceae* were expressed in *E.coli*; of these, the *nirS* candidate and an octaheme cytochrome c reductase showed the strongest nitrite-reducing activities, whereas the cloned equivalent of a previously tested multifunctional orange octaheme cytochrome showed lesser activity below the levels that could be obtained with native cell extract. We hypothesize that these enzymes are active in different physiological contexts.

In ^{15}N -labelling experiments, the orange and white *Beggiatoaceae* turned out to have distinctive capabilities. Both types were capable of denitrification and of nitrate reduction to ammonia, but the white *Beggiatoaceae* produced predominantly N_2 and the orange type generated predominantly ammonia. Nitrate-reducing pathways in these *Beggiatoaceae* appear to be affected by selective gene loss and horizontal gene transfer.

In the context of our initial metagenomic survey of Guaymas Basin that has yielded numerous anaerobic bacterial and archaeal lineages, the visually conspicuous *Beggiatoaceae* represent minority populations that have adapted to a highly specific environmental niche of respiratory sulfur oxidation at the micro-oxic, cool or temperate sediment-water interface.

THE MULTIPLE ROLES OF NITRATE AS AN OXIDANT

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After oxygen, nitrate is the most energetically favourable oxidant of abundant presence in the biosphere, and it is used for respiration by a vast diversity of microbes that couple nitrate reduction to the oxidation of a wide range of both organic and inorganic compounds. Reduction to nitrite appears to be the first step in all nitrate-reducing organisms while from nitrite several reductive pathways branch out, including the conversion to N_2O and N_2 , which renders nitrogen unavailable as nutrient for most organisms.

Despite the important role of nitrogen as nutrient and the multiple interactions of nitrogen transformations with the biogeochemical cycling of other elements, we have only a rudimentary understanding of how different nitrate- and nitrite-reducing processes are controlled and compete in natural environments, which organisms play the dominant roles in the nitrogen transformations, and how these transformations impact the cycling of elements such as carbon, manganese, iron, and sulfur. This presentation focuses on recent discoveries concerning the role of electron donors such as ferrous iron and methane in the reduction of nitrate and nitrite in aquatic sediments and anoxic waters.

TRANSCRIPTOMICS OF THE CABLE BACTERIUM *CANDIDATUS* ELECTRONEMA NIELSENII

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Cable bacteria are filamentous members of the Desulfobulbaceae family capable of conducting electrons via long distance electron transport. They couple anodic sulfide oxidation and cathodic oxygen or nitrate reduction over centimeter distances in sediments. This process, named electrogenic sulfide oxidation (e-SOx) leads to the development of a suboxic layer, devoid of both sulfide and oxygen. Although supported by biogeochemical analyses, e-SOx as their means of energy metabolism remains paradoxical, as cable bacteria are phylogenetically affiliated with sulfate reducing bacteria. Accordingly, cable bacteria genomes reconstructed from both single filaments and metagenomes showed the complete sulfate reduction pathway and none of the canonical sulfide oxidation pathways. Reversed steps in the sulfate reduction pathway are therefore proposed to be part of the sulfide oxidation pathway. To test this hypothesis, and to evaluate potential differential gene expressions in the different biogeochemical zones, gene expression of the candidate species *Electronema nielsenii* via RNA-Seq is compared between sediment zones with either anodic sulfide oxidation, cathodic oxygen and nitrate reduction, or electron transmission only.

MICROBIAL NITROGEN CYCLING POTENTIAL IN DEEP SEDIMENTS OF THE BALTIC SEA

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Recent studies evidence that microbial nitrogen (N) cycling processes such as nitrate reduction and protein degradation may play an important role in deep marine sediments (D'Hondt et al. 2004, Morono et al. 2011, Lloyd et al. 2013, Orsi et al., 2013). However, little is known about the N cycling potential and abundances of the various N cycling microorganisms in these sediments. Therefore, we investigated potential activities of exoenzymes hydrolyzing organic N compounds via incubations with fluorogenic substrates coupled to extraction and HPLC detection in Baltic Sea sediments down to a depth of 90 mbsf (IODP Expedition 347). In addition, we quantified abundances of marker genes for N cycling microorganisms via qPCR. Despite an improved extraction protocol for the fluorogenic substrates, exoenzyme activities of N-acetylglucosaminidase, alanine-aminopeptidase and phenylalanine-aminopeptidase were close to or below the detection limit for most samples. Nevertheless, our results suggest that microorganisms of these deep sediments possess the potential for hydrolyzing complex N compounds such as proteins or chitin. The marker gene abundances (in gene copies per g dry weight) of nitrate reducers (narG, up to 4.2×10^7), nitrite reducers (nirS, up to 3.2×10^7 ; nrfA, up to 7.3×10^6), and diazotrophs (nifH, up to 2.8×10^7) decreased with sediment depth and showed similar trends as archaeal and bacterial 16S rRNA gene abundances. Surprisingly, we also detected genes for ammonia-oxidizing archaea (down to ~ 6 mbsf, 1.9×10^5) and bacteria (down to ~ 17 mbsf, up to 3.2×10^6). Further, genes for chitin-degrading microorganisms (chiA, up to 7.2×10^5) were detected down to ~ 8 mbsf. Thus, our results indicate a diverse potential for microbial N cycling in deep Baltic Sea sediments and future analysis will provide an insight into the diversity of different N cycling communities.

A NEW PERSPECTIVE ON MICROBES FORMERLY KNOWN AS AMMONIA- AND NITRITE-OXIDIZERS

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Nitrification, the aerobic oxidation of ammonia via nitrite to nitrate is a central component of the biogeochemical nitrogen cycle in the world's oceans and is almost exclusively catalysed by bacteria and archaea. In the oceans, nitrification is responsible for the formation of most of the nitrate and dominates production of the potent greenhouse gas N₂O that is also depleting atmospheric ozone. Since their discovery more than 100 years ago, nitrifying microbes were always thought to be metabolically confined by gaining energy for growth exclusively from oxidation of ammonia and nitrite, respectively. We recently demonstrated that nitrifying microbes are actually metabolically much more versatile and can even grow unconnected to the nitrogen cycle (Koch et al. 2014; Koch et al. 2015). Furthermore, we identified ammonia-oxidizing archaea that can use cyanate as the only source of energy, nitrogen and reductant (Palatinszky et al. 2015) and have now first evidence that cyanate is indeed an environmentally important substrate for nitrifiers. Interestingly, nitrifiers can also reverse their canonical interaction pattern and perform reciprocal feeding between nitrite and ammonia-oxidizers – this new interaction pattern which starts with the activity of the nitrite-oxidizers allows joint use of substrates like cyanate and urea, even if the ammonia-oxidizers are not enzymatically equipped for it (Palatinszky et al. 2015; Koch et al. 2015).

The oxidation of ammonia via nitrite to nitrate, has always been considered to be a two-step process catalysed by chemolithoautotrophic microorganisms oxidizing either ammonia or nitrite. Recently, we discovered complete nitrifiers (comammox) belonging to the genus *Nitrospira* (that was always thought to contain exclusively strictly nitrite-oxidizing bacteria) (Daims et al. 2015) and showed that they are abundant and diverse in many terrestrial and aquatic ecosystems. These comammox microbes are perfectly adapted to oligotrophic systems and kinetic analyses revealed that they outcompete all ammonia-oxidizing bacteria and most ammonia-oxidizing archaea at low substrate concentrations. Perplexingly, comammox microbes – despite being so competitive in oligotrophic systems, have not yet been detected in marine samples and possible reasons for this will be discussed.

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STABLE ISOTOPE PROBING AND METAGENOMICS IDENTIFIES DIVERSE AND UNCHARACTERISED BACTERIA THAT DEGRADE DNA IN ANOXIC MARINE SEDIMENTS

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Nucleic acids are substantial components of marine biogeochemical cycles and are available as nutrients for microorganisms in sediments. Nevertheless, the identities of microorganisms that mineralize DNA in marine sediments are unknown and we hypothesized unique niches maybe filled by unknown DNA-degrading microorganisms. Here, we identified DNA-degrading bacteria in anoxic Arctic sediments by combining information from stable-isotope probing and metagenomics. Microcosms were amended with ^{13}C -labelled archaeal DNA or with unlabelled nucleobases and nucleosides. Evolution of $^{13}\text{CO}_2$ and decreasing archaeal DNA in sequence analyses demonstrated mineralisation of supplemented DNA within days. Sequencing 16S rRNA genes from density gradient fractions revealed DNA-derived carbon was incorporated by diverse phylotypes affiliated *Shewanella* and largely uncharacterised clades of *Tenericutes* ('NB1-n') and *Firmicutes* (Clostridial Family XI/'Fusibacter-sister clade'). Multiple genes for extracellular nucleases and catabolic pathways for DNA subcomponents were identified in the *Tenericutes* and *Shewanella* genomes, supporting their active involvement in DNA degradation. The *Firmicutes* organisms instead appeared to be efficient at scavenging nucleobases, but not necessarily hydrolysing DNA. Together, this study reveals functional niches of several poorly understood bacterial groups that may contribute to the key ecosystem function of mineralising nucleic acids in the marine benthos.

ARCHAEA ACTIVATE SHORT-CHAIN HYDROCARBONS BY THE FORMATION OF ALKYL-CoM IN HIGHLY DIVERGENT METHYL-CoM REDUCTASES

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Anoxic marine sediments are rich in natural gas, mostly methane, but also up to 20% short-chain alkanes (SCA). The anaerobic oxidation of methane (AOM) is performed by archaea that activate and completely oxidize methane using methyl-coenzyme M reductase (MCR) and other enzymes of the methanogenesis pathway. Reducing equivalents are transferred to sulfate-reducing bacteria. The fate of short-chain hydrocarbons in sediments was so far poorly assessed. Bacterial hydrocarbon oxidizers such as the only isolate BuS5 activate their substrate via addition to fumarate, but they are rare in sediments. We established thermophilic butane-degrading enrichment cultures (Butane50) from hydrothermally-heated sediments. This culture is dominated by two strains of *Ca. Syntrophoarchaeum* (GoM-Arch87) and the bacterium HotSeep-1. The archaea activate butane via the formation of alkyl-CoM. This before unknown reaction is catalyzed in methyl CoM reductases. Strikingly, *Ca. Syntrophoarchaeum* contains four, highly divergent, and also expressed *mcr* genes, which suggested a possible extended substrate range of these organisms. Indeed, from Butane50 we established an enrichment of a before less abundant strain of *Ca. Syntrophoarchaeum* that is able to oxidize propane. This strain shows a different MCR expression pattern. Our data suggests the need of highly specific MCR enzymes for the activation of each hydrocarbon. On a so far unknown pathway the archaea transform the alkyl moieties into butyryl-CoA, which is oxidized on a fatty acid oxidation pathway. Acetyl-CoA is fully oxidized on the Wood-Ljungdahl and the upstream methanogenesis pathway. Analogous to AOM electrons are transferred to partner bacteria. The recent detection of similar *Mcr* genes in multiple anoxic environments points towards an important role of the described hydrocarbon-degradation pathway in nature.

THE DYNAMIC DEEP BIOSPHERE – LINKING CHANGING PALEO-ENVIRONMENTAL CONDITIONS, RATES AND PATHWAYS OF MICROBIAL PROCESSES, AND DIAGENETIC SIGNALS IN THE SEDIMENTARY RECORD

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Microbial activity and linked biogeochemical processes in the deep biosphere are more dynamic than previously thought, reflecting the variability of a range of factors, including amount and quality of organic matter input, availability of reactive mineral phases, and progressive diagenetic overprint. On short time scales, changes in these factors can result in transient geochemical signatures in the pore-water and solid-phase, and a non-traditional redox zonation. Some signals persist over geological timescales; however, questions regarding their interpretation and further diagenetic alteration remain. New approaches to disentangle past and present biogeochemical processes and to examine the evolution and potential preservation of diagenetic signals in sediments over time include the use of reaction-transport modelling and multi-isotope analyses of pore-water and diagenetic minerals archived in the sedimentary record. We use results from IODP Expedition 323 Site U1341, drilled in the Bering Sea, as an example to discuss these approaches. At this site, variability in opal export and productivity over the last 4.3 Ma (März et al., 2013) resulted in changes in organic carbon respiration rates and transient geochemical signals. Results from an inverse reaction-transport model indicate a high deposition flux of extremely labile organic matter at ~2.58–2.51 Ma ago (Wehrmann et al., 2013). The model gives insight into the evolution of diagenetic processes over time, including the onset and decline of methanogenesis and anaerobic oxidation of methane. Profiles of Mg and Ca concentrations in the pore-water and Sr and Ca isotope values of the pore-water and diagenetic carbonates, provide evidence for the occurrence of carbonate precipitation at sulfate-methane transition zones, volcanic ash alteration in the former methanogenic zone, and ammonium-calcium exchange on clay minerals during time periods of higher organic carbon turnover rates (Wehrmann et al., 2016).

METHYLOTROPHIC METHANOGENESIS FUELS CRYPTIC METHANE CYCLING IN SURFACE SEDIMENT OF AARHUS BAY, DENMARK

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Methane concentrations are generally very low in marine surface sediments and indicate net CH₄ oxidation and methane flux out of the sediment. Yet, methanogenic archaea are present in those sediments, suggesting a potential for methanogenesis. An isotope dilution method based on sediment bag incubation and spiking with ¹³C-CH₄ was used to quantify CH₄ turnover rates in surface sediment from Aarhus Bay, Denmark. Highest CH₄ production and oxidation rates (>200 pmol cm⁻³ d⁻¹) were repetitively found in the top 0-2 cm, below which rates dropped below 100 pmol cm⁻³ d⁻¹ (2-16 cm), leading to a cryptic cycling of CH₄. Parallel ¹⁴C-labelling experiments revealed that methanogenesis from the hydrogenotrophic pathway was below 20 pmol cm⁻³ d⁻¹ throughout the surface sediment, and that there was no apparent contribution from the acetoclastic pathway. Moreover, in sediment slurry incubations with excess substrates (hydrogen, acetate, and trimethylamine) addition, dramatic increase of CH₄ was only detected in those serum bottles amended with trimethylamine, indicating highest potential of methanogenesis from the methylotrophic pathway. Our results show the existence of enhanced methanogenic activity and a dynamic recycling of CH₄ at low concentration in sulfate-rich marine surface sediment, where methanogenesis was dominated by the methylotrophic pathway.

ASYMMETRIC, SYNCHRONIZED CELL DIVISION DECIDES THE CELL SIZE DIFFERENCES IN CABLE BACTERIA

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Cable bacteria are long, multi-cellular filamentous bacteria; cells in sulfidic sediment oxidize sulfide and produce electrons, which are transported centimeter away to cells in oxic zone for reducing oxygen. This study explored cable bacterial cell heterogeneity of the two ends for the first time: large cell size differences were recorded from the opposite ends of the same filaments. Moreover, asymmetric cell division was observed and was proposed to be the main reason of the cell length variation. We hypothesized the asymmetric cell division is determined by cell pole-age, and established a synchronized cell division and cell growth model. The model can successfully predict cell length change in cable fragments, indicating the asymmetric, synchronized cell division decides cable cell size differences. Furthermore, cable cells contained bio-controlled distribution patterns of polyphosphate granules, an intracellular energy storage, suggesting polyphosphate could play important roles on the cell division and cell size at energy level.

Welcome to the workshop

Registration and information during the workshop

Registration, will take place in the reception, which is situated between The Stable (C) and the restaurant Magasinet (B). Lectures will take place in the Auditorium in The Stable (C) and poster sessions will take place in The Distillery (H). The registration desk is open from Monday 15:00.

Breakfasts, lunches, dinners, mixer and Workshop Dinner will all be served in Magasinet (B). Breakfasts, lunches, dinners and mixer are all served buffet style. Cultural Evening Dinner will be served at Sønderborg Castle in the Great Hall's eastern antechamber, Sønderbro 1, 6400 Sønderborg. Participants will be transported by bus to the Castle.

Working group sessions will take place in the meeting rooms at the Manor House (A), The Tenants farmer's House (G) and the Meadow House (J). Participants will be guided to these rooms.



Overview of Meeting Rooms & Conference Rooms at Sandbjerg Manor

Information for speakers

There will be 30 minutes available for invited speakers. Please note that this allotted time encompasses presentation, questions and time for change-over between speakers. It is therefore recommended that speakers target their presentations to be 25 minutes. Please give your PowerPoint presentation on USB memory stick to André Pellerin (PC-users) or Caroline Scholze (Mac-users) at the latest in the morning or the lunch break before your presentation. Caroline and André will be ready in the lecture room from 8:00 a.m. and also during the last half hour of the lunch break. A PC and a Mac laptop will be available. You may also connect your laptop to the projector via a serial interface. If you have a video presentation, please inform Caroline or André well ahead of time.

Information for poster presentations

Poster sessions will take place in The Distillery (H). Posters should be mounted as soon as possible after arrival. There is no particular order or numbering of the posters. Poster pins are available in the poster room. All posters will be displayed throughout the workshop. Presenters should be available at their posters during poster sessions.

WiFi

There is free WiFi access at Sandbjerg Manor. Please note that there is limited WiFi access in the basement of the Manor House.

Banks

Banks in Denmark are generally open from 09:30 to 16:00 on weekdays with late hours until 18:00 on Thursdays (closed Saturdays and Sundays). Most banks have ATMs outside their building. There are bank ATMs at Copenhagen and Billund Airports and in Sønderborg. There is no ATM at Sandbjerg Manor.

Currency

The currency in Denmark is the Danish Krone (DKK). One Krone is divided into 100 Øre. Rates on August 10, 2017: 100.00 USD = 629.64 DKK. 100.00 EUR = 743.86 DKK.

Credit Cards

In most places VISA, Eurocard and Mastercard are accepted. If you have American Express we recommend that you withdraw cash before arrival as only a few accept this credit card. E.g. the Danish Railway systems and most restaurants do not accept it.

Emergency phone number

(+45 only when calling from outside Denmark)

Police, fire, ambulance: 112

Falck rescue services: (+45) 70 10 20 30

Police: 114

Doctor, outside normal working hours: (+45) 70 11 07 07

Emergency room at Sønderborg Hospital: (+45) 7418 2500 Sydvang 1, 6400 Sønderborg. To get treatment you need referral from a Doctor (+45) 70 11 07 07

Dentist, outside normal working hours: (+45) 6541 4551/99 44 08 09

Pharmacy, outside normal hours: (+45) 7442 3502 (Jernbane Apoteket: Jernbanegade 10, 6400 Sønderborg) or 7442 2000 (Løve Apoteket, Grundtvigs Alle 179, 6400 Sønderborg)

Electricity

Denmark, like most other European countries, has 220 Volt AC, 50 Hz current and uses two-pin continental plugs. If you visit from the UK or Ireland, you will need an adaptor for electric appliances, whereas North Americans need a transformer in order to use their 110/125V appliances. [Plug and socket types.](#)

Language

The mother tongue in Denmark is Danish, which is closely related to Swedish and Norwegian. In general, Danes speak English very well, and some also speak German and/or French.

Time Zone

Denmark follows Central European Time (CET), which is one hour ahead of Greenwich Mean Time (GMT) and six hours ahead of Eastern Standard Time (EST).

Tipping

Tipping is appreciated, but not expected, and you should only do so if you feel you are getting exceptionally good service. If you do so 10 percent of the bill is sufficient. Tipping is included in taxi fares.

Drinking water

In Denmark you can drink the water straight from the tap.

Beverages, tobacco and kiosk items

Beverages, tobacco and kiosk items can be purchased at the Sandbjerg Manor. Purchase of beverages is self service and can be paid directly upon purchase (cash only) or upon check out (credit card or Danish Kroner cash). This means participants should register every purchase on a list and note whether they have paid up front or wish to bill it. Beverages are in a fridge in Magasinet (B).

Sandbjerg only accepts Danish Kroner and credit cards.

Printing

Laser printing is available in the lobby at Sandbjerg Manor for a minor fee (DKK 2 per page).

Conference website

<http://conferences.au.dk/geomicrobiology2017/>

Sponsors

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[Aarhus University Research Foundation](#): The foundation's objective is to support scientific research at Aarhus University. The foundation awards grants to concrete research projects and larger multi-year projects and initiatives that strengthen research at Aarhus University

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The [Danish National Research Foundation](#) (DNRF). The DNRF is an independent organization with the objective to promote and stimulate basic research. The Center of Excellence program is the main funding objective.



The [Center for Geomicrobiology](#) (CfG). The CfG at Aarhus University is co-financed by the DNRF and the ERC. The Center is the main organizer of the workshop and is also an important sponsor.



Welcome to Sandbjerg Manor

The history of Sandbjerg Castle can be traced back to the 16th century. In 1564, the estate became the property of Duke Hans the Younger (1545–1622) as his brother King Frederik II allotted one third of the royal share of the duchies to him - an area which included the islands of Ærø and Als and the Sundeved peninsula in the duchy of Schleswig.

The Duke left his mark on the landscape. Towards Alssund the Duke commissioned a dike built, which still exists today. With the establishment of the dike, a cove of the sound was converted into a lake, Møllesøen (the Mill Pond). The remains of his water mill can still be seen. The mill was operational until it burnt down in 1916.



The Sandbjerg Estate is situated in a scenic area directly to Alssund (Als Sound) about 7 km northwest of Sønderborg

On the death of Duke Hans, Sandbjerg was inherited by the Sønderborg line of his family. After a bankruptcy in 1667, the estate returned for a short while to the crown before it in 1673 was sold to Prefect (later Chancellor) Conrad Reventlow of Haderslev (1644–1708), with permission to establish a province out of Sandbjerg and his other possessions in Sundeved: the county of Reventlow-Sandbjerg.

Duke Hans' Sandbjerg was situated on the site of the present-day Sandbjerg Farm, on the other side of the Mill Pond.

In 1788, Conrad Georg Reventlow built a manor house on the headland facing Alssund. The builder was Christian August Bohlsmann from Sønderborg who also participated in the construction of Augustenborg Castle (and most likely also Gråsten Castle). The Mansion together with the Tenant's Farmer House, which was erected in 1783, the other utility buildings and the park constitute a total complex between Møllesøen and Alssund – the present-day Sandbjerg Estate.

Sandbjerg remained in the hands of the Reventlow family right up until 1930. For a period in the 1850s, the Mansion was the honorary residence of General Frederik Bülow, victor of the Battle of Fredericia in 1849. He died at Sandbjerg in 1858 and lies buried at Dybbøl Cemetery.

During the war of 1864, the Germans bivouacked in Storskoven wood – the Danish army was on the other side of Alssund. On the morning of 28 June, the great clock at Sandbjerg gave the signal at 2 o'clock for the invasion. Conservation boat runways and canon emplacements can still be seen along the coast, and there are also remains of column markers in the oldest trees.

Sandbjerg Manor today

After the death of the last Reventlow in 1929, Sandbjerg was sold to the Copenhagen barrister Knud Dahl and his wife, Ellen Dahl, née Dinesen - sister to the Danish author Karen Blixen. In 1954 she donated the estate to Aarhus University and after her death in 1959, the university took over the full rights of the entire Sandbjerg Estate.



The old Manor House



The Manor House today

Sønderborg and Sønderborg Castle

Sønderborg (Sonderborg) is an old town with a population of 27,000. It is located in Southern Denmark close to the German border, and it has been at the center of many important events in Denmark's history.

Sønderborg was founded in 1256 and is beautifully situated at the coast on both sides of Alsund (Als Sound) linked together with two bridges. The town grew up around Sønderborg Castle, which was founded during the 1200's and became one of the kingdom's strongest castles. Sønderborg is among other things well-known for the castle and for the recurring "Tilting-at-the-Ring".



Sønderborg Castle



Historical Tilting at the Ring at Sønderborg Castle

Sønderborg Castle

Sønderborg Castle was founded by the Danish king Valdemar the Great in 1158 as a fortified tower to provide protection against attacks by the Wends and it became one of the kingdom's strongest castles.

Around 1350, the castle was expanded significantly with an addition of the Blue Tower and with the construction of massive outer walls. In 1490, the fortress became the property of the Crown and both King Hans (1455-1513) and his son Christian II (1481-1559) made extensions to Sønderborg Castle. In the years from 1532-49 the deposed King Christian II (reigned from 1513 until 1523) was held captive in the castle.

In 1549 -71 King Christian III and Queen Dorothea transformed the castle and converted it into a four-wing Renaissance complex. After Christian III's death in 1559, Hercules von Oberberg built the castle chapel in 1568 -70 for the Queen dowager, - Queen Dorothea's Chapel – today one of Europe's few preserved princely chapels from the Reformation. The chapel houses Denmark's oldest Renaissance interior.

After Dorothea's death the castle became the residence of the Dukes of Sønderborg. After the Swedish wars 1657-1660, the Duchy of Sønderborg returned to the crown. In 1718-26, Frederik IV had the castle simplified in baroque style, - it is said to be due to disrepair. Renaissance gates, towers and spikes were removed, new roofs and windows were installed in straight, even rows, and Sønderborg Castle got its present day appearance. In 1764 the castle passed into the hands of the local dukes again and was rented out as a warehouse. After the Second Schleswig War in 1864, the province and the castle became Prussian property and served as army barracks until the reunification in 1920 where the castle was bought by the Danish state and thoroughly restored from 1964-73. Today it houses a museum of Southern Jutland history.

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