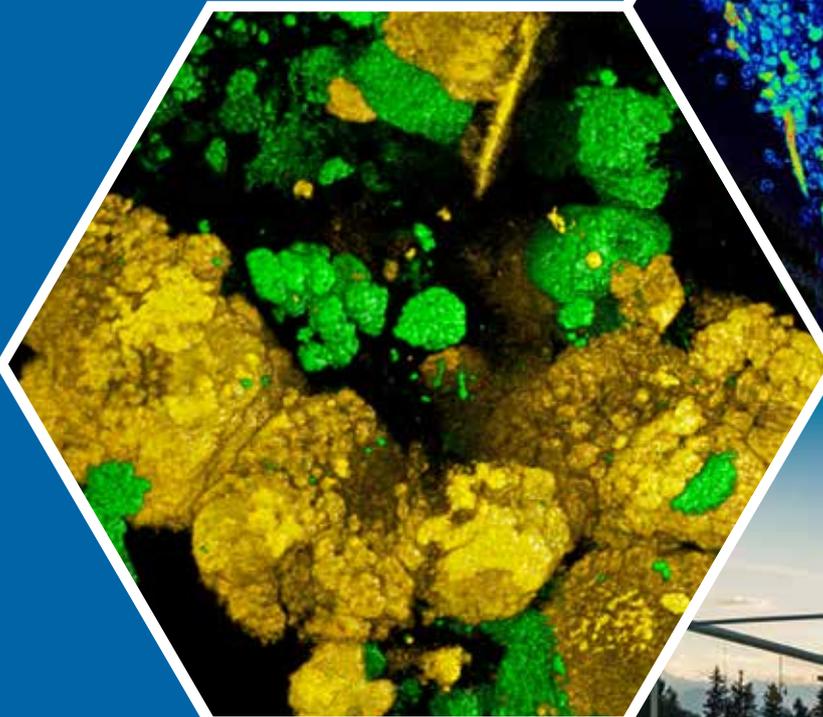
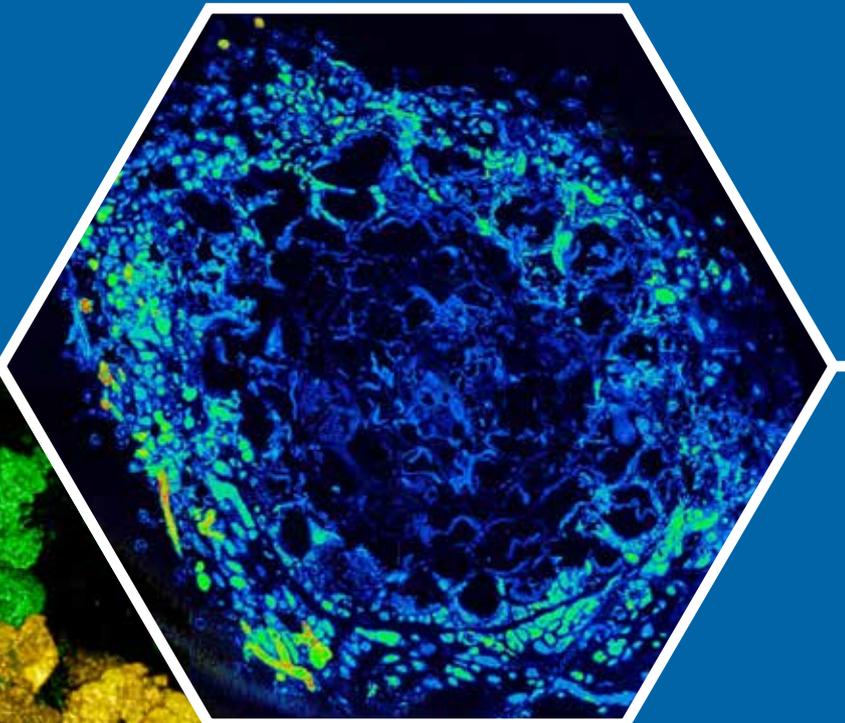


Centre for Microbiology and Environmental Systems Science
UNIVERSITY OF VIENNA

CMESS



CMESS

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MISSION STATEMENT

Microorganisms play a key role in sustaining life on Earth, yet are the least studied of all life forms. Their manifold functions shape natural and man-made ecosystems. Humans also shape the environment, an environment that is experiencing rapid global change due to pressures we exert in the Anthropocene. These pressures range from emerging contaminants to altered biogeochemical cycles and climate change. Furthermore, the health of plants, animals and humans is directly linked to the function of their microbiomes. Recent progress in method development allows us to study the complex interactions between hosts and microbes, between chemicals and the environment, and between microbes and climate.

The mission of CMES, the Centre for Microbiology and Environmental Systems Science, is to conduct excellent research at an internationally leading level. We develop cutting-edge methods for structure-function analyses of microbial communities in environmental and medical systems. We perform functional microbiome research to obtain a comprehensive understanding of host-microbe interactions, which also offers exciting opportunities for prophylaxis, diagnosis and treatment of many diseases. We investigate the role of microbial communities for the functioning of complex ecological systems as well as the impact of human activities on environmental systems in a changing world. This understanding can be used to solve some of the most pressing environmental and medical problems of today and tomorrow.

CUBE

The Division of Computational Systems Biology is

a group of bioinformaticians and computational biologists. CUBE focuses on understanding biological systems, ranging from single species to multi-species systems and ecosystems. The research is based on data from large-scale bioanalytical methods. Researchers in this group develop, improve and apply computational methods for the interpretation of molecular information in biology. They establish and analyse quantitative mathematical models.

DOME

The Division of Microbial Ecology seeks to under-

stand the role of microorganisms in Earth's nutrient cycles and as symbionts of other organisms. Researchers at DOME study the biodiversity, the ecology, and the evolutionary history of microbes. Their research ranges from ecophysiology, genomics, and evolution of key microorganisms in diverse environments to interactions of microbes among themselves and with eukaryotes, including the complex microbiomes of humans and animals.

CMESS

The Centre for Microbiology and Environmental Systems Science (CMESS) consists of four Research Divisions.

EDGE

The Division of Environmental Geosciences investigates key pro-

cesses controlling the natural environment and anthropogenic impacts. Researchers at EDGE combine field observations with experimental work, linking molecular scale mechanisms at environmental interfaces with complex large-scale environmental processes using quantitative modelling. EDGE accepts the challenges posed by the release of known and emerging pollutants and the need to understand their impact on soils, ground- and surface waters by process-based and mechanistic research.

TER

The Division of Terrestrial Ecosystem Research aims to

advance the fundamental understanding of how plants and soil microorganisms respond to and in turn shape their abiotic and biotic environment, and what consequences these interactions have for the functioning of Earth's ecosystems. Researchers at TER address pressing environmental issues, such as the impact of climate change on ecosystem functioning and the role of soils in the global carbon cycle and in food security.

DIRECTORS' STATEMENT



Andreas Richter
Head of CMESS



Thilo Hofmann
Vice Head of CMESS



Michael Wagner
Vice Head of CMESS



Annina Müller Strassnig
CMESS Administrative Head

In March 2021 we celebrated the second birthday of CMESS, the Centre for Microbiology and Environmental Systems Science. Established by the University of Vienna in 2019 as an organisational unit with full faculty status, we have spent the last two years building new structures and procedures, and growing together. Obviously, this wasn't always an easy task in the midst of the pandemic that has accompanied us for more than half of our existence. Despite the challenges, we can now look back on two very inspiring, stimulating and successful years, which encourage us to tackle the exciting scientific endeavors ahead of us with full enthusiasm.

CMESS does research in areas that are highly important, topical and relevant. In the past few years, it has become abundantly clear how important fundamental research in microbiology is for our society. Our research in this field encompasses topics related to the human microbiome and health, as well as to the role of microbes in global biogeochemical cycles, and microbe-host interactions. The other main area of research at CMESS is related to environmental systems science, in which we address pressing questions regarding the impact of human activities on environmental systems in a changing world, with research topics ranging from emerging contaminants to climate change. The bold and progressive decision of the University of Vienna to combine these two large research areas in one Centre with the establishment of CMESS has opened

up entirely new perspectives and opportunities, which we look forward to exploring in the coming years.

This report, the first CMESS Report ever, highlights our research areas and provides an introduction to our faculty and their achievements. The completion of this report is also a fantastic opportunity to thank all our staff and other members, about 200 in total from 33 different countries. It is only thanks to the great personal commitment, creativity, and friendship of our members - our fantastic administrative and technical support team, our dedicated and skilled students and post-doctoral researchers and world-class faculty - that we were able to successfully build up the Centre and to weather the pandemic well under the given circumstances.

Finally, we want to thank the organisations that fund our research, first and foremost the Austrian Science Fund (FWF) and the European Union (ERC, Horizon 2020, MSCA), and the University of Vienna, for believing in our research and giving us the opportunity to do cutting-edge-research that contributes to solving some of the most pressing challenges for humanity.

Andreas Richter
Michael Wagner

Thilo Hofmann
Annina Müller Strassnig

KEY NUMBERS

Funding

CMESS researchers are very successful in the acquisition of third-party funding year after year. In 2020, they raised EUR 4.9 million in third party funding, of which EUR 2.9 million came from the Austrian Science Fund (FWF), and EUR 1.4 million from the EU. In total, 22 research projects received funding in 2020.

4.9

102

Publications

In 2020, CMESS scientists published 102 publications in peer-reviewed journals. The vast majority of these publications was published in Q1 journals. You can access our publication database by scanning the QR-code.



Citations

The 430 publications that professors at CMESS have written during the last 5 years (2015-2020) have been cited more than 13,800 times. 30 of these 430 publications are listed as highly cited papers in Web of Science.

>13,800

Highly Cited

4

Early Career Researcher Awards

13

A large talent pool of highly qualified and highly motivated early stage researchers thrives at CMESS. Their success and future potential is reflected by the prizes and grants they receive: In 2020/21, we welcomed five Marie Skłodowska-Curie Fellows and three Re-Wire Fellows. Additionally, we host one

FWF Lise Meitner, one FWF Hertha Firnberg project, two FWF Young Independent Researcher Groups with five members including the project leader for one of them from CMESS, and one Ambizione Fellowship from the Swiss National Science Foundation (SNSF).

CMESS researchers are frequently cited, showing the global impact of their research. Of the 37 Highly Cited Researchers in Austria that were listed by Clarivate Analytics in 2020, 4 (more than 10%) are researchers at CMESS. The Highly Cited Researcher list contains scientists who are among the top 1% most cited researchers in their fields.

Research Platforms

Networking and collaboration, also across disciplines, play an important role. Researchers at CMESS are involved in 7 research platforms of the University of Vienna: *The Challenge of Urban Futures: Governing the complexities in European cities*, *The Comammox Research Platform*, *Mineralogical Preservation of the Human Biome from the Depth of Time*, *Plastics in the Environment and Society*, *Responsible Research and Innovation in Academic Practice*, *Secondary Metabolomes of Bacterial Communities*, and *Vienna Metabolomics Center*.

7

Awards / Grants

1+7

We are proud to have a Wittgenstein Award winner in 2019 among our scientists. The FWF Wittgenstein Award is the most prestigious Austrian research award. In addition, CMESS researchers are repeatedly among those scientists who acquire highly competitive grants of the European Research Council (ERC). In total seven ERC grants at all levels have been awarded to the 15 professors at CMESS, three of them to women.

International

The research and the research groups at CMESS are truly international: We are proud that the approximately 200 researchers and staff at CMESS come from 33 different countries from 5 continents.

33

PhD School

The newly established Doctoral School in Microbiology and Environmental Science already comprises 86 PhD students and 29 faculty members. Most students are funded by third-party funding.

86

Scientists and Staff

202

It is the people and their team spirit that make CMESS special. As of March 2021, more than 200 people are contributing to research, teaching and administration. These include 15 professors, 36 PostDocs, 9 staff scientists, more than 50 PhDs, around 40 Master's students, nearly 30 technicians, a dozen administrative employees, and 10 guests and scholarship holders.



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Microbiome, Symbiosis and Evolution

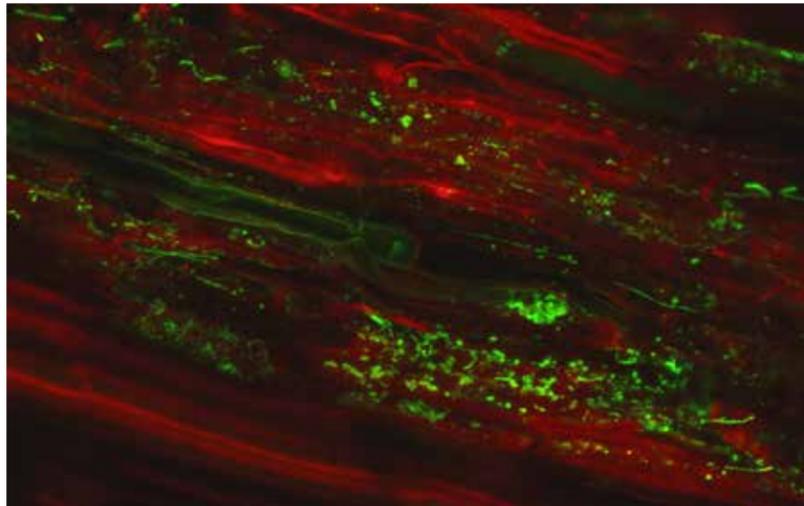
UNDERSTANDING THE VITAL ROLES OF MICROBES FOR OUR PLANET

Microbes are the dominant form of life – they are the most abundant and diverse organisms, and collectively microbes carry out functions that are vital for all life. Such functions include oxygen production, nitrogen cycling and degradation of organic carbon. Because microbes are also the most ancient organisms, all other life evolved on a planet that already contained complex microbial communities. The lives of modern plants and animals, including humans, are therefore intricately intertwined with those of the smallest organisms around them, and microbes often are key to the wellbeing of their larger hosts.

At CMESS, we study a wide range of topics to understand how microbial communities perform their functions



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



Microorganisms (in green) associated with rice plant root.

in a variety of natural and man-made ecosystems and how they have evolved to encode these functions. Particularly, we focus on the evolution of mutualism and parasitism, the ecology and biology of marine symbioses, and the interaction of microorganisms with each other, with their predators and with plants. Finally, an important and growing topic is how the actions of microbes influence the health of humans and other organisms.

Microbiomes, Microbial Symbionts and Pathogens

The term microbiome describes the microbes associated with a specific environment such as ocean water or desert soil, and also encompasses microbes growing in and on the human body. These communities are often highly diverse, consisting of eu-

karyotes, bacteria, archaea and viruses, and their interactions with each other and with their environment determine functions that include large-scale ecosystem processes and global nutrient cycles. Moreover, many of these functions can also be exploited as biological solutions to waste and pollution.

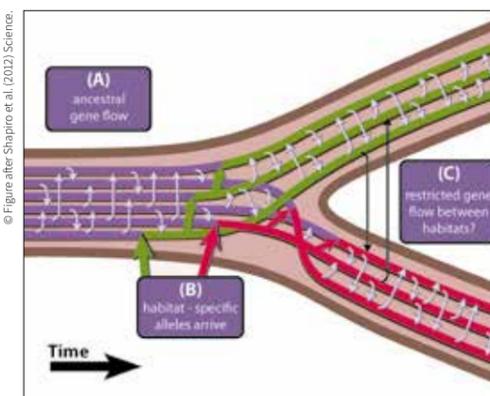
Animal- and plant-associated microbiomes can also include microbes that are highly specific and either benefit (mutualistic symbionts) or harm the host (pathogens). Beneficial symbionts may provide essential nutrients to their hosts, in exchange for an optimised environment. Bacterial pathogens exploit their hosts as part of their life cycle, sometimes with fatal consequences. 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.

We study a wide range of systems to elucidate general ecological mechanisms as well as system-specific interactions. Our ultimate goal is to translate fundamental knowledge into a better understanding of how global change will affect ecosystem services, and how we can influence the health of plants, animals and humans.

Selected microbiomes under investigation at CMESS

- Environmental microbiomes
- Microbiomes in biotechnology and industry
- Human and animal microbiota
- Beneficial symbionts in animals
- Intracellular microbes and pathogens
- Microbe-plant interactions
- Bacteria-virus (phage) dynamics in the wild



Visualisation of gene flow: Microbiologists at CMESS study how gene flow structures microbial genomes and how adaptation spreads within populations.



Sampling in the sea at Elba.

Microbial Evolution

The process of evolution underlies adaptation of organisms to ever-changing environmental conditions. Because microbes have fast generation times, evolutionary change happens on shorter time scales than in plants and animals, making microbes important model systems to understand the causes and consequences of evolution in general terms. However, the modes of evolution also differ in bacteria and archaea from those in eukaryotes in that horizontal gene

transfer between unrelated individuals can introduce entirely novel sets of genes to genomes, and it is such genes that may, for example, turn a harmless bacterium into a pathogen, allow a microbe to utilise a new nutrient, or introduce antibiotic resistance to entire communities of organisms. Because evolution in microbes is fast, it can happen on ecological timescales, thus influenc-

ing how populations and communities of organisms change under different conditions.

We cover diverse topics in microbial evolution, ranging from reconstruction of evolutionary history of genes and pathways to how species and populations arise and change. This also includes understanding of how organisms adapt to each other such as how resistance to viruses evolves in microbes in the wild. Finally, we use experimental evolution to ask to what extent outcomes of evolutionary processes are reproducible and predictable.

Research topics related to microbial evolution at CMESS

- Population genomics
- Evolution of resistance in hosts and counter resistance in viruses
- Horizontal gene transfer rates and bounds in the wild
- Mobile genetic elements

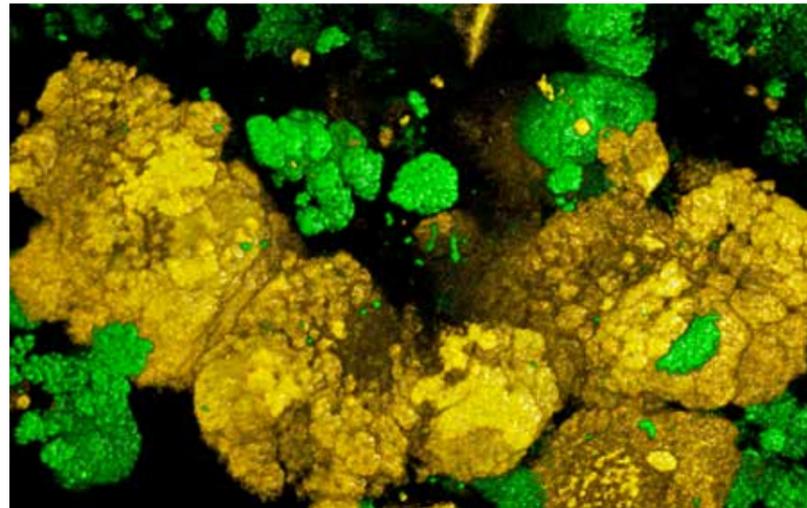
Microbial Ecology and Ecosystems

UNDERSTANDING BIOGEOCHEMICAL CYCLES THAT ENABLE LIFE

Microorganisms are of central importance for all global biogeochemical cycles and for food cycles in terrestrial, aquatic and technical ecosystems. This research area focuses on the structure and function of environmental microbiomes and the resulting flows of nutrient elements such as carbon, nitrogen, phosphorus and sulfur. The insights gained into the ecology, interaction and evolution of microorganisms are the basis for a better understanding of their contributions to ecosystem functions and for the optimised use of environmental microbiomes in technical systems.

Microbial N/S Cycling

All living organisms on our planet need nitrogen (N) and sulfur (S) for the biosynthesis of nucleic acids, proteins, and other cellular components and thus are directly connected to, and dependent upon, the biogeo-



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

chemical N and S cycles. These cycles consist of multiple processes, many of which are catalysed exclusively by bacteria and archaea.

Humans strongly impact the global N cycle by burning fossil fuels, cultivating plants that live in symbiosis with atmospheric N₂-fixing microbes, and most importantly by using artificial

nitrogen fertilisers. These transformations of the N cycle continue at a record pace. More than two billion people could not be fed without artificial nitrogen fertilisers, but as fertilisation efficiency is often below 50%, enormous amounts of anthropogenic ammonium affect the N cycle. Ecological consequences range from biodiversity loss, eutrophication

and dead zones in water bodies to increased emission of the greenhouse and ozone-depleting gas N₂O. Management strategies are urgently



Profile of a grassland soil showing different soil horizons.

needed to ensure a more efficient use of fertilisers and to reduce N₂O emissions.

The S cycle is intimately intertwined mainly through microbial activities with the cycles of other elements. Sulfate in the oceans represents the largest reservoir of biologically available sulfur on Earth. Microbial sulfate respiration thus fuels up to 50% of the mineralisation of organic carbon in marine sediments. The S cycle in terrestrial wetlands has an important control function on emission of the greenhouse gas methane.

CMESS includes internationally leading labs in N cycle and S cycle research. Our research aims at illuminating the complex biology of these biogeochemical cycles, from the level of whole processes in different

ecosystems to the ecophysiology and biochemistry of single microbial species. Our discoveries contribute to a holistic picture of these cycles, which is indispensable for predicting and mitigating environmental threats caused by human activities and global change.

Research topics related to N/S Cycling at CMESS

- Nitrogen fixation by free-living and plant-associated microbes
- Ecophysiology, biochemistry, and evolution of nitrifying microorganisms in terrestrial, aquatic, and engineered ecosystems
- Interactions of nitrifying microbes and plants in the rhizosphere
- Utilisation of organic and inorganic nitrogen compounds by plants and microorganisms
- Physiology and evolution of organic and inorganic sulfur-compound-utilising microorganisms in marine sediments and terrestrial wetlands
- Development of isotope techniques to quantify nitrogen and sulfur cycle processes

Microbiology of Soils

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 addresses fundamental questions on the factors governing

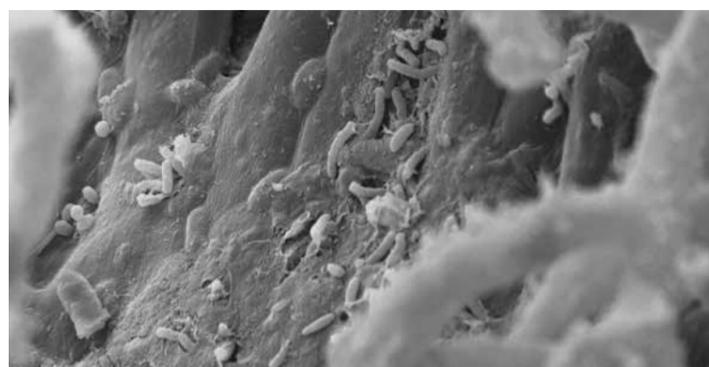
this extensive microbial diversity, on the mechanisms for microbial survival, and on the function of microorganisms in their environment. We aim to illuminate the role that microorganisms play in the terrestrial C cycle by decomposing, transforming and stabilising soil organic matter, the largest reservoir of organic carbon on Earth. And we 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 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).

Research topics related to the microbiology of soils at CMESS

- Microbial dormancy and resuscitation
- Soil organic matter formation and soil carbon storage
- Extracellular decomposition and microbial utilisation 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



Cross section of a marine tidal sediment showing oxic/suboxic (brown) and sulfidic (black) layers.



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

Global Change and Environmental Processes

UNDERSTANDING ENVIRONMENTAL SYSTEMS IN A CHANGING WORLD



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

Environmental systems are in a state of constant change, especially due to human activities. The aim of this research area is to identify, elucidate and model processes in terrestrial and aquatic systems and understand how they are impacted by anthropogenic influence. More specifically this research area focuses on questions concerning changes in biogeochemical cycles of matter, feedback to the climate, and the dynamics of pollutants. This allows a comprehensive understanding of complex environmental processes and the human influence on them, which is vital for future social decisions.

Microbes and Climate

Microorganisms have shaped the climate throughout Earth's history but microbial communities are also affected by climate change. Microorganisms

may acclimate or adapt in response to changing environmental and climatic conditions, leading to shifts in the composition and function of microbial communities, which may cause cascading alterations in biogeochemical cycles. The functional plasticity and diversity of microbes in the environment and the complex interplay of microbes with other organisms make the prediction of future effects of climate change on microbially-mediated ecosystem functions and services one of the most challenging frontiers of today's ecology research.

Research at CMESS focuses on the understanding which microorganisms respond to climate change in the upcoming decades and how, e.g. warming induced changes in soil organic matter breakdown may lead to soil-climate feedbacks through altered greenhouse gas production. We identify genetic

and metabolic properties of microbial key players of biogeochemical cycles, which have a disproportional negative or positive impact on climate change, and unravel their complex metabolic interactions. To address these questions, we apply the entire modern tool kit of molecular, analytical and stable isotope techniques.

Selected climate and global change topics at CMESS

- Soil warming, microbial acclimation and soil-climate feedbacks
- Impact of sulfur-cycling microorganisms on wetland methane emission
- Interactive effects of elevated atmospheric CO₂, warming and drought on soil processes
- Nitrogen fertilisation/ eutrophication and nutrient imbalances

Environmental Interfaces

Interfaces between the geosphere, biosphere, hydrosphere, and atmosphere are locations of intense biological activity, where pollutants are transformed, mobilised or immobilised, and where information about current or ancient biomes is archived. Interfaces may be truly global in scale or define the boundaries of nanoparticles. However, in order to understand interfacial processes, we focus on an even smaller scale: the molecular domain. Our goal is to arrive at quantitative models that are needed to underpin potentially costly decisions regarding environmental remediation or protection.

The investigation of processes on a range of spatial and time-scales poses challenges that we are well equipped to tackle. We develop novel analytical methods for the investigation of nanoparticles, we are using advanced spectroscopic methods, probing radiation from X-ray to IR, and we use mass spectrometry, including non-traditional isotope geochemistry in order to trace and elucidate interfacial processes.

Research on environmental interfaces at CMESS

- Mineral surfaces as information archives for past biomes
- Biological processes at environmental interfaces
- Interfacial processes mobilising or immobilising pollutants
- Natural nanoparticles, their (bio-)synthesis and their role in pollutant transport



In situ flumes field study to elucidate changes in microbial biofilm functioning following pulsed inputs: In this experiment CMESS researchers investigated post-fire changes to river functioning.

Emerging Environmental Pollutants

Chemical pollution is among the nine planetary boundaries that define Earth's stress limits. Pollutants therefore have the potential to irreversibly affect all ecosystems and are a threat to human and environmental health. Anthropogenic and naturally occurring chemicals are linked to complex sources and reactions in the environment, including their formation, transport, transformation and degradation.

Our overall goal is to understand the complexity of environmental systems and to apply those fundamental insights for solving the most pressing environmental problems of tomorrow.

We investigate threats of global concern like micro- and nanoplastics, manufactured and incidental nanoparticles, or freshwater contamination. Equally important to us are pollutants of natural origin. For instance, redox-driven uranium pol-

lution, asbestos in road construction, or persistent free radicals formed in wildfires. Our research aims to elucidate the occurrence, fate and (bio-)transformation of these substances from the molecular scale to a system understanding, fundamental prerequisites for accurate risk management. This knowledge is essential for safe use of existing and future products and required to design competitive remediation strategies and environmentally benign chemicals.

Research topics related to environmental pollutants

- Understanding the impact of engineered and incidental nanoparticles
- Micro- and nanoplastics in the environment
- Biotransformation of anthropogenic chemicals
- Behaviour of emerging environmental pollutants and innovative remediation strategies



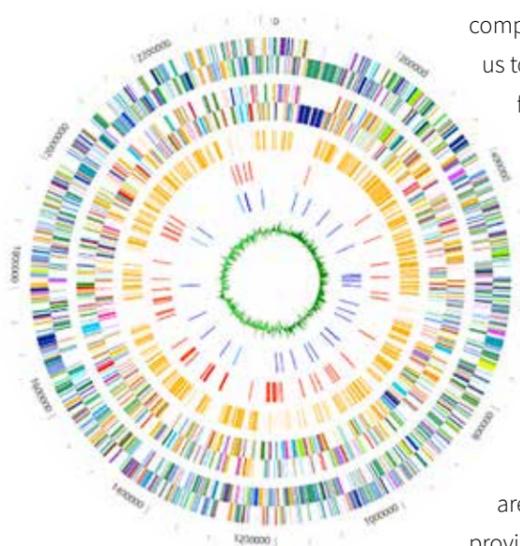
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Comparative Genomics

Life on Earth has been evolving for billions of years. Living organisms are found in virtually every environment, surviving and thriving under extreme heat, cold, radiation, pressure, salt, acidity, and darkness. Many of these environments are exclusively colonised by “simple” microorganisms, and the only nutrients available come from chemical compounds that only microbes can use. Their unparalleled genetic and metabolic diversity and range of environmental adaptations indicate that microbes long ago “solved” many problems for which scientists and engineers are still actively seeking solutions including carbon capture and nitrogen fixation.

The secrets to these adaptations are encoded in their genomes, which contain all the necessary instructions for



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

building functioning organisms. The first complete bacterial genome was deciphered in 1995. Since then, the number of complete genomes sequenced has grown exponentially. Powerful computers and sophisticated bioinformatics software are the key to unlocking the potential of these massive amounts of genomic data for medical and environmental applications.

The majority of microorganisms and viruses cannot be cultivated in the laboratory so far. We therefore use culture-independent approaches such as amplicon sequencing and metagenomics, which can be applied directly to nucleic acids isolated from any environment, to study the diversity, structure, and functional potential of microbial communities. State-of-the-art sequencing technologies combined with computational methods often allow us to reconstruct complete genomes from metagenomes, and to predict phenotypic traits from these genome sequences.

CMESS is involved in a wide range of genome sequencing and metagenomics projects and has established efficient tools and workflows for interpreting (meta)genomic data. 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.



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 CMESS

- **High-throughput community profiling using short- and long-read amplicon sequencing**
- **Genome annotation: EffectiveDB, SIMAP, pCOMP, GenSkew, ConsPred**
- **Functional genomics: NVT**
- **Comparative Genomics: Gepard, PICA, PhenDB, DeepNOG, VOGDB**
- **Metagenomics: probeBase, probeCheck, HoloVir**

Microbial Community Modelling

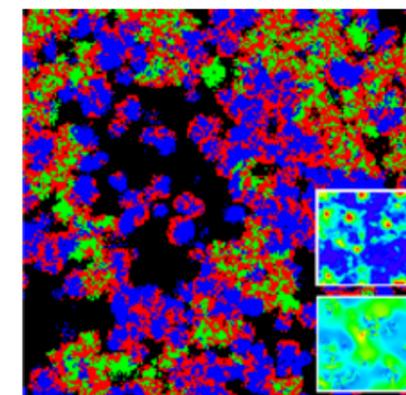
Microbial communities in natural environments consist of a multitude of functionally different individuals that interact with each other in a structured space. The wealth of microbial interactions in natural communities can be due to direct competition or predation but also through fairly indirect interactions such as exchanges of metabolites. The sum of these complex microbial interactions drive community metabolism and system behaviour on ecological and evolutionary time scales, eventually shaping the system’s response, resistance, and resilience to environmental change. However, the outcome of these interactions is often not predictable from properties of the individual organisms, and collective phenomena can emerge and modify system behaviour beyond our understanding of its individual parts. Therefore, at CMESS, we use mathematical modelling as a tool to explore the mechanisms that drive dynamics and functioning of complex microbial communities.

Different types of mathematical modelling enable us to understand the dynamics of microbial genome evolution in the light of microbial interactions, and to detect and quantify ecological forces that play a role in microbial community assembly. We use individual-based modelling to simulate competitive and synergistic interactions among microbial decomposers in spatially structured micro-environments, to explore how emerging system properties affect community behaviour. We model



Interacting soil bacterial community colonising the surface of a root.

microbial interaction networks using Lotka-Volterra dynamics and other approaches such as time series analysis to evaluate how diverse interactions affect community properties such as stability and resilience. We use meta*omic data to predict the structure of metabolic pathways, phenotypic roles, and growth rates of species in microbial communities. We develop steady-state metabolic models for microbial species and communities to predict how communities respond to changing nutrient availability and microbiome host factors.



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

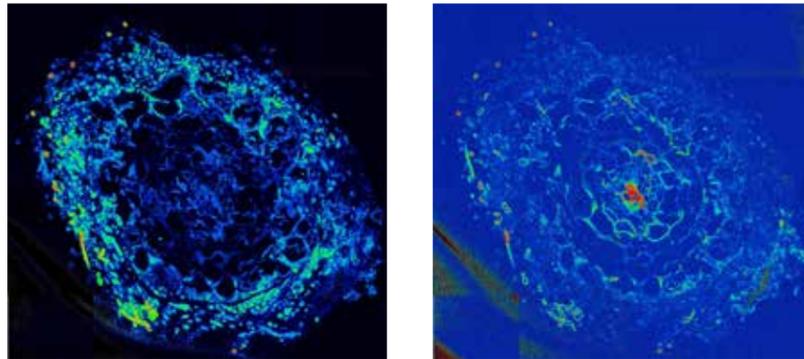
Methods and resources developed or applied at CMESS

- **Individual-based microbial community modelling**
- **Co-occurrence networks in environmental samples**
- **Computational models for molecular inter-species interactions**
- **Computational prediction of phenotypic roles of bacterial species**
- **Steady-state modelling of the metabolism of species and microbial communities**

Isotope Biogeochemistry

Measurements of isotope compositions are indispensable tools in microbial ecology, ecosystem science and environmental research. They are essential for linking microbes to functions, exploring the roles of uncultivable microorganisms, following host-microbe interactions and quantifying ecosystem and environmental processes or ancient human migration patterns. Our labs are equipped with a wide range of methods allowing us to probe light and heavy stable isotopes, as well as radiogenic and radioactive isotopes. This includes, for example, light elements that constitute the largest fraction of living organisms and water (H, C, N, O, S, and P), and heavy elements that are potent pollutants (e.g., Hg), or that serve as tracers for human migration (e.g., Sr). CMESS has developed and pioneered isotope methodology, including:

- Stable isotope probing (SIP) of nucleic acids, proteins and phospholipid fatty acids to identify not yet cultured environmental microbes that are actively processing target compounds
- Radioisotope approaches using isotope microarrays and fluorescence in situ hybridisation (FISH)-microautoradiography to link microbial community structure with function, and to measure soil and microbial P dynamics
- NanoSIMS and Raman spectroscopy approaches for chemical



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

- imaging of isotope incorporation within single cells
- Isotope tracing of processes such as N₂ 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
- Application of natural stable isotope abundances for in situ, minimally-invasive tracing of matter flow, and source-sink process investigations
- Isotope hydrology
- Non-traditional isotope geochemistry for process tracing in complex environments
- Sr-isotope geochemistry as tracer for early human migration



Mercury from an industrial pollution source undergoes chemical transformation reactions that are reflected in the isotopic composition of the element.

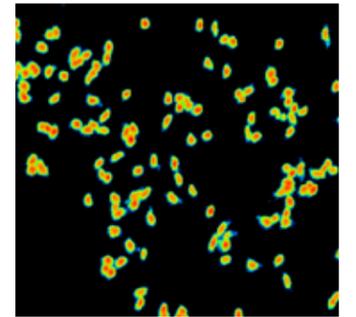
Single Cell Analysis

Virtually all microbial communities on our planet are dominated by a great diversity of uncultured microorganisms, which cannot be studied by traditional approaches in microbiology. In their habitats, microbes often coexist in spatially complex assemblies colonising 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 (e.g., fluctuations in nutrient concentrations) and involved in a plethora of biotic interactions.

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 can we decipher the in situ metabolic activities and symbioses of uncultured microbes. However, single-cell microbi-

ology is an enormous methodological challenge if we consider the tiny size of a microbial cell and the ultra-low amounts of substrates that are taken up, utilised, and exchanged by single cells.

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



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

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

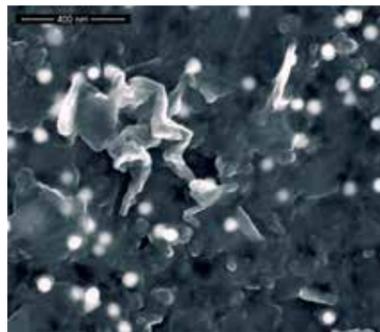
- Single-cell isotope probing using NanoSIMS, Raman microspectroscopy & microautoradiography
- Visualising and quantifying uncultured microbial cells by fluorescence in situ hybridisation (FISH) and confocal laser scanning microscopy
- 3D visualisation and image analysis software 'daime' (developed in-house)
- Single cell manipulation and sorting by laser microdissection
- Flow cytometry and fluorescence activated cell sorting
- Raman-activated microfluidic cell sorting



A Raman microspectrometer that is used for analysing 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.

Nanoparticle Analysis

In many environmental processes, nanoparticles and colloids represent the link between solutes and solids. Their small size (1–1000 nm) results in a large specific surface area, high reactivity, fast particle dynamics and potential mobility in marine and freshwaters, groundwater, soils, and sediments. Pollutants adsorb to nanoparticle surfaces or co-precipitate during particle formation. Manufactured nanoparticles may themselves be potential pollutants.



Gold nanoparticles (30 nm) among natural soil-derived nanoparticles in a scanning electron microscope.

The investigation of environmental processes involving nanoparticles or colloids requires specialised instruments and methodologies typically not available in environmental chemistry. We pioneer the development of methods to detect, identify, quantify and characterise natural, incidental and manufactured nanoparticles. This includes sampling, sample preparation and analysis with laser-based

particle sizing techniques, particle separation and sizing with different field flow fractionation systems, as well as multi-elemental analysis on a single nanoparticle level using the only available inductively coupled plasma-time of flight mass spectrometer (ICP-TOF-MS) in Austria (operated together with the Faculty of Chemistry). This ICP-TOF-MS collects full elemental spectra for each nanoparticle hence overcoming shortcomings of standard ICP-MS

instruments that may only detect one isotope in time-resolved mode and lose their multi-element capabilities. Among others, our methods include:

- Laser-based particle sizing techniques based on beam shading, static and dynamic light scattering determine particle size distributions from 0.6 nm to 600 µm in aqueous samples including information about particle shape and fractal dimension of particles and particle aggregates.
- Zeta potential and isoelectric point can be determined by dynamic light scattering/laser doppler anemometry in dispersions or by determination of streaming potential in porous media or on membranes.
- In our world-leading laboratory for field flow fractionation (FFF) analysis we operate five different instruments (symmetric flow-, asymmetric flow-, hollow fiber- and centrifugal FFF) in conjunction with multi-detection systems.
- We operate our ICP-MS instruments either in normal acquisition mode when coupled to FFF or in time resolved (single particle) mode when determining size and concentration of nanoparticles directly. In single particle mode nanoparticles down to below 20 nm can be quantified, this equals only ~ 80 attogram of gold in a single gold nanoparticle.



Field Flow Fractionation nanoparticle separation system coupled to various detection systems for detailed characterisation (UV-DAD, Fluorescence, DRI, static & dynamic light scattering and ICP-MS/MS).

Environmental Trace Analysis

The emission of hazardous and persistent contaminants such as synthetic organic compounds, heavy metals, and radioactive materials is a major threat for environmental and human health. Our goal is to obtain insights into these pressing environmental challenges. Therefore, we perform environmental trace analysis by using state-of-the-art instruments and by developing complementary methods that enable the reliable and efficient collection of high-quality data. To account for the complexity of environmental systems of interest, we take an interdisciplinary approach combining a wide range of methods including fieldwork, experiments under controlled laboratory conditions, and state-of-the-art computational approaches for data analysis. We use quantitative and qualitative approaches to explore the fate of organic and inorganic trace compounds at the molecular scale and to decipher the processes that control aquatic and terrestrial environments. Our methods cover the full analytical circle starting from sampling and sample preparation (digestion, extraction and preconcentration) to data acquisition and analysis. Examples are:

- Gas- and liquid chromatographic separation coupled to triple quadrupole tandem mass spectrometry to quantify target organic pollutants ranging from non-polar pollutants leaching from plastic to emerging persistent, mobile and potentially toxic substances such



Accelerated Solvent Extraction – Organic pollutants are extracted from solid samples as soil or sediments at high temperature and pressure.

- as tire additives, pharmaceuticals, pesticides, and per- and polyfluoroalkyl substances (PFASs).
- Liquid chromatography coupled to high-resolution mass spectrometry for the detection of suspects and the identification of unknown organic chemicals in complex environmental samples: Among other applications, we combine this technique with enzyme extraction methods to decipher biotransformation pathways of pollutants and promising alternatives.
- Inductively coupled plasma optical emission spectrometry (ICP-OES) for high-throughput analysis (ppb-range) of main and trace elements in a wide variety of matrices and single quadrupole inductively coupled plasma mass spectrometry (ICP-MS) for ultratrace analysis (ppt-range) of main and trace metals and metalloids.

- Triple quadrupole inductively coupled plasma mass spectrometry (ICP-MS/MS) for ultratrace analysis of metals, metalloids, sulfur and phosphorus at ppt levels; equipped with quadrupole mass filters before and after the collision/reaction cell to remove interferences and an automated matrix removal and pre-concentration system for the analysis of rare earth elements at ppq levels.

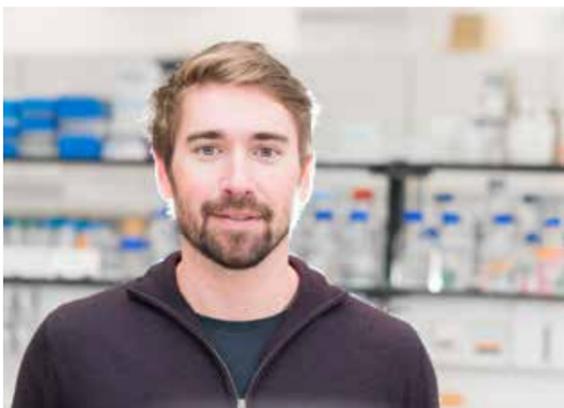


Soil extracts containing organic contaminants on an auto sampler for analysis via liquid chromatography-mass spectrometry (LC-MS/MS).



Research Groups

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David Berry

DOME – DIVISION OF MICROBIAL ECOLOGY

Full Professor

+43 1 4277 91212

david.berry@univie.ac.at

Since 2018: Full Professor for Intestinal Microbiology, University of Vienna

Since 2018: Operational Director of the Joint Microbiome Facility of the Medical University of Vienna and the University of Vienna

2016–2017: Associate Professor, University of Vienna

2012–2016: Assistant Professor, University of Vienna

2009–2012: Postdoctoral Researcher, University of Vienna

2009: PhD in Environmental Engineering, University of Michigan

Main research areas

- Ecology and evolution of the human microbiome
- Intestinal microbiota in health and disease
- Modelling approaches to study microbial communities
- Development of novel methods to study microorganisms in situ

Research in the group of David Berry (DB) is focused on understanding the biology of the human microbiota and its role in health and disease. He has pioneered the development of novel experimental and computational tools to reveal the function of microbial communities and has developed single cell isotope labelling techniques to characterise functional guilds in the intestinal ecosystem. The main research aims of DB are to gain a fundamental understanding of the assembly and interactions of the intestinal microbiota and to uncover how the microbiota affects host physiology. He is active in translational and clinical research in several fields, including chronic inflammation, nutrition, metabolic syndrome, cancer, and gut-immune-brain axis development in neonates.

DB holds a European Research Council (ERC) Starting Grant to elucidate functional networks and keystone species in the gut microbiota.

Selected publications

Rational design of a microbial consortium of mucosal sugar utilizers reduces *Clostridiodes difficile* colonization.

Pereira FC, Wasmund K, Cobankovic I, Jehmlich N, Herbold CW, Soo Lee K, ... Berry D. 2020 – Nat Commun, 11: 5104.

A fiber-deprived diet disturbs the fine-scale spatial architecture of the murine colon microbiome.

Riva A, Kuzyk O, Forsberg E, Siuzdak G, Pfann C, Herbold C, ... Berry D. 2019. Nat Commun, 10: 4366.

Mucispirillum schaedleri protects mice against non-typhoidal *Salmonella colitis* by interfering with virulence factor expression.

Herp S, Brugiroux S, Garzetti D, Ring D, Jochum L, Beutler M, ... Berry D,

Stecher B.

2019 – Cell Host Microbe, 25(5): 681-694.e8.

Genome-guided design of a defined mouse microbiota that confers colonization resistance against *Salmonella enterica* serovar Typhimurium.

Brugiroux S, Beutler M, Pfann C, Garzetti D, Ruscheweyh HJ, Ring D, ... Berry D, Stecher B. 2016 – Nat Microbiol, 2: 16215.

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

Berry D, Mader E, Lee TK, Woebken D, Wang Y, Zhu D, ... Wagner M. 2015 – Proc Natl Acad Sci USA, 112(2): E194–203.

Thomas Böttcher

JOINT PROFESSORSHIP CMES AND FACULTY OF CHEMISTRY



Full Professor

+43 1 4277 0

thomas.boettcher@univie.ac.at

Since 2020: Full Professor for Microbial Biochemistry, University of Vienna

2014–2020: Emmy-Noether Group Leader, Department of Chemistry, University of Konstanz

2011–2014: Postdoctoral Researcher, Harvard Medical School, Boston

2010–2011: Cofounder and Project Leader of start-up AVIRU GmbH, Munich

2010: Postdoctoral Researcher, Technical University Munich

2009: PhD in Chemical Proteomics, LMU Munich

Main research areas

- Chemistry of microbial interactions
- Discovery of microbial metabolites
- Species-specific antibiotics and anti-virulence strategies
- Chemical strategies for modulating microbial behaviour and signalling
- Development of chemical probes and customised enzyme inhibitors
- Chemistry of microbe-phage interactions

Research in the group of Thomas Böttcher (TB) focuses on the chemistry of microbial interactions and chemical strategies for modulating coordinated population behaviours of microbes. TB and his team elucidate chemical structures of metabolites that mediate and control interactions between microbes and with their human host. The research of the TB group exploits these compounds by synthetic chemistry in order to develop species-specific antibiotics and anti-virulence compounds. Additionally, his group is interested in chemical probes for active-site directed labelling of virulence-related enzymes and the development of customised inhibitors. The goal of TB's research is to improve the understanding of chemical interactions of microbes and to create chemical tools for precision interventions in complex microbiomes with the ultimate vision of chemical microbiome engineering.

TB was recently awarded an ERC Consolidator grant to investigate the chemistry of prophage induction.

Selected publications

A ligand selection strategy identifies chemical probes targeting the proteases of SARS-CoV-2.

Peñalver L, Schmid P, Szamosvári D, Schildknecht S, Globisch C, Sawade K, Peter C, Böttcher T. 2021 – Angew Chem Int Ed, 60(12): 6799-6806.

Competitive metabolite profiling of natural products reveals subunit specific inhibitors of the 20S proteasome.

Pawar A, Basler M, Goebel H, Alvarez Salinas G, Groettrup M, Böttcher T. 2020 – ACS Cent Sci, 6(2): 241-246.

A thiochromenone antibiotic derived from *Pseudomonas* quinolone signal selectively targets the Gram-negative pathogen *Moraxella catarrhalis*.

Szamosvári D, Schuhmacher T, Hauck C, Böttcher T. 2019 – Chem Sci, 10: 6624-6628.

Competitive live-cell profiling strategy for discovering inhibitors of the quinolone biosynthesis of *Pseudomonas aeruginosa*.

Prothiwa M, Englmaier F, Böttcher T. 2018 – J Am Chem Soc, 140(43): 14019-14023.

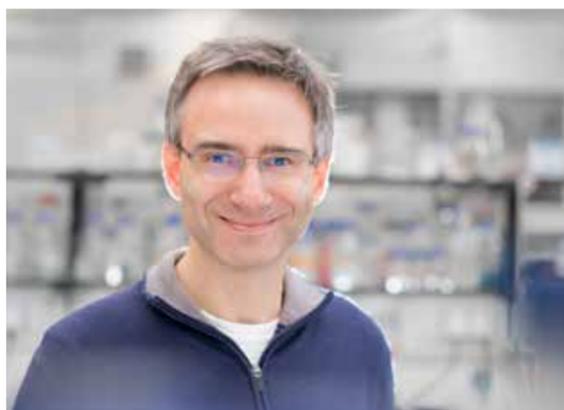
An unsaturated quinolone N-oxide of *Pseudomonas aeruginosa*

modulates growth and virulence of *Staphylococcus aureus*.

Szamosvári D, Böttcher T. 2017 – Angew Chem Int Ed, 56(25): 7271-7275.

One Enzyme, Three Metabolites: *Shewanella* algae controls siderophore production via the cellular substrate pool.

Rütschlin S, Gunesch S, Böttcher T. 2017 – Cell Chem Biol, 24(5): 598-605.



Holger Daims

DOME – DIVISION OF MICROBIAL ECOLOGY

Full Professor

+43 1 4277 91204

holger.daims@univie.ac.at

Since 2018: Head of the Comammox Research Platform, University of Vienna

Since 2017: Full Professor for Ecophysiology of Microorganisms, University of Vienna

2012–2017: Associate Professor, University of Vienna

2010–2012: Assistant Professor (Tenure Track), University of Vienna

2003–2010: Assistant Professor, University of Vienna

2001–2003: Postdoctoral Researcher, Technical University Munich (TUM)

2001: PhD in Microbiology, TUM

Main research areas

- Evolution and ecophysiology of nitrite-oxidising 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

Selected publications

Genomic and kinetic analysis of novel Nitrospinae enriched by cell sorting.

Mueller AJ, Jung MY, Strachan CR, Herbold CW, Kirkegaard RH, Wagner M, Daims H. 2021 – ISME J, 15: 732–745.

Exploring the upper pH limits of nitrite oxidation: diversity, ecophysiology, and adaptive traits of haloalkalitolerant Nitrospira.

Daebeler A, Kitzinger K, Koch H, Herbold CW, Steinfeder M, Schwarz J, ... Daims H. 2020 – ISME J, 12: 2967–2979.

Low yield and abiotic origin of N₂O formed by the complete nitrifier Nitrospira inopinata.

Kits KD, Jung M-Y, Vierheilig J, Pjevac

P, Sedlacek CJ, Liu S, ... Daims H. 2019 – Nat Commun, 10: 1836.

Kinetic analysis of a complete nitrifier reveals an oligotrophic lifestyle.

Kits KD, Sedlacek CJ, Lebedeva EV, Han P, Bulaev A, Pjevac P, ... 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, ... Wagner M. 2015 – Nature, 528: 504–509.

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

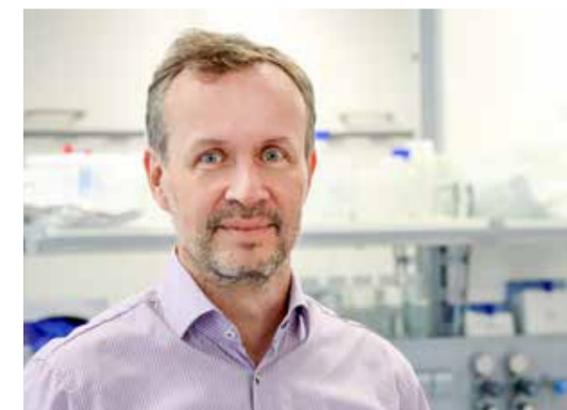
Koch H, Lückner S, Albertsen M, Kitzinger K, Herbold C, Spieck E, ... Daims H. 2015 – Proc Natl Acad Sci USA, 112: 11371–11376.

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 water treatment facilities. Key research goals of HD are to understand how the analysed microorganisms interact and maintain their activities in fluctuating environmental conditions. The resulting knowledge helps improve strategies to utilise and control N-cycling microorganisms in soils and engineered systems. HD and his team have revealed a hidden metabolic versatility of nitrite-oxidising bacteria and made key contributions to the discovery and characterisation of complete ammonia oxidisers (comammox).

An additional research area is the development and application of in situ labelling and imaging methods to characterise microorganisms in spatially complex environments, such as environmental and medical biofilms. Software developed by HD is among the most widely used programs for digital image analysis in microbial ecology, with applications in >300 studies worldwide.

Thilo Hofmann

EDGE – DIVISION OF ENVIRONMENTAL GEOSCIENCES



Full Professor

+43 1 4277 53320

thilo.hofmann@univie.ac.at

Since 2019: Vice Head of CMESS

Since 2018: Guest Professor, Nankai University

Since 2017: Adjunct Full Professor, Duke University

Since 2015: Director of the University of Vienna “Environmental Science Research Network”

2012–2016: Dean, Faculty of Geosciences, Geography and Astronomy, University of Vienna

Since 2005: Full Professor for Environmental Geosciences, University of Vienna

2003–2005: Lecturer (C2), University Mainz

1999–2003: Research Associate (C1), University Mainz

1998: PhD in Aquatic Geochemistry, University of Bremen

Thilo Hofmann's (TH) group focuses on nanogeosciences, investigates trace contaminants and sorption to carbonaceous materials and microplastics, and works in hydrogeology, including vulnerability analysis and modelling. His research aims to elucidate the mechanisms involved in interactions between organic contaminants and natural and synthetic sorbents, to develop prediction methods, to understand the impact of nanotechnology on the environment, and to analyse consequences in terms of environmental fate and remediation strategies. His group started to work intensively with microplastics, paying special attention to the release of additives and plasticisers, tire wear, and adsorption phenomena.

TH is director of the University of Vienna's Environmental Research Network, which includes more than 220 scientists from natural sciences, social sciences, humanities, law, and economics, aiming to tackle today's environmental challenges. He has received awards from the German Academic Scholarship Foundation, Berlin Technical University, and the German Water Chemical Society. He is adjunct/visiting professor at Duke (NC, USA) and Tianjin (China) University.

Main research areas

- Nanogeosciences: Understanding natural, incidental and engineered nanoparticles in the environment
- Pollution: Understanding the fate of contaminants from the molecular scale to soil and groundwater remediation
- Hydrogeology: Flow and transport modelling, risk assessment

Selected publications

Environmentally persistent free radicals are ubiquitous in wildfire charcoals and remain stable for years.

Sigmund G, Santín C, Pignitter M, Tepe N, Doerr SH, Hofmann T. 2021 – Nature Communications Earth & Environment, 2(68).

Technology readiness and overcoming barriers to sustainably implement nanotechnology-enabled plant agriculture.

Hofmann T, Lowry GV, Ghoshal S, ... Wilkinson KJ. 2020 – Nature Food, 1: 416–425.

Anthropogenic gadolinium in freshwater and drinking water systems.

Brünjes R & Hofmann T. 2020 – Water Research, 182: 115966.

A deep learning neural network approach for predicting the sorption of ionizable and polar organic pollutants to a wide range of carbonaceous materials.

Sigmund G, Gharasoo M, Hüffer T & Hofmann T. 2020 – Environmental Science & Technology, 54 (7): 4583–4591.

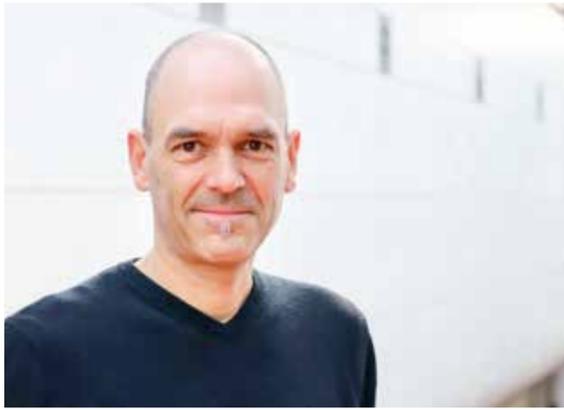
Sorption of organic substances to tire wear materials: Similarities and differences with other types

of microplastic.

Hüffer T, Wagner S, Reemtsma T & Hofmann T. 2019 – TrAC Trends in Analytical Chemistry, 113: 392–401.

Legal and practical challenges in classifying nanomaterials according to regulatory definitions.

Miernicki M, Hofmann T, ... Praetorius A. 2019 – Nature Nanotechnology, 14: 208–216.



Matthias Horn

DOME – DIVISION OF MICROBIAL ECOLOGY

Full Professor

+43 1 4277 91208

matthias.horn@univie.ac.at

Since 2019: Head of the Department of Microbiology and Ecosystem Science

Since 2007: Full Professor for Microbial Symbioses, University of Vienna

2005: Professor, University of Vienna

2003: Assistant Professor, University of Vienna

2001: PhD in Microbiology, Technical University 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 group of Matthias Horn (MH) focuses on bacteria infecting and residing within eukaryotic cells. Using an array of molecular and computational methods, his group discovered novel intracellular microbes, and deciphered molecular mechanisms and evolutionary processes underlying these associations. Bacteria living within eukaryotic host cells comprise important pathogens as well as symbionts of humans and diverse animals. Yet, intracellular microbes have long been underestimated with respect to diversity, distribution in nature, and their ecological importance. To address this knowledge gap, the group investigates selected non-model organisms, including symbionts of amoeba and viruses infecting protists. Current studies include the effects of co-infections with multiple intracellular microbes, ancestral genome reconstruction and evolution experiments to better understand (the evolution of) microbe-host interactions.

MH has received an ERC Starting Grant (Consolidator Track) and the START Award of the Austrian Science Fund FWF. He is currently coordinating a FWF-funded PhD program on Microbial Symbiosis.

Selected publications

Coevolving plasmids drive gene flow and genome plasticity in host-associated intracellular bacteria.

Köstlbacher S, Collingro A, Halter T, Domman D, Horn M. 2021 – Curr Biol, 31(2): 346-357.e3.

Molecular causes of an evolutionary shift along the parasitism-mu-

tualism continuum in a bacterial symbiont.

Herrera P, Schuster L, Wentrup C, König L, Kempinger T, Na H, Schwarz J, Köstlbacher S, Wascher F, Zojer M, Rattei T, Horn M. 2020 – Proc Natl Acad Sci U.S.A., 117: 21658-66.

Chlamydiae in the environment.

Collingro A, Köstlbacher S, Horn M. 2020 - Trends Microbiol, 11: 877-888.

The cooling tower water microbiota: Seasonal dynamics and co-occurrence of bacterial and protist phylotypes.

Tsao HF, Scheikl U, Herbold CW, Indra A, Walochnik J, Horn M. 2019 - Water Res, 464-479.

Symbiont-mediated defense against Legionella pneumophila in amoebae.

König L, Wentrup C, Schulz F, Wascher F, Escola S, Swanson MS,

Buchrieser C, Horn M. 2019 – mBio, 10: e00333-19.

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.

Christina Kaiser

TER – DIVISION OF TERRESTRIAL ECOSYSTEM RESEARCH



Assistant Professor (Tenure Track)

+43 1 4277 91263

christina.kaiser@univie.ac.at

Since 2018: Assistant Professor (Tenure Track), University of Vienna

Since 2014: Group Leader and Assistant Professor (Univ. Ass.), TER, University of Vienna

2014-2018: Guest Researcher at the International Institute for Applied Systems Analysis (IIASA), Laxenburg

2012-2014: IIASA Postdoctoral Fellow

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

2010: PhD in 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's (CK) work combines soil microbial ecology and theoretical modelling with ecosystem biogeochemistry. Looking at the soil from the perspective of complex system science CK's group utilises both mathematical modelling and experimental approaches to explore how microbial processes and interactions at the microscale govern organisation and regulation of microbial communities, and how this, in turn, affects soil organic matter turnover. 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 visualise 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 was recently awarded an ERC Consolidator grant to study self-organisation of microbial soil organic matter turnover.

Selected publications

Persistence of soil organic carbon caused by functional complexity. Lehmann J, Hansel CM, Kaiser C, ... Kögel-Knabner I. 2020 – Nature Geoscience, 13: 529-534.

Nitrogen and phosphorus constrain the CO₂ fertilization of global plant biomass.

Terrer C, Jackson RB, Prentice IC, Keenan TF, Kaiser C, ... Franklin O. 2019 – Nature Climate Change, 9: 684-689.

Rapid transfer of plant photosynthates to soil bacteria via ectomycorrhizal hyphae and its interaction with nitrogen availability.

Gorka S, Dietrich M, Mayerhofer W, ... Kaiser C. 2019 – Front Microbiol, 10: 168.

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 Bio Biochem, 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, Murphy DV. 2015 – The New Phytologist, 205(4): 1537-1551.



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Stephan Krämer

EDGE – DIVISION OF ENVIRONMENTAL GEOSCIENCES

Full Professor

+43 1 4277 53463

stephan.kraemer@univie.ac.at

Since 2012: Head of the Department of Environmental Geosciences

Since 2006: Full Professor for Environmental Geosciences, University of Vienna

2005: Habilitation, Environmental Geochemistry, ETH Zürich

2000–2006: ETH-Oberassistent, Department of Environmental Sciences, Swiss Federal Institute of Technology Zürich

1998–1999: Guest Scientist, Department of Environmental Science, Policy and Management, University of California, Berkeley

1997: PhD in Geosciences, TH Darmstadt

Main research areas

- aDNA and eDNA preservation at mineral surfaces
- Mobilisation and immobilisation of inorganic contaminants in soils and sediments
- Biological trace nutrient acquisition
- Mineral surface chemistry
- Rhizosphere chemistry

The research of Stephan Krämer (SK) focuses on the interactions of the biosphere with earth materials. Taking a process-oriented approach, his group is studying these processes in various contexts: From an environmental perspective, they study pollution mobilisation and immobilisation. From an agricultural perspective, they investigate how these processes lead to plant nutrient acquisition or the excessive loss of nutrients to surface waters. From a biogeochemical perspective, they elucidate key chemical mechanisms involved in element cycling. From an anthropological perspective, they investigate how interactions between DNA and minerals lead to the preservation of ancient human or pathogen DNA over long timescales.

The Krämer group uses modern methods such as non-traditional stable isotope geochemistry and synchrotron X-ray adsorption spectroscopy to study these problems on a molecular scale.

Selected publications

Copper limiting threshold in the terrestrial ammonia oxidizing archaeon *Nitrososphaera viennensis*. Reyes C, Hodgskiss LH, Baars O, Kerou M, Bayer B, Schleper C, Kraemer SM. 2020 – Res Microbiol, 171: 134-142.

Low Fe(II) concentrations catalyze the dissolution of various Fe(III)

(hydr)oxide minerals in the presence of diverse ligands and over a broad pH range.

Kang K, Schenkeveld WDC, Biswakarma J, Borowski SC, Hug SJ, Hering JG, Kraemer SM. 2019 – Env Sci Technol, 53: 98–107.

The effect of pH and biogenic ligands on the weathering of chrysotile asbestos; the pivotal role of tetrahedral Fe in dissolution kinetics and radical formation.

Walter M, Schenkeveld WDC, Reissner M, Gille L, Kraemer SM. 2019 – Chemistry, 25(13): 3286-3300.

A density functional theory investigation of oxalate and Fe(II) adsorption onto the (010) goethite surface with implications for ligand- and reduction-promoted dissolution.

Kubicki JD, Tunega D, Kraemer SM. 2017 – Chem Geol, 464: 14-22.

Synergistic effects between biogenic ligands and a reductant in Fe acquisition from calcareous soil.

Schenkeveld WDC, Wang Z, Giammar DE, Kraemer SM. 2016 – Env Sci Technol, 50: 6381-6388.

Alexander Loy

DOME – DIVISION OF MICROBIAL ECOLOGY



Full Professor

+43 1 4277 91205

alexander.loy@univie.ac.at

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

Since 2016: Co-founder, AMICI – Austrian Microbiome Initiative

2013–2017: Associate Professor, University of Vienna

Since 2013: Faculty member, APRI – Austrian Polar Research Institute

2009–2013: Assistant Professor, University of Vienna

2006–2009: Group Leader, University of Vienna

2003–2006: Postdoctoral Researcher, University of Vienna

2000–2003: PhD in Microbiology, Technical University Munich

Main research areas

- The complex symbiotic microbiota of animals and humans in health and disease
- 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 the role of the intestinal microbiota in health & disease and ecology & evolution of sulfur-compounds-utilising 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.

Research activities of AL aim at understanding how the myriad of physiological interactions among complex microbiota members impact sulfur & carbon cycling in their environment and nutrition & health of their animal and human host. This knowledge should ultimately translate to the design of microbiome-based strategies for improved health management, including nutritional and probiotic interventions. Current projects focus on microbial sulfur metabolism in wetlands and the intestinal tract and the development of defined microbial communities for production of new secondary metabolites such as antibiotics.

Selected publications

Hair eruption initiates and commensal skin microbiota aggravate adverse events of anti-EGFR therapy.

Klufa J, Bauer T, Hanson B, Herbold CW, Starkl P, ... Loy A, Sibilina M. 2019 – Sci Transl Med, 11: eaax2693.

Long-term transcriptional activity at zero growth by a cosmopolitan rare biosphere member.

Hausmann B, Pelikan C, Rattei T, Loy A, Pester M. 2019 – mBio, 10: e02189-18.

Peatland Acidobacteria with a dissimilatory sulfur metabolism. Hausmann B, Pelikan C, Herbold CW, Köstlbacher S, Albertsen M, ... Loy A. 2018 – ISME J, 12: 1729-1742.

Bottled aqua incognita: Microbiota assembly and dissolved organic matter diversity in natural mineral waters.

Lesaulnier CC, Herbold CW, Pelikan C, Gérard C, Le Coz X, ... Loy A. 2017 – Microbiome, 5: 126.

Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses.

Roux S, Brum JR, Dutilh BE, Sunagawa S, Duhaime MB, Loy A, ... 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.



Jillian Petersen

DOME – DIVISION OF MICROBIAL ECOLOGY

Associate Professor

+43 1 4277 91206

jillian.petersen@univie.ac.at

Since 2020: Associate Professor, University of Vienna

Since 2015: Vienna Research Group Leader of the Vienna Science and Technology Fund (WWTF)

2016–2020: Assistant Professor, University of Vienna

2009–2015: Postdoctoral Researcher & Senior Scientist, Max Planck Institute for Marine Microbiology, Bremen

2009: PhD in Marine Microbiology, University of Bremen

Main research areas

- Beneficial host-microbe interactions
- Ecology, evolution and development of marine symbioses
- Microbial metabolism
- In situ imaging of microbial identity and function
- Meta-omics analyses of host-associated microbes

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-oxidising bacterial symbionts. The goal 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 hydrothermal vents to shallow-water seagrass beds. Recent highlights include the discovery that in addition to fixing carbon and providing this for their host’s nutrition, the symbionts also fix nitrogen, and can provide this limiting nutrient to the surrounding seagrass habitats.

JP received an ERC Starting Grant 2018, and is a Board Member for the Austrian Science Foundation (FWF).

Selected publications

The symbiotic ‘all-rounders’: Partnerships between marine animals and chemosynthetic nitrogen-fixing bacteria.

Petersen JM, Yuen B.
2021 – Applied and Environmental Microbiology, 87: e02129–20.

Chemosymbiotic bivalves contribute to the nitrogen budget of seagrass ecosystems.

Cardini U, Bartoli M, Lee R, Luecker S, Mooshammer M, Polzin J, Weber M, Petersen JM.
2019 – ISME Journal, 13: 3131–3134.

Diversity matters: Deep-sea mussels harbor multiple symbiont strains.

Ansorge R, Romano S, Sayavedra L, Kupczok A, Tegetmeyer HE, Dubilier

N, Petersen JM.
2019 – Nature Microbiology, 4: 2487–2497.

Chemosynthetic symbionts of marine invertebrate animals are capable of nitrogen fixation.

Petersen JM, Kemper A, Gruber-Vodicka H, Cardini U, van der Geest M, Mussmann M, Bulgheresi S, Seah BKB, Chakkiath PA, Herbold C, Liu D, Belitz A, Weber M.
2016 – Nature Microbiology, 2: 16195.

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.

Martin Polz

DOME – DIVISION OF MICROBIAL ECOLOGY



Full Professor

+43 1 4277 91207

martin.f.polz@univie.ac.at

Since 2020: Full Professor for Microbial Population Biology and Genetics, University of Vienna

2009–2019: Full Professor, Massachusetts Institute of Technology

2004–2009: Associate Professor, Massachusetts Institute of Technology

1998–2004: Assistant Professor, Massachusetts Institute of Technology

1998: Postdoctoral Fellow, Harvard University

1997: PhD in Organismic and Evolutionary Biology, Harvard University

Main research areas

- Microbial population genomics
- Microbial viruses
- Evolutionary ecology
- Microbiomes

Microbes are the most abundant and diverse organisms on the planet. Yet how this diversity is structured in the environment remains poorly understood. Martin Polz’s (MP) group is broadly interested in structure-function relationships within microbial communities. What are the ecological and evolutionary dynamics of microbial populations? How do environmental interactions and selection structure populations? What are the rates and bounds of gene transfer?

The MP lab addresses these questions by a combination of in situ molecular approaches, environmental genomics, traditional physiological and genetic techniques and modelling. It studies patterns of diversity among co-occurring microbes from the level of the entire community to the individual genome. The model systems investigated by the MP group include marine microbes as well as animal microbiomes. The latest projects focus in particular on microbe-virus interactions and on growth dynamics under environmental conditions.

Selected publications

Diarrheal events can trigger long-term Clostridium difficile colonization with recurrent blooms.

VanInsberghe D, Varian B, Erdman S, Polz MF.
2020 – Nature Microbiol, 5(4): 642–650.

A reverse ecology approach based on a biological definition of microbial populations.

Arevalo P, VanInsberghe D, Elsherbini J, Gore J, Polz MF.
2019 – Cell, 178(4): 820–834.e14.

High resolution time series reveals cohesive but short-lived communities in coastal plankton.

Martin-Platero A, Cleary B, Kauffman KM, Preheim SP, McGillicuddy DJ, Alm EJ, Polz MF.

2018 – Nature Comm, 9(1): 266.

A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria.

Kauffman KM, Hussain FA, Yang J, Arevalo P, Brown, ... Polz MF.
2018 – Nature, 554(7690): 118–122.

Adaptive radiation by waves of gene transfer leads to fine-scale resource partitioning in marine microbes.

Hehemann J-H, Arevalo P, Datta MS, Yu A, ... Polz MF.
2016 – Nature Comm, 7: 12860.

Ecological populations of bacteria act as socially cohesive units of antibiotic production and resistance.

Cordero OX, Wildschutte H, Kirkup B, Proehl S, ... Polz MF.
2012 – Science, 337: 1228–1231.



Thomas Rattei

CUBE - DIVISION OF COMPUTATIONAL SYSTEMS BIOLOGY

Full Professor
+43 1 4277 91280
thomas.rattei@univie.ac.at

Since 2020: Head of the Doctoral School Microbiology and Environmental Science
Since 2019: Vice Head of the Department of Microbiology and Ecosystem Science
Since 2010: Full 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

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

TR's team maintains and develops internationally relevant resources in computational biology, such as the web portals phendb.org, vogdb.org and effectivedb.org for microbial trait prediction, virus orthologous groups and protein families, and bacterial secreted proteins and secretion systems.

Selected publications

DeepNOG: Fast and accurate protein orthologous group assignment.

Feldbauer R, Gosch L, Lüftinger L, Hyden P, Flexer A, Rattei T. 2020 – Bioinformatics, 36(22–23): 5304–5312.

Conserved Secondary Structures in Viral mRNAs.

Kiening M, Ochsenreiter R, Hellingner HJ, Rattei T, Hofacker I, Frishman D. 2019 – Viruses, 11(5): 401.

eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses.

Huerta-Cepas J, Szklarczyk D, Heller D, Hernández-Plaza A, Forslund SK,

Cook H, Mende DR, Letunic I, Rattei T, Jensen LJ, von Mering C, Bork P. 2019 – Nucleic Acids Res, 47(D1): D309–D314.

Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software.

Sczyrba A, Hofmann P, Belmann P, ... Rattei T, McHardy AC. 2017 – Nat Methods, 14(11): 1063–1071.

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, Vigil 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, 351(6269): 162–165.

Andreas Richter

TER - DIVISION OF TERRESTRIAL ECOSYSTEM RESEARCH



Full Professor
+43 1 4277 91260
andreas.richter@univie.ac.at

Since 2020: Head of CMESS
Since 2011: Full 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

Main research areas

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

Microbial communities are key components of all global biogeochemical cycles and play a central yet poorly understood role in climate change biology. Research in the group of Andreas Richter (AR) is focused on understanding how growth and turnover of microbial communities control the deconstruction and mineralisation of organic matter in terrestrial ecosystems in the current and in a future climate.

AR's research group has redefined and expanded the concept of microbial carbon use efficiency and nitrogen use efficiency and linked it to the theory of ecological stoichiometry. AR also pioneered the development of methods to estimate microbial growth and carbon use efficiency based on stable oxygen isotopes.

AR's group has extensively worked on soil organic matter storage in arctic ecosystems and permafrost-climate feedbacks. Another main research interests of AR's group are the interactive effects of climate change (i.e., global warming, elevated CO₂, drought) on microbial processes and community composition, as well as on plant-microbe interaction. AR is also currently exploring the development of synthetic soil ecosystems to address fundamental questions about the link between the structure/diversity of microbial communities and their function.

Selected publications

Microbial carbon limitation – the need for integrating microorganisms into our understanding of ecosystem carbon cycling.

Soong JL, ... Richter A. 2020 – Global Change Biology, 26: 1953–1961.

Microbial growth and carbon use efficiency show seasonal responses in a multifactorial climate change experiment.

Simon E, ... Richter A. 2020 – Communications Biology, 3: 584.

Increased microbial growth, biomass and turnover drive soil organic carbon accumulation at higher plant diversity.

Prommer J, ... Richter A.

2020 – Global Change Biology, 26: 669–681.

Microbial temperature sensitivity and biomass change explain soil carbon loss with warming.

Walker TWN, ... Richter A. 2018 – Nature Climate Change, 8: 885–889.

Decoupling of microbial carbon, nitrogen and phosphorus cycling in response to extreme temperature events.

Mooshammer M, ... 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, ... Richter A. 2016 – Soil Biology and Biochemistry, 97: 168–175.



Frank von der Kammer

EDGE – DIVISION OF ENVIRONMENTAL GEOSCIENCES

Senior Scientist

+43 1 4277 53380

frank.kammer@univie.ac.at

2012: Guest Professor, University of Aix-Marseille

Since 2009: Senior Scientist, University of Vienna

2006: Guest Professor, University of Pau

2005–2009: University Assistant, University of Vienna

1996–2005: Scientific Assistant, University of Technology Hamburg-Harburg

2005: PhD in Natural Sciences, Hamburg University of Technology (TUHH)

Main research areas

- Analysis of sub-micron particles in complex samples, single-particle elemental fingerprinting
- Understanding the behaviour of nanoparticles in the environment
- Development of regulatory risk assessment tools for the risk management of engineered nanomaterials
- Interaction of trace metals with particulate phases in the environment
- Trace metal dynamics and remediation

Frank von der Kammer's (FK) group focusses on nanogeo-sciences and environmental colloid chemistry. This includes, but is not limited to natural, incidental and engineered/ manufactured nanoparticulate/colloidal systems in soils, sediments, fresh- and groundwater. FK's research activities have pioneered the understanding of manufactured nanoparticles in the environment. They span from the development of sophisticated analytical tools and methods for the detection, identification and characterisation of nanoparticles and colloids in complex samples as soil, sediment, food and cosmetics, elucidating nanoparticle behaviour, fate and interactions in the environment to the development of regulatory tools for the environmental risk assessment of engineered nanoparticles on ISO and OECD level.

FK's group has developed the first validated methods to quantify manufactured nanoparticles in food and sun-screen and the first OECD guideline for the safety testing of nanomaterials. Currently FK develops multi-element single-particle elemental fingerprinting with ICP-TOF-MS to trace particulate pollutants from fuel additives, automotive catalysts, brake and tire wear and fly ash in the environment at ultra-trace levels.

Selected publications

Key principles and operational practices for improved nanotechnology environmental exposure assessment.

Svendsen C, ... von der Kammer F, van den Brink NW, Mays C, Spurgeon DJ. 2020 – Nature Nanotechnology, 15: 731–742.

Strategies for determining heteroaggregation attachment efficiencies of engineered nanoparticles in aquatic environments.

Praetorius A, Badetti E, Brunelli A, ... von der Kammer F. 2020 – Environmental Science-Nano, 7: 351–367.

Legal and practical challenges in classifying nanomaterials according to regulatory definitions.

Miernicki M, Hofmann T, Eisenberger

I, von der Kammer F, Praetorius A. 2019 – Nature Nanotechnology, 14: 208–21.

Where is the nano? Analytical approaches for the detection and quantification of TiO₂ engineered nanoparticles in surface waters.

Gondikas A, von der Kammer F, Kaegi R, Borovinskaya O, Neubauer E, Navratilova J, Praetorius A, Cornelis G, Hofmann T. 2018 – Environmental Science-Nano, 5: 313–326.

Single-particle multi-element fingerprinting (spMEF) using inductively-coupled plasma time-of-flight mass spectrometry (ICP-TOFMS) to identify engineered nanoparticles against the elevated natural background in soils.

Praetorius A, Gundlach-Graham A, ... von der Kammer F. 2017 – Environmental Science-Nano, 4: 307–314.

Isabella Wagner

JOINT PROFESSORSHIP CMES, FACULTY OF PSYCHOLOGY, AND VIENNA COGNITIVE SCIENCE HUB



Assistant Professor (Tenure Track)

+43 1 4277 47133

isabella.wagner@univie.ac.at

Since 2021: Assistant Professor (Tenure Track), University of Vienna

2017–2021: Postdoctoral Researcher, University of Vienna

2017: PhD in Medical Sciences, Donders Institute for Brain, Cognition and Behaviour, Radboud University Medical Center, Nijmegen

Main research areas

- Cognition-brain-microbiome interactions
- Neurobiology of learning and memory
- Social, cognitive and affective neuroscience
- Brain network interactions
- Advanced fMRI analysis methods

Research in the group of Isabella Wagner (IW) focuses on understanding interactions at the interface of the brain, cognition, and the human microbiome. Specifically, her work aims at elucidating how gut microbial characteristics affect brain function and cognitive processes such as learning, memory, and social behaviour. While primarily focusing on healthy individuals, IW's group aims to understand how age, genetic predisposition, and clinical conditions can affect the cognition-brain-microbiome link, and how targeted interventions influence the communication between these complex systems. IW has a strong background in cognitive neuroscience and tests her questions using functional magnetic resonance imaging (fMRI), combined with advanced analysis methods such as brain connectivity techniques and pattern recognition.

IW was awarded a Veni grant from the Dutch Research Council (2020, NWO Talent Programme Veni) and holds a Stand-Alone Project Grant (2021) by the Austrian Science Fund (FWF) to investigate the role of grid-cell representations for social memory in healthy individuals at genetic risk for Alzheimer's disease.

Selected publications

Durable memories and efficient neural coding through mnemonic training using the method of loci.

Wagner IC, Konrad BN, Schuster P, Weisig S, Repantis D, Ohla K, Kühn S, Fernández G, Steiger A, Lamm C, Czisch M, Dresler M. 2021 – Science Advances, 7(10): eabc7606.

Imaging empathy and prosocial emotions.

Lamm C, Rütgen M, Wagner IC. 2019 – Neuroscience Letters, 693: 49–53.

Mnemonic training reshapes brain networks to support superior memory.

Dresler M, Shirer WR, Konrad BN, Müller NCJ, Wagner IC, Fernández G, Czisch M, Greicius MD. 2017 – Neuron, 93: 1227–1235.

Physical exercise performed four hours after learning improves memory retention and increases hippocampal pattern similarity during retrieval.

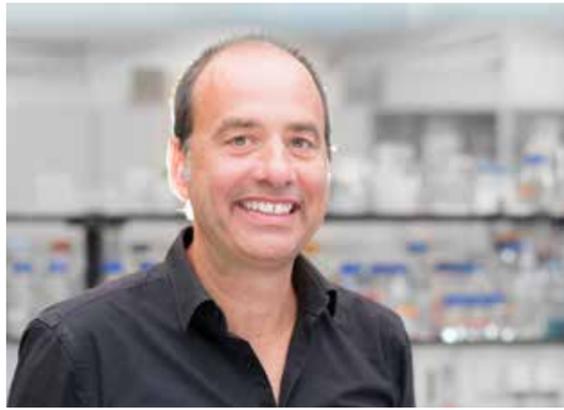
van Dongen EV, Kersten IHP, Wagner IC, Morris RG, Fernández G. 2016 – Current Biology, 26: 1722–1727.

Parallel engagement of regions associated with encoding and later retrieval forms durable memories.

Wagner IC, van Buuren M, Bovy L, Fernández G. 2016 – Journal of Neuroscience, 36(30): 7985–95.

Schematic memory components converge within angular gyrus during retrieval.

Wagner IC, van Buuren M, Kroes MCW, Gutteling T, van der Linden M, Morris RG, Fernández G. 2015 – Elife, 4: e09668.



Michael Wagner

DOME – DIVISION OF MICROBIAL ECOLOGY

Full Professor

+43 1 4277 91200

michael.wagner@univie.ac.at

Since 2020: Vice Head of CMESS

Since 2019: Distinguished Prof. (20%), Aalborg University

Since 2019: Visiting Professor in Engineering Science, University of Oxford

2019–2020: Head of CMESS

2009–2019: Member of the senate, University of Vienna

Since 2003: Full Professor for Microbial Ecology, University of Vienna

2001–2003: Associate Professor, Technical University Munich (TUM)

1996–2000: Assistant Professor, TUM

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

Main research areas

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

Selected publications

An automated Raman-based platform for the sorting of live cells by functional properties.

Lee KS, Palatinszky M, Pereira FC, Nguyen J, Fernandez VI, Mueller AJ, Menolascina F, Daims H, Berry D, Wagner M, Stocker R. 2019 – Nat Microbiol, 6: 1035–1048.

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, Lagkouravdos I, Karst SM, Galushko A, Koch H, Berry D, Daims H, Wagner M. 2015 – Nature, 524: 105–108.

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.

Current research in the Wagner lab focuses on the ecology, physiology, and evolution of nitrifying microorganisms. Humans are strongly impacting the global nitrogen cycle by the massive use of nitrogen fertilisers. Nitrification contributes to fertiliser loss, eutrophication and greenhouse gas emission, but is essential for efficient wastewater treatment. The Wagner lab has discovered, cultured, and characterised important new nitrifying bacteria and archaea including the long sought after complete nitrifiers and has described unexpected physiological traits of these organisms. Furthermore, the lab is developing single cell tools to investigate functional properties of microbes in their natural environment. These methods are based on stable isotope probing in combination with Raman microspectroscopy, microfluidics, and NanoSIMS.

MW is an EMBO member, has received an ERC Advanced Grant, the Wittgenstein Award of the FWF (highest Austrian science award), the Jim Tiedje Award of the International Society for Microbial Ecology, and the Schrödinger Prize of the Austrian Academy of Sciences.



Wolfgang Wanek

TER – DIVISION OF TERRESTRIAL ECOSYSTEM RESEARCH

Full Professor

+43 1 4277 91262

wolfgang.wanek@univie.ac.at

Since 2019: Full Professor for Physiological Ecology and Ecosystem Research, University of Vienna

2006–2019: Associate Professor, University of Vienna

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

2001–2006: Assistant Professor, University of Vienna

1996–2001: Research Assistant, University of Vienna

1996: PhD in Plant Sciences, University of Vienna

As a terrestrial ecosystem ecologist, Wolfgang Wanek (WW) focuses 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 centre on the biogeochemistry of grasslands and forests in the tropical and temperate biome, with a focus on N and P cycling in the soil-plant-microbe system. Applying ecophysiological and isotope methods he seeks to understand how ecosystems 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 gross C, N and P cycle processes that previously could not be measured.

Main research areas

- Stable isotope fractionation in plants, microorganisms and ecosystems
- Nutrient cycling in temperate and tropical grasslands and forests, with focus on nitrogen and phosphorus
- Global change effects on biogeochemical cycles and plant-microbe-soil interactions
- Development of isotope tracing methods to study gross nutrient cycle processes in soils
- Soil metabolomics and fluxomics

Selected publications

Nitrogen Isotope Fractionation During Archaeal Ammonia Oxidation: Coupled Estimates from Measurements of Residual Ammonium and Accumulated Nitrite. Mooshammer M, Alves RJE, Bayer B, ... Wanek W. 2020 – Frontiers in Microbiology, 11: 1710.

Quantifying microbial growth and carbon use efficiency in dry soil environments via ¹⁸O water vapor equilibration. Canarini A, Wanek W, Watzka M, ... Schnecker J. 2020 – Global Change Biology, 26: 5333–5341.

A novel isotope pool dilution approach to quantify gross rates of key abiotic and biological processes in the soil phosphorus cycle.

Wanek W, ... Prommer J. 2019 – Biogeosciences, 16: 3047–3068.

Soil multifunctionality is affected by the soil environment and by microbial community composition and diversity. Zheng Q, Hu Y, Zhang S, Noll L, ... Wanek W. 2019 – Soil Biology & Biochemistry, 136: 107521.

Wide-spread limitation of soil organic nitrogen transformations

by substrate availability and not by extracellular enzyme content. Noll L, Zhang S, Zheng Q, Hu Y, Wanek W. 2019 – Soil Biology & Biochemistry, 133: 37–49.

Decoupling of microbial carbon, nitrogen, and phosphorus cycling in response to extreme temperature events. Mooshammer M, Hofhansl F, Frank AH, Wanek W, ... Richter W. 2017 – Science Advances, 3: e1602781.



Photo: O.W./Daniel Hintermayer

Dagmar Wöbken

DOME – DIVISION OF MICROBIAL ECOLOGY

Assistant Professor (Tenure Track)

+43 1 4277 91213

dagmar.woebken@univie.ac.at

Since 2018: Assistant Professor (Tenure Track), University of Vienna

2012–2017: Group Leader, University of Vienna

2008–2011: Postdoctoral Researcher, Stanford University/ NASA Ames Research Center/ Lawrence Livermore National Laboratory (LLNL)

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

2007: PhD in Marine Microbiology, University of Bremen and Max Planck Institute for Marine Microbiology, Bremen

Main research areas

- Survival mechanisms of soil microorganisms
- Communities and processes in biological soil crusts and microbial mats
- Plant-microbe interactions
- Ecophysiology of soil acidobacteria
- Microorganisms involved in biological fixation of atmospheric N₂
- Application of single-cell methods to terrestrial and plant-associated systems

Selected publications

Distribution of mixotrophy and desiccation survival mechanisms across microbial genomes in an arid biological soil crust community.

Meier DV, Imminger S, Gillnor O, Wöbken D. 2021 – mSystems, 6(1): e00786–20.

Acidobacteria are active and abundant members of diverse

atmospheric H₂-oxidizing communities detected in temperate soils.

Giguere AT, Eichorst SA, Meier D, ... Wöbken D. 2021 – The ISME Journal, 15: 363–376.

Genomic insights into the Acidobacteria reveal strategies for their success in terrestrial environments.

Eichorst SA, Trojan D, Roux S, ... Wöbken D. 2018 – Environmental Microbiology, 20: 1041–1063.

Advancements in the application of NanoSIMS and Raman microspectroscopy to investigate the activity of microbial cells in soils.

Eichorst SA, Strasser F, Woyke T, ... Wöbken D. 2015 – FEMS Microbiology Ecology, 91: fiv106.

Revisiting N₂ fixation in Guerrero Negro intertidal microbial mats with a functional single-cell approach.

Wöbken D, Burow LC, Behnam F, ... Bebout BM.

2015 – The ISME Journal, 9: 485–496.

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

Berry D, Mader E, Lee TK, Wöbken D, ... Wagner M. 2015 – Proc Natl Acad Sci USA, 112(2): E194–203.

The goal of Dagmar Wöbken's (DW) research is to elucidate active microbial participants in key soil processes and the genomic and physiological features that allow their success in the challenging soil habitat. More specifically, DW investigates the factors that govern the activities of soil microorganisms in the C and N cycle, their survival and persistence strategies, as well as the interactions between microorganisms and plants. DW integrates the concepts of ecological theory into the realm of microbial ecology to address fundamental questions about niche differentiation, dormancy and microbial seed bank. DW aims to gain a holistic view on the function of the "soil microbiome" through the combination of process-level measurements, molecular techniques, stable isotope probing and single-cell approaches (such as FISH and NanoSIMS). DW's research group is constantly developing and improving methods for single-cell investigations in terrestrial ecosystems.

DW has received an ERC Starting Grant and is a member of the Board of Directors of the Young Academy of the Austrian Academy of Sciences.

Junior Research Groups

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CMESS JUNIOR RESEARCH GROUP LEADERS



Elizabeth (Liz) Hambleton

Liz Hambleton's (LH) group studies the evolution and molecular mechanisms of diverse 'photosymbioses' between the dominant symbiotic algae Symbiodiniaceae and ecologically important marine invertebrates. Main research questions include: how do different host organisms interact on the cellular level with the same intracellular algal symbiont? What are the molecular mechanisms underlying these symbioses, particularly complex metabolic exchange? To address this, LH's group combines functional experimentation in model systems, single-cell transcriptomics, metabolomics/lipidomics, and mass-spectrometry-based metabolic imaging.

Throughout her career, LH has been an expert in developing the sea anemone *Aiptasia* as a laboratory model to investigate the molecular mechanisms of the environmentally crucial coral-algal symbiosis, including the exchange of essential sterol nutrients in symbiosis. Her group is continuing work in *Aiptasia* in addition to establishing a new model system with the symbiotic acoel flatworm *Waminoa*. The LH group's ultimate aim is to understand globally widespread and evolutionarily important photosymbioses and their responses to environmental change.

Since 2020: Junior Research Group Leader, DOME, University of Vienna

2014–2020: Postdoctoral Researcher, University of Heidelberg

2013–2014: Early Career Fellow, Center for Ocean Solutions, Stanford University

2013: PhD in Biology, Stanford University



François-Xavier Joly

François-Xavier Joly's (FXJ) research focuses on elucidating the diverse roles of soil organisms on soil and ecosystem functioning, with a specific focus on soil fauna. His research spans across a wide range of ecosystems from drylands to boreal forests and particularly aims at disentangling the dominant mechanisms by which soil fauna contribute to plant litter decomposition and soil organic matter formation. He has instigated new research on the role of litter-feeding soil animals on organic matter turnover through a focus on animal faeces as important decomposition by-products.

His research activities aim to develop a mechanistic and predictive understanding of soil fauna contribution to soil processes in future climatic scenarios. FXJ is also involved in projects determining the processing of fire-residues by soil organisms and their contribution to carbon storage in fire-prone ecosystems.

Since 2021: Junior Research Group Leader, TER, University of Vienna

2017–2021: Postdoctoral Researcher, University of Stirling

2016–2017: Postdoctoral Researcher, Arizona State University

2015: PhD in Functional Ecology, University of Montpellier



Dimitri Kits

Research in the group of Dimitri Kits (DK) is centred on the study of the physiology of microbes that inhabit the gastrointestinal tract. Research projects of DK aim to understand fundamental mechanisms that microbes in the gut use to efficiently ferment dietary and host compounds and how the metabolic end-products of fermentation influence host and microbe physiology. In particular, DK is leading projects to unravel the pathways that lead to the formation and dissipation of important gases – such as hydrogen and hydrogen sulfide – by the intestinal microbiota and how the accumulation of these gases influences host health.

DK is also involved in studies to construct artificial human gut communities in an effort to understand community assembly of the intestinal microbiota and how the resident gut microbiota provides long term protection from pathogens (called colonisation resistance). In addition to culture dependent methods such as anaerobic cultivation, the research group of DK increasingly relies on bioinformatics/computational tools to analyse large scale microbiome data, and single cell culture-independent cell labelling/sorting methods to identify and characterise new pathways and organisms of the gut microbiota.

Since 2020: Junior Research Group Leader, DOME, University of Vienna

2018–2020: Marie Skłodowska Curie Postdoctoral Fellow, University of Vienna

2016–2018: Postdoctoral Researcher, University of Vienna

2016: PhD in Microbiology and Cellular Biotechnology, University of Alberta



Michael Zumstein

The junior research group of Michael Zumstein (MZ) studies the biotransformation and biodegradation of anthropogenic chemicals in natural and engineered environments. A focus lies on the transformation of structural and functional polymers, as well as of antibiotics, by extracellular enzymes that are present in receiving environments. The MZ group combines techniques from environmental analytical chemistry and molecular biology to obtain a fundamental understanding of the activity, the specificity, and the identity of these enzymes. The resulting knowledge offers possibilities to inform the design of green chemicals that are stable where needed and eliminated on their way into the natural environment.

MZ was recently awarded an Ambizione Fellowship from the Swiss National Science Foundation (SNF) to study extracellular wastewater peptidases and their role in the biotransformation of peptide-based pharmaceuticals.

Since 2021: Junior Research Group Leader, EDGE, University of Vienna

2019–2020: Postdoctoral Researcher and SNF Ambizione Fellow, Eawag

2018–2019: SNF Postdoctoral Researcher, Cornell University

2017: PhD in Environmental Chemistry, ETH Zurich

DIVISION JUNIOR RESEARCH GROUP LEADERS



Richard Kimber

Richard Kimber's (RK) research involves investigating interactions that occur at biogeochemical interfaces. The group particularly focuses on the microbial synthesis of biominerals by environmental microorganisms, including the study of microbial transformations of copper by pure cultures of model metal-reducing bacteria as well as cultures from contaminated soils. The primary goals are to understand microbial controls on the fate of inorganic contaminants in the environment and to develop 'green' synthesis methods for functional nanomaterials for remediation and catalysis. To achieve this, RK's group adopts a multi-disciplinary approach combining geochemical, microbiological, imaging, and spectroscopic techniques.

RK is also involved in projects investigating the interactions of ancient DNA with mineral surfaces and the use of strontium isotopes for studying human migration.

Since 2020: Junior Research Group Leader, EDGE, University of Vienna

2019–2020: Research Fellow, University of Manchester

2015–2019: Postdoctoral Researcher, University of Manchester

2013–2014: Postdoctoral Researcher, University of Vienna

2012: PhD in Geomicrobiology, University of Manchester



Naresh Kumar

Naresh Kumar's (NK) research focuses on mechanistic understanding of redox processes at mineral-water-organic matter (OM) interfaces and their implications on fate and mobility of contaminants and nutrients in the environment. To decipher mechanisms at molecular scale, NK's work relies on application of synchrotron-based X-ray spectroscopy and microscopic techniques at atomic-scale resolution to help determine chemical speciation and bonding environment at environmental interfaces.

Recent focus in NK's research has also been on mineral-biomolecule interactions to understand the role of mineral surfaces in the storage of biological information over time, a key question that has direct implications in tracing origin of life and human evolution and migration history. NK contributed to the establishment of the MINERVA (Mineralogical Preservation of the Human from the Depth of Time) platform at the University of Vienna.

Since 2018: Junior Research Group Leader, EDGE, University of Vienna

2014–2018: Postdoctoral Researcher, Stanford University

2013: PhD in Environmental Geosciences, Aix-Marseille University



Gabriel Sigmund

Gabriel Sigmund (GS) is interested in the multiple facets of pyrogenic carbon (i.e., wildfire charcoal, biochar, activated carbon) and emerging organic contaminants. GS's group aims to decipher processes in natural environments (post-fire landscapes), semi-engineered systems (agricultural soils), and engineered systems (remediation applications). Processes are investigated from batch-scale under controlled laboratory conditions to field scale, including the use of in situ river flumes to examine the effects of wildfire charcoals on microbial cycling of riverine organic matter.

Ongoing research focuses on (i) effects of pyrogenic carbon in post-fire landscapes on organic matter cycling and the occurrence of persistent free radicals, (ii) biochar and wood-based activated carbon for sustainable contaminant remediation, and (iii) mobility of ionic and ionizable organic contaminants, which is critical for assessing the emerging contaminant class of persistent mobile and toxic (PMT) substances.

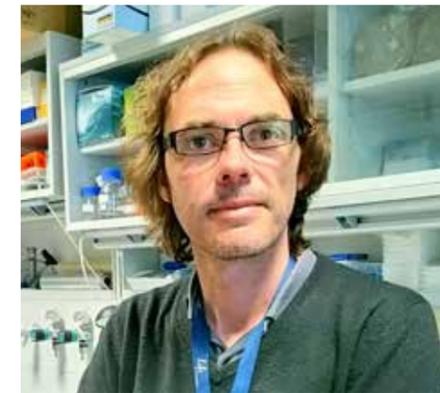
Since 2020: Junior Research Group Leader, EDGE, University of Vienna

2019: Invited Guest Scientist, Nankai University

2019: Postdoctoral Researcher, Agroscope Zurich

2018: Postdoctoral Researcher, Technical University of Munich

2017: PhD in Environmental Science, University of Vienna



Adrian Tett

Adrian Tett's (AT) group focuses on the development and utilisation of computational approaches combined with metagenomics to understand the human microbiome in fine detail. Specifically, the group explores the hidden diversity in novel species and sub-species and its relationship to health or disease.

AT's group exploits the thousands of available metagenomes and uses large-scale metanalyses to identify and target potentially important microbiome members for further analysis and characterisation. For instance, the group members were involved in revealing the gut bacterium *Prevotella copri* to be far more diverse than appreciated, which, with further ongoing characterisation, may explain the conflicting reports of *P. copri* in human health. Another interest of the group is utilising ancient microbial fossils and pre-industrialised populations to determine how the process of industrialisation has dramatically and rapidly changed the co-evolved human microbiome and the potential implications this may have to human health.

Since 2020: Junior Research Group Leader, CUBE, University of Vienna

2014–2020: Postdoctoral Researcher, CIBIO, University of Trento

2012–2013: Postdoctoral Researcher, Quadram Institute

2008–2011: Postdoctoral Researcher, John Innes Centre

2007: PhD in Microbiology and Bioinformatics, UK Centre for Ecology and Hydrology

CMESS People

Stephanie Eichorst 52 **Petra Pjevac** 53

Craig Herbold 52 **Arno Schintlmeister** 53

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SENIOR SCIENTISTS



Stephanie Eichorst

soil microorganisms, microbial physiology, acidobacteriota

One gram of soil contains over a million microorganisms, yet much of their function remains unknown. This has fascinated me since my PhD (Michigan State University, USA) and continued during my time at LANL (New Mexico, USA) and JBEI (California, USA). Since 2012, I have been at the University of Vienna investigating soil microorganisms (i.e. Acidobacteriota) via cultivation, '-omics' methods and metabolic process measurements. Recently, I am exploring their relationship to oxygen and involvement in atmospheric gas oxidation.



Petra Pjevac

microbiome, niche differentiation, chemolithoautotrophs

As staff scientist in the Joint Microbiome Facility, I support clinical and environmental studies with sequencing-based microbiome analyses. I aim to understand factors that shape microbial communities and drive niche differentiation between microorganisms. Besides sequencing-based approaches, I use physiological experiments and biogeochemical data to address these questions. I am particularly interested in chemolithoautotrophic microbes in complex environments, mainly those involved in nitrogen and sulfur cycling.

Craig Herbold

evolution, bioinformatics, phylogenetics

Life originated nearly four billion years ago and has increased in diversity and complexity ever since. I want to understand how major evolutionary and climatic events during this journey imprint into microbial genomes and what these patterns in turn can tell us about microbial evolution. I have been at the University of Vienna since 2014 where I apply my expertise in computational biology into being a resource for scientific collaboration as well as advising and teaching students.



Arno Schintlmeister

NanoSIMS, multimodal imaging, stable isotope probing (SIP)

Topochemical analysis deals with the simultaneous structural and chemical characterisation of materials. Since its establishment at the University of Vienna in 2010, I am working with nanoscale secondary ion mass spectrometry (NanoSIMS). After graduation in physical chemistry in 1999 (Innsbruck University), I spent seven years in industry (Plansee SE) before returning to academia (TU Wien). Today, I enjoy collaborating with colleagues from various fields, ranging from microbiology to materials sciences.



Thorsten Hüffer

particulate contaminants, plastic fragmentation, leaching

Chemical pollution is among the planetary boundaries irreversibly affecting ecosystems. Phase-transfer processes largely govern the fate of these chemicals in the environment. After my PhD (University of Duisburg-Essen) in 2014, I started investigating how biotic and abiotic processes change plastics – xenobiotics interactions in aquatic and terrestrial systems. Recently, I am exploring the interplay between the release of additives from plastics and tire materials and the continuum of macro-, micro- and nanoplastics.



Markus Christian Schmid

laboratory safety, microscopy, raman spectroscopy

In the beginning of my career I worked on the detection of microorganisms involved in the nitrogen cycle. As I moved from the University of Nijmegen to the University of Vienna in 2008 I continuously strengthened my expertise in microscopy techniques and I am now responsible for all aspects of microscopy as well as Raman spectroscopy. From 2010 on I took over several responsibilities regarding lab safety, which cumulated in receiving a diploma as work safety officer in 2017.

Marc Mußmann

marine sediment, element cycling, woeseiaceae

Marine coastal sediments are gigantic biocatalytic filters, where countless microbes break down organic matter and pollutants such as nitrate and hydrogen sulfide. Understanding this invaluable ecosystem service drives my research since my PhD and Post-Doc at the MPI Bremen (Germany). Currently, I aim to reveal the function of a globally abundant group of microorganisms in marine sediments, the Woeseiaceae. In my group, we study these 'hard-to-get' bacteria using cultivation and diverse molecular tools.



Hannes Schmidt

microbiome, imaging, synthetic soil ecology

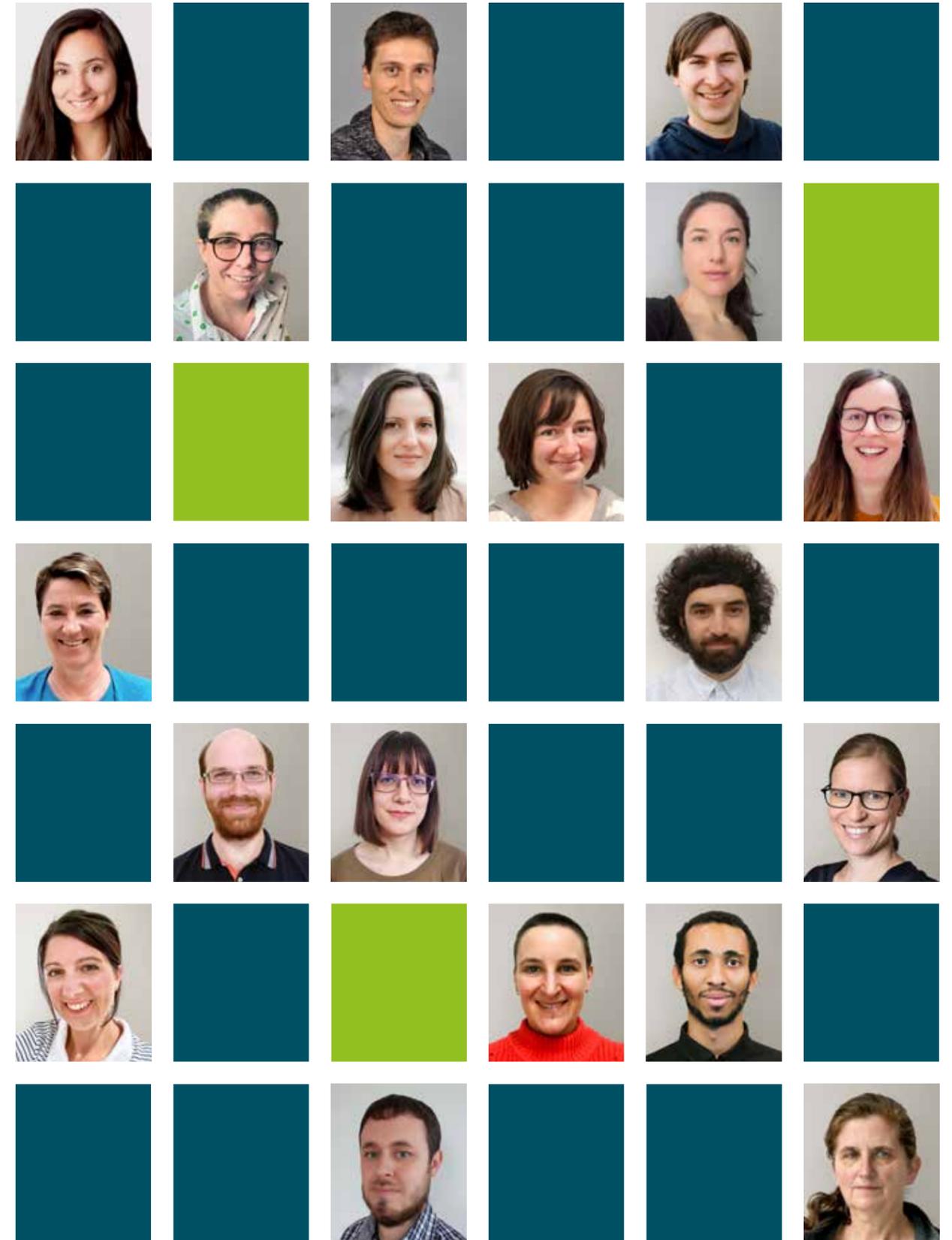
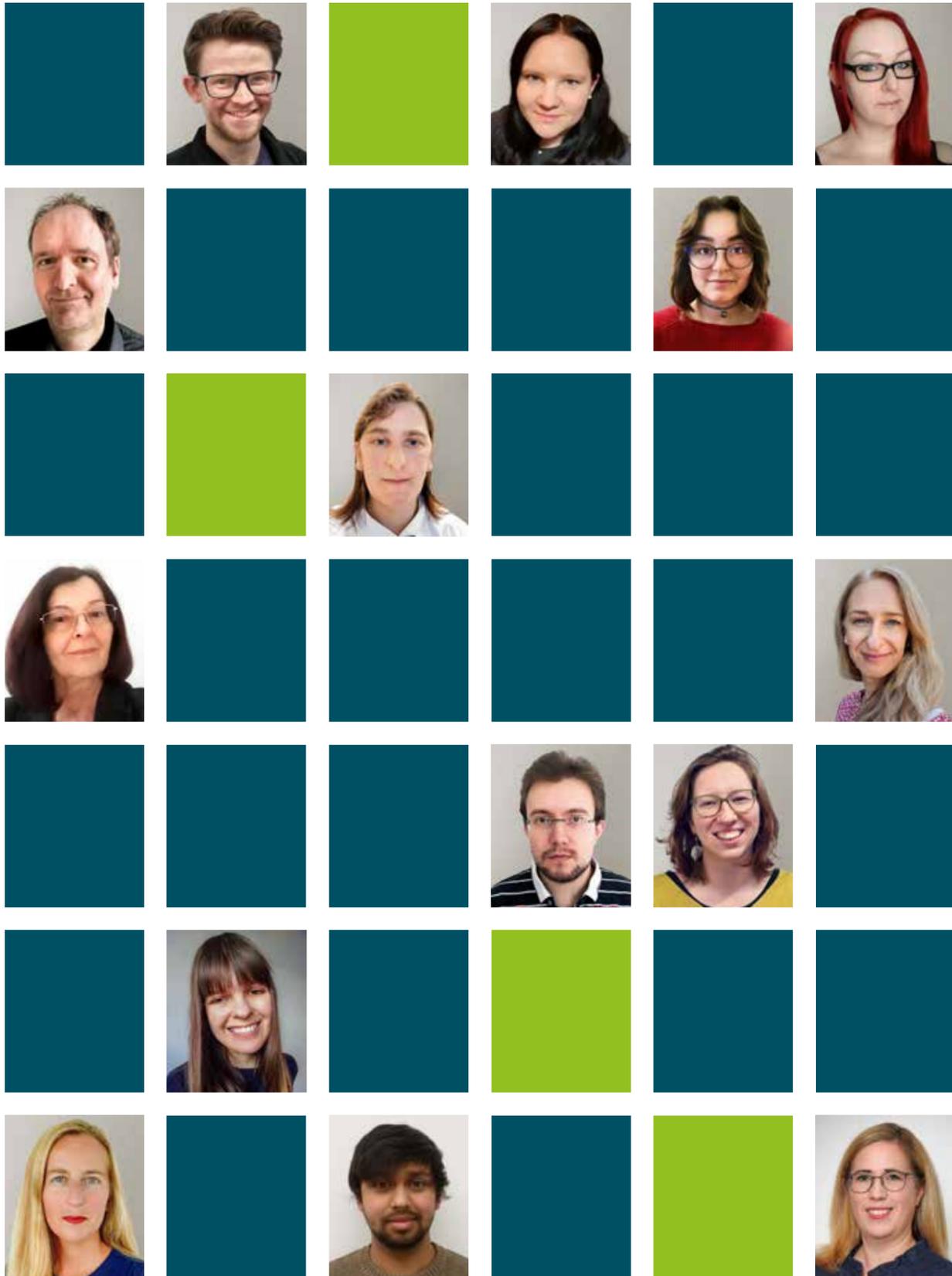
Soils harbour a myriad of (micro)organisms and are fundamental to plant growth. Initiated during my PhD at the University of Bremen (Germany), I have been studying rhizosphere-associated archaea and bacteria via multi-scale imaging, sequencing, and stable isotope techniques. I am fascinated by observing microbial cells within their habitat through a microscope. Currently, I am delving into fundamental questions of soil ecology via reductionist approaches using defined minimal microbial communities and artificially composed soils.



STUDENTS & EARLY CAREER RESEARCHERS

Cristina Alcaraz Chloe Allo
Lauren Alteio Patrick Arthofer Johanna Auer
Michaela Bachmann Veronica Barrajon Santos
Marcello Barylli Nada Basic Franziska Bauchinger Theresa Böckle
Maria de Fatima Cardoso Pereira Stephanie Castan Kyle Chardi Sampriti Chaudhuri
Songcan Chen Sean Darcy Renate Degen Marlies Dietrich Sara El Youbi Klaus Erlmeier
Florian Exler Denisa Finta Nathalie Friedl Lucia Fuchslueger Christoph Gall Niklas Gallati
Andrew Giguere Bettina Glasl Stefan Gorka Bosco Gracia Richard Grusek Ksenia Guseva
Philipp Gündler Leila Hadziabdic Tamara Halter Luzian Hämmerle Andreas Heberlein Nathalie Heldwein
Lukas Helmlinger Paulo Andres Herrera Ricci Isabella Hinger Julia Horak Astrid Horn Huifeng Hu
Peter Hunyadi Stefanie Imminger Deniz Inan Kian Jenab Rasmus Hansen Kirkegaard Anna Kistler
Katharina Klawatsch Sigrid Koizar Alexander König Julia Krasenbrink Julius Krämer Jannie Munk Kristensen
Jonas Lamprecht Michaela Lang Lukas Leibrecht Anna Lopatina Tamara Löwenstern Alejandro Manzano Marín
Miguel Angel Marazuela Calvo Klara Maritsch Victoria Sophie Martin Simon Merschroth Rouven Metz Dennis Andre Metze
Moritz Mohrlock Anna Julia Mueller Maximilian Ohmacht Jay Osvatic Anne Nicole Joelle Overbeeke Marton Palatinszky
Florian Panhölzl Ruoting Peng Alex Pfundner Bruna Yuri Pinheiro Imai Michael Predl Paul Prinz Dania Randi Christian Ranits
Antoine Raoult Hamid Rasoulimehrabani Katharina Reinhold Sofie Marie Reiter Sören Risse Alessandra Riva Lena Rohrhofer
Paula Andrea Rojas Pinzon Benjamin Robert Roller Cornelia Rottensteiner Dimitra Sakoula Erika Kristel Salas Hernandez
Rahul Samrat Jörg Schneckner Jan Schüürman Angelika Schwarzahns Christopher Sedlacek Eva Simon Julius Simonis
Alisa Socolov Natalia Solntceva Boyoung Song Kerrin Steensen Christiane Steindl Lucie Stetten Andreas Sparer
Felix Spiegel Marta Sudo Nathalie Tepe Ye Tian Dagmar Tiefenbrunner Lovro Trgovec-Greif Anna Ullrich Tobias Viehböck
Margaret Vogel Hary von Rautenkranz Susanne Wagner Helene Walch Kenneth Wasmund Natalie Wichmann
Julia Wiesenbauer Anouk Willemsen Teresa Maria Rosa Winter Xiaoqian Yu Benedict Yuen Artur Zaduryan
Cathrine Zaknun Sarah Zauner

TECHNICIANS & ADMINISTRATIVE STAFF



SOCIAL LIFE



Vienna 2019



Vienna 2020 (left) and Hohe Tauern 2019 (right)



Vienna 2019



Rabat an der Thaya 2019



Vienna 2020



Vienna 2018

Teaching at CMESS

FOR A NEW GENERATION OF PROFESSIONALS

Empowering a new generation of professionals and scientists with the skills to solve the challenges ahead: To this end, we are engaged at all levels of teaching, from Bachelor's and Master's to PhD curricula in disciplines tackling the pressing problems of our present and the future. Teaching in molecular biology and microbiology, in ecology and environmental sciences, including state of the art computational techniques in bioinformatics, we have a student-centred mind-set that aims at creating an interactive and motivating learning environment. With the highest level of training, we create opportunities for scientific careers and ensure high student employability.

We are contributing to the Bachelor's Program in **Biology** – a broad program with the possibility to focus on diverse disciplines, e.g., molecular biology or ecology – and are



Hands on field training at one of our test sites: Students take a water sample from a well they drilled themselves.

Ensuring teaching during the pandemic

During the SARS-CoV-2 pandemic, members of the Centre took a leading role in setting up the in-house testing service at the University of Vienna. Frequent tests of both staff and students ensured safety in teaching and kept scientific projects running. We have been very innovative in times of distant-learning: PhD students from the Centre won the University of Vienna “2020 Corona Teaching Award” for their outstanding commitment.

involved in the Bachelor and Master's programs in **Earth Sciences**. These degree programs introduce modern concepts of environmental geochemistry, aquatic chemistry, pollutant dynamics, and hydrogeology. Our Centre is particularly engaged in teaching at Master's level. The Master's program in **Computational Science** specifically focuses on computer methods within the natural sciences enabling the students to master computationally relevant aspects of research and data processing in biology. In **Bioinformatics** the Master's students focus on methods from computer science, biology and mathematics to be able to answer questions relating to biology and medicine. The English-language Master's program **Molecular Microbiology, Microbial Ecology, and Immunobiology** is a joint program with the Max Perutz Labs and the Faculty of Life Sciences. It offers interdisciplinary training at the interfaces of microbiology, ecology, and immunology. In another joint degree program with the Faculty of Life Sciences – the

English-language Master on **Ecology and Ecosystems** – we address fundamental problems in ecology, focusing on biogeochemistry and biodiversity research. Core topics include the role of organisms in the functioning of ecosystems. The English-language interdisciplinary Master's program **Environmental Sciences** addresses students who want to understand environmental aspects of the Earth system and apply deep scientific thought to solve some of its most urgent problems; from emerging pollutants to natural contaminants to anthropogenic disturbed biogeochemical cycles.

With the **International FISH Course**, the Centre offers an annual summer school for researchers at all degree levels interested in fluorescence in situ hybridisation (FISH) and advanced molecular methods to study structure and function of microbial communities. For more than a decade, this course has been a hub for transnational scientific exchange and collaboration.

Training through Research

THE DOCTORAL SCHOOL IN MICROBIOLOGY AND ENVIRONMENTAL SCIENCE



Our Doctoral School offers fully funded PhD positions for talented young scholars doing research in research areas ranging from molecular microbiology, ecology, and computational biology to environmental geosciences.

The Doctoral School in Microbiology and Environmental Science, established in July 2020, offers interdisciplinary training at the interfaces of microbiology, ecology, and environmental science. PhD students benefit from the collaboration of two research institutions with an internationally recognised scientific reputation: The Centre for Microbiology and Environmental Systems Science and the Max Perutz Labs, a joint venture of the University of Vienna and the Medical University of Vienna.

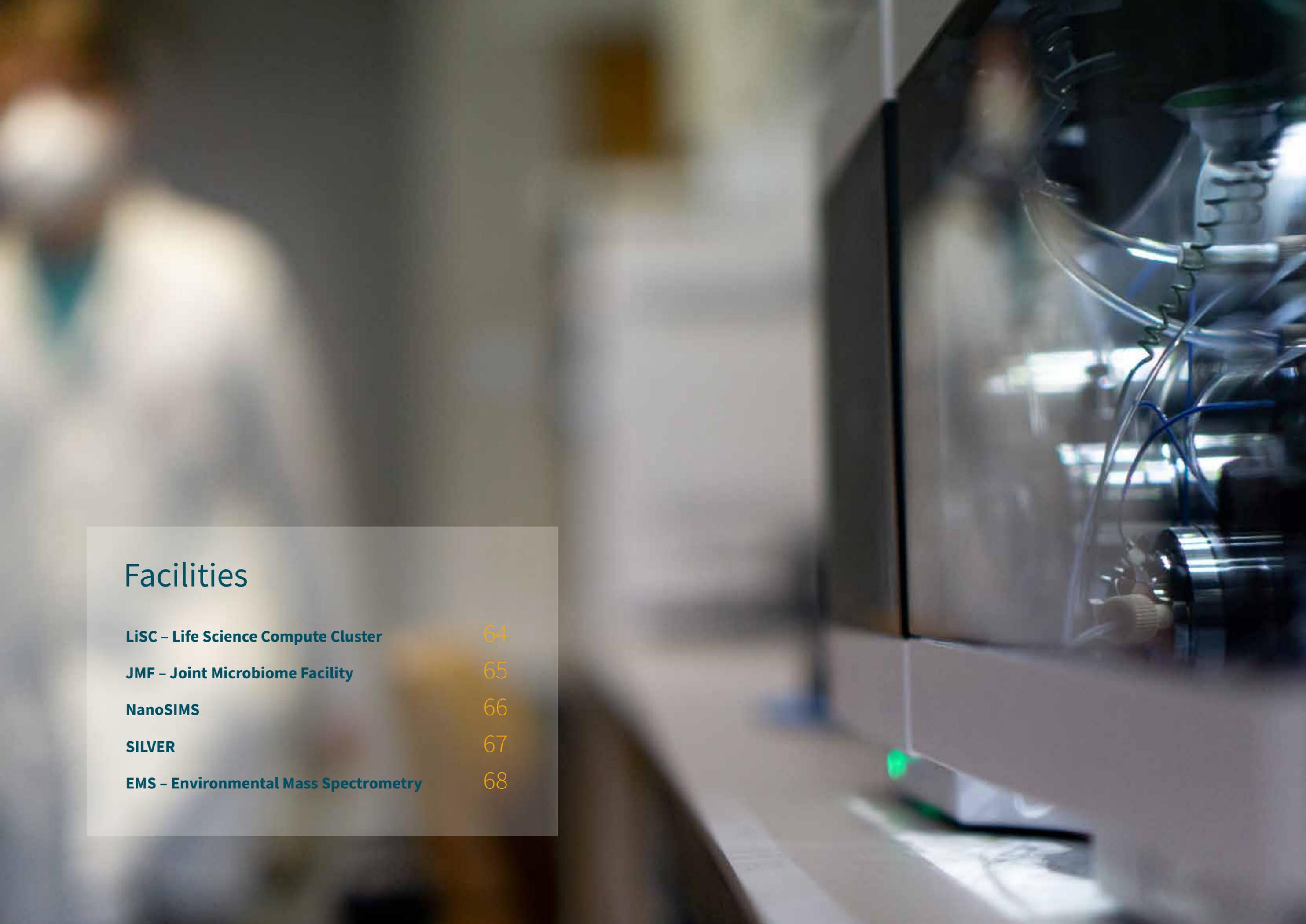
Since operations began in October 2020, doctoral students are offered an inspiring environment to address current challenges of the 21st century regarding the state of the environment, global change, and human, animal and plant health. In an international setting with members from

more than 25 different countries, PhD students perform cutting-edge research in areas such as adaptation and resistance mechanisms, microbiomes, biogeochemistry, emerging pollutants, molecular microbiology, and evolutionary and computational biology using state-of-the-art infrastructure. They acquire a comprehensive understanding of microbes at all levels, from molecular circuits determining the fate of single cells to microbial communities and ecosystem processes. Our students combine these insights with a molecular scale understanding of chemical mechanisms to solve complex problems of pollutant dynamics, nutrient acquisition and geochemical cycles.

Training through research is a basic principle of the school. Thus, all

PhD students are fully integrated into the faculty's research groups. Moreover, we offer advanced training in cutting-edge methods through workshops and seminars, research stays in partner labs, annual retreats, regular team meetings as well as individual meetings with the supervisor. In additional seminars hosted by the participating organisations, students can interact with high-profile international speakers and leading scientists in the field.

We place very high value on an active feedback culture and motivate students to improve our program by providing input. Student representatives are in constant exchange with the two heads and the coordinator of the doctoral school. Their ideas have considerably shaped past and ongoing events, courses, and workshops.



Facilities

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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.

CMESS operates a medium-sized high-performance compute cluster specialised 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 data processing. This system allows most users to analyse their data without any software installation, simply 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 1000 CPU cores and up to 2 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 about one PetaByte based on redundant, network attached disk arrays and parallel filesystems. As additional resources, we operate two dedicated database servers and three redundant virtualisation servers. Virtual machines are used to operate our publicly available resources, such as web portals, databases and user-friendly visualisation tools.

The Life Science Compute Cluster is frequently used by CMESS members and is jointly operated with the Faculties of Chemistry and 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, CMESS provides a user help-desk and software installation support.



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

JMF

JOINT MICROBIOME FACILITY

The Joint Microbiome Facility (JMF) provides advanced facilities and expertise to researchers working in clinical, environmental, and other basic research fields to characterise and understand complex microbial communities. The JMF is a joint venture of the Medical University of Vienna and the University of Vienna. Our goal is to facilitate the investigation of clinically-relevant and environmental microbiomes by offering individualised consulting and state-of-the-art services in study design, sequencing, bioinformatic analyses, and data interpretation. Additionally, the JMF is advancing the field of microbiome research by benchmarking existing approaches and developing new technological and analytical strategies.

In recent years, scientists have begun to appreciate the critical importance of human and microbial symbiosis for human health. Imbalances in the composition and activity of the microbial communities of the human body (the microbiome) correlate with a variety of diseases, and the microbiome has been recognised as an important modulator of the immune system. In addition, the huge diversity and importance of environmental microbiomes, both in natural and engineered systems, has also become increasingly recognised. In result, microbiome research is rapidly developing internationally and new research programs and institutions in this area are currently being established worldwide.

In this context, the JMF offers a range of cost-effective, high-throughput services to enable researchers to comprehensively assess microbial composition and activity in their system. These include DNA/RNA extraction from diverse sample types, amplicon sequencing, full-length primer-free rRNA profiling, and metagenomic and metatranscriptomic shotgun sequencing. We have extensive expertise in microbial community characterisation in various habitats, ranging from human, animal, and plant microbiomes to soils, sediments, aquatic environments and hot springs. We support researchers interested in clinically-relevant and environmental microbiome research during all stages of DNA and RNA sequencing based microbiome research – from experimental design, to sample processing and data analysis.

The high-throughput sequencing services available include:

- Illumina MiSeq-based highly multiplexed gene amplicon sequencing (e.g. 16S rRNA genes, 18S rRNA genes, ITS region)
- Illumina MiSeq-based microbial isolate genome sequencing
- Illumina HiSeq-/NovaSeq-based (meta-)genome and (meta-)transcriptome sequencing
- Oxford Nanopore MinION and PromethION technologies for long-read sequencing



The Oxford Nanopore PromethION System enables high throughput long read sequencing, allowing the JMF to generate high quality (meta)genomic datasets.



An array of Thermocyclers allows for highly parallelised sample processing.



The Illumina MiSeq System, our high quality short read sequencing technology of choice, is applied for data generation in the JMFs amplicon sequencing pipeline.

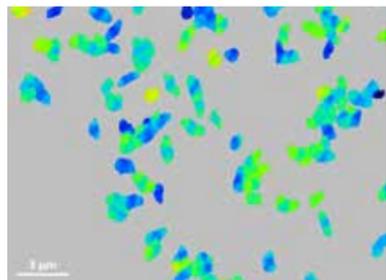
NanoSIMS

NANOSCALE SECONDARY ION MASS SPECTROMETRY



Panoramic view of the NanoSIMS laboratory.

NanoSIMS is an acronym for an advanced type of dynamic secondary ion mass spectrometer 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 ionisation 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 spectrom-



NanoSIMS visualisation of CO_2 fixation by single cells of nitrite-oxidising bacteria after ^{13}C stable isotope incubation.

ter, 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 visualise the distribution of virtually any element and their stable isotopes of interest in biological material at the sub-cellular level. Established in 2010 as part of the Large-Instrument Facility for Advanced Isotope Research, CMESS runs a CAMECA NanoSIMS 50L. This instrument is the only one in Austria. Hence, we support research groups across the Faculty, University and multiple national and international institutions in their chemical imaging efforts. Beyond performing measurements, CMESS offers extensive support to all users with respect to study design, sample preparation and pre-characterisation, data evaluation and data interpretation, which are key-steps in an efficient NanoSIMS analysis.

Research conducted at CMESS primarily focuses on microbial ecology: Here,

NanoSIMS is combined 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 hybridisation (FISH) for obtaining yet inaccessible information about the phylogenetic identity and functional role of microorganisms in their environment. With this approach, previously unrecognised 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.

Recently, the NanoSIMS received an upgrade: Being equipped with a cutting-edge oxygen ion source (type RF-plasma), it has reached the next level in ultra-trace metal analysis, which opens the door for novel applications such as microbial metallomics on the single cell level.

SILVER

STABLE ISOTOPE FACILITY OF THE UNIVERSITY OF VIENNA FOR ENVIRONMENTAL RESEARCH



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.

SILVER, the Stable Isotope Facility of the University of Vienna for Environmental Research, is the largest facility in Austria for analysing the ratios of stable isotopes of light elements in environmental samples. It is one of the leading laboratories for ecological research with stable isotopes in Europe.

Isotopes of an element differ in their number of neutrons and therefore in mass, but exhibit the same chemical behaviour. All of the light chemical elements that constitute the biosphere (hydrogen, carbon, nitrogen, oxygen, sulfur) 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 matter and 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 is part of the Large Instrument Facility for Advanced Isotope Research. This facility currently encompasses six state-of-the-art continuous flow isotope ratio mass spectrometers with



The elemental analyser-isotope ratio mass spectrometer represents the workhorse for carbon and nitrogen stable isotope analyses in bulk materials, such as in soils, plants and microbes.

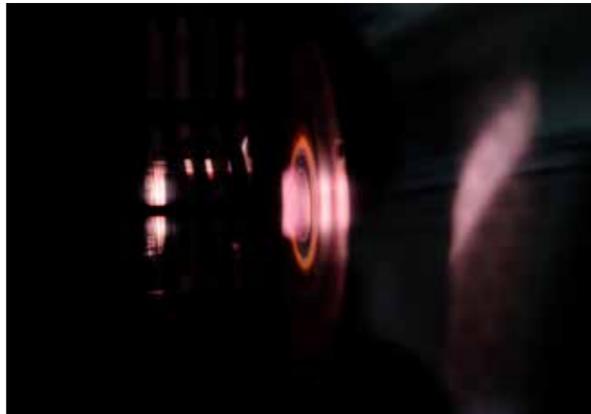
a range of front ends that allow for bulk and compound-specific analysis of hydrogen, carbon, nitrogen and oxygen isotopes in almost any type of environmental sample.

Instrumentation of the SILVER facility

- EA – IRMS: Elemental analyser for ^{13}C and ^{15}N in solid environmental samples
- Pyrolysis-IRMS: High-temperature pyrolysis system for ^2H and ^{18}O in solid samples and water
- Gasbench-IRMS: Trace gas pre-concentrator for ^{15}N analysis of N_2O , and for ^{13}C analysis of CO_2 and ^{18}O and ^2H analysis of water
- LC-IRMS: HPLC-Isolink for ^{13}C analysis of organic solutes
- GC-IRMS: GC-Isolink for ^{13}C , ^{15}N and ^2H analysis in organic analytes

EMS

ENVIRONMENTAL MASS SPECTROMETRY



A 6500°C hot Argon plasma ionises elements for mass spectrometric analysis. Within 5 cm the ions pass from atmospheric pressure to ultra-high vacuum and from 6500°C to room temperature.



Inductively coupled plasma mass spectrometry (ICP-MS) for simultaneous ultratrace analysis of metals and single-particle nanomaterial analysis.

The Centre's Environmental Mass Spectrometry Facility (EMS) provides state-of-the-art mass spectrometers for tracing environmental processes down to the nano- and molecular scales. The EMS has pioneered methodology tailored to challenging environmental samples. Natural and anthropogenic contaminants represent an extremely wide group of organic and inorganic substances, including unknown structures and transformation products. The EMS enables us to not only identify and detect these substances down to ultra-trace levels, but also to detect stable isotope fractionation for source tracing and the identification of processes controlling the biogeochemical cycling of metals.

Mass Spectrometry (MS) is the most efficient method for detecting, identifying, and quantifying contaminants and naturally occurring ultra-trace substances and isotope composition in environmental samples. Recent

advances in developing MS has led to an increasing use of advanced and sophisticated instruments for complex environmental samples. The great benefit of MS is its ability to identify and quantify many different analytes from complex mixtures in one run. We focus on the reliability of analyses involving high-resolution MS (HRMS), time-of-flight MS, tandem MS (MS/MS) to achieve faster high-throughput analyses with minimum sample preparation, and multicollector ICP-MS for stable isotope ratio measurements. Our EMS currently offers a suite of advanced analytical capabilities:

- Inductively coupled plasma – time-of-flight mass spectrometry (ICP-TOF-MS) for ultra-fast recording of full mass spectra can reveal large numbers of compounds in a sample down to attogram levels in single nanoparticles (hosted together with the Faculty of Chemistry).

- LC-MS/MS combines liquid chromatography and mass spectrometry for increased selectivity and fewer false-positive results.
- GC-MS/MS combines gas chromatography and mass spectrometry. It includes a compact benchtop triple quad (MS/MS) system, a PAL3 autosampler with HS-, SPME-, and ITEX for sample extraction and pre-concentration, and a multi-mode inlet for Large Volume and On-column injection, cryo-trap.
- ICP-QQQ-ICP-Triple quad offers flexibility in method development and provides unrivalled control of interferences in reaction mode delivering greater accuracy and more consistent results.
- MC-ICP-MS-High precision measurements of stable metal isotope ratios using a cold vapor introduction system and desolvating nebuliser for simultaneous introduction of standards.

Fighting the Pandemic

SARS-COV-2-RELATED ACTIVITIES AT CMES



At a press conference in August 2020, Michael Wagner (in the middle) and Federal Minister of Education Heinz Faßmann (on the right), together with partners from FH Campus Wien (on the left: Marina Fondi) presented the Ministry of Education's measures for the start of school: During this event, the Austrian SARS-CoV-2 school monitoring study coordinated by Michael Wagner was introduced that provides important prevalence data that are used nationally and internationally as basis for political decisions.

In March 2020 Michael Wagner (MW) initiated, together with colleagues from the Vienna BioCenter, the Vienna Covid-19 Detection Initiative (VCDI) that repurposed existing resources and expertise to build a high-throughput RT-qPCR testing pipeline. Furthermore, the VCDI developed a smart testing concept that combines gargling, pooling, and RT-qPCR. Based on this approach, members of CMES have been offered free SARS-CoV-2 tests at the VCDI during the last year, and since fall 2020 this offer was extended to

other faculties of the University of Vienna. Inspired by this text concept, the City of Vienna now offers gargling-based pooled PCR assays free of charge to its citizens, and this convenient home-sampling based testing has become a major pillar in the fight against the pandemic in Austria. Petra Pjevac and Hannes Schmidt from our Centre made major contributions to many of these activities.

Based on the gargling approach, MW coordinated a successful pilot study

Publication

Prevalence of RT-qPCR-detected SARS-CoV-2 infection at schools: First results from the Austrian School-SARS-CoV-2 prospective cohort study

Willeit P, Krause R, Lamprecht B, Berghold A, Hanson B, Stelzl E, Stoiber H, Zuber J, Heinen R, Köhler A, Bernhard D, Borena W, Doppler C, von Laer D, Schmidt H, Pröll J, Steinmetz I, Wagner M. 2021 – The Lancet Regional Health – Europe, 5:100086

for monitoring SARS-CoV-2 in 11 Viennese schools in June 2020. Subsequently, he initiated and coordinates a nationwide SARS-CoV-2 monitoring study in 250 Austrian schools that determines the prevalence of infected pupils and teachers several times per year ('dark figure' study) in a representative sample consisting of almost 15,000 people. This study is financed by the Austrian Federal Ministry of Education, Science and Research and represents a collaborative effort between four Austrian universities.

The school monitoring study provided new insights into the role of children and schools in the pandemic and the results from the first two rounds were published in *Lancet Regional Health – Europe*. The findings were used for policy briefings in Austria, Denmark and Germany and were covered extensively in the national and international media.

As a member of the Future Operations Platform, MW has developed together with other scientists a concept paper that suggests mandatory gargling PCR tests for all Austrian pupils in the new school year and this concept is currently piloted in ten schools in Vienna.

To download the concept paper (in German) please scan the QR code.



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Responsible for the content

Andreas Richter, Head of CMESS

Editors

Annina Müller Strassnig,
Pamela Nölleke-Przybylski,
Jillian Petersen

Layout & Design

Christian Högl, www.creativbox.at

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Gabriel Sigmund:
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