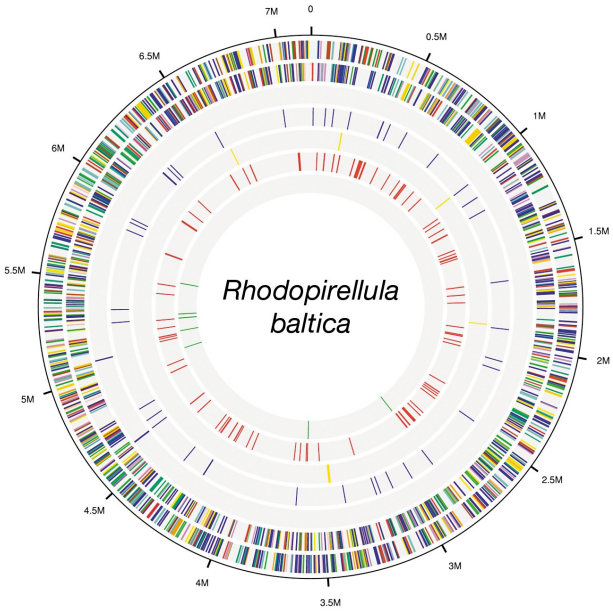
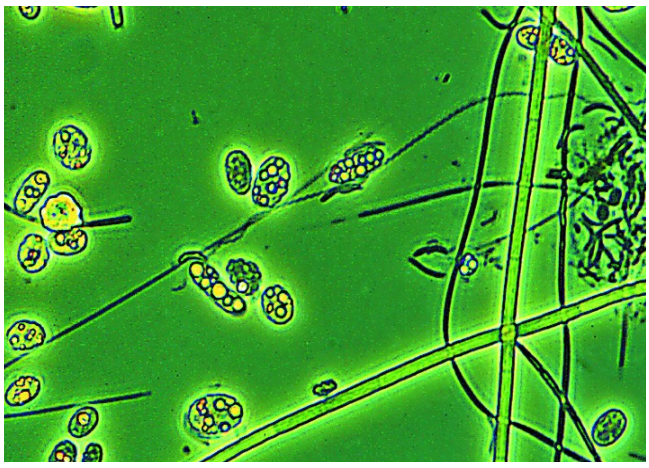
NoE Marine Genomics Europe - Exploratory Workshop: Marine Genomics Meets Marine Diversity

Max Planck Institute for Marine Microbiology
June 7 – 9, 2006





Welcome to the Workshop "Marine Genomics Meets Marine Diversity"

First of all we would like to welcome you to the Max Planck Institute for Marine Microbiology in Bremen and wish you a pleasant stay and many fruitful discussions.

The ecosystem-centred exploration of marine biodiversity has already a long tradition. Over the past two decades an unexpectedly large diversity of marine microbes (defined as microscopic pro- and eukaryotes) has been disclosed by molecular biological techniques, often based on comparative sequence analysis of single genes, such as the small subunit rRNA. Since few years high-throughput sequencing technologies are adding a new genomic perspective of marine microbes. Already the first preliminary insights into these blueprints of life revealed unexpected findings which provide hints on niche adaptations and key functions of the organisms in the global cycling of matters.

It is now time to **bridge the gap between marine diversity research and marine genomics**. An integration of (i) data on **diversity and spatio-temporal abundance** of microorganisms with (ii) **genomic data** and (iii) further **oceanographic information** on the chemistry, physics, geology and biology of the habitat can be readily achieved based on geographic location and sampling time. Whereas it is the task of computer scientists to provide searchable integrated datasets, it is up to the ecologists to raise and answer questions that have been out of reach so far, e.g.: "How does the microbial community change from a coastal to an open ocean site, how over different oceanic provinces?", "What is the seasonal variability and the influence of change in water temperature and nutrient availability?" "How does the interface between biosphere and geosphere – the famous biological pump removing carbon from the atmosphere - work on the molecular level?"

Large **geographically integrated datasets** will undoubtedly change the way marine biology is done today and it's now time to define the questions, expectations and technology that needs to be addressed. The meeting will bring together experts in the field of **Marine Diversity, Genomics, Ecology, Technology and Bioinformatics** to explore common interests and steps that have to be done.

Again a warm welcome from the organisation committee

Frank Oliver Glöckner (Head of Microbial Genomics Group),
Rudolf Amann (Department of Molecular Ecology)
Johanna Wesnigk and Rebecca Ludwig (Organisation team, EMPA-Bremen)

The organising committee

Contact information:

Frank Oliver Glöckner

Professor of Bioinformatics

International University Bremen and MPI for Marine Microbiology

Celsiusstrasse 1

28359 Bremen

Phone: +49 421 2028 970

Fax: +49 421 2028 580

fog@mpi-bremen.de

www.microbial-genomics.de

www.ribocon.com

Frank Oliver Glöckner

Max Planck Institute for Marine Microbiology and International University Bremen

Frank Oliver Glöckner's research focus is to investigate the genetic potential of marine bacteria by whole genome analysis and functional genomics to reveal the mechanisms coded in the genome enabling them to adapt to changing environmental conditions. He studied biology at the Technical University Munich, where he received his Diploma in Biology in 1995 with molecular microbiology as his main subject. He carried on research as a Ph. D. student in Munich and the Max Planck Institute for Marine Microbiology in Bremen and received his doctorate in 1998. From 1999-2000 he was a research scientist in the Dept. of Molecular Ecology at the MPI Bremen. In 2001 he got the head of the independent Microbial Genomics Group and joined 2004 the International University Bremen as an associate professor for Bioinformatics. He is member of the technological platform of the "International Census of Marine Life" initiative and bioinformatic representative of the microbial node within the Network of Excellence "Marine Genomics Europe". Since 2005 he is one of the founders of the company Ribocon, a spin-off of MPI Bremen focussed on knowledge transfer and product development in the field of molecular microbial diagnostics.

The organising committee

EMPA is a European project management company for environmental research projects. Its four service aspects are (i) giving strategic advice, (ii) writing proposals, (iii) performing project management, and (iv) training customer`s staff in project skills. EMPA offers a full service (one-stop-shop) with a focus on European cooperation within marine research. This includes the organisation of workshops and conferences, mainly in a project context. We strongly believe that coordinating an EC-funded project can be fun as well as successful, leading to worthwhile scientific and other results. EMPA offers ample experience in increasing the client's visibility, Europe-wide contacts and chances of further funding.

Dr. Johanna Wesnigk, the founder of EMPA, has a background in marine biology and degradation of pollutants. Since 1987 she has worked on promoting environmental, marine, and maritime research as scientist, coordinator and project manager. From 2002 – 2004 she has been the EU liaison officer and coordinator for European proposals and projects at the MPI Bremen. In 2005 she started her agency, the Environmental & Marine Project Management Agency EMPA.

Dr. Rebecca Ludwig, EMPA's part-time project assistant, has studied at Osnabrück university. During a stay in Eilat in 1997, she discovered her interest in cyanobacterial mats. She developed proposal writing skills by successfully applying for three stipends. These enabled here to work with prestigious research groups at the University of Warwick, UK, and Rutgers University, USA. In 2004 she finished her Ph. D. thesis at the Max-Planck-Institute for Marine Microbiology in Bremen. She works for EMPA as a freelancer since July 2005 to combine her marine research background and her strong organisational skills with an interest in personnel and project management.

Agenda

NoE Marine Genomics Europe Exploratory Workshop:

Marine Genomics Meets Marine Diversity

Wednesday, 07.06.2006

20:00 Speakers Dinner Restaurant Palmyra

Am Lehester Deich 81, 28357 Bremen, Tel.: 0421 / 566 388 0
Tram station „Am Lehester Deich" with Tram line 4 to Borgfeld
Web: http://www.restaurant-palmyra.de/index.html

Thursday, 08.06.2006

8:45 Short Welcome and Introduction by Host Frank Oliver Glöckner

9:00 – 11:00 Session 1: Diversity Chair: Ramon Rosselló-Mora

each presentation 30 min. including discussion

Carlos Pedrós-Alió (CSIC, Institut de Ciències del Mar, Barcelona, Spain)
Marine microbial diversity: is it knowable?

Ramon Rosselló-Mora (Institut Mediterrani d'Estudis Avançats, Esporles, Spain)
The impact of genomics in prokaryotic taxonomy

Wiebe Kooistra (Stazione Zoologica Anton Dohrn, Naples, Italy)
The success of the diatoms in the modern marine plankton

Bernhard Fuchs (Max Planck Institute for Marine Microbiology, Bremen, Germany)
Bacterioplankton composition in the namibian upwelling system as revealed by 16S rRNA cloning and fluorescence in situ hybridisation (FISH)

11:00– 11:15 Coffee Break

11:15 – 13:30 Session 2: Genomics Chair: David Scanlan

each presentation 20 min. including discussion

David Scanlan (Dept. of Biological Sciences, University of Warwick, UK)
Niche partitioning of picocyanobacteria - an ecological and genomic perspective

Klaus Valentin (Alfred Wegener Institute for Polar & Marine Research, BHV, Germany)
Algal genomics - present and future trends - an overview about finished, ongoing and planned genome projects and their most important outcomes

Uwe John (Alfred Wegener Institute for Polar & Marine Research, BHV, Germany)
Functional genomics meets harmful algal bloom research: insights into toxin synthesis and growth control

Gurvan Michel (Station Biologique de Roscoff, France)
Structural and functional census of the polysaccharidases from *Rhodopirellula baltica*: a key polymer degrader in marine environment

Hanno Teeling (Max Planck Institute for Marine Microbiology, Bremen, Germany)
Novel aspects of marine ecological metagenomics – clustering of metagenomic fragments by intrinsic DNA signatures

Oded Béjà (Technion-Israel Institute of Technology, Haifa, Israel)
The quest for viral 'photosynthesis' using both metagenomics and environmental genomics

13:30– 15:00 Lunch Break (Snacks are served at the MPI)

15:00 – 17:00 Session 3: Ecology Chair: Ian Joint

each presentation 30 min. including discussion

Klaus Jürgens (Baltic Sea Research Institute (IOW), Warnemünde, Germany)
Diversity of microbial communities and their biogeochemical functions in marine pelagic redoxclines

Ian Joint (Plymouth Marine Laboratory, UK)
Microbial metagenomics and marine biogeochemical cycles

Jakob Pernthaler (Limnological Station, University Zurich, Switzerland)
Diversity and seasonal dynamics of Cytophaga-like bacteria in coastal North Sea waters

Gerhard J. Herndl (Royal Netherlands Institute for Sea Research, NIOZ, Netherlands)
Bacterial and archaeal diversity and function in the major deep water masses of the North Atlantic

Agenda

17:00 – 17:15 Coffee Break

17:15 – 18:15 Bridging talk (30 min.) and discussion

Feng Chen (Livermore Biolaboratory, Walnut Creek, USA)
454 sequencing technology and its application in microbial and metagenomic community sequencing at US DOE Joint Genome Institute

18:15 Dinner at the MPI

Friday 09.06.2006

8:30 – 10:30 Session 4: Technology Chair: Jean Weissenbach

each presentation 30 min. including discussion

Jean Weissenbach (Genoscope, Evry, France)
A metagenomic approach of wastewater processing

Alexander Loy (Universität Wien, Austria)
Functional probing of microbial communities with rRNA-targeted oligonucleotide microarrays

Thomas Schweder (EMA-Universität Greifswald, Germany)
Proteome analyses of marine bacteria

Phillip Neal (Marine Biology Laboratory (MBL), Woods Hole, USA)
Estimating marine microbial diversity: lots of data, lots of problems, a few solutions

10:30– 10:45 Coffee Break

10:45 – 12:30 Session 5: Bioinformatics Chair: Ed Vanden Berghe

each presentation 20 min. including discussion

Edward Vanden Berghe (VLIZ, Oostende, Flanders Marine Institute, Belgium)
Marine biodiversity databases – an overview

Francisco Rodriguez-Valera (Universidad Miguel Hernández, Alicante, Spain)
Biogeography of marine bacteria, genes, spacers and genomes

Andrea de Bono (*UNEP/DEWA/GRID-Europe, Châtelaine*, Switzerland)
GRID: The Global Resource Information Database

Anton Güntsch (Botanic Garden and Botanical Museum, FU Berlin, Germany)
Integration of heterogeneous biodiversity data sources using BioCASE and ABCD

Thierry Lombardot (Max Planck Institute for Marine Microbiology, Bremen, Germany)
The Genomes Mapserver: an integrative tool for ecological genomics and metagenomics

12:45 – approx. 14:00 Final Discussion **(Room 4021, Snacks will be served)**

Speakers

Carlos Pedrós-Alió

Institut de Ciències del Mar de Barcelona, CMIMA, CSIC

Contact information:

Carlos Pedrós-Alió

Research Professor

Institut de Ciències del Mar, CMIMA, CSIC

Ps Marítim de la Barceloneta 37-49

08003 Barcelona, Spain

Phone: +34932309597

Fax: +34932309555

cpedros@icm.csic.es

Carlos Pedrós Alió' s research interests include understanding the organisation of planktonic microbial communities from two different perspectives: trophic mode and genetic diversity. Widely different systems are used to determine the range of possible in situ situations: oligotrophic springs, solar salterns, karstic lakes with anaerobic hypolimnia or oligotrophic oceanic waters. Molecular techniques are used to determine the genetic diversity of pico- and nanoplankton assemblages. Current work focuses on gene expression in the field and comparative genomics of marine bacteria.

He studied Biological Sciences at the Universitat Autònoma de Barcelona (UAB), where he received his Licenciado (≈ Bachelor) in 1975. After predoctoral work in the UK and Portugal he did his dissertation work with a Fulbright-Hays grant and a Research assistantship at the Department of Bacteriology, University of Wisconsin-Madison, USA. He received a Ph.D. in Bacteriology in 1981 and a Doctor of Biological Science from UAB in 1982. From 1981 he worked as Postdoctoral fellow at the Department of Microbiology, UAB and became assistant professor in 1985. Since 1989 he works in the Institut de Ciències del Mar, CSIC (National Council for Scientific Research), Barcelona, where he was Head of the Department of Marine Biology and Oceanography from 1995 to 1997. In 1999 he was awarded the City of Barcelona Prize for scientific research.

Marine microbial diversity: is it knowable?

Carlos Pedrós-Alió

Estimates of the order of magnitude for the total number of microbial species on Earth range from 10^3 to 10^9. Despite global dispersal of microorganisms, the number is probably rather large. The total biodiversity of an ecosystem is composed of two elements. First, a set of abundant taxa that carry out most ecosystem functions, grow actively and suffer intense losses through predation and viral lysis. These taxa are retrievable with molecular techniques, but difficult to grow in culture. And second, there is a seed-bank of many rare taxa. These taxa are not growing or grow very slowly, do not experience viral lysis and predation is reduced. These taxa are seldom retrieved by molecular techniques, but many can be grown in culture, thus explaining why "everything is everywhere".

Speakers

Ramon Rosselló-Mora

Institut Mediterrani d'Estudis Avançats, CSIC-UIB

Contact information:

Ramon Rosselló-Mora

Tenured Scientist CSIC

Institut Mediterrani d'Estudis Avançats; CSIC-UIB

C/ Miquel Marqués 21

07190 Esporles

Illes Balears, Spain

Phone: +34971611826

Fax: +34971611761

rossello-mora@uib.es

The main research focuses of Ramon Rosselló-Mora are microbial taxonomy and marine microbial diversity. He specialized in theoretical aspects of the concept of prokaryotic species as well as in practical aspects of molecular microbial taxonomy. In addition, he has been researching on diversity and autoecology of extreme halophilic Bacteria, and marine anaerobic benthic prokaryotes. He studied Biology and defended his PhD thesis in 1992 at the University of the Balearic Islands, Mallorca. His postdoctoral tracks had been performed at the Technical University Munich under the supervision of Prof. Schleifer (1993-1995); the University of the Balearic Islands under the supervision of Prof. Lalucat (1995-1997); and at the Max Planck Institute for Marine Microbiology in Bremen under the supervision of Prof. Amann (1997-1999). In 2000 he became Professor at the University of the Balearic Islands, and in 2001 he started his current position as Tenured Scientist of CSIC at the IMEDEA in Mallorca. He is now group leader of a small team of PhD students and postdoctoral fellows. Finally since early 2006 he is Executive Editor of the journal Systematic and Applied Microbiology (http://www.elsevier.de/syapm).

The impact of genomics in prokaryotic taxonomy

Ramon Rosselló-Mora

Taxonomy may be regarded as one of the most boring subjects in microbial research. However, most non taxonomists directly or indirectly exploit taxonomy by using either the established nomenclature to identify their study organisms, or by the use of the created categories (e.g. species or family) to describe the diversity. Taxonomy is generally made by taxonomists, who try to develop a classification system and rules that are pragmatic and operational for the whole scientific community. However, the system and the conceptual basis of prokaryotic taxonomy are heavily criticised by ecologists and evolutionary microbiologists because what has been established does not fit their needs. The pitfalls of the classification system are mainly derived from the vast diversity of the prokaryotic world that impedes the finding of universal objective criteria. Despite of it, there is a common agreement that it has been achieved the best that was achievable in regard to the hitherto technological developments.

Prokaryotic taxonomy, with less than 200 years of existence, has been improved by the exploration of new methodologies. The first big impact was made by the discovery of DNA and the genomes. 30 years later, the possibility to reconstruct phylogenies based on molecular clocks, and esp. those of 16S rRNA gene sequence constituted the second breakthrough in prokaryotic taxonomy, and the classification system is now strongly influenced by such reconstructions. In both cases long debates followed before those conceptual bases were accepted by the community.

Now, 30 years after the second breakthrough in taxonomy, genomics appear to be the next step forward into the improvement of the classification system. Based on the hitherto accumulated information, first suggestions appeared and claim to be of better accuracy for constructing the classification system. Parameters as Average Nucleotide Identity, or Multilocus Sequence Analysis are suggested to substitute whole genome hybridisations. In addition, whole genome phylogenies, or multigene concatenates are suggested to substitute rRNA phylogenies. Here it will be argued that all such improvements may be of important help in establishing a stable system. But taxonomy, which is set on a pragmatic basis, may still be away from an absolute benefit from genomics. Much has to be discussed in the following years before understanding the real impact of genomics into prokaryotic taxonomy. And a 3rd 30-year discussion lapse is possibly approaching.

Speakers

Wiebe H.C.F. Kooistra

Stazione Zoologica Anton Dohrn

Contact information:

Wiebe Kooistra
Staff researcher
Stazione Zoologica Anton Dohrn
Villa Comunale
I-80121 Naples, Italy
Phone: +390815833271
Fax: +390817641355
kooistra@szn.it
www.szn.it

The research of Wiebe Kooistra focuses on the evolution of form, ecological strategies, phylogeographic patterns and life histories in algae, in particular diatoms. Thereto he infers molecular phylogenies of the groups of interest and compares these trees with whatever else is known from these organisms (fossil record, ecology, morphology). There are two major research lines; one focuses on the apparent success of the diatoms in the modern plankton and on what factors are responsible for their apparent success, the second focuses on speciation in diatoms. Wiebe Kooistra studied marine biology at the Rijksuniversiteit Groningen, The Netherlands and received his doctorate in 1993. From 1993 to 1996 he was postdoctoral researcher at the AWI in Bremerhaven and from 1996 to 2000 at the Smithsonian Tropical Research Institute in Panama. Since 2000 he is staff researcher in marine botany at the Stazione Zoologica Anton Dohrn. Dr. Kooistra is active in several European projects and leads an RMP in the NoE MarBEF.

The success of the diatoms in the modern marine plankton

Wiebe Kooistra

Diatoms constitute the most diverse eukaryote microalgal group in the modern marine plankton. Their hallmark is the compound silica cell wall, called frustule, which covers the cell completely, while at the same time permitting growth and mitotic division. First, I briefly review the evolutionary history and ecological diversity of the diatoms. Then, I will explain the traits that have given the diatoms a cutting edge over plankton groups such as silicoflagellates, haptophytes (coccolithophorids), dinoflagellates, and the green and red marine phytoplankton. Diatoms have a superior photo-system, the possibility to take up organic material, the ability to form resting stages, low quotas of trace elements needed, possibly a C-4 mode of carbon fixation, a large central vacuole for nutrient storage, the silica encasing, advanced biochemical defences, and last but definitely not least, high ecological diversity. During the course of their evolution several originally benthic lineages adopted a planktonic lifestyle secondarily, over and over again, making use of new designs. In the last part, I show what genome projects (Thalassiosira, Phaeodactylum) and EST-library projects teach us about diatom evolution.

Speakers

Bernhard Fuchs

Max Planck Institute for Marine Microbiology

Contact information:

Bernhard Fuchs

Senior Group Leader

MPI for Marine Microbiology

Celsiusstrasse 1

28359 Bremen

Phone: +49 421 2028 935

Fax: +49 421 2028 790

bfuchs@mpi-bremen.de

Bernhard Fuchs' research is focused on the development and application of new methods to explore the diversity and function of marine bacterioplankton.

Bernhard Fuchs studied biology at the Technical University of Munich, where he received his Diplom in the year 1998 with microbiology as his main subject. He started his Ph.D. work in Munich which he continued and finished at the Max Planck Institute for Marine Microbiology in Bremen in 1998. From 1999-2002 he worked as a research scientist (PostDoc) in the Dept. of Molecular Ecology at MPI Bremen. Since 2003 he is a senior group leader in the Dept. of Molecular Ecology. In 2005 he was appointed as a lecturer of the faculty of the International Max Planck Research School MarMic.

Bacterioplankton composition in the Namibian Upwelling system as revealed by 16S rRNA cloning and fluorescence in situ hybridisation (FISH)

Bernhard M. Fuchs, D. Wöbken, T. Stührmann, Y. Haile, M. Kuypers, R. Amann

Few studies have been conducted to determine the composition of bacterioplankton in upwelling waters so far. Here we present first results of the diversity and composition of the heterotrophic bacterioplankton in the water column of the Namibian Shelf. First, from representative water depths 16S ribosomal RNA gene clone libraries were constructed and more than 350 clones were sequenced. The observed diversity was high and generally similar groups as compared to an open ocean environment were found. However in suboxic and anoxic water layers also other groups like relatives to sulphur-oxidising bacteria and groups involved in the nitrogen cycle (Nitrospina, Anammox) have been found. The bacterioplankton composition was determined by specific staining of bacterial and archaeal groups with fluorescence in situ hybridisation. The composition of the bacterioplankton changed significantly along a transect from the coast to the shelf break. At stations near the coast those bacterioplankton groups were dominating, which are characteristic for eutrophic conditions like members of the Cytophagales. Further to the open ocean the alpha-Proteobacteria were dominating. The gamma- Proteobacteria showed a maximum at stations in the middle of the shelf. Detailed results with more specific probes will be reported. A correlation analysis of the occurrence of specific organisms to biogeochemical data will be presented.

David Scanlan

Dept. of Biological Sciences, University of Warwick

Contact information:

Dave Scanlan

Reader in Microbiology

Dept. of Biological Sciences, University of Warwick

Gibbet Hill Road, Coventry CV4 7AL, UK

Phone: +44 24 76 528363

Fax: +44 24 76 523701

d.j.scanlan@warwick.ac.uk

http://www2.warwick.ac.uk/fac/sci/bio/research/micro/

http://www2.warwick.ac.uk/fac/sci/bio/research/margenes/

The principal aim of Dave Scanlan's group is to understand the structure and function of picocyanobacterial assemblages in the open ocean and identify the factors that have led to the ecological success of these organisms using a synthesis of expertise in microbial molecular ecology, photosynthetic/ nutrient physiology & biochemistry, and genomics.

Areas of particular interest are nutrient acquisition, regulatory and sensing mechanisms, especially with respect to bacterial niche adaptation, and factors controlling marine photo-synthesis. Most recently his work with the genera *Prochlorococcus* and *Synechococcus* has led to a much more detailed understanding of why these organisms dominate the world's oceans. This has included, in collaboration with other European research laboratories, the formal description and complete genome sequencing of several marine picocyanobacterial isolates and paves the way for further characterisation of the physiological processes that underlie the ecological success of these organisms. The research of his group is currently funded by NERC, BBSRC and the EU.

Brief Academic profile: 2004 - date Reader in Microbiology, University of Warwick; 2003 - 2004 Lecturer in Microbiology, University of Warwick; 1995 – 2003: Royal Society University Research Fellow. The molecular ecology of photosynthesis in the oceans.

Niche partitioning of picocyanobacteria - an ecological and genomic perspective

David Scanlan

Marine cyanobacteria are the most abundant photosynthetic organisms on Earth with only two genera numerically dominating most oceanic waters, *Prochlorococcus* and *Synechococcus*. Both genera are genetically diverse e.g. the marine *Synechococcus* lineage contains at least ten genetically distinct clades and includes isolates with a wide range of pigmentation (Fuller *et al*., 2003, *Appl. Environ. Microbiol*. 60: 2430-2443).

Molecular ecological studies indicate that the phylogenetic microdiversity seen within *Synechococcus* and *Prochlorococcus* correlates with the partitioning of genotypes into specific spatial environments. With the idea that it is the environmental gradients of light and nutrients that dictate this niche partitioning we have employed mutagenesis and transcriptomics to begin to define the molecular basis for such niche adaptation mechanisms focusing particularly on nutrient (P) acquisition and cell signaling networks.

Comparative genomics highlight differences in P sensing, storage and acquisition strategies, which, to an extent, have been verified and elaborated by culture studies with two model *Synechococcus* spp., reflecting mesotrophic (WH 7803) versus oligotrophic (WH 8102) ecotypes. Targeted gene deletions of regulatory components demonstrate a role for both PhoB and PtrA (a regulator of previously unknown function) in regulation of the P acquisition machinery in WH 8102. These regulatory genes are however, missing or non-functional in some sequenced picocyanobacterial genomes, suggesting they are not required under the set of environmental conditions that such genotypes proliferate, reiterating the niche adaptation idea.

Klaus Valentin

Alfred Wegener Institute for Polar and Marine Research

Contact information:

Klaus Valentin
Senior Researcher
Alfred Wegener Institute
Am Handelshafen 12
27570 Bremerhaven, Germany
Phone: +49 173 3241067
Fax: +49 471 4831 1425
kvalentin@awi-bremerhaven.de

Klaus Valentin's research focus is to investigate the genetic potential of marine algae by whole genome analysis and functional genomics to reveal the mechanisms coded in the genome enabling them to adapt to changing environmental conditions. He studied biology at the Justus Liebig University Giessen, where he received his Diploma in Biology in 1985. He did research on plastid evolution as a Ph. D. student in Giessen and received his doctorate in 1990. From 1991- 1992 he was a research scientist in the Dept. of Botany of the University of Washington, Seattle. Between 1992 and 1999 he established a group working on the evolution of biochemical pathways of the plastid. In 2000 he joined the Alfred Wegener Institute (AWI) to work on the molecular diversity of the marine Picoplankton. Since 2003 he is a Senior researcher at the AWI with a main focus on genomics. He is member of the technological platform and the algal node committee of the Network of Excellence "Marine Genomics Europe". Since 1988 he is on the editorial board of the European Journal of Phycology and since 2004 he is editor for molecular biology of the same journal.

Algal Genomics - present and future trends - an overview about finished, ongoing and planned genome projects and their most important outcomes

Klaus Valentin

Genomics has reached phycology through the publication of the first two algal genomes from a diatom and a primitive red algae. However, the term "alga" only vaguely describes the diversity seen in this taxon. Looking at the tree of life recently published by Sandra Baldauf it appears that algae can be found in 5 out of 8 major eukaryote groups. Additionally there are the haptophytes and cryptophytes which do not group with any of the 8 aforesaid. So more than half of the major eukaryote groups contain algae. The term alga is even more confused by the fact that algae may contain primary, secondary, or even tertiary plastids. From a developmental biology point of view it is also important, that of the five lineages producing complex multicellular organisms three are algae: red algae, brown algae, and green algae (later giving rise to land plants), next to animals and fungi.

Consequently, there are ongoing efforts to sequence more algal genomes. Genome projects are next to completion, or under way, for a number of algal species, including *Ostreococcus tauri* and *Chlamydomonas reinhardii* (green algae), *Galdieria sulphuraria* (primitive red alga), *Phaeodactylum tricornutum* and *Pseudonitzschia multiseries* (Diatoms), *Ectocarpus siliculosus* (brown alga), and *Emiliania huxleyi* (Haptophye). For other species there are projects submitted or seriously planned: *Chondrus crispus* (multicellular red alga), *Fragilariopsis cylindrus* (Polar diatom), 5 *Ostreococcus* species, *Cyanophora paradoxa* (Glaucophyte), and *Cryptomonas* (Cryptophyte). Within the next few years we therefore can expect to see huge amounts of data on algal genomes allowing conclusions on the evolution of eukaryotic genomes, the evolutions of eukaryotic photosynthesis and the development of complex multicellularity.

A challenging task will be to analyse and understand these data. New bioinformatic tools for phylogenomic analyses will be necessary and new molecular tools to elucidate gene functions.

Uwe John

Alfred Wegener Institute for Polar and Marine Research

Contact information:

Uwe John

Research Scientist

Alfred Wegener Institute for Polar and Marine Research

Am Handelshafen 12

27570 Bremerhaven

Phone: +494714831-1841

Fax: +49 471 4831-1425

ujohn@awi-bremerhaven.de

Web: http://www.awi-bremerhaven.de/People/show?ujohn

Uwe John is a research scientist at the Alfred Wegener Institute (AWI) for Polar and Marine Research, Bremerhaven, Germany. His research emphasis is on the molecular regulation of toxin synthesis and growth regulation of marine protists, combining ecological and physiological experiments with functional genomics to reveal the mechanisms behind the phenomenon of algal bloom formation. He studied biology at the University of Hannover, where he received his Diploma in Biology in 1997, and worked on post-transcriptional gene regulation as his thesis subject. Subsequently, he moved to the AWI and finished his PhD dissertation in 2002 on the molecular biology of two toxigenic species within the algal molecular genetics group. From 2002-2005, he was a post-doctoral scientist in the Biological Oceanography Section; in addition, since 2003 he has been instrumental in establishing a programme on the molecular aspects of chemical ecology within the new Section Ecological Chemistry directed by Prof. Cembella. In 2005, he was appointed as a research scientist within this section with leading responsibilities for molecular ecology. Uwe John is involved as a consortium member and research scientist in several EU-projects, including EUKETIDES, Marine Genomics, MARBEF (AWI molecular biology representative), and ESTTAL, for which he is also acting as scientific manager.

Functional genomics meets harmful algal bloom research: insights into toxin synthesis and growth control

Uwe John

In marine ecosystems the interactions among protists and prokaryotes (eubacteria and cyanobacteria) and effects on zooplankton play a dominant role in food web ecology and trophodynamics. Among protists and cyanobacteria, species considered to be "harmful algae" can cause harm by forming aggregations of cells known as harmful algal blooms (HABs). Certain harmful algae can cause negative ecological effects even at relatively low cell concentrations by production of potent phycotoxins, thereby killing or incapacitating micro-grazers and diverse organisms such as fish, sea-birds and marine mammals by vectorial transfer through marine food webs. Although the ecological role of phycotoxins is poorly understood, the obvious ability of toxic protists to survive, thrive and occasionally to dominate the plankton via the formation of blooms, supports the hypothesis that these bioactive secondary metabolites have a distinct function in the ecological success and evolution of the species.

A key component for defining the factors responsible for bloom development is the biochemical and molecular regulation of the toxic and other allelochemical interactions among grazers, prey, and competitors. Knowledge of the genes and enzymes involved in phycotoxin production and their metabolic regulation within the cell, and molecular regulation of other secondary metabolites that may function as allelochemicals, is very limited. Functional genomic and proteomic studies on regulation of phycotoxins/allelochemicals are crucial for our understanding of the molecular ecology of toxigenic microalgae. Studies on genetic regulation and intrinsic control mechanisms of growth and cell proliferation are also required. During the last few years, rapid advances in molecular technologies are allowing us to begin to address this lack of knowledge. Whole genome sequencing and limited genomic approaches, such as expressed sequence tags (ESTs), complemented with the development of DNA-microarrays, are powerful tools to address questions in functional genomics. Application of a spectrum of molecular methods has begun to yield valuable insights into the genetic regulation of processes such as growth and toxin synthesis in marine protists.

Gurvan Michel

Station Biologique de Roscoff

Contact information:

Gurvan Michel

Senior Scientist

Station Biologique de Roscoff, UMR7139 (CNRS/UPMC)

Place Georges Teissier BP74, 29682 Roscoff, France

Phone: +33 2 98 29 23 30

Fax: +33 2 98 29 23 24

gurvan@sb-roscoff.fr

http://www.sb-roscoff.fr/UMR7139/en/interaction.html

Gurvan Michel's research focuses on the identification and characterisation of enzymes involved in the degradation and the biosynthesis of algal polysaccharides. He studied biology at the Institut National Agronomique Paris–Grigron and received his Engineer diploma in 1997. As a Ph. D student, he learnt protein crystallography with Otto Dideberg at the Institut de Biologie Structurale in Grenoble and obtained his doctorate in 2000. From 2001-2002, he was a research associate in Miroslaw Cygler's group at the Biotechnology Research Institute in Montreal, Canada. Since 2003 he is a CNRS permanent scientist and has joined the Station Biologique in Roscoff to develop with Mirjam Czjzek a new protein crystallography group. His current strategy is to combine genomics approaches with structural methods to investigate the function of novel polysaccharidases from marine bacteria and algae.

Structural and functional census of the polysaccharidases from *Rhodopirellula baltica*, a key polymer degrader in marine environment

Gurvan Michel

Marine algae are characterised by their abundance of anionic polysaccharides which have no equivalent in land plants. These polymers are sulfated (agars, carrageenans, fucoidans) or rich in uronic acids (alginates). They display great chemical complexity, which gives rise to unique physicochemical and biological properties. The algal carbohydrates constitute a crucial carbon resource for numerous heterotrophic marine bacteria. Among these microorganisms, the *Planctomycetes* likely play a central role in the global carbon cycle as mineralisers of organic carbon. The genome of *Rhodopirellula baltica*, a Planctomycete isolated from marine snows, has revealed the presence of numerous polysaccharidases and more than 100 sulphatases!

We have demonstrated that *R. baltica* displays carrageenolytic activity confirming that this marine bacterium is a good model to identify enzymes specific for sulphated polysaccharides from algae. We have thus started a medium-throughput project to study the function and the 3D structure of the polysaccharidases from *R. baltica*. Its genome contains 29 glycoside hydrolases, 4 polysaccharide lyases, 17 carbohydrate esterases and 59 glycoside transferases (http://www.cazy.org/CAZY/). Using various bioinformatics tools, we have established that these 109 proteins are constituted by 165 independent structural modules. We have selected 96 target-genes, based on their structural and/or functional significance combined with their compatibility with our cloning strategy. For each gene, one single PCR-product has been cloned in parallel into two expression vectors (cloning success: His-tag vector, 92/96 targets; GST-tag vector: 73/96 targets). These 165 plasmids have been transformed into *E. coli* strains, which have been incubated at low temperature (20°C) in an auto-inducer culture medium. The expression and the solubility of the recombinant proteins have been tested by SDS-PAGE and Dot-Blot analyses. At least 30 target-proteins have been expressed under a soluble form with the His-tag vector. The expression tests with the GST-Tag vector are underway. A panel of soluble polysaccharidases has been purified by affinity chromatography. The first activity tests and crystallographic results will be discussed.

Speakers

Hanno Teeling

Max Planck Institute for Marine Microbiology

Contact information:

Hanno Teeling
Postdoctoral Researcher
MPI for Marine Microbiology
Celsiusstrasse 1
28359 Bremen
Phone: +494212028 976
Fax: +49 421 2028 790
hteeling@mpi-bremen.de
www.mpi-bremen.de/en/Microbial_Genomics_Group.html

Hanno Teeling achieved diplomas in Chemistry and Biology at the University of Oldenburg in 1996 and 1997, respectively, with a focus on Microbiology, Biochemistry and Environmental Analytics. After doing some molecular work on Green Sulfur Bacteria at the Institute for Chemistry and Biology of the Marine Environment (Oldenburg) and a nearly two year excursion to the field of clinical psychology of asthmatics at the Center for Clinical Psychology and Rehabilitation (Bremen), he started a Ph.D. at the Max Planck Institute for Marine Microbiology (Bremen) in late 2000, which he finished in early 2004. During that time, he worked on the bioinformatic analysis of the first completely sequenced Planctomycete, *Rhodopirellula baltica*, and ever since, cell biology, evolution and comparative genomics of Planctomycetes remained one of his major interests. During his ongoing postdoctoral research at the Max Planck Institute for Marine Microbiology, Hanno Teeling works on clustering and phylogenetic classification of metagenome fragments, and the bioinformatic side of diverse genome, comparative genomic and metagenome projects of marine bacteria. He is involved in the setup and programming of bioinformatic pipelines and meanwhile has published two standalone applications (TETRA, RibAlign). Hanno Teeling relates to the Network of Excellence Marine Genomics Europe (NoE MGE) in being the contact person for bioinformatics of the Microbial Node, and has been tutor in two bioinformatic courses held within the framework of the NoE MGE.

Novel aspects of marine ecological metagenomics - clustering of metagenomic fragments by intrinsic DNA signatures

Hanno Teeling

In recent years, the analysis of collectively sampled and sequenced microbial genomes has emerged as one of the key techniques in the field of environmental genomics and has become widely-known under the term 'metagenomics'. The most prominent metagenome study to date is the Sargasso Sea project, which lead almost to a twofold increase of the sequenced genes stored in public databases. Many similar projects are on the way and are expected to increase the sequence information such that metagenome sequences soon will exceed those coming from whole genome sequencing projects.

In order to transform this wealth of sequence information into biological meaning, techniques are required that cluster non-overlapping sequences that originate from one or closely related species. It has been known for long that species differ regarding the frequencies of short oligonucleotides within their DNA, and more recently it has been shown that these intrinsic DNA signatures carry a weak phylogenetic signal.

This talk will focus on some of the more recent advances in the extraction of such intrinsic signatures and their application to the metagenome of the symbionts of *Olavius algarvensis. Olavius* spp. are marine oligochaetes that have completely reduced their gut, digestive tract and nephridia and have shifted the respective tasks to a complex microbial community that they carry under their cuticle. These symbionts have recently been subjected to a community shotgun sequencing approach, and some outcomes of the respective study will be discussed.

Speakers

Oded Béjà

Technion - Israel Institute of Technology

Contact information:

Oded Béjà
Senior Lecturer
Department of Biology,
Technion - Israel Institute of Technology,
Haifa 32000, Israel.
Office: +972-4-8293961
Lab: +972-4-8293410
Fax: +972-4-8225153
beja@tx.technion.ac.il

Oded Béjà received his Ph.D. from the Weizmann Institute of Science, Rehovot, Israel for his thesis on: "Structure and function of Multidrug Resistance protein expressed in *Escherichia coli*". From 1998 – 2001 he was Postdoctoral fellow at the Monterey Bay Aquarium Research Institute, California, USA. In 2001 he became Senior Lecturer at the Technion -Israel Institute of Technology, Israel

He is member of the Board of the Israel Society for Microbiology and member of the Editorial Board of "Environmental Microbiology" and "Biotechnology Journal".

The quest for viral 'photosynthesis' using both metagenomics and environmental genomics

Oded Béjà

Genes that encode the photosystem II D1 protein (*psbA*) were recently found in several cultured cyanophage genomes. These viral photosynthesis genes may provide a beneficial trait to the viruses or to their photosynthetic cyanobacterial hosts, or even represent a previously unrecognised gene pool for formation of photosynthetic apparati.

Using both BAC based approaches (environmental Genomics) and Metagenomics we observe that between 44% (Sargasso Sea) to at least 59% (Atlantic Ocean) of environmental D1 sequences are of viral origin. Moreover, viral signatures were also detected in D1 mRNA, indicating that these photosynthetic viral genes are actively expressed in the marine environment. Overall, our environmental observations raise the possibility that marine viruses actively participate in and influence oceanic photosynthesis on a global scale. The possible implications to oceanic photosynthesis and to the carbon cycle will be discussed.

Klaus Jürgens

Baltic Sea Research Institute Warnemünde (IOW)

Contact information:

Klaus Jürgens

Professor of Biological Oceanography

Baltic Sea Research Institute Warnemünde (IOW)

Seestrasse 15

18119 Rostock

Germany

Phone: +49 381 5197 250

Fax: +49 381 5197 211

klaus.juergens@io-warnemuende.de

www.io-warnemuende.de

The actual research focus of Klaus Jürgens and his group at the IOW is the role of microorganisms in biogeochemical cycles, with emphasis on the Baltic Sea ecosystem. He studied Biology at the University of Konstanz, where he received the Diploma in Biology with Limnology as the main subject. He performed his PhD thesis on trophic interactions and microbial food webs in plankton communities at the Max Planck Institute for Limnology in Plön and received the doctorate from the University of Kiel in 1994. From 1994-1995 he was guest research scientist at the National Environmental Research Institute in Silkeborg, Denmark, participating in research projects on the ecology of shallow lakes. From 1995-2002 he was research scientist at the MPI in Plön, focussing mainly on mechanisms of predator-prey interactions between bacteria and bacterivorous protists. In 2003 he became head of the Biological Oceanography department at the Baltic Sea Research Institute Warnemünde and professor at the University of Rostock.

Diversity of microbial communities and their biogeochemical functions in marine pelagic redoxclines

Klaus Jürgens

Pelagic redoxclines are a common feature of many shelf- and marginal seas. This is mostly related to a combination of topography, water exchange and organic input. In the case of the central Baltic Sea a pronounced salinity gradient at 60-80 m depth inhibits vertical mixing. Oxygen deficiency and sulphide accumulation occurs in the deep water below the halocline. The redoxcline, characterised by steep vertical gradients of oxygen, nitrogen and sulphur compounds and trace metals, is a site of biogeochemically important transformations, mostly driven by microorganisms, and of enhanced microbial activities (e.g., dark CO_2 fixation). Here distinct functions can often be related to responsible key microorganisms. By an interdisciplinary approach, our actual research aims at (1) quantifying rates of element transformation, particle formation and transport across the redox gradient and understanding the regulating mechanisms, and (2) elucidating the structure and functions of the microbial communities and identifying key players for the different transformation processes. Some major results of our recent redoxcline research include new insights into the structure and activity of denitrifying bacteria, functioning of the manganese shuttle, the vertical distribution of microbial diversity and the identification of abundant chemolithoautotrophic bacteria. However, several open questions are also evident, for which to answer we a need a combination of in situ experimental approaches, culturing and metagenomics.

Speakers

Ian Joint

Plymouth Marine Laboratory

Contact information:

Ian Joint

Group leader

Plymouth Marine Laboratory, Prospect Place, The Hoe, Plymouth, PL1 3DH, UK

Phone: +44 1752 633476

Fax: +44 1752 633101

i.joint@pml.ac.uk

www.pml.ac.uk

Ian Joint is an Individual Merit Promotion (IMP Band 2) at the Plymouth Marine Laboratory; this scheme recognises the best scientists employed by the UK Research Councils. His research has focussed on determining the productivity of natural assemblages of autotrophic and heterotrophic microbes in the sea. Recent work has been concerned with cell-to-cell signalling in marine biofilms and with applying metagenomics to natural assemblages of marine microbes. In the last 5 years, he has been PI or co-PI on 7 Natural Environment Research Council (NERC) research grants, including leading this consortium of 12 microbial ecology groups in the NERC Postgenomics and Proteomics Directed Programme. He is a member of the NERC Peer Review College.

Microbial metagenomics and marine biogeochemical cycles

Ian Joint

I will report on a project funded by the UK Natural Environment Research Council, which is part of the Post-genomics and Proteomics Directed Programme. The research involves a consortium of microbial ecologists from 10 UK Universities and research institutes; it has a duration of 3 years, and a budget of £2.4 million. There are 3 broad areas of research that utilise microbial metagenomics approaches to investigate marine biogeochemical cycles. The first question asks if microbes exist in definable communities in the ocean and how biogeochemical fluxes might depend on microbial community structure. The second topic area concerns the nitrogen cycle, and it investigates if the scale of nitrogen limitation is a function of interactions between microbes in the assemblage. The third broad area of research concerns the role of microbial activity in the production of atmospheric biogases.

In this talk I will concentrate on one specific aspect of climate change – ocean acidification. A significant proportion of anthropogenic CO_2 has, and will continue to, dissolve in the oceans. When CO_2 dissolves, it forms carbonic acid, which reduces the pH of sea water. Within the next 100 years, with the 'business as normal scenario' of the IPCC, the pH of seawater is projected to fall to 7.8. This is the lowest ocean pH for ~25 million years. It is not known how marine microbial activity will be affected by this change in pH. Certain groups of phytoplankton, such as coccolithophores, have received most attention because calcite deposition will be greatly reduced at pH 7.8. But bacteria and other microbes may be significantly affected. At pH 7.8 the concentration of free ammonia (as distinct from ammonium ions) will be about half that existing at present. Since ammonia (not ammonium) is the substrate for ammonia oxidising bacteria, what will be the effect on marine nitrification rates?

To answer this and other questions about microbial functional diversity, the consortium will carry out a mesocosm experiment in May 2006 at the large scale facility of the University of Bergen. 3 enclosures of 12 m^3 will be bubbled with 750 ppm CO_2 to reduce the pH to ~7.8 and microbial activity will be compared with that in 3 mesocosms that have not been supplemented with CO_2. We will determine changes in microbial diversity during a bloom of phytoplankton induced by adding nitrate and phosphate and will determine if the variation in pH has a significant effect on microbial function. The major approaches used will involve fosmid libraries, stable isotope probing and microarrays. I will present preliminary findings from this experiment.

Speakers

Jakob Pernthaler

Limnological Station, University Zurich

Contact information:

Jakob Pernthaler

Professor

Limnological Station, Inst. Plant Biol, Univ. Zurich

Seestrasse 187, 8802 Kilchberg, Switzerland

Phone: +41 1 716 1210

Fax: +41 1 716 1225

pernthaler@limnol.unizh.ch

Jakob Pernthaler is professor at the University of Zürich where he acts as head of the Limnological Station of the Institute of Plant Biology. A central focus of his research lies upon studying the role and fate of different water column microbes in marine and freshwater habitats in the context of microbial food webs and substrate availability. This is founded upon three sets of techniques: (i) A suite of molecular biological approaches for the identification and staining of common environmental microbes without prior cultivation based upon comparative rRNA gene cloning and sequence analysis. In his laboratory methods have been improved for the determinative whole-cell fluorescence in situ hybridisation (FISH) of small slowly-growing water column microbes with rRNA-targeted probes in oligotrophic offshore or freshwater environments. (ii) Strategies for the rapid quantification of population sizes, biovolumes and activities of FISH-stained microorganisms by automated motorised microscopy, image analysis, and flow cytometry. (iii) Cytochemical and autoradiographic techniques to measure the DNA synthesis and specific substrate uptake of individual microbial populations in mixed communities at the single-cell level, to establish a link between the phylogenetic identification of microbial populations and their growth patterns in situ. Current research topics in his lab focus on the effects of predator-induced mortality on the composition of microbial assemblages, and the potential adaptations of microbial species to compensate or to avoid such losses, and on the life strategies of so-called "opportunistic" bacterial species (i.e. bacterial ecotypes that are superior competitors in steep environmental gradients or during rapid changes of growth conditions) in coastal marine waters.

Diversity and seasonal dynamics of Cytophaga-like bacteria in coastal North Sea waters

Jakob Pernthaler

Bacteria of the Cytophaga-Flavobacterium (CF) lineage of Bacteroidetes are amongst the most abundant single phyla in coastal marine waters, but they are conspicuously underrepresented in 16S rRNA gene clone libraries. Thus, little is known about the seasonal population dynamics of different CF lineages as determined by fluorescence in situ hybridisation (FISH). We constructed two clone libraries from coastal North Sea waters and screened the libraries for CF-related sequence types by a specific PCR assay. The local diversity at the sampling site was subsequently compared with the global diversity of almost complete 16S rRNA gene sequences of marine Bacteroidetes. Although 55 almost complete sequences were obtained, an index of coverage indicated that CF diversity in our samples remained undersampled. More than half of our sequences formed unique groups at the species level (97% similarity), representing 3% of the total diversity of marine Bacteroidetes . Specific probes for the analysis of different CF clades by FISH were designed and applied to weekly samples from a 1-year study. Bacteria from the different CF groups were generally rare throughout the year except for few sampling dates. Our findings point to a high diversity of CF in marine waters that appears to be still largely undescribed at the level of almost complete 16S rRNA gene sequences. CF in the coastal North Sea appear to be structured in numerous small, coexisting populations that may form short-lived blooms at certain environmental conditions.

Gerhard J. Herndl

Royal Netherlands Institute for Sea Research (NIOZ)

Contact information:

Gerhard J. Herndl

Professor of Biological Oceanography

Royal Netherlands Institute for Sea Research (NIOZ)

P.O. Box 59

1790AB Den Burg

The Netherlands

Phone: +31 222 369 507

Fax: +31 222 319 674

herndl@nioz.nl

www.nioz.nl

Gerhard J. Herndl received his PhD degree at the University of Vienna (Austria) in 1982. After a Post Doc in the lab of Prof. Farooq Azam at Scripps Institution of Oceanography (USA) he established a marine microbial ecology working group at the Dept. of Marine Biology at the Univ. of Vienna. In the year 1993, G.J. Herndl became Associate Professor at the Department of Marine Biology of the University of Vienna and in 1997, Head of the Department Biological Oceanography at the Royal Netherlands Institute for Sea Research (NIOZ). Since 1999, he is also Professor of Biological Oceanography at the University of Groningen.

Bacterial and archaeal diversity and function in the major deep water masses of the North Atlantic

Gerhard J. Herndl

The abundance and cell production of Archaea and Bacteria in the meso- and bathypelagic North Atlantic were determined along a S-N transect from 65°N to 7°N following the North Atlantic Deep Water. Using catalysed reporter deposition-FISH (CARD-FISH) and specific oligonucleotide probes, Archaea were found to be consistently more abundant than Bacteria below 100 m depth. Combining microautoradiography with CARD-FISH (MICRO-CARD-FISH) revealed that the percentage of *Eury*- and *Crenarchaeaota* taking up leucine did not follow a specific trend with depth. The fraction of *Crenarchaeota* taking up inorganic carbon increased with depth, while *Euryarchaeota* taking up inorganic carbon decreased from 200 m to 3000 m depth. The ability of Archaea to take up inorganic carbon was used as a proxy to estimate archaeal cell production. We estimate that archaeal production in the meso- and bathypelagic North Atlantic contributes between 10-84 % to the total prokaryotic production in the deep Atlantic water masses. The recently emerging notion that *Crenarchaeota* are ammonia oxidisers was tested using RT-PCR to quantify the *amoA* gene copy numbers. Crenarchaeal *amoA* copy numbers decreased from the bottom of the euphotic layer to the bathypelagic realm by three orders of magnitude while the abundance of *Crenarchaeota* determined by MICRO-CARD-FISH and RT-PCR decreased only by one order of magnitude over this depth range. Thus, we conclude that bathypelagic *Crenarchaeota* are actively growing in the dark ocean, however, it is likely that, in contrast to recent observation on *Crenarchaeota* from the upper water column, bathypelagic *Crenarchaeota* are not oxidising ammonia in significant amounts. Sequence information on the 16S rRNA gene of the *crenarchaeotal* community indicates that those potentially harbouring the *amoA* gene and those lacking it are very closely related.

Feng Chen

US DOE Joint Genome Institute

Contact information:

Feng Chen

Group Leader

US DOE Joint Genome Institute

2800 Mitchell Dr., B400;

94598; Walnut Creek, CA USA

phone: +01 925 296 5733

fax: +01 925 296 5620

fchen@lbl.gov

www.jgi.doe.gov

The US DOE Joint Genome Institute's mission is to serve as a national resource for large-scale, cost effective sequencing of DNA from organisms of scientific, political and economic importance, and to make a significant contribution to genomic sciences. Feng Chen is a group leader in the Genomic Technologies Department and is in charge of developing technologies related to Genomics in general and in particular, DNA isolation and sequencing. One of his major research interests is to evaluate and validate new sequencing technologies available through early collaboration with companies such as 454 Life Science, Solexa, Helicos and Agencourt Bioscience and to develop applications for these new technologies. His group is working on developing methods to apply these newly available sequencing platforms particularly on high-throughput sequencing of microbial genomes, metagenomic samples, expression tags, and ancient DNA samples. He holds a B.S. in Genetics and Genetic Engineering from Fudan University in 1989 and a Ph.D. in Biochemistry from University of Oklahoma in 1997. He was appointed as Assistant Director of Advanced Center for Genomic Technology at University of Oklahoma from 1999 to 2000 to oversee the center's participation in NIH's Human Genome Project. His own research focus was comparative Genomics of human chromosome 22 and syntenic mouse chromosome regions. From 2000 to 2004, he was Senior Research Scientist and Production Leader at Exelixis, Inc. He was involved in various research projects in plant and insect genomics and human cancer genomics. He joined Joint Genome Institute in later 2004.

454 Sequencing Technology and Its Application in Microbial and Metagenomic Community Sequencing at US DOE Joint Genome Institute

Feng Chen

The US DOE Joint Genome Institute (JGI) is a high-throughput sequencing centre involved in a myriad of sequencing projects. A major effort at JGI is the sequencing of microbial genomes and microbial community samples of relevance to the DOE missions of carbon sequestration, bioremediation and energy production. The JGI Microbial Program is responsible for the generation of over 300 microbial genomes and metagenomic samples and we are interested in utilising new technologies to increase capacity and efficiency. The 454 sequencing platform is an integrated system of emulsion-based PCR amplification of hundreds of thousands of DNA fragments linked to high throughput parallel pyrosequencing in picoliter-sized wells. The 454 sequencing platform can deliver 30 to 50 million base pairs (mbp) from a single run. The quality of raw reads is about 99% and the assembly quality is about 0.05% at raw coverage of about 20X. It lacks of paired-end information currently. The traditional Sanger sequencing method is lower in throughput and more costly but it provides high quality sequencing results and more accurate assemblies. The paired-end information from Sanger sequencing is proven to be crucial in scaffolding and gap closure. For whole genome shotgun sequencing, we developed a strategy to combine the Sanger sequencing data with 454 sequencing data to achieve better assembly with less cost. Two technologies are complementary with each other in terms of coverage and quality. Using 454 technology to sequence pooled clones covering Sanger sequencing gaps is an effective way for gap closing. Different strategies have been developed to increase the efficiency of sequencing fosmid clones from metagenomic samples. Efforts have been taken to develop in-house informatics tools for data analysis. Selected data and results from these areas will be presented.

This work was performed under the auspices of the US Department of Energy's Office of Science, Biological and Environmental Research Program, and by the University of California, Lawrence Livermore National Laboratory under Contract No. W-7405-Eng-48, Lawrence Berkeley National Laboratory under Contract No. DE-AC02-05CH11231and Los Alamos National Laboratory under Contract No. W-7405-ENG-36.

Jean Weissenbach

Genoscope and Université d'Evry Val d'Essonne

Contact information:

Jean Weissenbach

Director of Research,

GENOSCOPE

2 rue Gaston Crémieux,

CP5706 , 91057 EVRY,

France

Phone: +33 1 6087 2502

Fax: + 33 1 6087 2532

jsbach@genoscope.cns.fr

www.szn.it

Jean Weissenbach was born on February 13, 1946 in Stasbourg. He entered the French National Research Organisation (CNRS) in 1970 and is now Director of Research. He has directed several CNRS laboratories as well as a research unit at the Pasteur Institute. He headed the programme for the human genetic linkage map at Genethon and was Scientific Director of Genethon from 1993 until 1997. Since 1997 he has been the director of Genoscope - Centre National de Sequencage.

His career has been centred on molecular biology. He received his Ph.D. from the Louis Pasteur University in Strasbourg in 1977, where he studied the sequencing and coding properties of transfer RNA. He did a post-doctoral fellowship from 1977 to 1981 at the Weizmann Institute, and then at the Pasteur Institute where he worked on cloning the genes for human interferons. This led him to human molecular genetics, his research interest since 1982.

During the last 20 years, his work has included:

1. Molecular genetics of human sex chromosomes and sex determination.
2. Jean Weissenbach and his research group at the Genethon laboratory created a human genetic linkage map which consists of over 5000 highly polymorphic genetic markers.
3. With his group, or in collaboration with other groups, he has localised genes for numerous genetic diseases, and identified some of them.
4. Since 1997, Jean Weissenbach has directed the Centre National de Séquençage-Genoscope, which has participated in the sequencing of large genomes (human chromosome 14, Arabidopsis, Tetraodon, etc.) & genomes of microorganisms.
5. At present, Genoscope's research activities are mainly oriented toward the genomics of environmental microorganisms. These organisms play an essential role in the equilibria of the biosphere and they have important applications in bioremediation of waste and in biotechnology.

A metagenomic approach to wastewater processing

Denis Le Paslier, Eric Pelletier, Abdelghani Sghir, Rakia Chouari, Akila Ganesan, Sonda Guermazi, Delphine Rivière, Patrick Daegelen and Jean Weissenbach

Wastewater is processed through a number of biochemical pathways by microorganisms which progressively decompose organic matter into mineral components. Mineralisation is driven to a certain extent through a succession of steps which take place under aerobic or anaerobic conditions. We have only a partial view of the biochemical aspects and we know little about the prokaryotic florae involved and their exact contribution to the overall process. We have therefore applied genomic and metagenomic approaches to obtain more knowledge about the microbial actors and the biochemistry at work in wastewater processing.

We have successively used 16S rDNA analysis and constructed metagenomic DNA libraries of large insert fragments extracted from different basins of a municipal wastewater treatment plant. A fosmid library of more than one million clones of DNA extracted from an anaerobic mesophilic digester was screened by high density filter hybridisation using various 16S rDNA probes. Sequences of 16S rDNAs identified in the fosmids were compared to those obtained from PCR products from the DNA extracted from the florae of the basins. Though globally similar, some qualitative and quantitative differences were observed. New bacterial divisions that represent significant fractions (>5%) of the prokaryotic population of the digestor were identified and are being further characterised.

End sequences of the large insert clones have been obtained and are being analysed using several approaches including assembly, definition of open reading frames, coding sequence alignments etc. Preliminary results of such analyses will be presented.

Alexander Loy

University of Vienna

Contact information:

Alexander Loy

Group leader, University of Vienna

Department of Microbial Ecology

Althanstr.14, A-1090 Wien

Austria

Phone: +43 1 4277 54207

Fax: +43 1 4277 54389

loy@microbial-ecology.net

www.microbial-ecology.net/loy.asp

www.microbial-ecology.net/probebase

Alexander Loy's research focuses on investigating the ecology and evolution of microorganisms of the sulphur cycle and on the development of novel molecular methods, in particular DNA microarrays, for structure-function analyses of microbial communities. He studied biology at the Technical University Munich, where he received his diploma in Biology in 1999. He continued his research at the Department of Microbiology (headed by Prof. Karl-Heinz Schleifer) of the TU Munich and received his Ph.D. in 2003. In 2002, he has co-founded probeBase – an online resource for rRNA-targeted oligonucleotide probes. Since 2003, he is a postdoctoral fellow at the Department of Microbial Ecology (headed by Prof. Michael Wagner) at the University of Vienna, where he leads the "Microarray and Sulphur Cycle" group. Since 2004, he also regularly acts as an invited expert of the European COST action 853, focusing on microarray technology. From 2004 to 2006 his research was financed by a Marie Curie Fellowship within the Sixth European Framework Program.

Functional probing of microbial communities with rRNA-targeted oligonucleotide microarrays

Alexander Loy

The overwhelming extent of microbial diversity on our planet necessitates the development of novel techniques for rapidly and efficiently monitoring the dynamics and distribution of microbes in the environment. In principle, DNA microarrays fulfil all requirements in this regard. This talk will highlight important steps in the design and application of oligonucleotide microarrays targeting ribosomal RNAs or their genes (so-called PhyloChips) and discuss the major benefits and limitations of their use for identification and quantification of microorganisms in complex samples. Furthermore, the application of a new PhyloChip-based approach for monitoring consumption of a radioactively-labelled substrate by defined members of a microbial community will be presented. I anticipate that combining this so-called IsotopeArray approach with PhyloChips customised for a habitat of interest will allow comparative, phylogenetic and functional profiling of complex microbial assemblages over time and space in a highly parallel manner.

Speakers

Thomas Schweder

Institute of Marine Biotechnology and Institute of Pharmacy, EMA-University Greifswald

Contact information:

Thomas Schweder
Professor of Pharmaceutical Biotechnology
Institute of Marine Biotechnology and
Institute of Pharmacy,
EMA-University Greifswald
F.-L.-Jahnstr. 17
D-17487 Greifswald
phone: +49 3834 864212
Fax: +49 3834 864238
schweder@uni-greifswald.de
http://www.marine-biotechnologie.de
http://pharm1.pharmazie.uni-greifswald.de/index.html

Thomas Schweder's research focus is to investigate the biotechnological potential of marine and industrial bacteria by means of the techniques of functional genomics. This includes the characterisation of so called stress and starvation signatures of these bacteria by proteomics and transcriptome analyses. He studied biology at the Ernst-Moritz-Arndt-University Greifswald, where he received his Diploma in Biology in 1990 Applied Microbiology being his main subject. Until 1993 he was a Ph. D. student in the laboratory of Prof. Michael Hecker in Greifswald and received his doctorate in January 1994. From 1994-1995 he spent a postdoc time in the lab of Prof. A.C. Matin at Standford University (CA). From 1995 until 2001 he was a Postdoctoral Research Fellow in the laboratory of Professor Dr. Michael Hecker at the Institute of Microbiology. In 2001 he became the director of the Institute of Marine Biotechnology in Greifswald. Since 2004 Thomas Schweder is Professor for Pharmaceutical Biotechnology at the University of Greifswald.

Proteome analyses of marine bacteria

Thomas Schweder

The genome sequencing of marine bacteria provides new perspectives for the understanding of their unique physiological activities. Proteomics relying on two-dimensional (2-D) gel electrophoresis of proteins followed by spot identification with mass spectrometry is an excellent experimental tool for physiological studies allowing for a comprehensive analysis of gene expression and gene function of marine microorganisms. Currently three marine microorganisms are in our focus: (1.) the uncultivable bacterial endosymbiont of the deep sea tubeworm *Riftia pachyptila*, (2.) the planctomycete *Rhodopirellula baltica* and (3.) the psychrophilic Antarctic bacterium *Pseudoalteromonas haloplanktis*. Proteome studies provide information on the protein level which can be considered as the "working" level of the cells. We are thus able to explore the physiological capacity of even uncultivable bacteria like the endosymbiont of *R. pachyptila*. The determination of cellular proteome signatures during defined cultivation conditions (e.g. starvation and physical stress conditions) make it possible to affiliate so far unknown proteins to functional groups. Furthermore, proteome signatures visualise strictly regulated groups of the bacterial genes. The response to starvation and stress conditions give new insights into the physiological adaptation of the microorganisms to the changing marine environmental conditions.

Speakers

Phillip Neal

Marine Biology Laboratory, Woods Hole

Contact information:

Phillip Neal

Senior Research Assistant

Marine Biology Laboratory (MBL) Woods Hole

7 Water Street; Woods Hole, Ma.; USA

phone: +01 508 289 7153

pneal@mbl.edu

Phil Neal is a senior research assistant on the ICoMM project at the Marine Biology Laboratory in Woods Hole. His research interests are focused on developing-, implementing-, and testing new estimates of sequence similarity. He holds a bachelors degree in Conservation of Natural Resources from U.C. Berkeley and a Masters from the School of Fisheries at the University of Washington. He has worked in IT most of his professional career.

Estimating Marine Microbial Diversity: lots of Data, Lots of Challenges, a Few Suggestions

Phillip Neal

The International Census of Marine Microbes (ICoMM), a project of The Census of Marine Life (COML) has completed a prototype marine microbial project using the new '454' sequencing technology. The quantity (~118k sequences) and quality (~100 nt. avg. length) of data generated by the 454 technology created new challenges for the bioinformatics group at the Marine Biology Lab (MBL) at Woods Hole.

Some of these new challenges were to:

1. Develop a reference database to compare V6 regions of known 16s rDNA gene sequences against the 454 sequences
2. Develop a taxonomic database for the reference sequences
3. Pre-process the 454 sequences to optimise quality.
4. Map the 454 sequences to the sequences in the reference database
5. Generate diversity estimates

This talk will address different aspects of responses to these challenges.

Some of these aspects are:

1. Data sources for the reference database
2. Use of NCBI and RDP taxonomies
3. Blasting for primers
4. Alignments and Distance measures
5. Dotur and diversity estimates
6. Computing resources

Edward Vanden Berghe

VLIZ, Flanders Marine Institute

Contact information:

Dr Edward Vanden Berghe
Manager,
Flemish Marine Data- and Information Centre,
Flanders Marine Institute
Wandelaarkaai 7
B8400 Oostende
wardvdb@vliz.be
www.vliz.be
www.marbef.org

Edward Vanden Berghe has been involved in computer applications and statistical analysis in biology since finishing his MSc from the Free University of Brussels in 1978. His PhD was on theoretical models of Nematode morphology, from the same university. From 1993 to 1996, he was building a biogeographical information system for the National Museums of Kenya, to allow to document biodiversity in Kenya, and to support conservation efforts. From 1996 to 1999, he was managing a project on marine information, based in Mombasa, and documenting publications and species distributions in the Western Indian Ocean region. From 1999, he is heading the Data- and Information centre in the Flanders Marine Institute. Major applications developed are Integrated Marine Information System (IMIS), a modular knowledge management system documenting expertise, literature and datasets; the Integrated Marine Environmental Readings and Samples (IMERS); the European Register of Marine Species; the European Node of the Ocean Biogeographic Information System. VLIZ is responsible for data management of MarBEF network of excellence; the two latter data systems were developed on behalf of MarBEF.

Since 15 years, Edward Vanden Berghe has been teaching as a guest professor at the Free University Brussels, on data analysis and marine data management. He has also conducted several short training workshops, mostly on marine biodiversity data management, in conjunction with the Intergovernmental Oceanographic Commission of UNESCO.

MarBEF: lessons learned from data integration

Edward Vanden Berghe

Marine Ecosystem Biodiversity and Functioning (MarBEF) is a EU network of excellence, with now over 70 institutional partners, and representing 600 marine scientists. EU funding is in the first place meant to stimulate integration of science on a pan-European scale, rather than to fund new science. One of the important integrating activities is the development of databases, containing data and information on taxonomy and biogeography from a large number of partners.

One of the datasets under development focuses on soft-bottom macrobenthos. A total of over 450,000 distribution records, from 42 different sources, were brought together in a single access database. Integrating data from different sources brought to light several issues. Lack of proper data management procedures with several of the partners made integrating those data a labour-intensive exercise. Lack of standards in sampling methodology made strict comparison of measured densities and biomass across individual datasets difficult. Last but not least, differences in interpretation of taxonomy, differences in identifications, and numerous spelling variations would, if not corrected for, have lead to a serious overestimation of marine biodiversity.

In integrating biogeographical data from different sources, the European Register of Marine Species plays an important role. This register contains not only the valid names of species known to occur in Europe, but also synonyms and documented misspellings. ERMS is an essential tool to harmonise taxonomic names used in the different databases. Also, ERMS contains a taxonomic hierarchy, allowing to group taxa included in the database to any taxonomic rank, in order to avoid problems with uncertain identifications.

Francisco Eduardo Rodriguez Valera

Universidad Miguel Hernandez

Contact information:

Francisco Eduardo Rodriguez Valera

Professor

Universidad Miguel Hernandez,

Campus de San Juan, 03550 San Juan de Alicante, Spain

phone: +34965919451

Fax: +34965919576

frvalera@umh.es

http://miracle.umh.es/database/

The research group headed by Prof. Rodríguez-Valera studies the different aspects of Microbiology including the Microbial Ecology of hypersaline waters, taxonomy and biodiversity of halophilic Bacteria and Archaea, marine Microbial Ecology and other related fields such as molecular evolution, population genetics and biogeography of marine bacteria.

The research group started work related to microbial biodiversity by the molecular approach in 1993 within the European Project CLEAN, to analyse the biodiversity of coastal lagoons. The work was continued in the EU project ROBUST and MIDAS. Furthermore specific molecular markers such as the internal spacers of the ribosomal operons have been developed. Given the difficulties in classification of bacteria based on phenotypic features, an important attempt has been made to characterise prokaryotes from variable DNA sequences. For many years, the group has been involved in the acquisition and management of prokaryotic DNA sequence data, generating hundreds of sequence data that have been used to characterise and classify prokaryotic species. In particular, our lab has been an important contributor to the classification of bacterial species by means of the ribosomal intergene spacer region.

The group has created a novel free-access database for ribosomal spacer regions, with hundreds of visits per year, that manages over 2000 sequences of this highly-variable DNA sections used in phylogenetic studies (Nucleic Acid Research 2001, 29:178-180). We have also started a database from the European project MIRACLE, that is a primordial version of the MARINE-MICROBASE that we aim to create, but reduced to data from the MIRACLE project in European seas.

Biogeography of marine bacteria, genes, spacers and genomes

Francisco Rodriguez-Valera, Giuseppe D'Auria and Elena Ivars

Marine bacteria represent an excellent model in which to investigate issues related to biogeography, microdiversity and short-term evolution in prokaryotes. Simplicity and reproducibility of sampling, habitat characterisation and biomass, nucleic acids or even culture (for some groups) retrieval represent a great advantage. Besides, large amount of data are already available in databases. During the last 10 years we have been studying some case examples of off-shore picoplanctonic marine prokaryotes using direct PCR amplification of 16S rDNA and ITS, screening and development of databases (mostly of 16S rDNA but also of ITS's) and lately isolation and in-depth study of cultures by MLST, genome fingerprinting and (only in one case) whole genome sequencing. We have found very little influence of geography on genotype retrieval but many water bodies contain endemisms that are probably a reflection of habitat diversification.

Speakers

Contact information:

Andrea de Bono

Data processing and GIS analyst

UNEP/DEWA/GRID-Europe

International Environment House

11 Chemin des Anémones

1219 Châtelaine

Switzerland

Phone: +41 22 917 82 40

Fax: +41 22 917 82 40

debono@grid.unep.ch

www.grid.unep.ch

geodata.grid.unep.ch

metafunctions.grid.unep.ch

Andrea de Bono

UNEP/DEWA/GRID-Europe

Andrea de Bono joined the GRID-Europe team in 2001.

He currently works on data processing, metadata set-up, and database management for the Global Environment Outlook (GEO) Data Portal, and for environmental indicators of the GEO Yearbook. He is also participates in the redaction of the Early Warning Briefs on Emerging Environmental Threats.

He studied geology at the University of Torino (Italy). After obtaining a Ph.D. in Geology in 1998 (University of Lausanne, CH), he worked as field cartographer in a foreign geological company. He pursued further studies in geomatics at Geneva University (CH).

His research focus for the EU „Metafunctions" project includes: collecting and processing oceanic environmental parameters, performing GIS analysis to retrieve missing data, management of data storage in the ecological database, and development of the (Meta)genome map server.

GRID: The Global Resource Information Database

Andrea de Bono

The Global Resource Information Database (GRID) is a worldwide network of 15 environmental data centres. It is part of the Division of Early Warning and Assessment (DEWA) of the United Nations Environment Program (UNEP). The GRID network was launched in 1985 with various centres in the world. GRID-Europe is located in Geneva. Its principal activity is to provide high-quality environmental data and information, to underpin UNEP's review of the state of the environment and provide early warning on emerging environmental threats. It offers technical services and develops value-added environmental products to support the work of other entities on a case-by-case basis.

To advance the development of a Geographic Information System (GIS) combining genomic and ecological data, we offer competence in the following specific domains:

GIS, remote sensing, and modelling to provide: better insights to decision-makers, sustainable use of natural resources, analysis of emerging environmental problems and threats. Recent applications in this domain include: satellite imagery analysis to map chlorophyll concentration of Lebanon's coastal water as a response to land-derived pollution; evolution of the Mesopotamian marshlands ecosystem, and modelling of asymmetric wind speed.

Integration, dissemination and communication of geographic information visually on the World Wide Web through a GIS (webmapping). GRID-Europe is responsible for the complete design, data gathering and formatting, and on-line interface of several data portals and map servers.

GRID-Europe will be contributing through its work on this novel data-mining system: A 'Genomes MapServer' is under development, which will soon enable scientists around the world to access integrated genomic and ecological data, and clearly visualise the results of their analyses.

An innovative aspect is the use of GIS, which allow simulation and analysis of events from a geographical or spatial perspective. Novel patterns - for example, the physical clustering of genes within a genome - will be correlated to the contextual habitat data. E.g. a particular cluster of genes may be found in a number of genomes and metagenomes all taken from high-temperature environments. It would be reasonable to infer that the gene must play some role in enabling survival in extreme heat.

Anton Güntsch

Botanic Garden and Botanical Museum Berlin-Dahlem

Contact information:

Anton Güntsch

Head, Section of Biodiversity Informatics

Botanic Garden and Botanical Museum Berlin-Dahlem

Dept. of Biodiversity Informatics & Laboratories

Königin-Luise-Str. 6-8

D-14191 Berlin

Phone: +49 30 83850166

Fax: +49 30 84172955

a.guentsch@bgbm.org

http://www.bgbm.org/guentsch/

Anton Güntsch (MSc Computer Science – Technical University Berlin) graduated in 1994 with his study about neural networks and strategic games. From 1994 to 1999 he has been working for a private enterprise (ZLV-Berlin) in the area of Geographic Information Systems and database design. Since 1999, he works at the Department of Biodiversity Informatics and Laboratories of the Botanic Garden and Botanical Museum (BGBM) in Berlin, since 2003 as head of the Biodiversity Informatics and Documentation section. His scientific activities are centred to the design and implementation of collection and taxonomic databases at Meta and object level, the design of cooperative networks of distributed biodiversity information systems, and the digitisation of living and conserved biological collections. He was responsible for the implementation of the BioCISE collection catalogue and the European Natural History Specimen Information Network Pilot system (ENHSIN), an XML based World Wide Web access system for distributed heterogeneous collection databases. Present project and committee memberships: 1) CODATA Working Group on Biological Collection Data Access, 2) GBIF-Germany IT commission (chair), 3) BioCASE work package lead for the Central System implementation, 4) Euro+Med computer working group and 5) GBIF Science Subcommittee for Digitisation of Natural History Collection Data (DIGIT).

Integration of heterogeneous biodiversity data sources using BioCASe and ABCD

Anton Güntsch

The implementation of worldwide networks for exchanging and accessing primary biodiversity information resources has been hampered by the sheer diversity of these resources. Systems such as those containing collection, name- and taxon-related data come in a wide variety of operating systems, database management systems, and underlying data models. The problem has been tackled by several projects and initiatives aimed at providing common data standards and Internet query protocols. The ideal is a solid foundation for generic software modules enabling database holders to link their collections to international networks without having to modify the implementation of their systems.

The BioCASE project (http://www.biocase.org) initially delivered such standards and software with a focus on high resolution biological collection data, covering physical collection objects as well as observations and multimedia objects. Based on an XML query-specification (BioCASe-Protocol) and a comprehensive XML data definition schema (Access to Biological Collection Data, ABCD), various software modules have been implemented to support both data providers and clients in biodiversity networks. The protocol definition is completely generic and unconcerned with a given application's specific data schema, and as a result, the software has been put to new uses such as taxon- and name-oriented systems and metadata-networks.

Prominent users of the technology include the Biological Access Service for Europe (BioCASE), SYNTHESYS, the Global Biodiversity Information Facility (GBIF) and Species2000. All software components are freely available under the Mozilla licensing scheme. Additionally, the Botanic Garden and Botanical Museum Berlin-Dahlem offers data providers using BioCASe products a helpdesk, which can be reached at support@biocase.org.

Speakers

Thierry Lombardot

Max Planck Institute for Marine Microbiology

Contact information:

Thierry Lombardot

PostDoc in bioinformatics/ marine ecological genomics

MPI for Marine Microbiology

Celsiusstrasse 1

28359 Bremen

Phone: +49 421 2028 974

Fax: +49 421 2028 580

tlombard@mpi-bremen.de

www.microbial-genomics.de

www.metafunctions.org

www.megx.net

Thierry Lombardot's research interests are data integration in the field of genomic and metagenomic and biological /ecological interpretation of sequence data. His field of research currently focuses on marine ecological genomics of prokaryotic organisms.

After completing his study in Switzerland (Geneva, Bachelor in Biochemistry and Lausanne, Master in environmental sciences), he joined the Microbial Genomics Group headed by Frank Oliver Glöckner in 2001 at the Max Planck Institute in Bremen, Germany. Since his Ph. D. focusing on the bioinformatic analysis of the marine organism Rhodopirellula baltica in 2004, he works as a research scientist and co-initiated the EU-funded project MetaFunctions which includes partners from Germany, Poland and Switzerland.

The Genomes Mapserver: an integrative tool for ecological genomics and metagenomics

Thierry Lombardot, Renzo Kottmann and Frank Oliver Glöckner

Today, more than 20 genomes of marine prokaryotic organisms are available in public databases. This number is going to increase dramatically since the Moore Foundation is starting to release around 90 genome sequences of marine origin. Furthermore, large-scale metagenomic studies focus on marine habitats, revealing a plethora of new genes and high prokaryotic diversity (e.g. the Sargasso Sea project).
These sequencing efforts lead to the emergence of "marine ecological genomics", defined as the application of genomic sciences to understanding the structure and function of marine ecosystems. The exponentially growing genomic data source represents a huge potential to gain more insights into marine ecosystems by exploring possible correlations between the genetic potential and the corresponding habitat for prokaryotic key-organisms. Therefore, specialised bioinformatic platforms are needed to systematically acquire, store, analyse and visualise this deluge of sequence data within the ecological context.
The "Genomes Mapserver" is a Geographic Information System (GIS) to store and systematically analyse (meta-) genomic data in correlation with ecological information. It is developed within the framework of the EU-funded project MetaFunctions. Currently the focus is set to marine systems, but our framework can be expanded to integrate all kinds of ecological systems.
GIS are commonly used in the field of geology for data integration. A GIS is a combination of elements designed to store, retrieve, analyse and display geographic data. In our newly developed Genomes Mapserver, the sampling sites of marine (meta)-genomic studies are displayed within a browseable world map. Each sampling site can be selected to display the corresponding sequences and additional contextual information. The underlying database is designed to enable future data mining tasks to reveal possible gene patterns associated with a particular environmental context.
This integrative system is intended to support researchers to generate a better understanding of the functioning of ecosystems based on genomic and metagenomic sequence data.

Participants

Invited Speakers

Name		Organisation	country	email
Oded	Bèjà	Technion, Isreal Institute of Technology	Israel	beja@tx.technion.ac.il
Feng	Chen	US DOE Joint Genome Institute	US	fchen@lbl.gov
Andrea	de Bono	UNEP / DEWA / GRID-Europe	Switzerland	debono@grid.unep.ch
Bernhard	Fuchs	Max Planck Institute for Marine Microbiology	Germany	bfuchs@mpi-bremen.de
Anton	Güntsch	Botanic Garden & Bot. Museum, Berlin-Dahlem	Germany	a.guentsch@bgbm.org
Gerhard	Herndl	Royal NIOZ	Netherlands	herndl@nioz.nl
Uwe	John	Alfred-Wegner-Institute Bremerhaven	Germany	ujohn@awi-bremerhaven.de
Ian	Joint	Plymouth Marine Laboratory	UK	i.joint@pml.ac.uk
Klaus	Jürgens	Baltic Sea Research Inst. Warnemünde, IOW	Germany	klaus.juergens@io-warnemuende.de
Wiebe	Kooistra	Stazione Zoologica Anton Dohrn	Italy	kooistra@szn.it
Thierry	Lombardot	Max Planck Institute for Marine Microbiology	Germany	tlombard@mpi-bremen.de
Alexander	Loy	University of Vienna	Austria	loy@microbial-ecology.net
Gurvan	Michel	Station Biologique de Roscoff	France	gurvan@sb-roscoff.fr
Phillip	Neal	Marine Biology Laboratory (MBL) Woods Hole	US	pneal@mbl.edu
Carlos	Pedrós-Alió	Institut de Ciènces del Mar, CMIMA, CSIC	Spain	cpedros@cmima.csic.es
Jakob	Pernthaler	University Zurich, Limnological Station	Switzerland	pernthaler@limnol.unizh.ch
Francisco	Rodriguez-Valera	Universidad Miguel Hernandez	Spain	frvalera@umh.es
Ramon	Rosselló-Mora	Inst. Mediterrani d'Estudis Avançats, CSIC-UIB	Spain	rossello-mora@uib.es
David	Scanlan	University of Warwick	UK	D.J.Scanlan@warwick.ac.uk
Thomas	Schweder	EMA-University Greifswald	Germany	schweder@uni-greifswald.de
Hanno	Teeling	Max Planck Institute for Marine Microbiology	Germany	hteeling@mpi-bremen.de
Klaus	Valentin	Alfred-Wegner-Institute Bremerhaven	Germany	kvalentin@awi-bremerhaven.de
Edward	Vanden Berghe	VLIZ, Flanders Marine Institute	Belgium	wardvdb@vliz.be
Jean	Weissenbach	GENOSCOPE	France	jsbach@genoscope.cns.fr

Participants

Agnieszka	Rybarczyk	Poznan University of Technology	Poland	arybarczyk@cs.put.poznan.pl
Josefa	Antón	Universidad de Alicante	Spain	anton@ua.es
Edmund	Bäuerlein	MPI for Biochemistry (retired)	Germany	e_baeuerlein@yahoo.de
Beatriz	Diez Moreno	Stockholm University	Sweden	beatrizdiez.moreno@botan.su.se
Alexis	Dufresne	Station Biologique de Roscoff	France	dufresne@sb-roscoff.fr
Jane	Heywood	National Oceanography Centre, Southampton	UK	jlh4@noc.soton.ac.uk
Manfred	Höfle	GBF Braunschweig- Division Microbiology	Germany	mho@gbf.de
Olaf	Kaiser	Bielefeld University	Germany	olaf.kaiser@genetik.uni-bielefeld.de
Andreas	Krell	Alfred-Wegner-Institute Bremerhaven	Germany	akrell@awi-bremerhaven.de
Isabelle	Mary	National Oceanography Centre, Southampton	UK	imary@noc.soton.ac.uk
Martin	Ostrowski	University of Warwick	UK	M.Ostrowski@warwick.ac.uk
Frederic	Partensky	Station Biologique de Roscoff	France	partensky@sb-roscoff.fr
Marcin	Radom	Poznan University of Technology	Poland	marcin.radom@cs.put.poznan.pl
Gustaf	Sandh	Stockholm University	Sweden	sandh@botan.su.se

Local guests

Name		Organisation	country	email
Marga	Bauer	MPI for marine Microbiology	Germany	mbauer@mpi-bremen.de
Dietmar	Blohm	University Bremen	Germany	dhb@biotec.uni-bremen.de
Michael	Diepenbrock	Alfred-Wegner-Institute, University Bremen	Germany	mdiepenb@uni-bremen.de
Marc	Einsporn	Alfred-Wegner-Institute Bremerhaven	Germany	meinsporn@awi-bremerhaven.de
Paola	Gomez	MARMIC int. Ph D rearch school, Bremen	Germany	pgomez@marmic.mpg.de
Jens	Harder	MPI for marine Microbiology	Germany	jharder@mpi-bremen.de
Elisabeth	Helmke	Alfred-Wegner-Institute Bremerhaven	Germany	ehelmke@awi-bremerhaven.de
Otthein	Herzog	University Bremen	Germany	herzog@informatik.uni-bremen.de
Renzo	Kottmann	MPI for marine Microbiology	Germany	rkottman@mpi-bremen.de
Stefan	Kurtz	University Hamburg	Germany	kurtz@zbh.uni-hamburg.de
Katja	Metfies	Alfred-Wegner-Institute Bremerhaven	Germany	kmetfies@awi-bremerhaven.de
Uta	Passow	Alfred-Wegner-Institute Bremerhaven	Germany	upassow@awi-bremerhaven.de
Michael	Richter	MPI for marine Microbiology	Germany	mrichter@mpi-bremen.de
Regina	Schauer	MPI for marine Microbiology	Germany	rschauer@mpi-bremen.de
Meinhard	Simon	ICBM University Oldenburg	Germany	m.simon@icbm.de
Francesca	Simonato	MPI for marine Microbiology	Germany	fsimonat@mpi-bremen.de
Matthias	Ullrich	International University Bremen, IUB	Germany	m.ullrich@iu-bremen.de
Patricia	Wecker	MPI for marine Microbiology	Germany	pwecker@mpi-bremen.de
Nadine	Winkelmann	MPI for marine Microbiology	Germany	nwinkelm@mpi-bremen.de
Martin	Zacharias	International University Bremen, IUB	Germany	m.zacharias@iu-bremen.de

Organisors

Frank Oliver	Glöckner	MPI for marine Microbiology, IUB	Germany	fog@mpi-bremen.de
Rudolf	Amann	MPI for marine Microbiology	Germany	ramann@mpi-bremen.de
Rebecca	Ludwig	EMPA (Env. & Marine PM Agency, Bremen)	Germany	r.ludwig@empa-bremen.de
Johanna	Wesnigk	EMPA (Env. & Marine PM Agency, Bremen)	Germany	j.wesnigk@empa-bremen.de