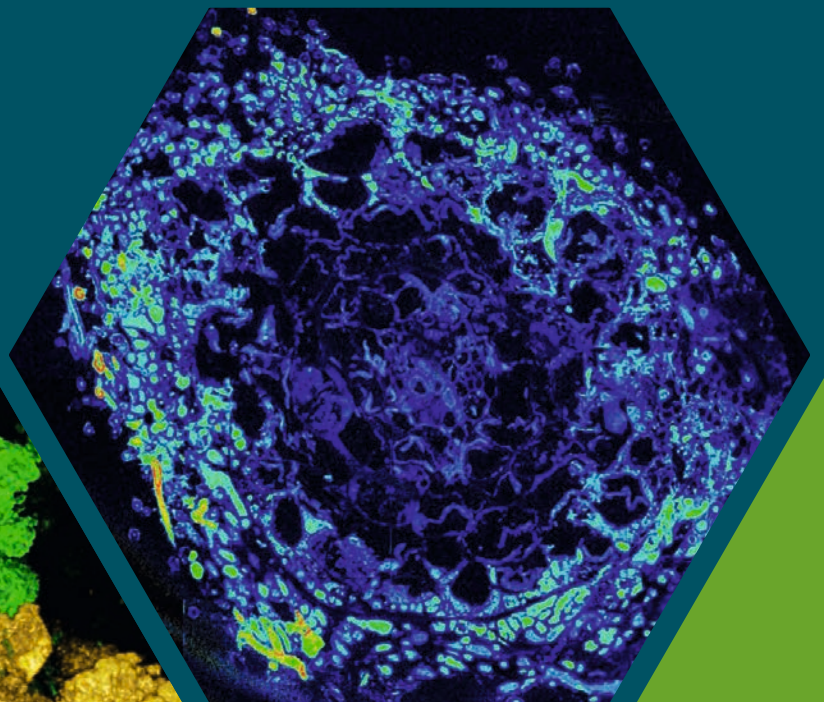
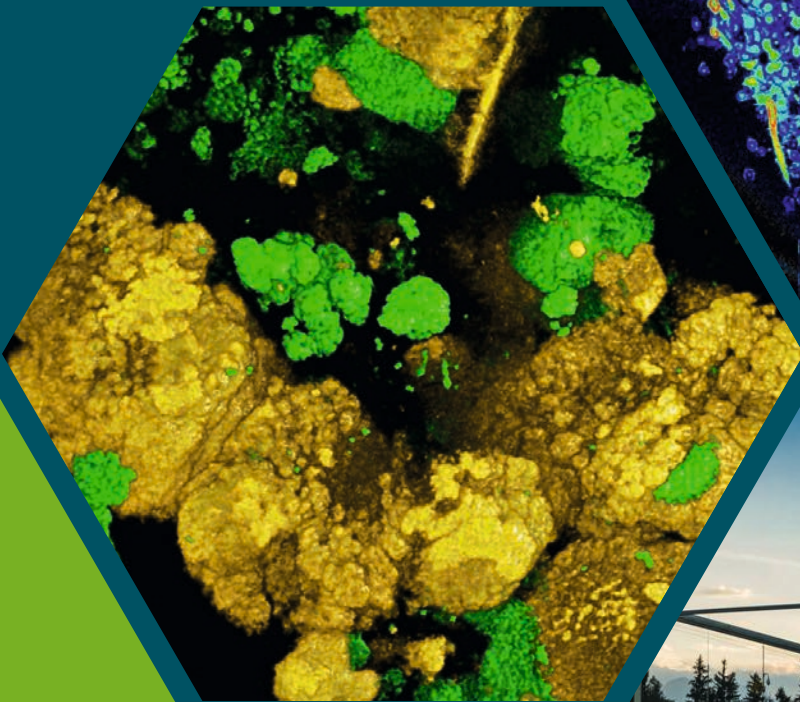


DEPARTMENT OF MICROBIOLOGY AND ECOSYSTEM SCIENCE
UNIVERSITY OF VIENNA

ANNUAL REPORT

2017



**Department of Microbiology and Ecosystem Science
Research Network “Chemistry meets Microbiology”
University of Vienna**

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INTRODUCTION

Our modern societies are facing numerous fundamental challenges. During the last decades we have learnt that several of these challenges are tightly linked to microbiology and ecosystem science. Microbial communities are of central importance for environmental and human health, for food security, sustainable agriculture and forestry, clean oceans and inland water resources, and provide fascinating opportunities for clean and efficient energy generation, climate action, and improved resource efficiency. Exploring the links between microbiology and ecosystems needs interconnected research, resources, and knowledge across different fields, technologies and disciplines.

The Department of Microbiology and Ecosystem Science (DMES) of the University of Vienna was founded in 2011 to create a tightly connected interdisciplinary research environment. It currently consists of three units: the Divisions of Microbial Ecology (DOME), Terrestrial Ecosystem Research (TER), and Computational Systems Biology (CUBE). The department's research centers around microbial communities and their theatres of activity – the microbiomes - in various aquatic and terrestrial ecosystems and their interaction with protozoa, plants, animals, and humans. We aim to provide a fundamental understanding of the links between microbiomes and their abiotic and biotic environment, and to determine the consequences for the functioning of Earth's ecosystems. For this purpose, we also develop, improve, and apply computational methods for the interpretation of molecular information, and establish and analyze quantitative mathematical models.

In this booklet, we introduce DMES and its achievements in 2017. We are a unique research unit in terms of scientific expertise, equipment, and techniques. Also in 2017, DMES was continuously growing. Within our 12 research groups and three research facilities, 117 employees and students from 24 nations look back to a productive, successful, and enjoyable year 2017. We hope you enjoy the tour to our research topics, methods and technologies, group leaders, and much more, provided by this booklet.



RESEARCH NETWORK: CHEMISTRY MEETS MICROBIOLOGY

DEPARTMENT OF MICROBIOLOGY AND ECOSYSTEMS SCIENCE (DMES)

Head of Department: Michael Wagner

Deputy Heads: Matthias Horn, Thomas Rattei, Andreas Richter

Division of Computational Systems Biology (CUBE)

Head: Thomas Rattei
Harald Marx

Division of Microbial Ecology (DOME)

Head: Michael Wagner
David Berry
Holger Daims
Stephanie Eichorst
Craig Herbold
Matthias Horn
Alexander Loy
Jillian Petersen
Markus Schmid
Dagmar Wöbken

Division of Terrestrial Ecosystem Research (TER)

Head: Andreas Richter
Christina Kaiser
Wolfgang Wanek

Administration & Technicians

Florian Goldenberg
Gabriele Kaindl

Administration & Technicians

Nadja Draxl
Tamara Matzhold
Cornelia Mazza
Gabriele Schwammel
Barbara Urbanic

Administration & Technicians

Sabrina Pober
Sabine Maringer
Christof Oberwalder
Ludwig Seidl
Margarete Watzka

Life Science Compute Cluster

Nano-SIMS

Arno Schintlmeister

SILVER –

Stable Isotope Facility

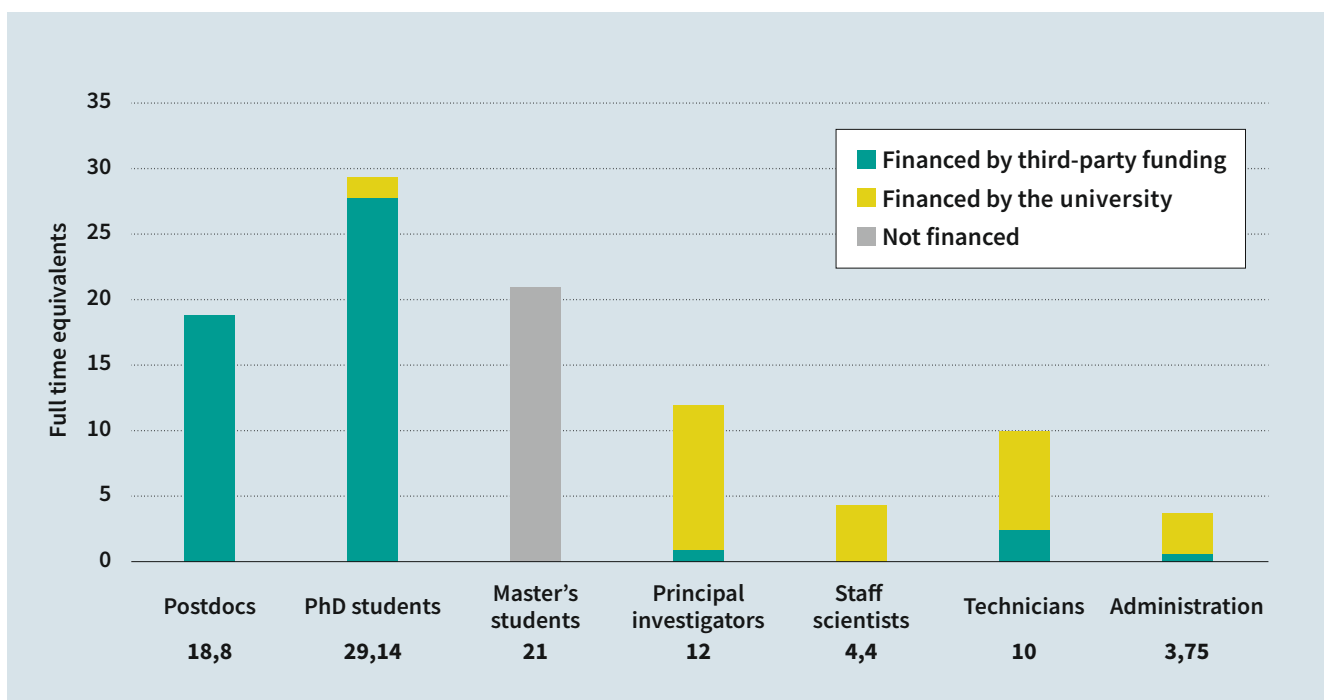


DMES IN BRIEF

THE UNITED NATIONS OF DMES (April 2017)

 Austria 56	 Croatia 1
 Germany 21	 Greece 1
 PR China 7	 Hungary 1
 USA 4	 Israel 1
 France 3	 Japan 1
 Italy 3	 Malta 1
 Australia 2	 Netherlands 1
 Canada 2	 Norway 1
 Portugal 2	 Romania 1
 Slovak Rep. 2	 Singapore 1
 Spain 2	 South Korea 1
 Brazil 1	 UK 1

PERSONNEL

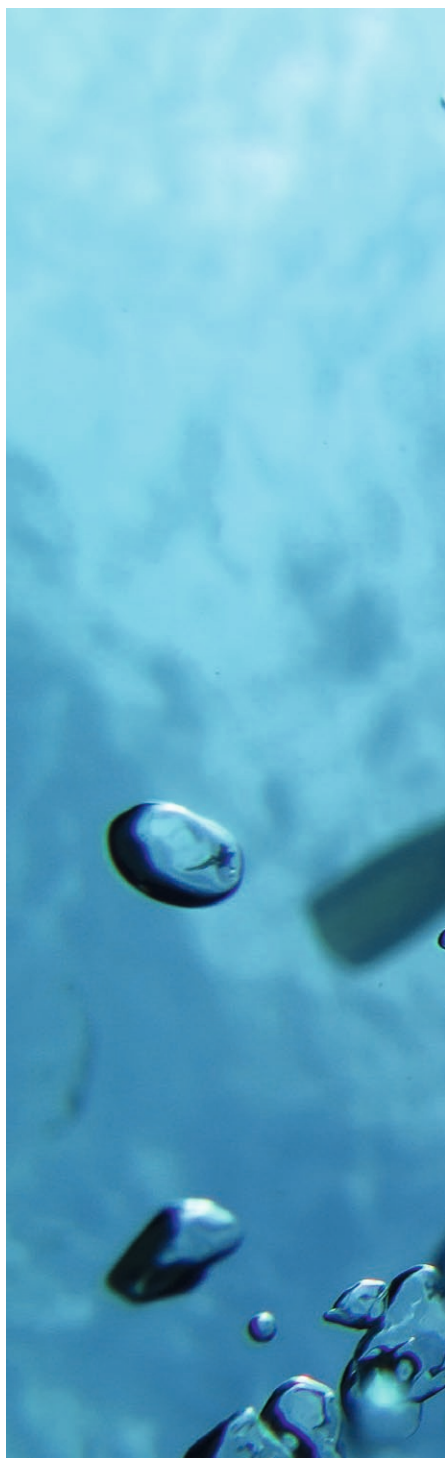
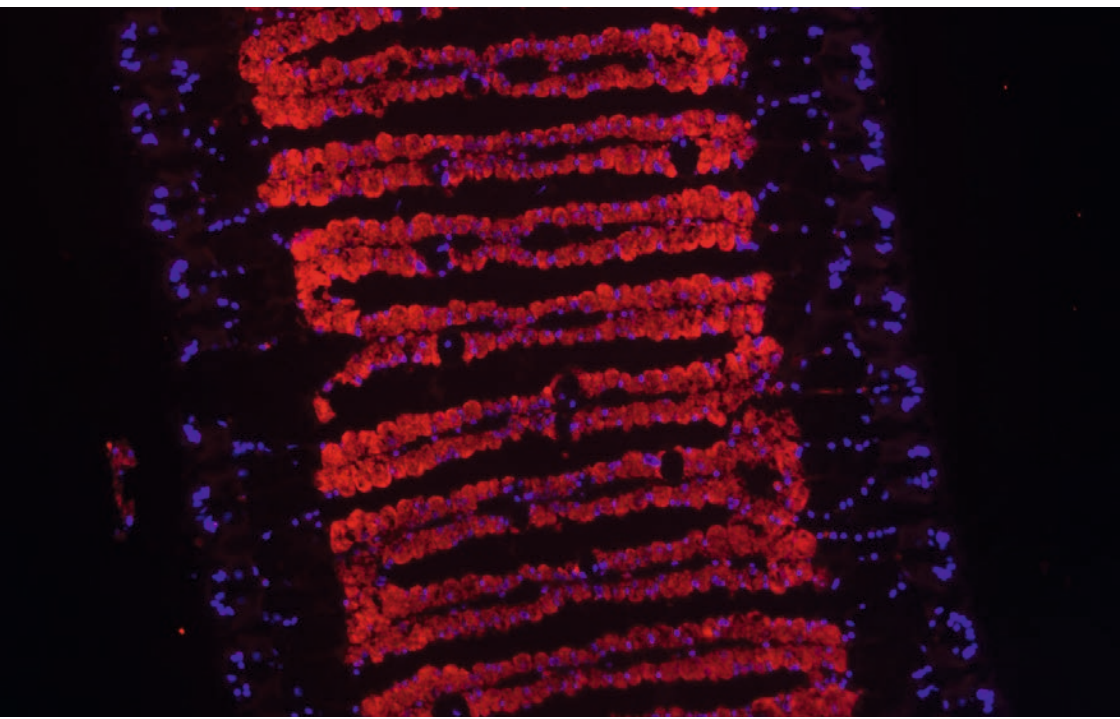


DIVISIONS

The **Division of Microbial Ecology** includes **seven research groups**. The group leaders are David Berry, Holger Daims, Matthias Horn, Alexander Loy, Jillian Petersen, Michael Wagner, and Dagmar Woebken. All groups share lab and office space, they are tightly connected through their research topics, joint projects, joint seminars, and the application of similar molecular methods. The Division is in charge of the NanoSIMS lab.

The **Division of Terrestrial Ecosystem Research** includes **three research groups**. The group leaders are Andreas Richter, Christina Kaiser and Wolfgang Wanek. The research groups are closely working together as evidenced by many joint publications and projects, by joint seminars and interrelated research areas (ecosystem ecology and global environmental change). TER runs the **SILVER laboratory** (Stable Isotope Laboratory of the University of Vienna for Environmental Research), the instruments of which are being part of the Large Instrument Facility for Advanced Isotopes in Life Sciences.

The **Division of Computational Systems Biology** includes **two research groups**. The group leaders are Harald Marx and Thomas Rattei. The Rattei group focuses on "In silico genomics" and the Marx group on "Computational peptidomics". Both groups share office space, an in-house IT infrastructure, and are tightly connected through their research topics, joint projects, joint seminars, and the application of similar bioinformatic methods.





RESEARCH TOPICS

Microbiome	8
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Microbiology of Soils	11
Microbial Symbionts and Pathogens	12

MICROBIOME

THE NEW FRONTIER IN BIOSCIENCE

Microorganisms are the dominant form of life on Earth – they are ubiquitous and the vast majority provide vital services for the environment or their host.

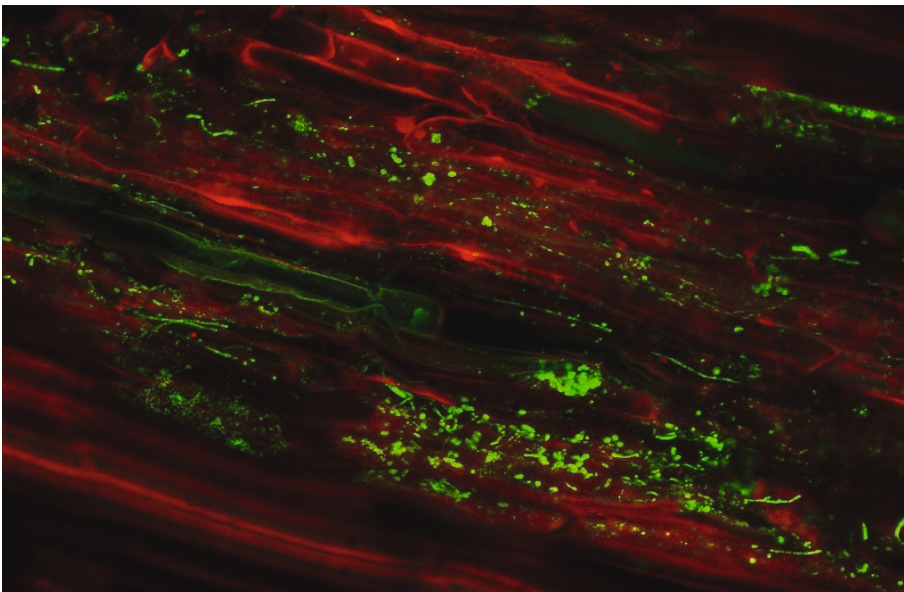
The term microbiota describes the community of microorganisms that inhabit a given environment. This includes environments as different as marine sediment, grassland soil, wastewater treatment plants, and the human body. This ecological community may be composed of commensal, symbiotic or pathogenic organisms that come from

The microbiota in biotechnological processes is responsible for cleanup of anthropogenic wastes or environmental pollution. The symbiotic microbiota is a vital determinant of the physiology and health of its host – be it a unicellular eukaryote, a plant, an animal or a human individual.

Research at DMES strives to unlock the secrets of diverse environmental and host-associated microbiomes and translate this fundamental knowledge into a better understanding of the



The human body hosts at least as many microbial cells as human cells.



Microorganisms (in green) associated with rice plant root

any of the domains of life – bacteria, archaea, eukaryotes or viruses. The sum of the genomic information of a given microbiota, which translates into its manifold functions and phenotypes, is called the microbiome.

The environmental microbiota is the driver of large-scale ecosystems processes and global nutrient cycles.

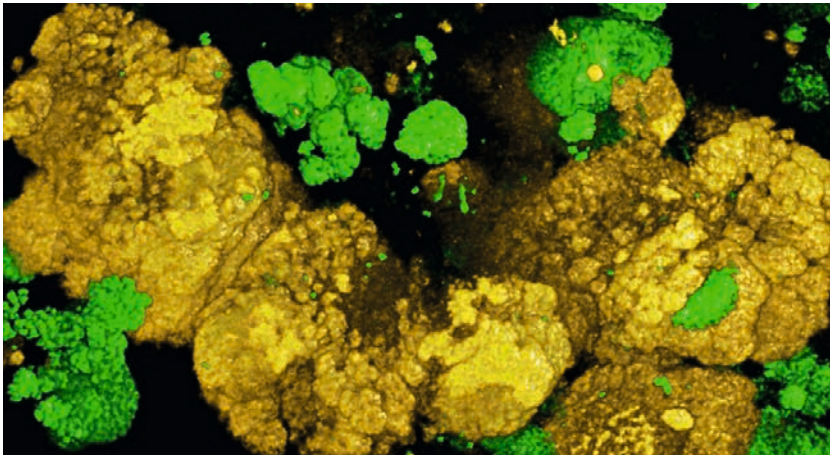
processes and factors that govern global changes of our planet and the health of plants, animals, and humans. Using holistic experimental approaches that integrate contemporary microbiome methods, we investigate the composition, dynamics, and functional roles of complex microbiota members and their reciprocal impact on their biotic and abiotic environment.

Selected microbiomes under investigation at DMES

- Host-associated microbiomes
 - Human
 - Vertebrate animals, e.g. mice, common marmosets
 - Invertebrate animals, e.g. bivalves, insects, sponges
 - Plants, e.g. rice
 - Protozoa
- Environmental microbiomes
 - Soils, e.g. wetland, grassland, permafrost, crusts
 - Marine sediments
- Microbiomes in biotechnology and industry
 - Wastewater treatment
 - Bottled water
- Ancient microbiomes
 - The iceman ‘Ötzi’

MICROBIAL NITROGEN CYCLING

CRUCIAL FOR LIFE AND ENVIRONMENTAL HEALTH



Visualization of ammonia-oxidizing bacteria (green) and nitrite-oxidizing bacteria (yellow) in biofilm from a wastewater treatment plant.

Research topics related to N-cycling at DMES

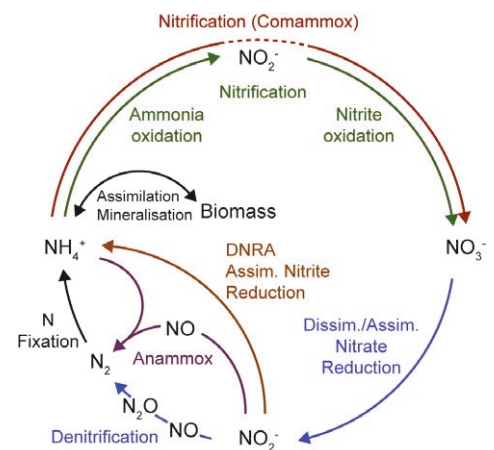
- Nitrogen fixation by free-living and plant-associated microorganisms
- Microbiology of nitrification
 - Physiology, biochemistry, and evolution of ammonia oxidizing archaea and bacteria, nitrite-oxidizing bacteria and the complete nitrifiers (comammox)
 - In soils, freshwater habitats, and the oceans
 - In wastewater treatment plants and drinking water treatment systems
- Utilization and degradation of organic nitrogen compounds by microorganisms
- Nitrogen use efficiency of terrestrial microbes and plants
- NO, N₂O emissions by nitrogen-cycling microorganisms
- Development of isotope techniques to quantify nitrogen cycle processes

All living organisms on our planet need nitrogen (N) for the biosynthesis of nucleic acids, proteins, and other cellular components and thus are directly connected to, and dependent upon, the biogeochemical N-cycle. It consists of multiple processes, including making inorganic nitrogen (atmospheric N₂) available to organisms, interconverting inorganic soluble and gaseous nitrogen forms, and ultimately recycling them back to atmospheric N₂. Many of the individual steps in this cycle are catalyzed exclusively by bacteria and archaea.

During the last century, humans have strongly impacted the global N-cycle by burning fossil fuels, cultivating plants that live in symbiosis with N₂-fixing microbes, and most importantly by using artificial nitrogen fertilizers. These anthropogenic transformations of the N-cycle continue at a record pace. More than two billion people could not be fed without artificial nitrogen fertilizers, but as fertilization efficiency is often below 50%, enormous amounts of anthropo-

genic ammonium affect the N-cycle. This has vast ecological and economical consequences ranging from biodiversity loss, eutrophication and dead zones in water bodies to increased emission of the potent greenhouse and ozone-depleting gas N₂O. In this precarious situation, management strategies are needed to ensure a more efficient use of fertilizers and to reduce N₂O emissions. However, these important measures are hampered by surprisingly large gaps in our fundamental understanding of the microbiology and ecology of N-cycling.

DMES includes internationally leading labs in N-cycle research. Our research aims at illuminating the complex biology of N-cycling, from the level of whole processes in different ecosystems to the ecophysiology and biochemistry of single microbial species. The obtained new insights contribute to a holistic picture of the N-cycle, which is indispensable for predicting and mitigating environmental threats caused by human activities and global change.



Schematic illustration of the Nitrogen-cycle

MICROBES AND CLIMATE

A RECIPROCAL INTERACTION



Microorganisms have shaped the climate throughout the Earth's history. And, the microbiomes of Earth's ecosystems have been and are currently affected by the climate. Individual microorganisms may acclimate or adapt to changing environmental conditions, leading to shifts in the composition and function of microbial communities, alterations in major biogeochemical cycles and, eventually, in feedback reactions to the climate. For example, global warming increases the breakdown and mineralization of organic matter in wetlands and permafrost soils, inducing a microbially-mediated soil-climate feedback through increased greenhouse gas production, the possible dimension of which is threatening, although still a matter of debate.

The functional plasticity and almost inconceivable diversity of microbes in the environment and the complex interplay of microbes with other organisms such as plants and soil fauna, make the prediction of future effects of climate change on microbially-mediated ecosys-

tem functions arguably one of the most challenging frontiers of today's ecology research.

Global change research at DMES focuses on the questions which and, more importantly, how microorganisms will respond to and influence climate change in the upcoming decades to centuries. To address these questions, we apply the entire modern tool kit of molecular and stable isotope techniques for studying complex microbial communities and their functions in their natural environment. Our research focuses on identification and revealing the genetic and metabolic features of microbial key players of the carbon, nitrogen, phosphorus and sulfur cycle that have a disproportional negative or positive impact on climate change. More specifically, we aim at unraveling the complex metabolic interactions during organic matter degradation and how individual microorganisms influence the production of specific greenhouse gases such as methane and carbon dioxide in terrestrial and aquatic environments.

Microbial responses to climate change are tested in a multifactorial grassland experiment.

Selected climate and global change topics under investigation at DMES

- **Soil Warming**
 - Physiological acclimation of microbial communities
 - Permafrost-Climate feedbacks
 - Impact of sulfur-cycling microorganisms on wetland methane emission
- **Interactive effects of elevated atmospheric CO₂, warming and drought**
 - Effects on microbial carbon and nutrient cycling in soil
 - Changes in plant-microbe interactions, such as mycorrhizal associations
- **Nitrogen fertilization/ eutrophication and nutrient imbalances**
 - Effects of nutrient imbalances on microbial processes

MICROBIOLOGY OF SOILS

FUNDAMENT OF THE TERRESTRIAL ECOSYSTEM

Soils play a pivotal role in the functioning of the Earth's terrestrial ecosystems and harbor an almost inconceivable diversity of microorganisms. Soil microorganisms are the drivers of global nutrient cycles (such as the carbon, nitrogen, phosphorus and sulfur cycles) and influence the Earth's climate. Our research in this area addresses fundamental questions on the factors governing this extensive microbial diversity and the function of microorganisms in their environment, specifically the role that microorganisms play in the decomposition, transformation and build-up of soil organic matter, the largest reservoir of organic carbon on Earth. We also address questions on interactions amongst microorganisms and of microorganisms with other organisms such as plants and soil fauna to better understand soil organic matter dynamics and nutrient cycling. Furthermore, we integrate concepts of ecological theory into the realm of microbial ecology



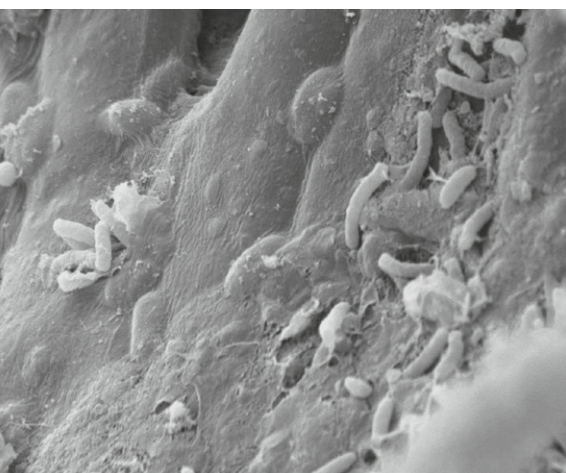
Sampling in the Negev desert

and investigate pressing environmental issues such as the impact of climate and land-use change on the functioning of soil ecosystems and potential repercussions on human wellbeing.

These questions are investigated at various scales; from the ecosystem process level (i.e. where microbial processes become evident) to the single-cell level (i.e. μm scale, where microorganisms operate). We use state-of-the-art techniques such as metagenome and metatranscriptome sequencing, single-cell methods (fluorescence *in situ* hybridization, NanoSIMS and Raman microspectroscopy), stable isotope tracing and biomarker fingerprinting, various biogeochemical methods, isotope pool dilution techniques, and mathematical modelling. Focal environments that we study include permafrost soils, tropical rainforests, biological soil crusts and temperate soils in forests, grasslands, paddies and wetlands.

Research topics related to the microbiology of soils at DMES

- N_2 fixation (free-living diazotrophs in soil and plant-associated diazotrophs)
- Microbial dormancy and resuscitation
- Soil organic matter formation and soil carbon storage
- Extracellular decomposition and microbial utilization of soil organic C, N and P
- Microbial C and N use efficiency and ecological stoichiometry
- Plant-soil-microbe interactions
- Mathematical modelling of soil microbial communities



Bacteria colonizing a mycorrhizal root tip of a beech tree (Scanning electron microscopy image, in collaboration with the Core Facility for Cell Imaging and Ultrastructure research)

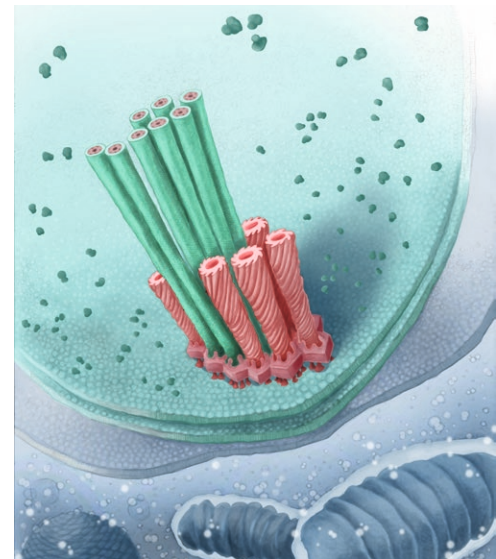
MICROBIAL SYMBIONTS AND PATHOGENS

No one lives alone – the life history of all organisms has forever been and still is affected by diverse interactions with microbes. These associations can range from mutualism to parasitism, with far-reaching consequences for both partners.

Beneficial symbionts may provide essential nutrients to their hosts, in exchange for shelter and an optimal niche. Bacterial pathogens exploit their hosts as part of their life cycle, sometimes with fatal consequences for their partners. Yet, there is a fine line between the two: The molecular mechanisms underlying microbe-host interactions are often similar between beneficial

symbionts and parasitic pathogens, and the outcome of many of these associations often depends on environmental conditions, and genetics and lifestyle (e.g. nutrition) of the host.

At DMES we investigate a number of model and non-model systems to better understand the interplay between microbes and their hosts. By focusing in from complex microbiomes to mainly bilateral interactions, we strive to unravel the molecular and physiological basis of microbial symbioses and their evolutionary histories using a comprehensive approach including state-of-the-art experimental methods and computational analyses.



Secretion system of *Amoebophilus asiaticus* (illustrated by Leo Popovich)



Sampling in the sea at Elba

Selected microbial symbionts and pathogens under investigation at DMES

- Human and animal microbiota
 - Microbial ecology of different body habitats (gut, skin, etc.)
 - Interactions between commensals and pathogens
 - Functional roles in health and disease
- Beneficial symbionts in animals
- Intracellular microbes and pathogens
 - Chlamydiae in the environment
 - Intranuclear bacteria
 - Bacterial symbionts of amoeba
- Microbe-plant interactions

SEMINAR SPEAKERS



Chantal Abergel
Centre National de la
Recherche Scientifique Marseille



Peer Bork
EMBL Heidelberg



Konstantin Gavazov
Umeå University



Eva Heinz
Sanger Institute



Gunda Köllensperger
University of Vienna



Harald Marx
University of Wisconsin-Madison



Alexander Moschen
University of Innsbruck



Dianne Newman
California Institute of Technology

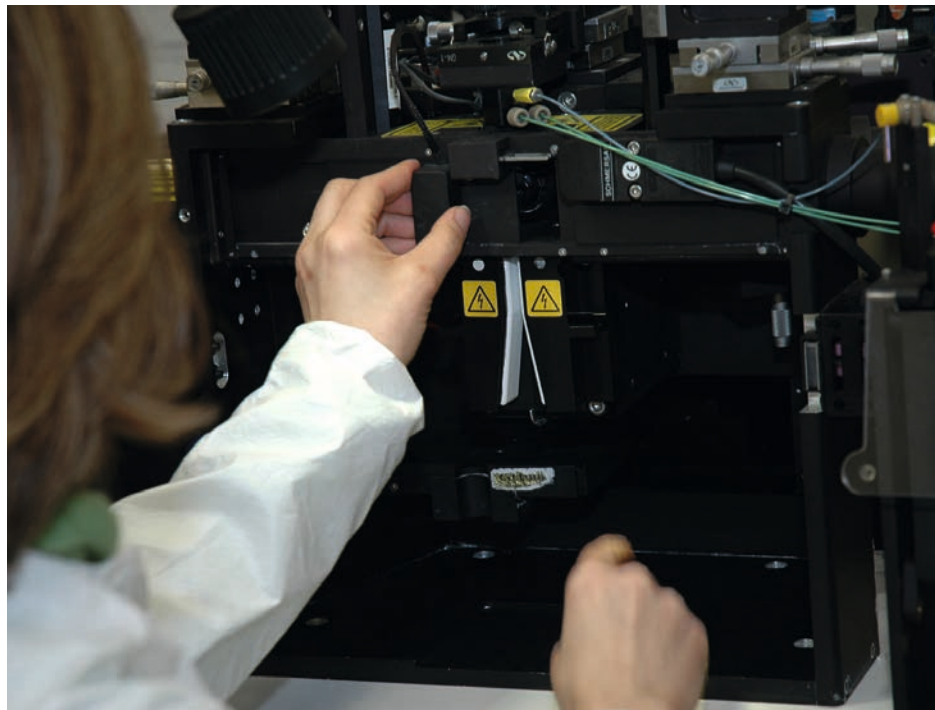
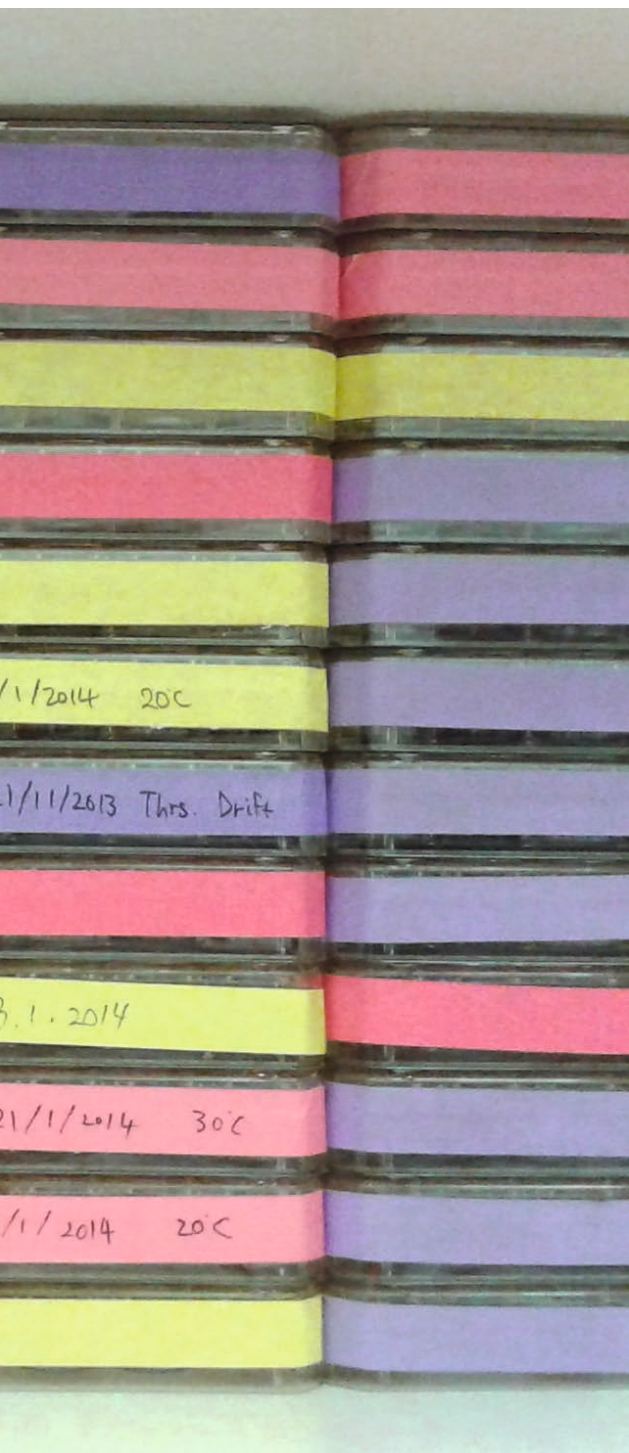


Christian Sieber
University of Berkeley



Sergey Zotchev
University of Vienna





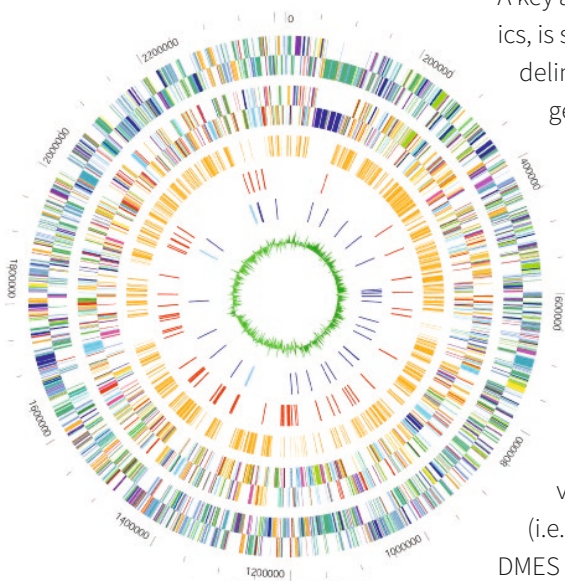
METHODS & TECHNOLOGIES

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COMPARATIVE GENOMICS

Life on Earth has evolved for some billion years. Living organisms are found in virtually every environment, surviving and thriving in extremes of heat, cold, radiation, pressure, salt, acidity, and darkness. Often in these environments, only “simple” microorganisms are found and the only nutrients come from inorganic matter. The diversity and range of environmental adaptations indicate that even tiny microbes long ago “solved” many problems for which scientists and engineers are still actively seeking solutions.

These secrets are enclosed in the genomes, which encode the construction plans of cells and organisms. The first complete bacterial genome was deciphered in 1995. Since then the number of complete genomes sequenced has been growing exponentially. Only powerful computers and sophisticated bioinformatics software allows us to investigate these massive data.



The chromosome of *Protochlamydia amoebophila* revealed insights into the early evolution of chlamydial pathogens and symbionts.

The majority of microorganisms and viruses cannot be cultivated in the laboratory so far. In order to study the diversity, composition and structure of microbial communities, amplicon sequencing and metagenomics are applied to nucleic acid sequences directly isolated from the environment. Specific computational methods allow to reconstruct nearly complete genomes from metagenomes, and to predict phenotypic traits from these genome sequences.

DMES is involved in many genome-sequencing and metagenomics projects and has established efficient tools and workflows. We are engaged in maintaining and improving genomic data in public databases. We also create new software to push the limits of accuracy and throughput in computational genomics.

A key aspect of computational genomics, is structural genome annotation to delineate genomic elements such as genes, promoters, regulatory elements and more recently (non-) coding elements in “junk” DNA. However, this process frequently fails to identify elements coding for bioactive peptides, like small open reading frames (smORFs), single exon genes, overlapping genes and genes with unconventional translation start sites (i.e. non-AUG), among others. Hence, DMES develops proteogenomic tools that leverage next-generation sequencing and mass spectrometry-based proteomics to advance present annotation efforts.



From the mummy of the Tyrolean Iceman we could reconstruct genome sequences of himself, his microbiome and even pathogens, including the stomach bacterium *Helicobacter pylori*.

Methods and resources developed by DMES

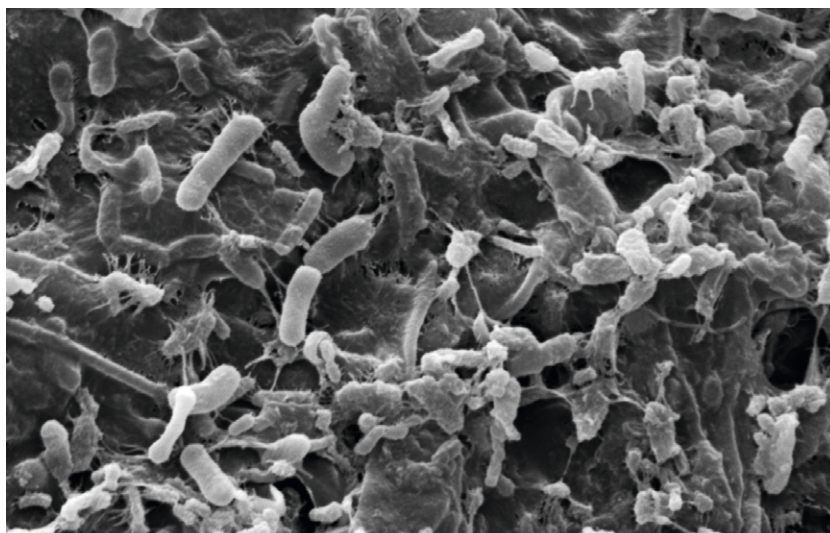
- Genome annotation
 - EffectiveDB
 - SIMAP
 - pCOMP
 - GenSkew
 - ConsPred
- Functional genomics
 - NVT
- Comparative Genomics
 - Gepard
 - PICA
- Metagenomics
 - probeBase
 - probeCheck
 - HoloVir
 - Viral Orthologous Groups

MICROBIAL COMMUNITY MODELLING

Microbial communities in natural environments consist of a plethora of functionally different individuals that interact with each other in a structured space. Without interactions among units of a system one could extrapolate from the behavior of the units to the behavior of the system. However once interactions occur, collective phenomena can emerge and modify system behavior beyond our understanding of its individual parts. In DMES, we use mathematical modelling as a tool to explore the mechanisms that drive dynamics and functioning of complex microbial communities.

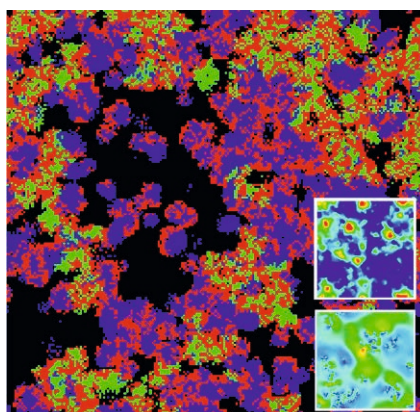
The wealth of microbial interactions in natural communities is rooted in their necessity to perform “leaky” functions. One example is microbial decomposition of complex organic matter. Microbes release specific extracellular enzymes that cleave complex organic molecules into smaller units which can then be taken up into microbial cells. As small molecules are readily diffusible in a liquid environment, this allows other nearby microbes to exploit these enzymatic products leading to a spectrum of social behaviors such as cooperation, “cheating” or “division of labour” by metabolic specialization. Social interactions among individual microbes lead to the emergence of collective system behaviors which determine not only community metabolism, but also the system’s response, resistance and resilience to environmental change.

We use individual-based modelling to simulate competitive and synergistic interactions among microbial organic matter decomposers in a spatially structured micro-environment, which allows us to explore how emerging



Interacting soil bacterial community colonising the surface of a root. (Scanning electron microscopy image in collaboration with Core Facility Cell Imaging and Ultrastructure Research, University of Vienna)

system properties affect community carbon and nitrogen turnover. We also model microbial interaction networks using Lotka-Volterra dynamics and other approaches to evaluate how diverse interactions affect community properties such as stability and resilience. Using environmental co-occurrence information from metagenomic datasets, we seek to reconstruct putative interaction networks in order to identify keystone species in microbial communities.



Methods and resources developed or applied in DMES

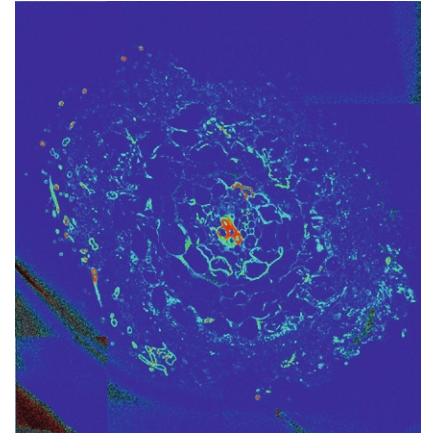
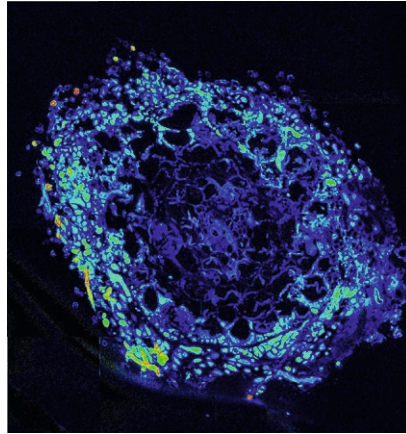
- ◆ Individual-based microbial community modelling
- ◆ Co-occurrence networks in environmental samples
- ◆ Computational approaches for studying molecular inter-species interactions

Snapshot of an individual-based model simulation of microbes belonging to three different functional groups decomposing leaf litter. Each coloured dot represents a microbe, insets show distribution of soluble metabolic products.

ISOTOPES

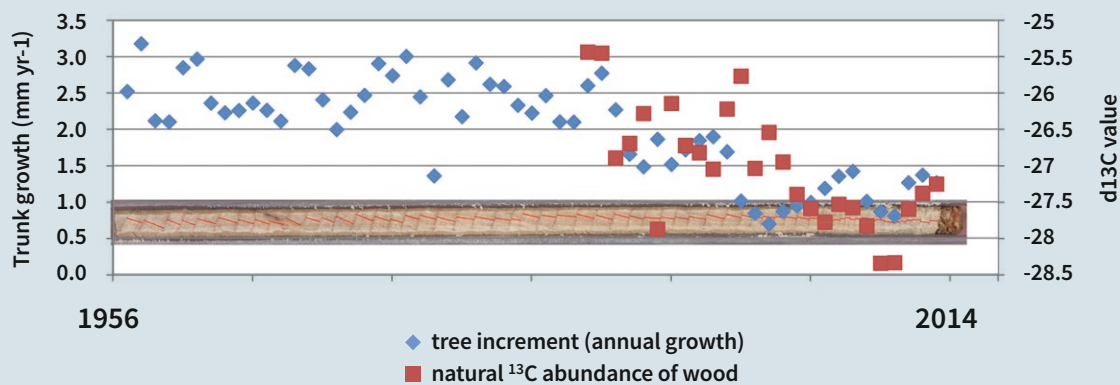
Isotopes are indispensable tools in microbial ecology and ecosystem research. Without them linking microbes to functions, exploring the roles of uncultivable microorganisms, following host-microbe interactions and quantifying ecosystem processes would not be possible. A wide range of stable isotopes and radioisotopes are applied, mainly of elements constituting the largest fraction of living organisms (H, C, N, O, S, and P), from the single cell to the ecosystem level. DMES has developed and pioneered isotope methodology, including:

- Stable isotope probing (SIP) of nucleic acids or PLFA to identify not yet cultured environmental microbes that are actively processing target compounds
- Radioisotope approaches using isotope microarrays and combined FISH-microautoradiography to link microbial community structure with function
- NanoSIMS and Raman approaches for chemical imaging of isotope incorporation within single cells
- Isotope tracing of processes such as N_2 fixation, cellulose breakdown, microbial metabolism in gut and soils, microbial growth in complex environments, and nitrogen cycling processes
- Isotope pool dilution measurements of processes such as microbial C, N, P and S cycling in soils and sediments
- Applications of natural stable isotope abundances for *in situ*, minimally-invasive, tracing of matter flow, and source-sink process investigations



NanoSIMS images of mycorrhizal C and N exchange.
On the left: Visualisation of nitrogen uptake by mycorrhizal fungi (as ^{15}N).
On the right: Visualisation of recent plant photosynthates (as ^{13}C) in a cross-section of an ectomycorrhizal beech root using NanoSIMS.

Increment width and stable isotope analyses in tree wood cores allow reconstruction of tree physiology and paleoclimate



Dating and stable isotope analysis of tree wood cores allow paleoclimate reconstructions.

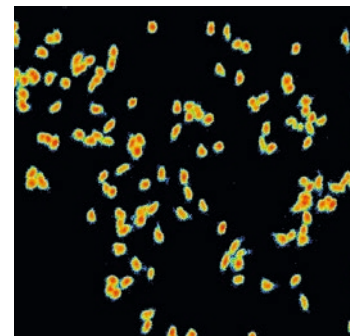
SINGLE CELL ANALYSES

Virtually all microbial communities on our planet are dominated by a great diversity of uncultured microorganisms, which cannot be studied by traditional approaches of microbiology. In their habitats, microbes often coexist in spatially complex assemblies like biofilms and flocs. They colonize sediments, soils, roots, teeth, the gut, and many other environments with an intricate three-dimensional architecture. Within these consortia, microbes are influenced by numerous abiotic factors such as fluctuations in nutrient concentrations and other physicochemical parameters, and they are involved in a plethora of biotic interactions with each other and eukaryotic hosts.

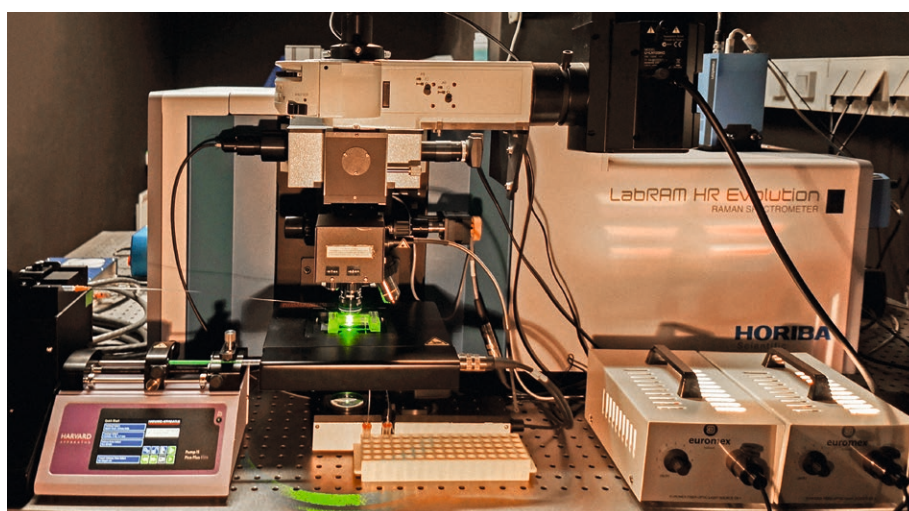
To understand this complex microbial life, we must literally dive into these microbial communities and look directly at the single cells and the microscopically small niches where they thrive and interact with other organisms. Only then we can decipher the *in situ* metabolic

activities and symbioses of uncultured microbes. However, single-cell microbiology is an enormous methodological challenge if we consider the tiny size of a microbial cell and the ultra-small amounts of substrates that are taken up, utilized, and exchanged by single cells.

DMES plays a leading role in the development and application of single-cell techniques to study uncultured microorganisms *in situ*. Our toolbox comprises cutting-edge methods for labeling cells with isotope tracers, detecting metabolic activities at the single cell level, monitoring the flow of substrates through microbial communities, resolving 3D localization patterns of microbial cells, and activity-based cell sorting for downstream analyses and single-cell genomics. All our research projects make heavy use of these approaches. We continually optimize and adapt our single-cell tools to address new research questions and push their limits of sensitivity, accuracy, and spatial resolution.



NanoSIMS visualization of the relative sulfur content within single cells of the nitrite-oxidizing bacterium *Nitrospira moscoviensis*.



A Raman microspectrometer that is used for analyzing the chemical and isotope composition of single microbial cells, and for sorting single cells based on their *in situ* metabolic activities in environmental and medical samples.

Single-cell methods and resources developed and/or maintained by DMES

- Detection and monitoring of metabolic activity; single cell stable isotope probing
 - NanoSIMS
 - Raman microspectroscopy
 - Microautoradiography combined with FISH
- Identification, visualization, and quantification of uncultured microbial cells
 - Fluorescence *in situ* hybridization (FISH)
 - Confocal laser scanning microscopy
 - In-house developed 3D visualization and image analysis software 'daimé'
- Single cell manipulation and sorting
 - Laser microdissection
 - FISH-based sorting
 - Raman microspectroscopy combined with microfluidics and optical tweezers



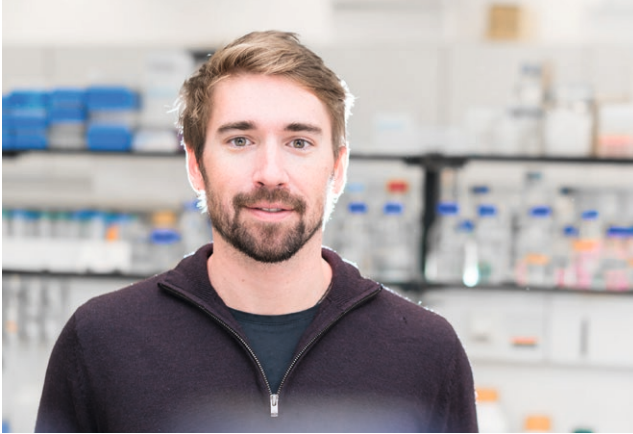


RESEARCH GROUP LEADERS

David Berry	22	Jillian Petersen	28
Holger Daims	23	Thomas Rattei	29
Matthias Horn	24	Andreas Richter	30
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Alexander Loy	26	Wolfgang Wanek	32
Harald Marx	27	Dagmar Wobken	33

DAVID BERRY

DOME – DIVISION OF MICROBIAL ECOLOGY



📌 Full Professor

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At DOME since 2009

since 2018: Full Professor, University of Vienna

2016–2017: Associate Professor, University of Vienna

2012–2016: Assistant Professor, University of Vienna

2009–2012: Postdoctoral Researcher, Univ. of Vienna

2009: Ph.D. in Environmental Engineering, University of Michigan

2006: M.S.E. in Environmental Engineering, University of Michigan

2005: B.S. in Bioresource Engineering, Rutgers University

Main research areas

- Ecology and evolution of the intestinal microbiota
- Intestinal microbiota and disease
- Modeling approaches to study microbial communities
- Development of novel methods to study uncultivated microorganisms *in situ*

Research in the group of David Berry (DB) is focused on the study of the intestinal microbiota and interactions of the microbiota with its host. He has pioneered the use of novel experimental and computational tools to reveal the function of the intestinal microbiota, and has developed single cell isotope labeling techniques to identify and characterize functional guilds in the intestinal ecosystem such as mucus-degrading microbiota. The research activities of DB include developing a fundamental understanding of the assembly and interactions of the intestinal microbiota. He is also involved in clinical studies related to chronic

intestinal inflammation and colorectal cancer, as well as the orchestrated assembly of the microbiota, maturation of the immune system, and neurodevelopment in premature neonates.

DB was recently awarded a European Research Council Starting Grant to study functional networks and keystone species in the gut microbiota. Publications authored by DB are mainly in Q1 (best 25% from the field) journals, including leading journals such as Nature and PNAS.

* At the time of the printing of this report in 2018, David Berry was already appointed Full Professor.

Selected publications

Lifestyle and horizontal gene transfer-mediated evolution of *Mucispirillum schaedleri*, a core member of the murine gut microbiota.

Loy A, Pfann C, Steinberger M, Hanson B, Herp S, Brugiroux S, Gomes Neto JC, Boekschoten MV, Schwab C, Urich T, Ramer-Tait A, Rattei T, Stecher B, Berry D.

2017 – *mSystems*, 2 (1) e00171–16

Pediatric obesity is associated with an altered gut microbiota and discordant shifts in Firmicutes populations. Riva A, Borgo F, Lascandro C, Verduci E, Morace G, Borghi E, Berry D. 2017 – *Environ Microbiol*, 19(1): 95–105

Tracking heavy water (D2O) incorporation for identifying and sorting active microbial cells.

Berry D, Mader E, Lee TK, Woebken D, Wang Y, Zhu D, Palitinszky M, Schintlmeister A, Schmid M, Hanson BT, Shterzer N, Mizrahi I, Rauch I, Decker T, Bocklitz T, Popp J, Gibson CM, Fowler PW, Huang WE, Wagner M.

2015 – *Proc Natl Acad Sci USA*, 112(2): E194–203

Deciphering microbial interactions and detecting keystone species with co-occurrence networks. Berry D, Widder S.

2014 – *Front Microbiol*, 5: 219

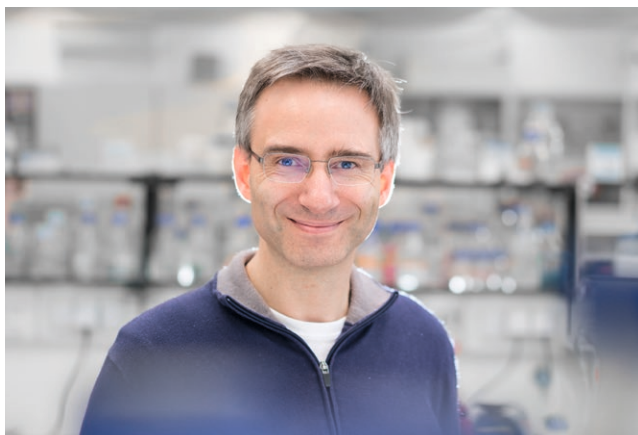
Temporal bacterial community dynamics vary among ulcerative colitis patients after faecal microbiota transplantation.

Angelberger S, Reinisch W, Makrathathis A, Lichtenberger C, DeJaco C, Papay P, Novacek G, Trauner M, Loy A, Berry D.

2013 – *Am J Gastroenterol*, 108: 1620–1630

HOLGER DAIMS

HOME – DIVISION OF MICROBIAL ECOLOGY



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At HOME since 2003

since 2017: Full Professor,
University of Vienna

2012–2017: Associate Profes-
sor, University of Vienna

2010–2012: Assistant Profes-
sor (tenure track), University
of Vienna

2003–2010: Assistant Profes-

sor, University of Vienna

2001–2003: Postdoctoral Re-
searcher, Technical Universi-
ty of Munich

2001: PhD in Microbiology,
Technical Univ. of Munich

1997: Diploma in Biology,
University of Technology of
the Rhineland, Aachen

Main research areas

- Evolution and ecology of nitrite-oxidizing bacteria and completely nitrifying organisms (comammox)
- Functioning of complex microbiota in engineered systems
- Microbial interactions in biofilms
- Development of methods to study microorganisms directly in their environment

Research in the group of Holger Daims (HD) addresses the diversity, ecophysiology, and evolution of nitrogen-cycling microorganisms that are functionally important in natural ecosystems, agriculture, and wastewater and drinking water treatment. An additional research area is the development and application of single-cell labeling and imaging methods to characterize microorganisms in spatially complex environments, such as environmental and medical biofilms. His expertise comprises (meta)genomics, isotope labeling and image analysis techniques, and physiological and molecular biological methods to study selected model organisms as well

as communities of uncultured microbes. Key research goals of HD are to understand how the analyzed microorganisms adapt to different environments and maintain their activities in fluctuating conditions, and how they interact with other microbes. The knowledge gained should help develop improved strategies to utilize microorganisms in engineered systems, and to control the composition and activities of complex microbiota in an environmental or medical context.

Most publications authored by HD are published in Q1 (best 25% from the field) journals, including leading journals such as Nature, Science, and PNAS.

Selected publications

Kinetic analysis of a complete nitrifier reveals an oligotrophic lifestyle. Kits KD, Sedlacek CJ, Lebedeva EV, Han P, Bulaev A, Pjevac P, Daebeler A, Romano S, Albertsen M, Stein LY, Daims H, Wagner M.

2017 – Nature, 549:269–272

Giant viruses with an expanded complement of translation system components. Schulz F, Yutin N, Ivanova NN, Ortega DR, Lee TW, Vierheilig J, Daims H, Horn M, Wagner M, Jensen GJ, Kyrpid-

es NC, Koonin EV, Woyke T.

2017 – Science, 356: 82–85

Complete nitrification by Nitrospira bacteria.

Daims H, Lebedeva EV, Pjevac P, Han P, Herbold C, Albertsen M, Jehmlich N, Palatinszky M, Vierheilig J, Bulaev A, Kirkegaard RH, von Bergen M, Rattei T, Bendinger B, Nielsen PH, Wagner M.

2015 – Nature, 528: 504–509

Cyanate as an energy source for nitrifiers.

Palatinszky M, Herbold C, Jehmlich N, Pogoda M, Han P, von Bergen M, Lagkouvardos I, Karst SM, Galushko A, Koch H, Berry D, Daims H, Wagner M.

2015 – Nature 524, 105–108

Expanded metabolic versatility of ubiquitous nitrite-oxidizing bacteria from the genus Nitrospira.

Koch H, Lückner S, Albertsen M, Kitzinger K, Herbold C, Spieck E, Nielsen PH, Wagner M, Daims H.

2015 – Proc. Natl. Acad. Sci. USA, 112: 11371–11376

Growth of nitrite-oxidizing bacteria by aerobic hydrogen oxidation.

Koch H, Galushko A, Albertsen M, Schintlmeister A, Gruber-Dorninger C, Lückner S, Pelletier E, Le Paslier D, Spieck E, Richter A, Nielsen PH, Wagner M, Daims H.

2014 – Science 345, 1052–1054

MATTHIAS HORN

HOME – DIVISION OF MICROBIAL ECOLOGY



📌 Full Professor

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At HOME since 2003
since 2015: Deputy Head of the Research Network “Chemistry meets Microbiology”
since 2007: Full Professor for Microbial Symbioses, University of Vienna

2005: Professor, University of Vienna
2005: START Award of the Austrian Science Fund (FWF)
2003: Assistant Professor, University of Vienna
2001: PhD in Microbiology, Technical University of Munich

Main research areas

- Microbial symbioses, with emphasis on bacterial symbionts of protists
- Evolution of intracellular bacteria
- Microbial genome evolution
- Molecular and cellular biology of intracellular bacteria
- Bacteria-host interactions

Research in the lab of Matthias Horn (MH) focuses on bacteria infecting and residing inside eukaryotic cells. Using an array of molecular and computational methods, his research led to the discovery of novel microorganisms, molecular mechanisms, and evolutionary processes governing these associations. Bacteria living within eukaryotic host cells comprise important pathogens and essential symbionts of humans and diverse animals, yet owing to the intracellular lifestyle their analysis is challenging. Our understanding of their biology is thus lacking behind, and they have long been underestimated with respect to their diversity and distribution in nature and their ecological

importance. MH’s lab aims to close this knowledge gap by investigating selected non-model organisms, such as symbionts of amoeba and insects, using a polyphasic approach aiming at a comprehensive understanding of evolution, ecology, biology, and host-interaction of obligate intracellular bacteria.

MH is author of 101 publications in peer-reviewed journals, with over 6,600 citations so far. He has received an ERC Starting Grant (Consolidator Track) and the START Award of the Austrian Science Fund FWF. His research is continuously funded by third-party grants (total budget since 2003: approx. 5 million Euro).

Selected publications

Convergent patterns in the evolution of mealybug symbioses involving different intrabacterial symbionts. Szabó G, Schulz F, Toenshoff ER, Volland JM, Finkel OM, Belkin S, Horn M.

2017 – ISME J. 3: 715–726

In situ architecture, function, and evolution

of a contractile injection system. Böck D, Medeiros JM, Tsao HF, Penz T, Weiss GL, Aistleitner K, Horn M, Pilhofer M.

2017 – Science, 6352: 713–717

Intranuclear bacteria: inside the cellular control center of eukaryotes. Schulz F, Horn M.

2015 – Trends Cell Biol. 6: 339–346.

Plastid establishment did not require a chlamydial partner. Domman D, Horn M, Embley TM, Williams TA.

2015 – Nature Comm. 6: 6421

Integrating metagenomic and amplicon databases to resolve the phylogenetic and ecological diversity of the Chlamydiae.

Lagkouravdos I, Weinmaier T, Lauro F, Cavicchioli R, Rattei T, Horn M.

2014 – ISME J. 8: 115–125

Discovery of chlamydial peptidoglycan reveals bacteria with murein sacculi but without FtsZ. Pilhofer M, Aistleitner K, Biboy J, Gray J, Kuru E, Hall E, Brun YV, VanNieuwenhze MS, Vollmer W, Horn M, Jensen GJ.

2013 – Nature Commun. 4: 2856

CHRISTINA KAISER

TER – DIVISION OF TERRESTRIAL ECOSYSTEM RESEARCH



📌 **Group Leader**

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At DOME since 2014

since 2014: Group leader, University of Vienna

since 2014: Guest Researcher at IIASA, Laxenburg

2012–2014: IIASA Postdoctoral fellow

2011: Postdoctoral fellow, University of Western Australia (UWA)

2010: PhD in Ecology, University of Vienna

2003: Master (Mag.) Ecology, University of Vienna

Main research areas

- Emergent phenomena of complex microbial communities
- The spatial aspect of rhizosphere priming
- Interactions between soil microarchitecture and soil microbial ecology
- Carbon and nitrogen exchange between plants, mycorrhizal fungi and soil bacteria
- Effect of mycorrhizal associations on soil organic matter decomposition

Christina Kaiser (CK)'s work combines soil microbial ecology and theoretical modelling with ecosystem biogeochemistry. Looking at the soil from the perspective of complex system science CK utilizes both mathematical modelling and experimental approaches to explore how microbial processes and interactions at the microscale govern organization and regulation of microbial communities, and how this, in turn, controls soil organic matter turnover. Her application of individual-based modelling to soil microbial communities has led to novel insights on self-regulation capacities of microbial decomposer communities in soil. CK's group furthermore investigates carbon and nitrogen exchange in the tripartite

symbiosis of plants, mycorrhizal fungi and soil microbial decomposers. They combine state-of-the-art stable isotope techniques with nanoscale secondary ion mass spectrometry (NanoSIMS) to trace carbon and nitrogen through the plant-soil system and visualize the in-situ flow of these elements at subcellular scales at the plant-microbe interface, which allow deeper insights in the controls of this exchange and its consequences for ecosystem carbon and nitrogen cycling. CK's work has been published in leading journals of the fields, such as Ecology Letters, Nature Communications, New Phytologist, and Soil Biology and Biochemistry, including several highly cited papers.

Selected publications

Synergistic effects of diffusion and microbial physiology reproduce the Birch effect in a micro-scale model. Evans S, Dieckmann U, Franklin O, Kaiser C.
2016 – Soil Biology and Biochemistry, 93: 28–37

Social dynamics within decomposer communities lead to nitrogen retention and organic matter build-up in soils. Kaiser C, Franklin O, Richter A, Dieckmann U.
2015 – Nature Communications, 6: 8960

Exploring the transfer of recent plant photosynthates to soil microbes: mycorrhizal pathway versus direct root exudation. Kaiser C, Kilburn MR, Clode PL, Fuchslueger L, Koranda M, Cliff JB, Solaiman ZM, Murphy D V.
2015 – The New Phytologist 205(4): 1537–1551

Microbial community dynamics alleviate stoichiometric constraints during litter decay. Kaiser C., Franklin O., Dieckmann, U., Richter A.
2014 – Ecology Letters, 17: 680–690

Belowground carbon allocation by trees drives seasonal patterns of extracellular enzyme activities by altering microbial community composition in a beech forest soil. Kaiser C., Koranda M., Kitzler B., Fuchslueger L., Schnecker J., Schweiger P., Rasche F., Zechmeister-Boltenstern S., Sessitsch A., Richter A.
2010 – The New Phytologist 187: 843–858

ALEXANDER LOY

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📌 Full Professor

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At DMES since 2003

since 2017: Full Professor for Microbial Communities, University of Vienna

since 2016: Managing director, Austrian Microbiome Initiative (AMICI)

2013–2017: Associate Professor, University of Vienna

2008–2013: Assistant Professor, University of Vienna

2006–2008: Group leader, University of Vienna

2003–2006: Postdoctoral Researcher (Marie Curie fellow), University of Vienna

2003: PhD in Microbiology, Technical Univ. of Munich

Main research areas

- Function of the complex symbiotic microbiota of animals and humans
- Evolution and ecology of sulfur microorganisms
- Development of novel methods to study microorganisms in their natural environments

Research in the group of Alexander Loy (AL) covers a diverse spectrum of topics in microbial ecology and symbiosis, such as functions of the intestinal microbiota in health and disease of their human or animal host and ecology and evolution of sulfur-compounds-utilizing microorganisms. He has long-standing expertise in developing and applying stable isotope-labelling and molecular biology methods for *in situ* analysis of complex host-associated and environmental microbiota. The research activities of AL aim at understanding how the myriads of physiological interactions among complex microbiota members impact sulfur and carbon cycling in their environment and nutrition and health

of their host. This knowledge should ultimately translate in the design of microbiome-based strategies for improved health management, including nutritional and probiotic interventions.

AL is co-founder and managing director of AMICI – the Austrian Microbiome Initiative. He is author of 74 peer-reviewed publications (> 5300 citations, H-index 35, Scopus) in mainly Q1 (best 25% from the field) journals, including leading journals such as Nature, Science, PLoS Biology, and PNAS. His research is continuously funded by third-party grants from diverse public and industrial sources (total budget since 2004: approx. 3.3 million Euro).

Selected publications

Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses.

Roux S, Brum JR, Dutilh BE, Sunagawa S, Duhaime MB, Loy A, Poulos BT, Solonenko N, Lara E, Poulain J, Pesant S, Kandels-Lewis S, Dimier C, Picheral M, Searson S, Cruaud C, Alberti A, Duarte CM, Gasol JM, Vaque D, Tara Oceans Coordinators, Bork P, Acinas SG, Wincker P, Sullivan MB.
2016 – *Nature*, 537: 689–693

Phylogenetic and environmental diversity of DsrAB-type dissimilatory (bi)sulfite reductases.

Müller AL, Kjeldsen KU, Rattei T, Pester M, Loy A.
2015 – *ISME J*, 9: 1152–1165

Host-compound foraging by intestinal microbiota revealed by single-cell stable isotope probing.

Berry D, Stecher B, Schintlmeister A, Reichert J, Brugiroux S, Wild B, Wanek W, Richter A, Rauch I, Decker T, Loy A, Wagner M.
2013 – *Proc. Natl. Acad. Sci. USA*, 110: 4720–4725

Phylotype-level 16S rRNA analysis reveals new bacterial indicators of health state

in acute murine colitis. Berry D, Schwab C, Milinovich G, Reichert J, Ben Mahfoudh K, Decker T, Engel M, Hai B, Hainzl E, Heider S, Kenner L, Müller M, Rauch I, Strobl B, Wagner M, Schleper C, Urich T, Loy A.
2012 – *ISME J*, 6: 2091–106

A constant flux of diverse thermophilic bacteria into the cold Arctic seabed.

Hubert C, Loy A, Nickel M, Arnosti C, Baranyi C, Brüchert V, Ferdelman T, Finster K, Christensen FM, Rosa de Rezende J, Vandieken V, Jørgensen BB.
2009 – *Science*, 325: 1541–1544

HARALD MARX

CUBE – DIVISION OF COMPUTATIONAL SYSTEMS BIOLOGY



📌 Group leader

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At DMES since 2017

since 2017: Group leader, Department of Microbiology and Ecosystem Science, University of Vienna, Austria

2014–2017: Postdoctoral scholar, Department of Chemistry, University of Wisconsin-Madison

2014: PhD in Computational Proteomics, Technical University of Munich

2009: Diploma in Bioinformatics, Technical University of Munich

Main research areas

- Host-microbe interactions
- Bioactive peptides
- Computational peptidomics and proteomics
- Metaproteomics and proteogenomics
- Mass spectrometry-based proteomics

Research in the lab of Harald Marx (HM) focuses on the structural and functional genome annotation of bioactive peptides to discover novel drugs to meet challenges in cancer treatment, infectious disease and microbiome health. Bioactive peptides are pervasive across the tree of life, playing a pivotal role in cell-cell communication, e.g., in bidirectional host-symbiont and host-pathogen interactions. To explore the peptidome in a systematic way, the

Marx group develops state of the art bioinformatic approaches and utilizes mass spectrometry-based proteomics. HM has expertise in dry and wet lab methods, including high-throughput proteomics, proteogenomics, and meta-proteomics.

HM has published in top tier journals, e.g. Nature and Nature Biotechnology and made major contributions to the proteomics field.

Selected publications

A proteomic atlas of the legume *Medicago truncatula* and its nitrogen-fixing endosymbiont *Sinorhizobium meliloti*. Marx H., Minogue C. E., Jayaraman D., Richards A. L., Kwiecien N. W., Sihapirani A. F., Rajasekar S., Maeda J., Garcia K., Del Valle-Echevarria A. R., Volkening J. D., Westphall M. S., Roy S., Sussman M. R., Ané J. M., Coon J. J. **2016 – Nat Biotechnol, 34(11), 1198–1205**

Mass spectrometry based draft of the human proteome. Wilhelm M., Schlegl J., Hahne H.,

Gholami A. M., Lieberenz M., Savitski M. M., Ziegler E., Butzmann L., Gessulat S., Marx H., Mathieson T., Lemeer S., Schnatbaum K., Reimer U., Wenschuh H., Mollenhauer M., Slotta-Huspenina J., Boese J.-K., Bantscheff M., Gerstmair A., Faerber F., Kuster B. **2014 – Nature, 509 (7502), 582–587**

A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. Marx H., Lemeer S., Schliep J. E., Matheron L., Mohammed S., Cox J., Mann M., Heck A. J. R., Kuster B. **2013 – Nat. Biotechnol. 2013, 31 (6), 557–564**

JILLIAN PETERSEN

DOME – DIVISION OF MICROBIAL ECOLOGY



Assistant Professor (tenure track)

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At DMES since 2015

since 2015: Assistant Professor and Head of the WWTF Vienna Research Group for Marine Symbiosis, University of Vienna

2010–2015: Postdoc and Senior Scientist, Max-Planck-Institute for Marine Microbiol-

ogy, Bremen

2009: PhD in Marine Microbiology, University of Bremen

2006: MSc in Marine Microbiology, University of Bremen

2004: BSc in Microbiology, University of Queensland

Main research areas

- Host-microbe interactions
- Metagenome, -transcriptome and -proteome analysis of host-associated microbes
- Microbial metabolism
- In situ* imaging of microbial identity and function
- Ecology, evolution and development of marine symbioses

Animals evolved in a ‘sea’ of microbes. It is therefore not surprising that the vast majority of animals have evolved to rely on microbes for numerous aspects of their health, development and nutrition. Jillian Petersen’s (JP) group contributes to this rapidly expanding research field. Her work focuses on beneficial interactions between marine invertebrate animals and their sulfur-oxidizing bacterial symbionts. The goal of this research is to understand how the symbiotic partners establish and maintain their intimate relationship from generation to generation, and how these associations evolved in such diverse and widespread marine habitats from deep-sea hydro-

thermal vents to shallow-water seagrass beds. The JP Group has established expertise in ‘omics’ analyses of host-associated microbes, in imaging symbiont identity and activity *in situ*, and develops bioinformatic methods for understanding the population genetic structure of natural co-infections with multiple symbiont strains. JP’s work has been internationally recognized through awards such as the Lindeman Award of the Association for the Sciences of Limnology and Oceanography, and the Wolf Vishniac Award for Young Investigators from the International Society for Environmental Biogeochemistry.

Selected publications

Chemosynthetic symbionts of marine invertebrate animals are capable of nitrogen fixation. Petersen JM, Kemper A, Gruber-Vodicka H, Cardini U, van der Geest M, Musmann M, Bulgheresi S, Seah BKB, Chakkiath PA, Herbold C, Liu D, Belitz A, Weber M
2016 – Nature Microbiology 2:16195
doi:10.1038/nmicrobiol.2016.195

A specific and widespread association be-

tween deep-sea Bathymodiolus mussels and a novel family of Epsilonproteobacteria. Assie A, Borowski C, van der Heijden K, Raggi L, Geier B, Leisch N, Schimak MP, Dubilier N, Petersen J
2016 – Environmental Microbiology Reports 8: 805–813 doi:10.1111/1758-2229.12442

An abundance of toxin-related genes in the genome of beneficial symbionts from deep-sea hydrothermal vent mussels. Sayavedra L, Kleiner M, Ponnudurai R, Wetzel S, Pelletier E, Barbe V, Shoguchi E, Satoh N, Reusch TBH, Rosenstiel P, Schilhabel MB, Becher D, Schweder T, Markert S, Dubilier N, Petersen JM
2015 – eLife e07966 doi:10.7554/eLife.07966

Bacterial symbionts of Bathymodiolus mussels and Escarpia tubeworms from Chapopote, an asphalt seep in the southern Gulf of Mexico. Raggi L, Schubotz F, Hinrichs K-U, Dubilier N, Petersen JM
2013 – Environmental Microbiology 15: 1969–1987 doi:10.1111/1462-2920.12051

Hydrogen is an energy source for hydrothermal vent symbioses. Petersen JM, Zielinski FU, Pape T, Seifert R, Moraru C, Amann R, Hourdez S, Girguis PR, Wankel SD, Barbe V, Pelletier E, Fink D, Borowski C, Bach W, and Dubilier N
2011 – Nature 476: 176–180

THOMAS RATTEI

CUBE – DIVISION OF COMPUTATIONAL SYSTEMS BIOLOGY



📌 Full Professor

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At DMES since 2010

since 2010: Professor for In Silico Genomics, University of Vienna

2001–2010: Group leader and Assistant Professor, Department of Genome Oriented Bioinformatics, Technical University of Munich

1999: PhD in Chemistry, Technical University Dresden

1995: Diploma in Chemistry, Technical University Dresden

Main research areas

- Computational and systems biology
- Genome and metagenome analysis
- Functional genomics
- Host-pathogen interactions
- Databases and infrastructure for bioinformatics

Work and experience of Thomas Rattei (TR) covers a wide spectrum of topics from bioinformatics, genome and metagenome analysis and systems biology. He has long-standing expertise in developing and applying computational methods for the interpretation of large-scale sequence information. The international reputation of his research group triggered their involvement in numerous international (meta-) genome sequencing and analysis consortia. The research activities of TR are not only covering individual, project-specific questions but also general problems in bioinformatics, computational infrastructure and large-scale biological databases. Furthermore, his group de-

velops novel computational approaches for studying molecular inter-species interactions, such as between hosts and pathogens, between symbionts or in microbial ecosystems.

Publications authored by TR are mainly published in Q1 (best 25% from the field) journals, including leading journals such as Nature, Science, and PNAS. TR's team maintains and develops internationally relevant resources in computational biology, such as the SIMAP database of protein sequence similarities and the web portal effectivedb.org predicting bacterial secreted proteins and secretion systems.

Selected publications

The 5300-year-old *Helicobacter pylori* genome of the Iceman.

Maixner F, Krause-Kyora B, Turaev D, Herbig A, Hoopmann MR, Hallows JL, Kusebauch U, Vigl EE, Malfertheiner P, Megraud F, O'Sullivan N, Cipollini G, Coia V, Samadelli M, Engstrand L, Linz B, Moritz RL, Grimm R, Krause J, Nebel A, Moodley Y, Rattei T, Zink A.
2016 – Science, 6269: 162-5

EffectiveDB-updates and novel features for a better annotation of bacterial secreted proteins and Type III, IV, VI secretion systems.

Eichinger V, Nussbaumer T, Platzer A, Jehl MA, Arnold R, Rattei T.

2016 – Nucleic Acids Res., D669-74

Prediction of microbial phenotypes based on comparative genomics.

Feldbauer R, Schulz F, Horn M, Rattei T.

2015 – BMC Bioinformatics, 14: S1

Sequence-based prediction of type III secreted proteins.

Arnold R, Brandmaier S, Kleine F, Tischler P, Heinz E, Behrens S, Niinikoski A, Mewes HW, Horn M, Rattei T.

PLoS Pathog. 2009 Apr; 5(4): e1000376. doi: 10.1371/journal.ppat.1000376.

MIPS: analysis and annotation of genome information in 2007.

Mewes HW, Dietmann S, Frishman D, Gregory R, Mannhaupt G, Mayer KF, Münsterkötter M, Ruepp A, Spannagl M, Stümpflen V, Rattei T.

Nucleic Acids Res. 2008 Jan; 36(Database issue): D196-201.

ANDREAS RICHTER

TER – DIVISION OF TERRESTRIAL ECOSYSTEM RESEARCH



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At TER since 2000

since 2011: Professor for Ecosystem Science, University of Vienna

since 2016: Guest Research Scholar at IIASA, Laxenburg

2013–2016: Director of the Austrian Polar Research Institute

2000–2010: Associate Professor, Institute of Ecology and Conservation Biology

1990–1999: University Assistant, Institute of Plant Physiology, University of Vienna

1989: PhD in Botany (major) and Geology (minor), University of Vienna, Austria

Main research areas

- Carbon use efficiency, growth and turnover of microbial communities
- Microbial communities, SOM composition and the breakdown of organic matter
- Ecological stoichiometry and nitrogen and phosphorus cycling
- Arctic soil carbon storage and the permafrost-climate feedback
- Effect of climate change and elevated CO₂ on soil processes

The research of Andreas Richter (AR) focuses on understanding how microbial communities deconstruct and mineralize organic matter, how growth and turnover of microbial communities is regulated and affects soil organic matter storage. During the last years, AR's research group has critically reviewed and expanded the concept of microbial carbon use efficiency and nitrogen use efficiency (i.e., the fraction of the organic carbon or nitrogen taken up by microorganisms, that is used for growth), and linked it to the theory of ecological stoichiometry. Additionally, his group has worked on soil organic matter storage in arctic ecosystems and questions of permafrost-climate

feedbacks, on the interactive effects of climate change on microbial processes and ecosystem functioning and on plant-microbe interaction in phosphorus and nitrogen cycling. AR is a renowned specialist on the application of stable isotope technique to ecological questions.

AR has authored and co-authored more than 170 publications in peer-reviewed journals (>105 publications since 2008), including publications in leading journals such as Nature, Science, PNAS, Nature Geoscience, Nature Communications, Science Advances and Ecology Letters.

Selected publications

Decoupling of microbial carbon, nitrogen and phosphorus cycling in response to extreme temperature events. Mooshammer, M., Hofhansl, F., Frank, A.H., Wanek, W., Hämmerle, I., Leitner, S., Schneckler, J., Wild, B., Watzka, M., Keiblinger, K. M., Zechmeister-Boltenstern, S., Richter, A.
2017 – Science Advances 3: e1602781

Soil microbial carbon use efficiency and biomass turnover in a long-term fertilization

experiment in a temperate grassland. Spohn, M., Pötsch, E.M., Eichhorst, S.A., Woebken, D., Wanek, W., Richter, A.

2016 – Soil Biology and Biochemistry 97: 168–175

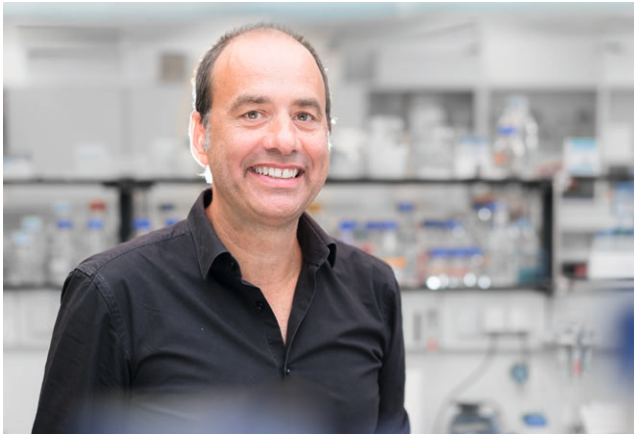
Plant-derived compounds stimulate the decomposition of organic matter in arctic permafrost soils. Wild, B., Gentsch, N., Čapek, P., Diáková, K., Alves, R., Bárta, J., Gittel, A., Hugelius, G., Knoltsch, A., Kuhry, P., Lashchinskiy, N., Mikutta, R., Palmtag, J., Schleper, C., Schneckler, J., Shibistova, O., Takriti, M., Torsvik, V., Urich, T., Watzka, M., Šantrůčková, H., Guggenberger, G., Richter, A.
2016 – Scientific Reports 6: 25607

Adjustment of microbial nitrogen use efficiency to carbon:nitrogen imbalances regulates soil nitrogen cycling. Mooshammer, M., Wanek, W., Hämmerle, I., Fuchsluger, L., Hofhansl, F., Knoltsch, A., Schneckler, J., Takriti, M., Watzka, M., Wild, B., Keiblinger, K.M., Zechmeister-Boltenstern, S., Richter, A.
2014 – Nature Communications 5: 3694

Carbon use efficiency of microbial communities: Stoichiometry, methodology and modeling. Sinsabaugh, R.L., Manzoni, S., Moorhead, D.L., Richter, A.
2013 – Ecology Letters 16: 930–939

MICHAEL WAGNER

DOME – DIVISION OF MICROBIAL ECOLOGY



📌 Full Professor

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✉ wagner@microbial-ecology.net

At DOME since 2003

since 2015: Head of the Research Network “Chemistry meets Microbiology”

2011: ERC Advanced Grant

since 2003: Head of the Division of Microbial Ecology and Full Professor for Microbial Ecology, University of Vienna

2001–2003: Associate Professor at TUM

1996–2000: Assistant Professor at TUM

1995–1996: Postdoctoral fellow, Northwestern University, Evanston, Illinois

1992–1995: PhD (Dr. rer. nat.) at TUM

Main research areas

- Nitrification with a focus on ammonia-oxidation and complete nitrification (comammox)
- Functional analyses of microbes using single-cell isotope probing

Current research in the lab of Michael Wagner (MW) focuses on the ecology, physiology, and evolution of nitrifying microorganisms that catalyze the aerobic oxidation of ammonium via nitrite to nitrate. During the last century, humans have strongly impacted the global nitrogen (N) cycle by the massive use of artificial nitrogen fertilizers. Nitrification contributes to massive eutrophication events, biodiversity loss, and dead zones in water bodies as well as human health risks. The MW lab has discovered, cultured, and characterized important new nitrifying bacteria and archaea including the long sought after complete nitrifiers and has described novel physiological traits of these environmentally and biotechnologically important

organisms. For more than two decades the Wagner lab is developing single cell tools to investigate functional properties of microbes while living in complex microbial communities in their natural environment. These methods are based on stable isotope probing in combination with Raman microspectroscopy, microfluidics, and nanoscale secondary ion mass spectrometry (NanoSIMS) and are now applied by numerous research groups worldwide.

MW is author of 230 publications in peer reviewed journals and has been recognized as a Highly Cited Researcher in 2014–2017. His papers have received over 30,000 citations so far and he has an H-index of 92 (Web of Science).

Selected publications

Kinetic analysis of a complete nitrifier reveals an oligotrophic lifestyle. Kits KD, Sedlacek CJ, Lebedeva EV, Han P, Bulaev A, Pjevac P, Daebeler A, Romano S, Albertsen M, Stein LY, Daims H, Wagner M.
2017 – *Nature*, 549:269–272

Complete nitrification by Nitrospira bacteria. Daims H, Lebedeva EV, Pjevac P, Han P, Herbold C,

Albertsen M, Jehmlich N, Palatinszky M, Vierheilig J, Bulaev A, Kirkegaard RH, von Bergen M, Rattei T, Bendinger B, Nielsen PH, Wagner M.
2015 – *Nature*, 528: 504–509

Cyanate as an energy source for nitrifiers. Palatinszky M, Herbold C, Jehmlich N, Pogoda M, Han P, von Bergen M, Lagkouvardos I, Karst SM, Galushko A, Koch H, Berry D, Daims H, Wagner M.
2015 – *Nature* 524, 105–108

Expanded metabolic versatility of ubiquitous nitrite-oxidizing bacteria from the genus Nitrospira. Koch H, Lücke S, Albertsen M, Kitzinger

K, Herbold C, Spieck E, Nielsen PH, Wagner M, Daims H.

2015 – *Proc. Natl. Acad. Sci. USA*, 112: 11371–11376

Tracking heavy water (D2O) incorporation for identifying and sorting active microbial cells. Berry D, Mader E, Lee TK, Woebken D, Wang Y, Zhu D, Palatinszky M, Schintlmeister A, Schmid MC, Hanson BT, Shterzer N, Mizrahi I, Rauch I, Decker T, Bocklitz T, Popp J, Gibson CM, Fowler PW, Huang WE, Wagner M.

2015 – *Proc Natl Acad Sci USA*, 112: E194–203

WOLFGANG WANEK

TER – DIVISION OF TERRESTRIAL ECOSYSTEM RESEARCH



Associate Professor

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At TER since 2001

since 2011: Associate Professor, University of Vienna

2006: Habilitation in Physiological Ecology and Ecosystem Research, University of Vienna

2001–2006: Group Leader and Assistant Professor, Head of SILVER laboratory, University of Vienna

1996: PhD in Plant Sciences, University of Vienna

1993: MSc in Botany, University of Vienna

Main research areas

- Stable isotope fractionation in ecosystems
- Nitrogen and phosphorus nutrition of plants and microorganisms
- Stoichiometric relationships in plants, microorganisms and the environment
- Controls of terrestrial nutrient cycling
- Global change effects on plant – soil – microbe relations

As a terrestrial ecosystem ecologist Wolfgang Wanek (WW) focuses his research on the linkage between plant and microbial functioning and ecosystem processes. He has long standing expertise in applying stable isotopes to unravel the role of plants and soil microbes and their interaction in controlling ecosystem processes. The research activities of WW center on the biogeochemistry of grasslands and forests in the tropical and temperate biome, with a focus on nitrogen and phosphorus cycling in the soil-plant-microbe system. Applying ecophysiological and isotope methods he seeks to understand how ecosys-

tems responded to past and how they respond to current and future global change, and how this feeds back on the functioning of ecosystems. His group has pioneered the development of an array of stable isotope based methods to enable the quantification of C, N and P cycle processes that previously could not be measured.

Publications authored by WW are mainly published in the best 25% of the journals from the field, and include publications in leading journals such as Nature, Science and PNAS.

Selected publications

Microbial physiology and soil CO₂ efflux after 9 years of soil warming in a temperate forest – no indications for thermal adaptation.

DA. Schindlbacher, J. Schnecker, M. Takriti, W. Borken, W. Wanek

2015 – *Global Change Biology* 21, 4265–4277

New insights into mechanisms driving carbon allocation in tropical rainforests.

F. Hofhansl, J. Schnecker, G. Singer, W. Wanek
2015 – *New Phytologist* 205: 137–146

Adjustment of microbial nitrogen use efficiency to carbon:nitrogen imbalances regulates soil N cycling.

M. Mooshammer, W. Wanek, I. Hämmerle, L. Fuchslueger, F. Hofhansl, A. Knoltsch, J. Schnecker, M. Takriti, M. Watzka, B. Wild, K. M. Keiblinger, S. Zechmeister-Boltenstern, A. Richter
2014 – *Nature Communications* 5: article no 3694

Stoichiometric imbalances between terrestrial decomposer communities and their resources: mechanisms and implications of microbial adaptations to their resources.

M. Mooshammer, W. Wanek, S. Zechmeister-Boltenstern, A. Richter

2014 – *Frontiers in Microbiology* 5: article 22

Pervasive change in the nitrogen cycle in tropical forests.

P. Hietz, B.L. Turner, W. Wanek, A. Richter, C.A. Nock, S.J. Wright

2011 – *Science* 334, 664-666

DAGMAR WOEBKEN

DOME – DIVISION OF MICROBIAL ECOLOGY



Assistant Professor (tenure track)

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At DOME since 2012

Since 2018: Assistant Professor, University of Vienna

2014: ERC Starting Grant

2012–2017: Assistant Professor (Univ. Ass.), University of Vienna

2008–2011: Postdoctoral Researcher, Stanford

University

2007–2008: Postdoctoral Researcher, Max-Planck Institute for Marine Microbiology, Bremen

2007: PhD in Marine Microbiology, University of Bremen

2003: Diploma in Biology, Leibniz University Hannover

Main research areas

- Diazotrophy in soils
- Processes in microbial mats and biological soil crusts
- Microbial dormancy and resuscitation
- Microbial mediated cellulose degradation in temperate soils
- Plant-microbe interactions
- Ecophysiology of the acidobacteria
- Application of single-cell methods to terrestrial and plant-associated systems

Terrestrial environments cover a substantial part of the Earth's surface, being home to a large fraction of our planet's microbial diversity. The goal of Dagmar Woebken's (DW) research group is to better understand the active microbial participants in key processes within the terrestrial C- and N-cycle and to identify the factors that govern these activities. Her research activities further address the physiologies that allow for the success of soil microorganisms and the interactions between plants and microorganisms. DW aims to gain a holistic view on the function of the soil microbiome. To achieve this, investigations combine process-level measurements

with molecular techniques, stable isotope probing and single-cell approaches (such as fluorescence *in situ* hybridization and NanoSIMS). As such, DW's research group is constantly developing and improving methods for single-cell investigations in terrestrial ecosystems. Publications authored by DW are mainly published in Q1 (best 25% in the field) journals, including journals such as PNAS, Cell, and the ISME Journal. DW has received an ERC Starting Grant and is a member of the Young Academy of the Austrian Academy of Sciences. Research in her group is continuously funded by third-party grants (total funding obtained since 2012: approx. € 3.2 million).

Selected publications

Genomic insights into the Acidobacteria reveal strategies for their success in terrestrial environments. Eichorst SA, Trojan D, Roux S, Herbold C, Rattei T, Woebken D.
2018 – Environ Microbiol

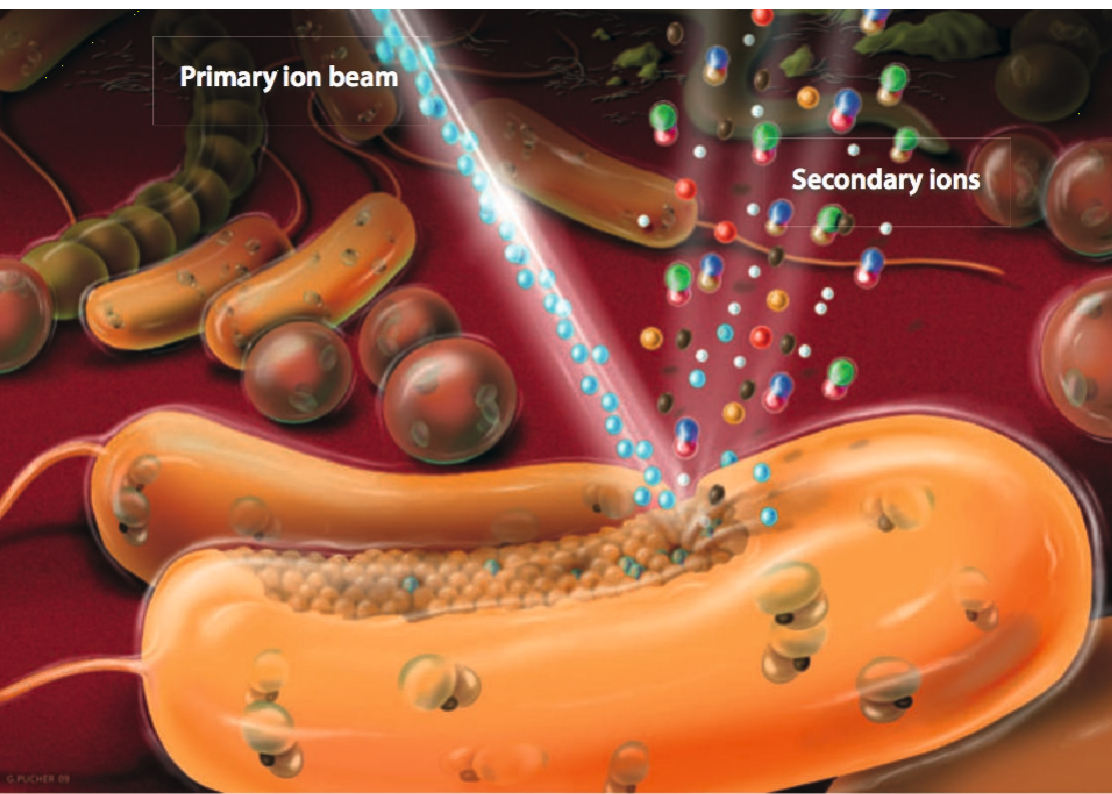
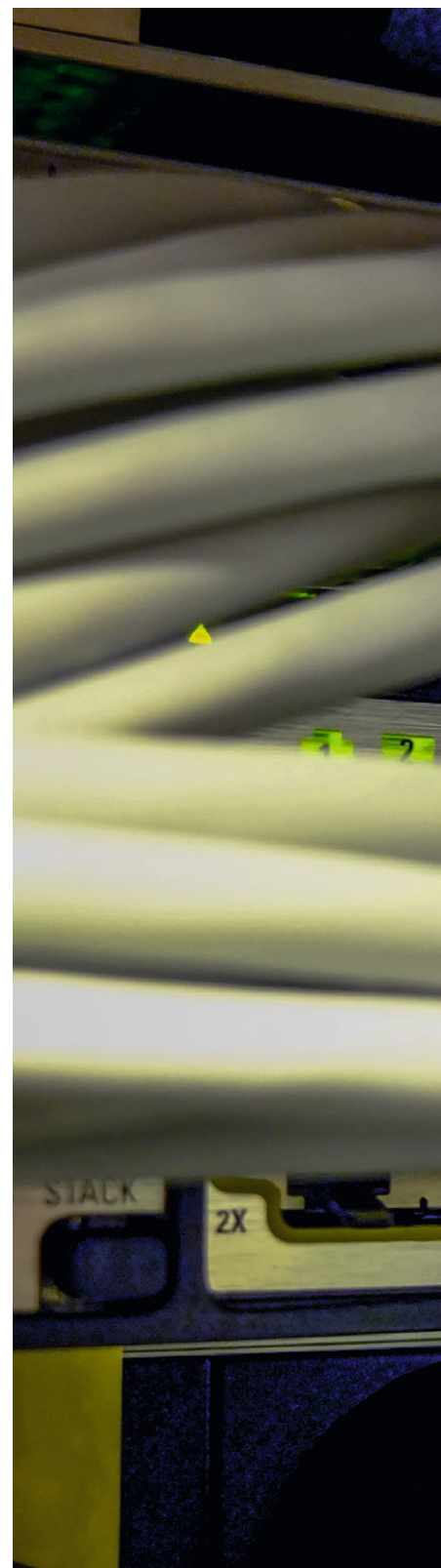
Application of stable-isotope labeling techniques for the detection of active diazotrophs. Angel R, Panhölzl C, Gabriel R, Herbold C, Wanek W, Eichorst SA, Woebken D.
2018 – Environ Microbiol, 1: 44-61

Advancements in the application of NanoSIMS and Raman microspectroscopy to investigate the activity of microbial cells in soils. Eichorst SA, Strasser F, Woyke T, Schintlmeister A, Wagner M, Woebken D.
2015 – FEMS Microbiol Ecol, 91: fiv106

Revisiting N₂ fixation in Guerrero Negro intertidal microbial mats with a functional single-cell approach. Woebken D, Burrow LC, Behnam F, Mayali X, Schintlmeister A, Fleming ED, Prufert-Bebout L, Singer SW, López Cortés A, Hoehler TM, Pett-Ridge J, Spormann AM, Wagner M, Weber PK, Bebout BM.
2015 – ISME J, 9:485-496

Anoxic carbon flux in photosynthetic microbial mats as revealed by metatranscriptomics and NanoSIMS. Burrow LC*, Woebken D*, Marshall IPG, Lindquist EA, Bebout BM, Prufert-Bebout L, Hoehler TM, Tringe SG, Pett-Ridge J, Weber PK, Spormann AM, Singer SW.
2013 – ISME J, 7:817-829 (*co-first authors)

Tracking heavy water (D₂O) incorporation for identifying and sorting active microbial cells. Berry D, Mader E, Lee TK, Woebken D, Wang Y, Zhu D, Palatinszky M, Schintlmeister A, Schmid MC, Hanson BT, Shterzer N, Mizrahi I, Rauch I, Decker T, Bocklitz T, Popp J, Gibson CM, Fowler PW, Huang WE, Wagner M.
2015 – Proc Natl Acad Sci USA, 112: E194-203





FACILITIES

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Overview of SILVER laboratory with five isotope ratio mass spectrometers allowing bulk and compound-specific analysis of hydrogen, carbon, nitrogen and oxygen in biological and environmental samples

Isotopes of an element differ in their number of neutrons and therefore in mass, but exhibit the same chemical behavior, allowing scientist to use them as powerful tools to uncover fluxes in the environment. All of the light chemical elements that constitute the biosphere (hydrogen, carbon, nitrogen, oxygen, sulfur, phosphorus) are found in more than one isotopic form, with most of these natural isotopes being stable, i.e. non-radioactive. The ratio between the heavy and light stable isotopes of an element (e.g., the ratio of ^{13}C over ^{12}C) varies in nature, bearing information on underlying physicochemical and biological processes, as well as of sources and sinks of the matter and/or compounds. Moreover, compounds highly enriched in heavy stable isotopes can be used to trace the fate and transformations of compounds in complex environmental systems, which is not possible by any other approach.

SILVER, the Stable Isotope Facility of the University of Vienna for Environ-

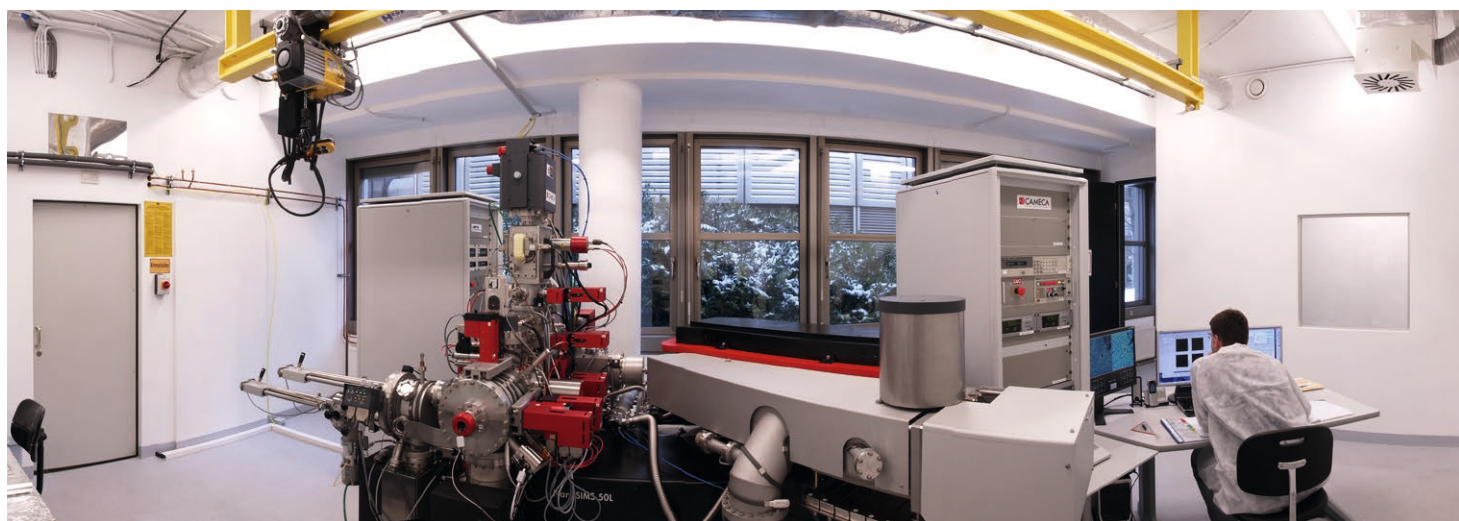
mental Research, is the largest facility in Austria for analyzing the ratios of stable isotopes of light elements in environmental samples and one of the leading laboratories for ecological research with stable isotopes in Europe. SILVER was founded in 2006 and is part of the Large Instrument Facility for Advanced Isotope Research and run by the division of Terrestrial Ecosystem Research at DMES.

In addition to determining the bulk isotopic composition of solid samples by elemental analysis – isotope ratio mass spectrometry (IRMS), SILVER is specialized in compound-specific isotope analysis in ecology and biology. SILVER currently encompasses five state-of-the-art continuous flow isotope ratio mass spectrometers with a range of front ends. The different configurations possible with these front-ends allow for bulk and compound-specific analysis of hydrogen, carbon, nitrogen and oxygen isotopes in almost any type of environmental sample.

Instrumentation of the SILVER facility

- EA – IRMS
 - Elemental analyzer for ^{13}C and ^{15}N in solid environmental samples
- Pyrolysis/Gasbench – IRMS
 - High-temperature pyrolysis system for ^2H and ^{18}O in solid samples and water
 - Head-space gas sampler for ^{13}C analysis of CO_2 and ^{18}O and ^2H analysis of water
 - Trace gas pre-concentrator for ^{13}C analysis of CH_4
- Cryotrap Gasbench - IRMS
 - Trace gas pre-concentrator
 - ^{15}N analysis of N_2O
- HPLC – IRMS
 - HPLC-Isolink
 - ^{13}C analysis of organic analytes
- GC – IRMS
 - GC-Isolink
 - ^{13}C , ^{15}N and ^2H analysis in organic analytes

NANOSIMS



Panoramic view of the NanoSIMS Laboratory (© Gregor Eder)

“NanoSIMS” is an acronym for an advanced type of dynamic secondary ion mass spectrometer particularly designed for trace element and high precision isotope analyses with sub-micrometer spatial resolution. Sample bombardment by a finely focused beam of energetic, chemically reactive primary ions (Cs^+ or O^- , spot-size down to 50 nm), leads to the ejection and ionization of atoms and short-fragmented molecules which are highly efficiently extracted by means of a strong electrostatic field and directed towards the entrance slit of a double focusing mass spectrometer, enabling the simultaneous detection of up to seven distinct secondary ion species at single-ion-counting sensitivity. Owing to these features, NanoSIMS imaging is perfectly suited to measure and visualize the distribution of virtually any elements and their stable isotopes of interest in biological material at the sub-cellular level.

Our research primarily focuses on microbial ecology, in which we combine NanoSIMS with stable isotope probing (e.g. $^2\text{H}/^1\text{H}$, $^{13}\text{C}/^{12}\text{C}$, $^{15}\text{N}/^{14}\text{N}$, $^{18}\text{O}/^{16}\text{O}$, $^{34}\text{S}/^{32}\text{S}$), high-throughput elemental analysis – isotope ratio mass spectrometry (EA-IRMS) and single cell identification techniques such as fluorescence *in situ* hybridization (FISH) for obtaining yet inaccessible information about the phylogenetic identity and functional role of microorganisms in their environment. Utilizing this approach, previously unrecognized physiological properties of bacteria and archaea thriving in soils, microbial mats, activated sludge, deep groundwater samples and within symbiotic relationships in marine ecosystems as well as the mammalian gut could be deciphered.

Established in 2010 as part of the Large-Instrument Facility for Advanced Isotope Research, DMES runs a CAMECA NanoSIMS 50L. Our instru-

ment is the only one in Austria and we support research groups in the faculty, university and many other national and international institutions in their chemical imaging efforts. Beyond performing measurements, DMES offers extensive support to all users with respect to study design, sample preparation and pre-characterization, data evaluation and data interpretation, which are key-steps in an efficient NanoSIMS analysis.

LiSC

LIFE SCIENCE COMPUTE CLUSTER



The Life Science Compute Cluster consists of login nodes, compute nodes, server nodes and storage nodes, which are all mounted in 19" racks. The housing of the machines is done in collaboration with the Technical University Vienna in the Arsenal area.

DMES operates a medium sized high-performance compute cluster specialized in bioinformatics and computational life science. The main difference to larger, generic computing facilities, such as the Vienna Scientific Cluster (VSC) is the rich, flexible and up-to-date bioinformatics software repository, the availability of major biological databases on-site and fast, local storage space for temporary files. This system allows most users to analyse their data without any software installation, just by using the pre-installed tools and databases.

The cluster is based on common PC architecture and contains several login nodes for job testing and submission, the actual compute nodes and a large storage array. It contains more than 800 CPU cores and from 128 GB to 1 TB RAM per node. Copies of relevant biological databases (such as NCBI nt and nr) are available on local high-speed disks in all compute nodes. Software is

provided via a modular environment, where needed applications and specific versions are activated and deactivated as needed. The storage system has a total capacity of more than 650TB based on redundant, network attached disk arrays.

As additional resources, we operate two dedicated database servers and two redundant virtualization servers. Several virtual machines are used to operate our publicly available resources, such as web portals, databases and tools.

The LiSC is frequently used by DMES members and is shared with the Faculty of Life Science and with collaboration partners inside and outside the University of Vienna. As most of the users are non-specialists in high-performance computing, DMES provides a user helpdesk and software installation support. By 2017, more than 500 bioinformatics programs are installed on LiSC.



Special hardware extensions, such as MIC and GPU processor, are available for evaluation and development of bioinformatic software.

TEACHING

1 BACHELOR PROGRAM BIOLOGY (comprises six semesters leading to a Bachelor's degree). DMES is involved in the Bachelor program Biology with a variety of lectures and practical courses. E.g. the lecture of Michael Wagner "Introduction to physiology: From microbes to plants and animals" – with about 500 Students – which takes place in the Audi-Max.

2 MASTER PROGRAM (comprises four semesters and leads to a Master's degree; with a deeper scientific approach). DMES contributes to the following master programs in biology:

Master in Molecular Microbiology, Microbial Ecology & Immunobiology: Students are trained in interdisciplinary sciences such as microbial ecology, symbiosis research, immunobiology, molecular biology, phylogeny and evolution, functional genomics and genetics and bioinformatics.

Master in Ecology and Ecosystems: This program addresses fundamental problems in ecology and takes both an organismic and an ecosystem-based approach to ecology. Core topics are the role of organisms in ecosystem functioning and biogeochemistry, and the factors responsible for spatial and temporal variations in biodiversity.

Master in Environmental Sciences: This applied program takes an interdisciplinary approach to the investigation of processes that control the earth environment.

Master in Computational Science: This program trains students in the MINT-fields (mathematics, informatics, astronomy, biology, chemistry, physics) to become experts in the computer-aided aspects of the natural sciences.

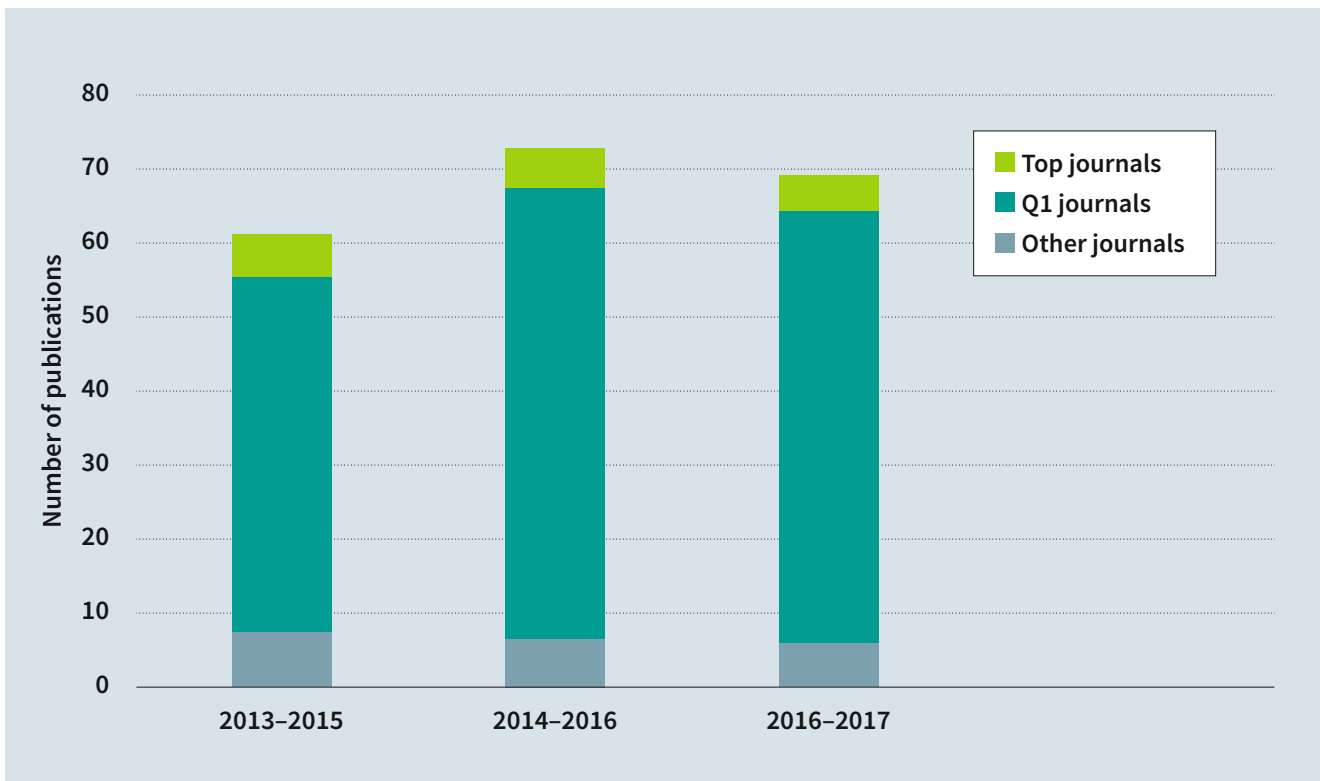
Master in Bioinformatics: This master program is open to students having a bachelor degree in life science, mathematics or computer science. In the first semester the students acquire the background in the relevant fields outside their degree, in the second and third semester the students specialize in bioinformatics, in the fourth semester the students work on their master thesis.

In addition DMES is involved in the master's programs *Molecular Biology* and *Genetics and Evolutionary Biology*.

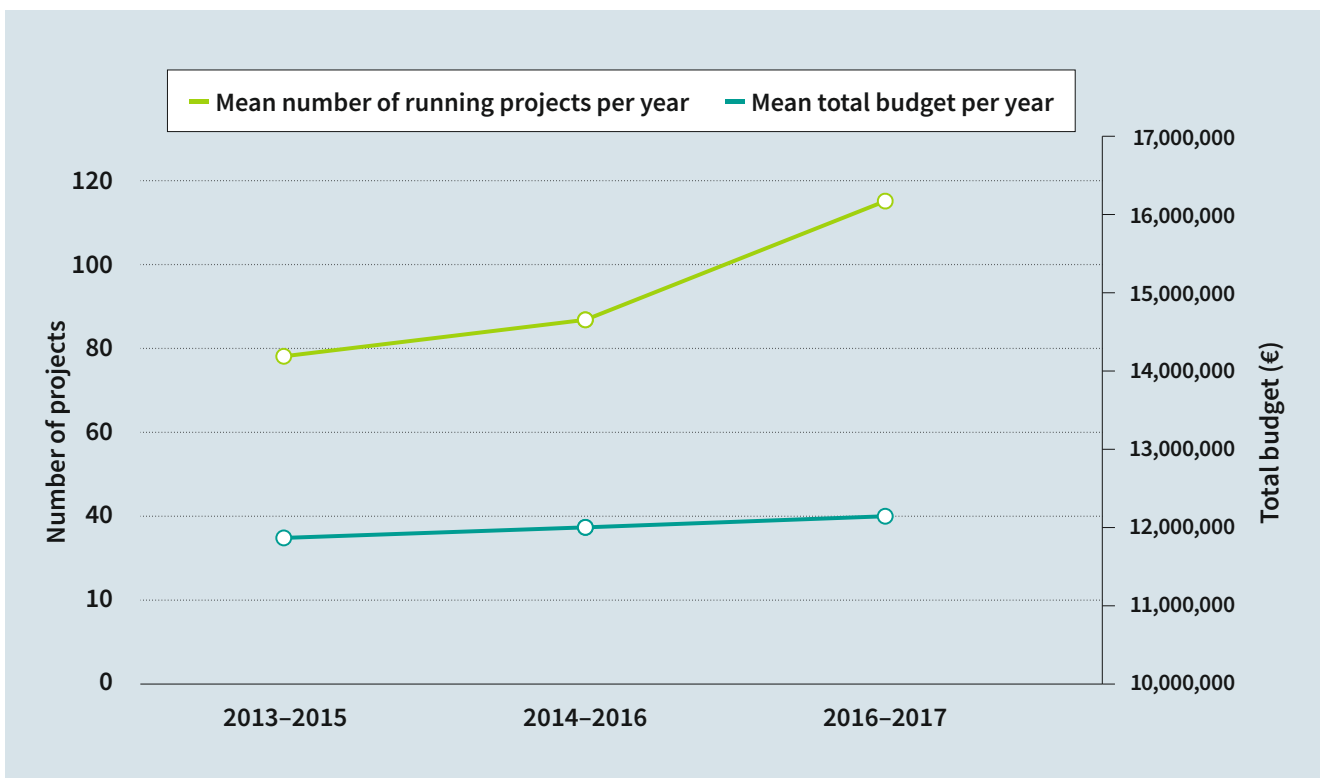
3 DOCTORAL/PHD PROGRAMMES: After having successfully completed the Diploma or Master program, the students can continue with a PhD program at DMES (comprises six semesters and leads according to the subject field of the dissertation to a PhD degree).



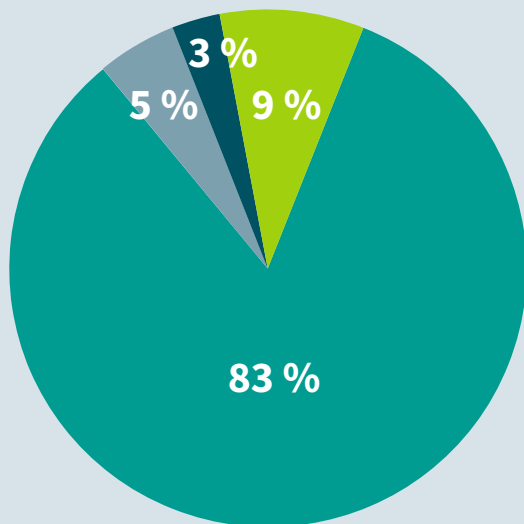
KEY FIGURES



Mean numbers of publications per year in interdisciplinary top journals, Q1 journals in the respective categories (according to the ISI Journal Citation Report), and other peer-reviewed journals.



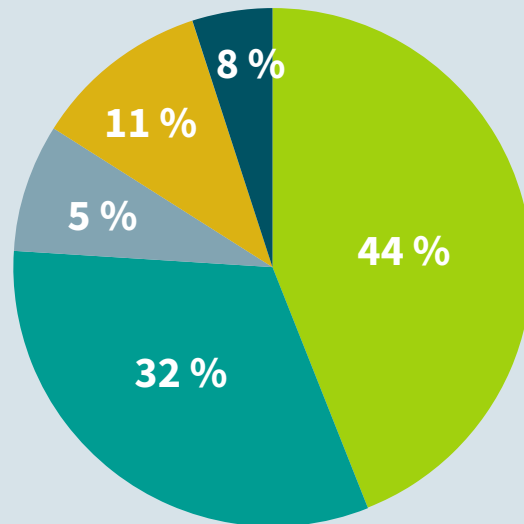
Mean number of third-party funded projects and mean total project budget per year.



■ Top journals*
■ Q1 journals
■ Q2 journals
■ Other journals

* Nature, Science, PLoS Biology, Nature Communications, Science Advances

In 2017 members of the Department published **59 papers in peer-reviewed journals, 2 book chapters, and 3 other publications**. In total **92%** of the papers appeared in the top 25% journals (**Q1**) in the respective subject categories.



■ Austrian Science Fund (FWF)
■ European Research Council (ERC)
■ European Union (except ERC)
■ Vienna Science and Technology Fund (WWTF)
■ Other sources

In 2017, research at the Department was funded by **44 external grants with a total volume of € 17,231,986**. The main funding sources were the **FWF** (23 grants), the **ERC** (3 grants), other programs of the **European Union** (6 grants), and the **WWTF** (2 grants).



In 2017, **4 PhD students and 13 Master's students finished** their thesis work at the Department and graduated.

Currently, 41 PhD students and 21 Master's students are conducting their thesis research at the Department. Members of the Department had functions in **11 external PhD committees** and were reviewers and/or examiners of 2 external PhD theses.



Members of the Department presented **30 public talks, interviews, TV and radio features, and articles**

in the general media and contributed with lectures and seminars to the **KinderUniWien** (children's university).



Key research publications by Department members were **covered by 31**

articles in major Austrian and international printed or online media, and were featured by numerous scientific or general internet news services.



Members of the Department received in 2017 in total **11 awards, highly competitive stipends, and other honors**.

In addition, two Department members (Holger Daims and Alexander Loy) were **promoted to Full Professors** and one member (David Berry) received his **Habilitation in Microbiology**.



In 2017, members of the Department presented their research in **60 invited oral presentations** at national

and international conferences, workshops, and institutional seminars.



In 2017, members of the Department **organized and co-organized 12 national and international conferences and workshops**.

These events included the **ASM Microbe 2017 Meeting** (>10,000 participants), the first symposium of the **Austrian Microbiome Initiative (AMICI)**, and **ICoN5** (the leading international conference on nitrification and related processes).

FUN@DMES



