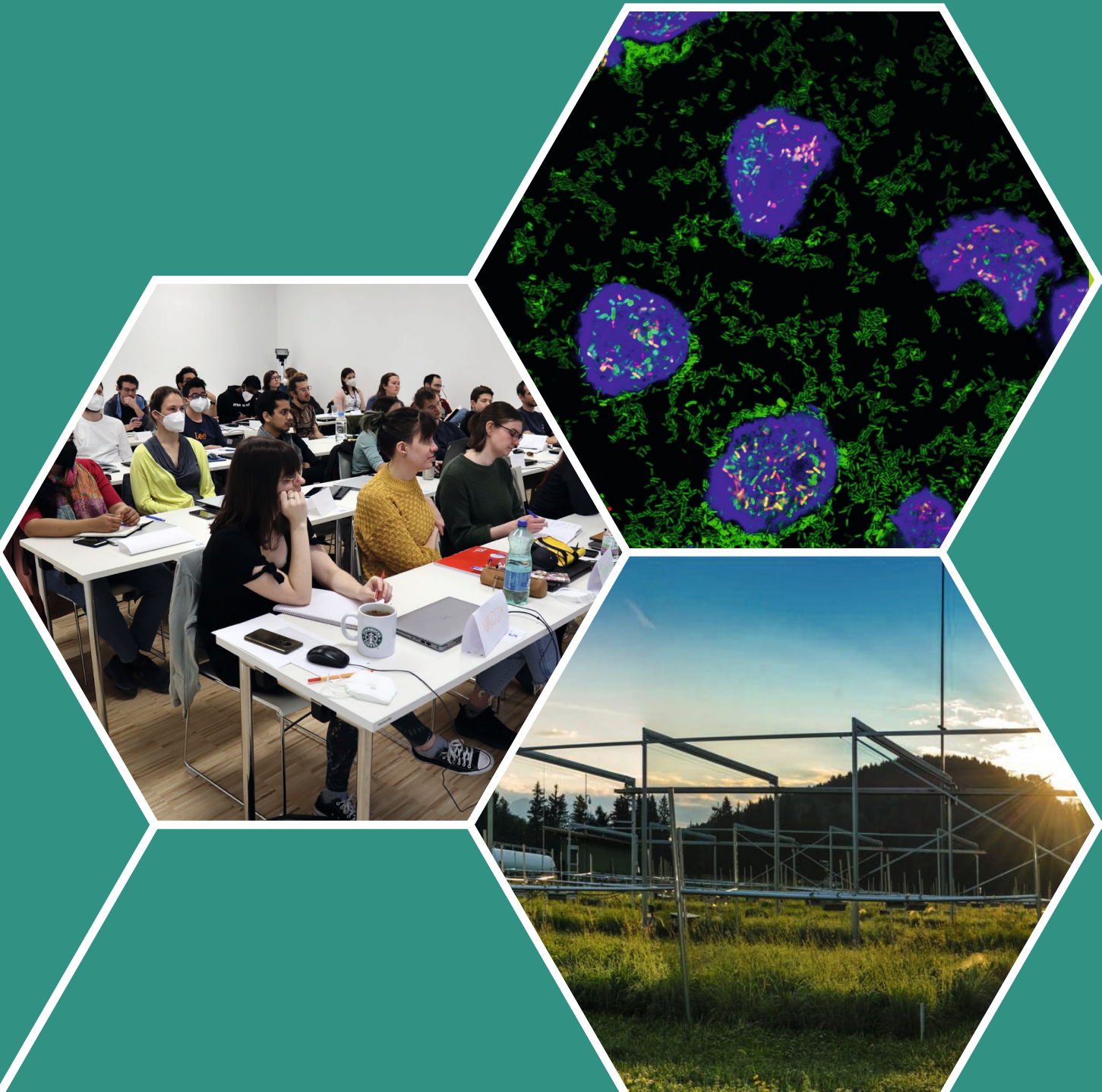


Centre for Microbiology and Environmental Systems Science
UNIVERSITY OF VIENNA

VDS-MES

Annual Report 2022



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Imprint

Doctoral School in Microbiology and Environmental Science
Centre for Microbiology and Environmental Systems Science

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Preface

You are reading the first annual report of the Doctoral School in Microbiology and Environmental Science (VDS-MES). In this report we summarize the school by numbers, introduce the persons behind the school, welcome students who joined the school in 2022 and highlight the graduates who left the school during that year.

The mission of our school is the advancement of education and research in microbiology and environmental science. Therefore, the central strategic goals of the doctoral school are (1) excellent training of PhD candidates, measured by the scientific achievements during the PhD thesis as well as their employability and career opportunities, and (2) advancing science through internationally competitive basic, translational and applied investigations, measured by the number and impact of publications and patents. Our aims comprise selective recruitment, consistent high quality of supervision, excellent training and infrastructure, and administrative as well as financial support to the students. In addition, the measures outlined below will improve the quality of doctoral education and reduce time-to-degree in the future. As you will read in this report, we followed these goals and established suitable structures and activities of our school since the founding of our school in mid-2020. In 2022 we have mainly focused on the admission standards to the school, the initial phase of the PhD (Thesis Advisory Committees and New PhD Science Days), student networking and peer exchange as well as teaching on the doctoral level. For the new year 2023, we have ambitious plans. E.g., we will implement a comprehensive “onboarding” curriculum for students joining our school, will improve the data management in PhD projects, will establish group and individual coaching for scientific writing and will establish an Alumni network.

Our school could only be that successful in 2022 because it was broadly supported by the organizational units, by the students and our faculty. We all enjoy an open culture of discussion, contribution and criticism – I hope we will keep this spirit also for the future. Special thanks to all who have supported the school in particular functions, such as our PhD representatives, our study conference or our study program advisors. Your activities have been invaluable for the development of the school.

I wish you a successful 2023 and look forward to another fruitful year for our school. Enjoy reading this annual report!

Thomas Rattei
Head of the VDS-MES

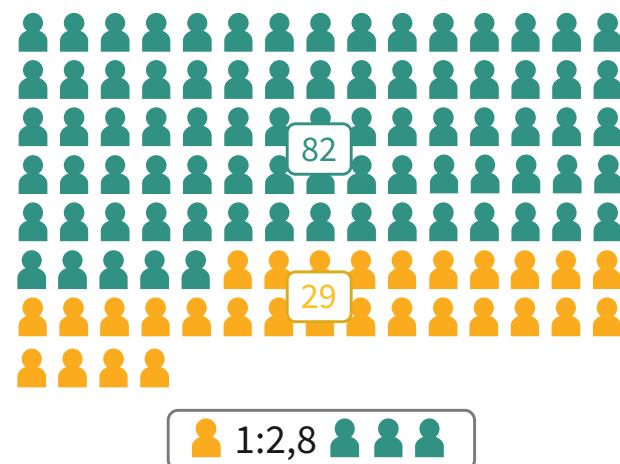
Facts and Figures

Who we are

- An **interdisciplinary** doctoral school at the interface of microbiology, molecular ecology and environmental geosciences
- Addressing **current challenges** in the 21st century society: the role of microbiomes, adaptation and resistance mechanisms, biogeochemistry, pollutant dynamics and nutrient fluxes – in global change and for human, animal, plant and environmental health
- Understanding **microbes** and the **networks** they shape at all levels – from molecular circuits to ecosystem processes and geochemical cycles

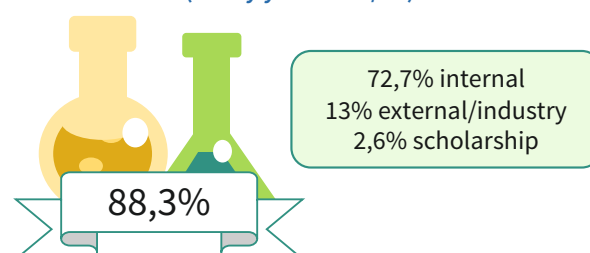
Faculty-Student ratio

(WiSe 2022)



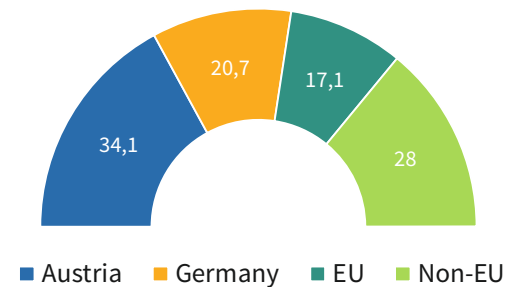
Financed students

(Study year 2021/22)



Student nationalities %

(WiSe 2022/2023)

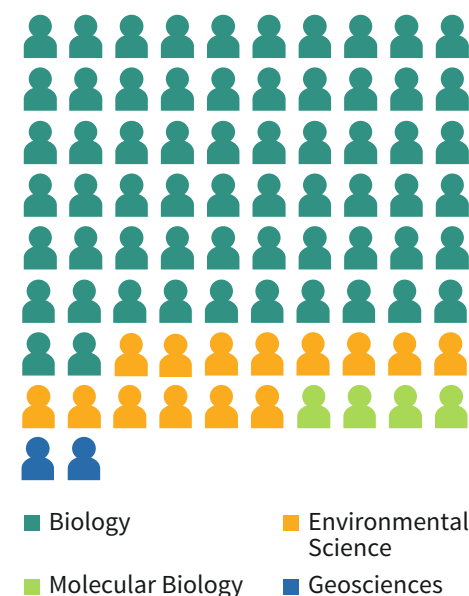


Sex ratio



Fields of study

(WiSe 2022)

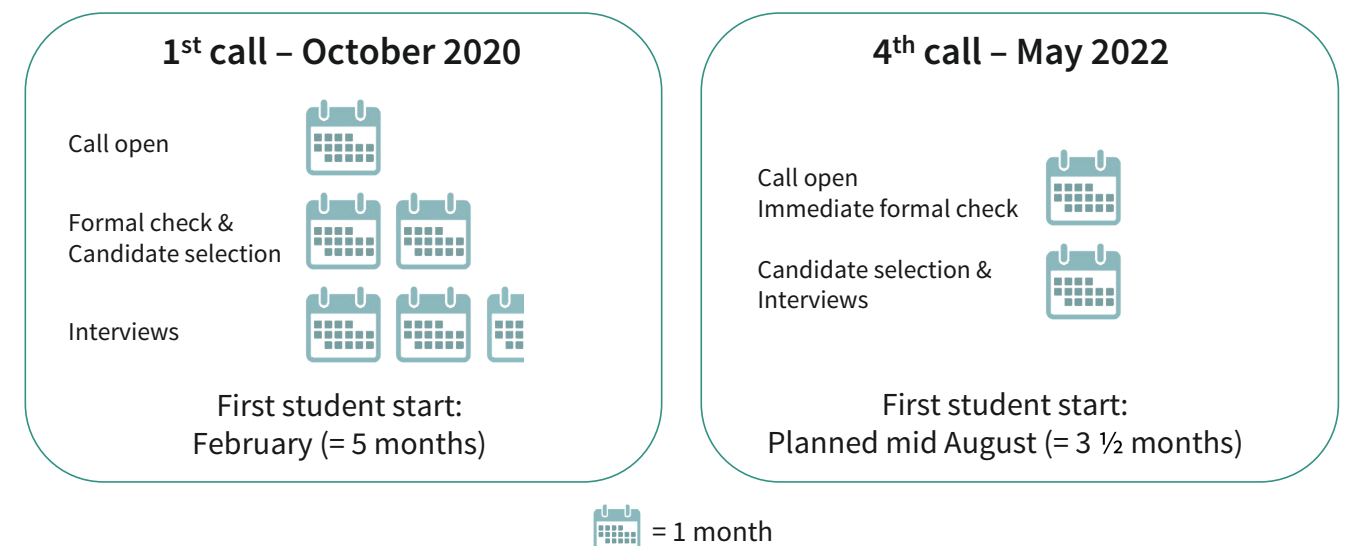


- ### Establishing new events
- First "New PhD Science Day"
 - Student newsletter
 - Doctoral School teaching
 - 2nd call
 - Election of PhD reps, integration into DS team

- ### Feedback and outreach
- Supervision survey
 - Outreach planning
 - 4th call
 - Finishing grants
 - Long Night of Research



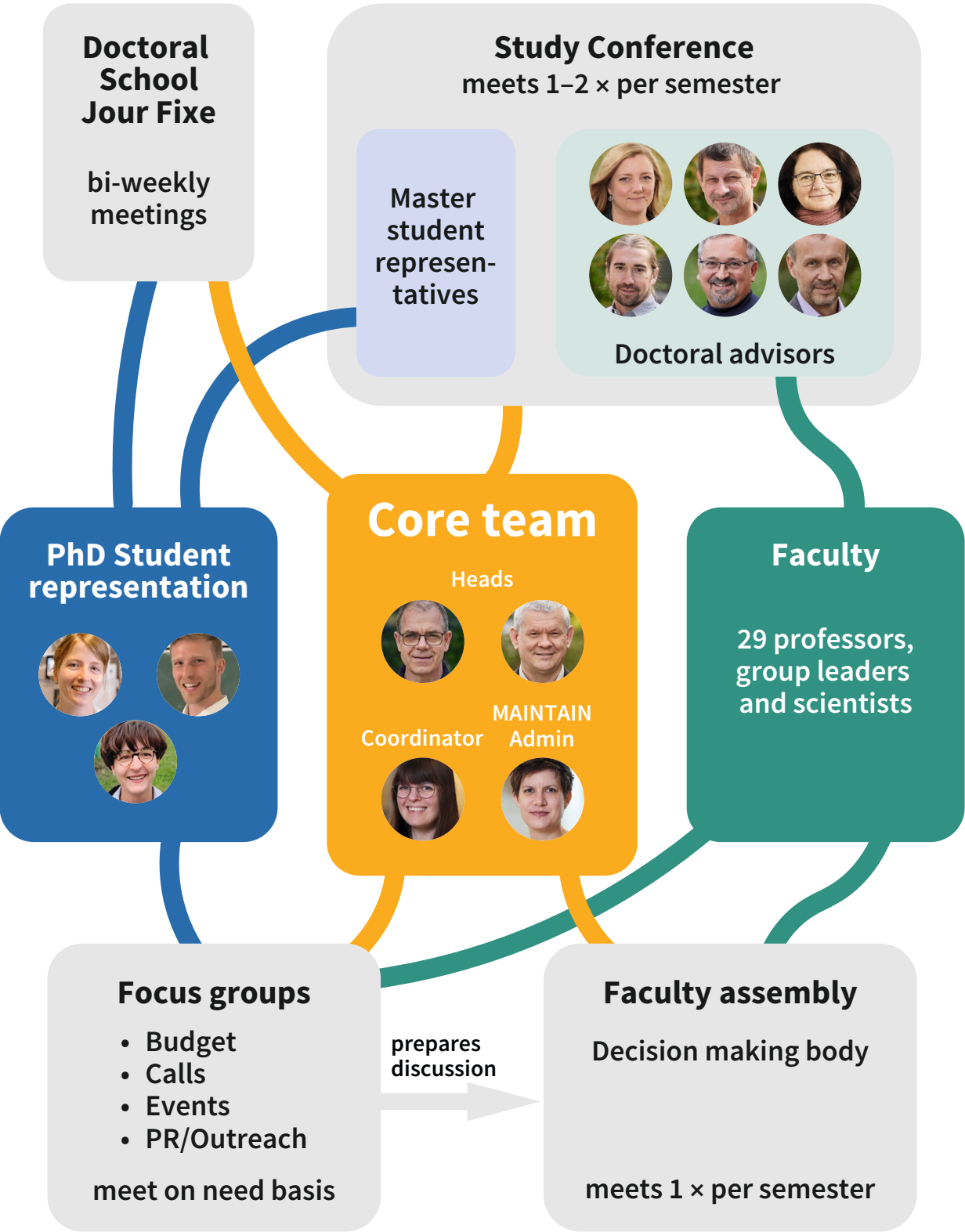
First and currently last call – Timeline



vds-mes.cmess@univie.ac.at

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Team and Structure



CORE TEAM

The doctoral school is led by **Thomas Rattei** and **Stephan Krämer** as head and vice-head, respectively. **Nadja Holzleitner** serves as coordinator of the school.

Franziska Bauchinger supports the core team in her role as administrative manager of the doctoral program MAINTAIN which employs 8 of the students in our school.

DOCTORAL ADVISORS

Biology: **Jill Petersen and Wolfgang Wanek**

Molecular Biology: **Isabella Moll and David Berry**

Environmental Sciences and Geosciences: **Andreas Richter and Thilo Hofmann**

Master students: **Thomas Moser, Jakob Habitzl**

PHD STUDENT REPRESENTATIVES

Our school’s elected student representatives **Charlotte Henkel, Jay Osvatic, and Eva Simon** support the team by taking part in our regular meetings as the voice of the student body.

FOCUS GROUPS

Our focus groups consist of a small number of faculty members as well as student representatives who take care of discussing and preparing ideas for certain topics which then are presented to the faculty assembly in at least biannual meetings.

Currently, the **budget focus group** meets at least once per semester.

Two more groups focusing on the topics of **recruitment calls** as well as **PR and events**, respectively, meet on a need basis.

STUDY CONFERENCE

The VDS MES study conference consists of our PhD student representatives, doctoral advisors as well as representatives of the master students. The study conference meets with the doctoral school team 1-2 times per semester and discusses teaching, services of the doctoral school and more.

FACULTY ASSEMBLY

The faculty assembly consists of all professors (assistant, associate and full) as well as senior scientists and postdocs involved in the school. It is the primary decision-making body of the doctoral school and meets once per semester to finalise discussion points that have been prepared within the focus groups.

Stephan Köstlbacher

24.03.2022

UNCOVERING THE HIDDEN DIVERSITY AND ANCESTRAL STATES OF CHLAMYDIAE GENOMES

Supervisor: **Matthias Horn**



Chlamydiae are an ancient group of bacteria, found in diverse eukaryotic hosts, that adapted an intracellular lifestyle more than a billion years ago. While much of the research has focused on animal pathogenic chlamydiae, our knowledge on the hidden diversity of chlamydiae in the environment is very limited. This work uses genomic and phylogenetic approaches to uncover the hidden genome diversity and biology of uncultured chlamydiae, and to model long evolutionary history.

Firstly, I studied the evolution of chlamydiae plasmids, uncovering evidence for a plasmid in the ancestor of all chlamydiae that has since coevolved with chlamydiae. Plasmid genes left an impact on chlamydial genomes due to increased mobility between chlamydial plasmids and chromosomes. Endosymbionts tend to be isolated from horizontal gene transfer (HGT) and therefore can suffer from degenerative effects, illustrating the importance of chlamydiae plasmids that might mitigate this effect.

Secondly, using pangenomics I was able to almost double the chlamydial genome-represented diversity and uncover a surprisingly widespread potential for anaerobic metabolism in several chlamydial groups.

Thirdly, I reconstructed ancestral chlamydiae genomes using state of the art phylogenetic methods. I presented evidence underpinning and more accurately delineating an endosymbiotic lifestyle already in the chlamydial last common ancestor. However, I inferred a facultative anaerobic lifestyle that is yet undescribed for obligate endosymbionts. The analyses presented here have far reaching implications for our understanding on chlamydiae diversity and evolution.

Robert Brünjes

08.04.2022

GADOLINIUM - A MARKER ELEMENT IN AQUATIC ENVIRONMENTS AND FORENSIC SCIENCE

Supervisor: **Thilo Hofmann**

The increasing use of gadolinium-based contrast agents (GBCAs) for magnetic resonance imaging (MRI) is leading to widespread contamination of water bodies and drinking water reservoirs around the world as conventional sewage treatments are unable to remove GBCAs.

Since MRI diagnostics are mainly carried out on weekdays, the discharge of anthropogenic gadolinium (Gdanth) into surface waters via sewage treatment plants is usually higher on those days than at weekends. This results in a transient signal that has been tracked in both surface water and groundwater within our study area. Due to on-site infiltration conditions, the propagation of the Gdanth signal from surface water to groundwater could be used to calibrate lumped parameter models. The ideal conservative behavior of Gdanth also provides an opportunity to reassess the behavior of other tracers in natural environments. Gdanth can therefore be used not only as a classically conservative tracer to assess fluxes from surface waters into groundwater, but also, because of the temporal variations in its release, as a transient tracer with which to determine the timescales of subsurface environmental processes.

Gadolinium is also used as a marker element for particles derived from gunshot residues (GSRs) of military and police firearms. A new method is proposed to analyze these GSRs, based on single-particle inductively coupled plasma time-of-flight mass spectrometry (sp-ICP-TOF-MS). This method can detect thousands of particles per minute, enables rapid sample screening for GSR particles, and can be used to support currently used GSR detection methods, especially when lead-free, antimony-free, or gadolinium-tagged ammunition has been used.





Daniela Trojan

01.07.2022

INVESTIGATING THE LIFESTYLE OF THE *ACIDOBACTERIOTA*, A PHYLUM UBIQUITOUS IN TERRESTRIAL ENVIRONMENTS – GENOMICS AND PHYSIOLOGICAL STUDIES

Supervisor: **Dagmar Wöbken**

Acidobacteriota represent one of the most abundant bacterial phyla in terrestrial environments worldwide. However, little is known about them. The overarching research goal of this PhD thesis was to elucidate the eco-physiology and thus the success of Acidobacteriota in soils by combining genomic, transcriptomic, functional gene expression and growth-based analyses.

An initial comparative genomic analysis of 24 genomes from acidobacterial isolates revealed traits that provide genomic, physiological and metabolic versatility, presumably allowing flexibility in the fluctuating soil environment. Mobile genetic elements, including temperate bacteriophages, influenced the structure and plasticity of these genomes. We detected the capacity to use a diverse collection of carbohydrates, as well as inorganic and organic nitrogen sources, both advantageous traits in environments with fluctuating nutrient environments.

We also identified soil Acidobacteriota with the potential to scavenge atmospheric concentrations of H_2 .

Respiratory flexibility can be attained by inducing branched-respiratory chains that terminate in multiple oxidases with different affinities for O_2 . Low-affinity as well as high-affinity TOs were detected in the genomes of terrestrial acidobacterial strains.

Using highly sensitive O_2 optodes, this PhD thesis presents apparent K_m values for O_2 for species outside the phylum Proteobacteria for the first time. Surprisingly, the expression of the conventional high-affinity TOs at micro- and nanomolar O_2 concentrations was not detected but rather the expression of low-affinity TOs. This challenges the standing hypothesis that a microaerobic lifestyle is exclusively imparted by the presence of high-affinity TOs.

Jay Osvatic

06.07.2022

A STUDY ON THE LIFE CYCLE OF LUCINID SYMBIONTS AND THEIR AVAILABILITY IN THE ENVIRONMENT: WHERE DID THEY COME FROM, WHERE DO THEY GO?

Supervisor: **Jill Petersen**

Chemosynthetic symbioses have been found in marine habitats across the entire world, from shallow water to great depths. One of the most successful hosts of these symbiotic relationships, by species count, is the bivalve family Lucinidae. Lucinidae have existed for 400 million years and have colonized a wide range of environments. The success of the hosts is due, in part, to their horizontally-acquired sulfur-oxidizing symbionts, whose diversity is understudied.

The goal of this thesis was to expand on the known lucinid symbiont diversity, elaborate on the variation in the metabolisms, and incorporate the complex evolutionary history of lucinids to better understand the host-symbiont relationship, using environmental context. Museum samples of rare specimens alongside fresh environmental samples from Elba, Italy formed the basis of this research. High-throughput metagenomic sequencing was used to generate putative metagenome-assembled genomes from over 30 lucinid species to investigate the biodiversity and metabolic variation between symbiont species. 16S rRNA gene sequencing was used to assess abundances of symbionts in the host and environmental samples.

In total, 20 novel species of lucinid symbiont were analyzed. These species include the most widely distributed symbiont species known thus far, *Candidatus Thiodiazotropha taylori* and *Ca. T. gloverae*, both of which were found in several host species. In addition to these species, instances of symbiont-switching to another bacterial family, related to symbionts of hydrothermal vent invertebrates, were found.

Environmental surveys that were conducted suggested that lucinid-associated habitats can be reservoirs of symbionts and that lucinids themselves may play a role in seeding the environment with symbionts upon death.





Joana Séneca Cardoso Da Silva

27.09.2022

THE IMPACTS OF SINGLE AND MULTIPLE GLOBAL CHANGE DRIVERS ON SOIL MICROBIAL COMMUNITIES AND FUNCTIONS

Supervisor: **Andreas Richter**

Atmospheric CO₂ concentrations and global temperatures have been steadily increasing as a consequence of anthropogenic activities. Future climate predictions forecast an increasing frequency of climatic extreme events such as droughts and heat waves. Microorganisms play a major role in terrestrial ecosystem functioning and there is growing evidence that ecosystem level responses to climate change can be tightly linked to changes in microbial physiology, community structure and composition.

In this thesis I assess the effect of single and combined climate change drivers on soil microbial communities, with a special focus on the terrestrial nitrogen cycle. Results showed that a summer drought caused a decrease in amoA transcription levels from ammonia-oxidizing archaea and complete nitrifiers, while ammonia-oxidizing bacteria remained relatively unaffected. One year after the end of the drought, significant differences in bacterial/archaeal and fungal community structure remained observable in soils previously exposed to drought, in comparison to controls. The effects of future climate conditions on community structure were more pronounced during spring and autumn, than in summer. Microorganisms exposed to long-term warming showed increased transcription levels of genes encoding secreted extracellular enzymes involved in the depolymerization of high molecular weight organic nitrogen such as proteins and peptidoglycan. This provides evidence of the importance of microbial necromass as a C and N source in response to sustained warming, where substrate depletion is a common phenomenon.

Tamara Halter

02.11.2022

ECOLOGY AND EVOLUTION OF CHLAMYDIAL SYMBIONTS OF ARTHROPODS

Supervisor: **Matthias Horn**

Chlamydiae are a phylum of obligate intracellular bacteria that found a niche in eukaryotes over a billion years ago and have successfully persisted to the present day.

The main aim of my research was to deepen our knowledge about Rhabdochlamydiaceae - the potentially largest, yet highly understudied group of chlamydiae infecting arthropod hosts.

Firstly, we used amplicon sequencing data to show that members of this group are highly abundant in soil and freshwater ecosystems suggesting also protists as their hosts. We used comparative genomics to reveal that the arthropod symbionts represent intermediate stages of adaptation of chlamydiae from protists to vertebrate hosts. In addition, we proposed a scenario for the evolution of arthropod infecting rhabdochlamydiae in which mobile genetic elements lead to streamlined genomes.

Secondly, we used *R. porcellionis* to investigate strain diversity in Rhabdochlamydia. Using comparative genomics, we identified outer membrane proteins and proteins containing eukaryotic-like domains as hot-spots of variation. Infection assays in insect cell cultures revealed that the two genetically most dissimilar strains differ in their infectivity. We used gene expression data to identify the type III secretion system, proteins with eukaryotic-like domains and outer membrane proteins as well as the transcription factor EUO to be involved in this difference.

Lastly, we analyzed *R. oedothoracis* and co-existing *Wolbachia*, *Cardinium* and 'Ca. Tisiphia' endosymbionts in a spider host. We show that the symbionts co-exist frequently in the spider. With comparative genomics we verify the involvement of mobile elements in genome reconstruction and evolution of Rhabdochlamydia, and suggest genes for *Wolbachia* to cause reproductive manipulation in the spider. We used phylogenetic reconstructions of shared mobile elements to show that the symbionts likely met each other in the past.





Maximilian Nepel

18.11.2022

N₂-FIXING MICROBIAL COMMUNITIES IN TWO DISTINCTIVE TERRESTRIAL ECOSYSTEMS – GRASSLAND SOILS AND ARBOREAL ANT NESTS

Supervisors: **Dagmar Wöbken** and **Michael Wagner**

Nitrogen (N) is one of the main building blocks of life on earth. Atmospheric N₂ is made biologically available by biological nitrogen fixation (BNF) performed by a specific microbial guild – the diazotrophs. They are highly phylogenetically diverse, display various physiologies and microbial lifestyles, and can be found in all major ecosystems. Due to the global importance of BNF, it is essential to further investigate this process and the diazotrophic community composition in understudied and diverse ecosystems, and identify environmental factors shaping them.

In this PhD thesis, this community was studied by amplicon sequencing of the dinitrogenase reductase gene in two distinctive terrestrial ecosystems, global grassland soils and arboreal ant nests in the Neotropics. To the best of our knowledge, this is the first study correlating seasonal climatic, edaphic and vegetation variables, and spatial distance with diazotrophic beta diversity on a global scale, spanning four continents. In grasslands, diverse and heterogeneous community composition across 23 sampling sites could be revealed, with best predictors seemingly related to seasonal water availability.

In rainforest canopies, ants associated with cecropia trees cultivate microbial “patches” in their nesting space, in which first evidence for arboreal ant-associated BNF could be provided, which can support ant population growth.

In conclusion, this thesis extends the current knowledge on the ecological importance of BNF in understudied ecosystems and also on environmental factors potentially shaping diazotrophic community compositions. Further, highly heterogeneous diazotrophic communities could be shown in distinctive ecosystems on both the global scale, or locally, in alleged specific ant-plant-microbe associations.

Annelieke Overbeeke

06.12.2022

BACTERIAL DEGRADATION OF POLYSACCHARIDES IN THE GUT MUCOSAL ECOSYSTEM

Supervisor: **David Berry**

A healthy diet is one of the main pillars of healthy living, where fibers play an important role in host health. Not only do fibers reduce chances of disease onset, fibers are also vital for a healthy digestive tract which includes the gut microbiome. In return the bacteria in the intestines provide the host with additional nutrients the host is unable to produce itself. In a healthy system a mucus layer covers the intestine in order to prevent bacteria from coming into direct contact with host cells and thus causing an inflammatory response. However, with many diseases this mucus layer is diminished.

The main focus of this thesis was to investigate bacterial interactions with the mucus layer. This was done in a holistic in vivo approach using mice models fed a fiber deficient diet investigating the entire mucosal ecosystem as well as in vitro.

The in vivo experiments showed, contrary to popular belief, mucus reduction is not a result of an increasing number of mucus degrading bacteria but rather a host-led response. Additionally, our results verified the loss of bacterial diversity upon the absence of fiber. Lastly, we showed physiological changes in the intestines resulting from a lack of fiber, including a shortened length.

Different taxa within the gut microbiome are vital to host health. We selected closely related *Bacteroides* species in order to investigate the mechanisms behind degradation of host glycosaminoglycans as well as the potential cooperation between species via cross-feeding. Here we found that closely related species have different degradation profiles yet do share degradation products in order to keep a balanced ecosystem.





Stephanie Castan

07.12.2022

FATE AND IMPACT OF ANTHROPOGENIC PARTICLES IN THE NATURAL ENVIRONMENT

Supervisor: **Thilo Hofmann**

The four studies in this thesis aimed to fill knowledge gaps regarding fate and behavior of anthropogenic particles in the environment. These include synthetic polymers (microplastics, tire wear), combustion products (soot, char), or engineered carbonaceous materials.

Micro- and nanoplastics are often proclaimed to influence the fate of organic contaminants in agricultural soils by mobilizing them within the soil. Possible transport and contaminant desorption scenarios were calculated to understand the role of micro- and nanoplastics as contaminant vector. We found that micro- and nanoplastics may be a source of organic contaminants to agricultural soil, eventually exposing edible plants to contaminants released within upper soil layers, rather than enhancing vertical contaminant transport through soil. Carbonaceous materials fractionate dissolved organic matter (DOM) upon sorption.

The interactions between DOM and carbonaceous materials were investigated with the key findings that molecular weight of DOM, sorbent surface area and surface functional groups determine to which extent aromaticity of DOM controls sorption to carbonaceous materials. Aromaticity of DOM remains the controlling factor for sorption when regarding distinctive molecular weight fractions. After its deposition in surface waters, soot can encounter and interact with herbicides like S-Metolachlor. Sorption of S-Metolachlor to soot decreases for NO₂-transformed soot but is not affected by DOM at environmentally relevant concentrations.

Biochar particles may be mobile in soil, counteracting their purpose to sorb and immobilize contaminants in soils. Aggregation of biochar particles was analyzed in dependence of solution chemistry in the presence of organic contaminants. Sorbed hydrophobic organic contaminants are expected to reduce the mobility of biochar particles in soil as high ionic strength and sorption of the model contaminant pyrene enhanced biochar aggregation by synergistic effects.

Kyle Chardi

16.12.2022

EFFECT OF ORGANIC LIGANDS ON THE STABILITY OF TETRAVALENT URANIUM UNDER ANOXIC CONDITIONS

Supervisor: **Stephan Krämer**

Uranium (U) from both anthropogenic uses and geogenic sources is a contaminant which poses threats to human health. The immobilization of U by bioreduction is a remediation strategy based on the reduction of soluble hexavalent U (U(VI)) to sparingly soluble tetravalent U (U(IV)). Yet, the stability of U bioreduction end products can vary drastically, ranging from recalcitrant crystalline phases such as uraninite (UO₂) to labile biomass-bound noncrystalline U(IV). The presence of chelating ligands which can complex and (re)mobilize U have the potential to compromise the stability of such immobilized U sources, thus undermining the efficacy of U remediation efforts, even under strictly anoxic conditions. Such organic ligands can be found in the environment from both anthropogenic applications (e.g., fertilizers) and natural sources (e.g., biogenic ligands exuded by plants and microorganisms).

In light of the vastly differing labilities of U(IV) phases and the potential for organic ligands to mobilize U from U(IV) phases even under anoxic conditions, the aim of this work was to unravel what processes and ligand properties control U mobilization under anoxic conditions. Ligand-induced U mobilization from UO₂ and noncrystalline U(IV) was directly compared, highlighting the significantly higher mobilized U concentrations from noncrystalline U(IV) at faster rates compared to UO₂. Combined effects of humic substances and other organic ligands were additionally probed, resulting in elevated U mobilization. Finally, the role of competitive complexation from cations commonly found in the subsurface was investigated in model batch reactor experiments as well as in bioreduced field sediments. Competing cations had varied effects on ligand-induced U mobilization depending on the cation-ligand combination, ranging from >99% U mobilization inhibition to no significant deviation from ligand-only treatments. The findings of this work bring attention to the implications organic ligands pose towards undermining the stability of immobilized U(IV) in the environment.





Boris Meisterjahn

21.12.2022

METHODS FOR THE INVESTIGATION OF THE FATE OF ENGINEERED NANOPARTICLES IN THE ENVIRONMENT AND COMPLEX MATRICES

Supervisor: **Thilo Hofmann**

The objectives of this thesis were to evaluate and investigate setups and methods for the assessment of the fate of nanomaterials in aquatic environmental systems. Specifically this comprised (i) the development, scientific justification and evaluation of a simplified standard test for the assessment of the dispersion stability of nanomaterials that would be applicable for most routine laboratories and (ii) the evaluation of analytical techniques on the applicability for detection and characterization of ENMs in a more complex system. Despite the necessary simplifications made, a powerful tool enabling a comparative assessment of ENM dispersion stability in different types of aquatic media reflecting the relevant composition of terrestrial surface waters was established. The applicability of Flow-Field-Flow Fractionation (Flow-FFF) coupled to a multi-detection setup was successfully demonstrated for the analysis of gold nanoparticles (AuNPs) in a complex matrix. The combination of different detection systems allows in principle the investigation of the interactions between ENMs and natural nanoparticles (NNPs). The comparison of samples with different concentrations of natural organic matter (NOM) mitigated the common assumption that hetero-agglomeration would always dominate the fate of ENMs in environmental matrices. The use of Flow-FFF for analysis of nanomaterial mixtures in complex matrices requires optimization of the parameters that influence the separation behavior. It was shown that the behavior of particles within Flow-FFF channels cannot be predicted or explained purely in terms of electrostatic interactions. In general, careful adjustment of separation conditions can result in acceptable, but not ideal, separation for different stabilized materials. However, the optimized conditions will not be ideal for any particle and results have to be interpreted carefully e.g. with respect to size determination.

Philipp Höhn

21.12.2022

THE POTENTIAL OF HYDROGEOPHYSICS AND DEEP REINFORCEMENT LEARNING FOR BETTER GROUNDWATER MANAGEMENT

Supervisor: **Thilo Hofmann**

In his PhD work, Philipp investigated (a) the comparison of streambed hydraulic conductivity from slug testing with imaging results of components of the streambed complex electrical conductivity derived from spectral induced polarization (SIP) measurements on a small sub-reach scale, and (b) the utility of estimates of streambed hydraulic conductivity, based on such imaging, on selected groundwater model predictive uncertainty at a groundwater management site. It highlighted the potential of waterborne SIP to depict streambed hydraulic conductivity magnitude variations better than to quantify it with every detail, while demonstrating value of respecting supportive SIP-derived information in reducing selected predictive uncertainties of groundwater models. Furthermore, the work tested (c) formulating and optimizing aquifer management tasks in a deep reinforcement learning framework. It demonstrated that reformulating management objectives in such a way and coupling them to optimization based on reinforcement learning using deep neural networks acting as policy models, can be a novel pathway for computational hydrogeology and can be well worth exploring further. In the three tested simulated environments, the optimized policy models surpassed the superiority of experienced human control over control from random actions in terms of average cumulative reward by 30.8 %, 25.1 % and 18.4 %, respectively.





Sean Darcy

(Mentor: Christina Kaiser)

In my research I combine modelling approaches and experimental data analysis to investigate how microbial community composition and structure relate to soil organic matter composition and decomposition. Through the lens of complex systems science I hope to detect imprints of microbial self-organization and describe and quantify potential emergent properties of soil systems.

To achieve this I combine insights gained from a model in which I simulate community assembly mechanisms with the analysis of how microbial communities and soil chemical fingerprints relate using co-occurrence network analysis. Then, in a large field experiment I will be applying this knowledge by investigating the effect of warming on soil chemistry and diversity and aim to distinguish patterns, such as non-linear responses indicative of self-organization processes in complex systems.



Leila Hadziabdic

(Mentor: Isabella Moll)

Within the scope of my PhD project, I am investigating the production and meaning of alternative protein isoforms produced from non-stop mRNAs in *E. coli*. Non-stop mRNAs do not permit correct termination of translation and lead to stalling of ribosomes. Primary ribosome rescue system to resolve stalled translation complexes in *E. coli* is trans-translation, a process which ultimately leads to degradation of truncated proteins produced from the non-stop mRNA. Under specific conditions, however, the ribosome rescue system may be switched to alternative rescue (AR). Unlike trans-translation, AR leads to stabilization and preservation of truncated proteins originating from non-stop mRNAs. If we consider that the switch to this rescue system is induced only under specific conditions, and if some of the alternative protein variants are functional, it could be speculated that AR-induced proteomic changes might be providing phenotypic heterogeneity to single cells in bacterial populations. The main objectives of my PhD thesis are to identify some of the alternative proteins isoforms produced by alternative rescue (AR) in *E. coli* and elucidate their meaning for the cell.

Lukas Helmlinger

(Supervisor: Matthias Horn, TAC members: Tamara Haselkorn / University of Central Arkansas, Thierry Soldati / University of Geneva, Jill Petersen / University of Vienna)

The amoeba *Dictyostelium discoideum* has a long history as a model system for a variety of cellular processes, such as chemotaxis, phagocytosis and recurring multicellularity. Only recently, the microbiome of wild *D. discoideum* strains and other closely related species has been elucidated, leading to the discovery of novel environmental chlamydiae. These chlamydiae are related to the well-known human pathogens but do not influence the fitness of their natural dictyostelid host under laboratory conditions. We hypothesize that the long-lasting symbiosis between chlamydiae and dictyostelids has led to distinct adaptations in the chlamydial phenotype- and genotypes. The availability of naturally infected dictyostelids and genetically manipulated strains make these symbioses the ideal system to study chlamydial evolution also with regards to the threats still posed by pathogenic chlamydiae.



Aaron Kintzi

(Supervisor: Michael Zumstein, TAC members: Thilo Hofmann / University of Vienna, Michael Sander / ETH Zurich)

Water-soluble polymers (WSPs) are an important class of chemicals used in a wide range of applications including everyday consumer products. The very nature of many WSP applications, be it in shampoos, detergents or cosmetics, leads to their direct discharge into the wastewater system. Since many conventionally used WSPs are known to be non-biodegradable, and because WSP recovery from wastewater is not feasible, biodegradability is a desired property for sustainable WSPs. The aim of my PhD project is to study the aerobic biodegradation and biotransformation of WSPs in domestic wastewater systems. To understand which WSPs are biodegradable in wastewater and how this relates to their polymer properties and the respective environmental conditions, I assess the biodegradability of promising WSPs (e.g. polyaminoacids) using incubation experiments coupled to respirometric analysis. Assuming that extracellular breakdown into small molecules is the limiting step before cellular uptake and subsequent metabolization of WSPs can occur, I will conduct biotransformation experiments using wastewater extracellular enzymes. Subsequently, I want to identify and characterize extracellular enzymes involved in WSP biodegradation.





Lukas Leibrecht

(Mentor: Jill Petersen)

Symbiosis is a widespread phenomenon in nature, ranging from very basic associations to the complex system of the human and its microbiome. An example for a rather simple form is the mutualistic association of clams from the family Lucinidae with chemoautotrophic bacteria. The clams acquire their symbionts horizontally at a certain life stage, specifically choosing one or a few bacterial species among countless others in the surrounding environment. The host animal profits from the sugars provided by the bacterial partners and the microscopic symbionts can thrive in a stable environment within the host cells (endosymbionts). The focus of my PhD project is to investigate the underlying mechanisms (e.g. transcriptional responses in symbiotic vs aposymbiotic hosts, identification of key genes upon initial colonization and more) of how this specific symbiosis is formed. The project includes different experiments, transcriptomic analysis, electron and confocal microscopy and quantitative PCR techniques.



Alexander Pfundner

(Supervisor: Thomas Rattei, TAC members: Alexander Probst / University of Duisburg/Essen, Claudia Plant / University of Vienna)

In my work, I investigate how microbial communities can be represented at different molecular levels and how this representation can be utilized to assign traits to these communities. For this, I utilize approaches from Bioinformatics and Machine Learning, e.g. multi-omics integration or predictive modeling. The main project behind my PhD aims to identify links between microbial communities in marine sediments and hydrocarbon seepage by looking at genomic, transcriptomic, proteomic and geochemistry data. In addition to that, I will evaluate and improve methods for feature engineering and dataset preparation in microbiome research.

Laura Quell

(Supervisor: Boris Görke, TAC members: David Berry / University of Vienna, Silvia Bulgheresi / University of Vienna)

Bacteria use a variety of two-component systems (TCS) to sense and react to their environment. The QseEF system, together with outer membrane anchored lipoprotein QseG, constitutes such a TCS. Albeit little is known in terms of the stimulus sensed by the QseEGF system, there are indications that it may represent an envelope stress response related signaling system. Additionally, the role of lipoprotein QseG within the QseEGF system remains largely unknown. My project tries to identify the stimulus (stimuli) sensed by QseEGF and to clarify the role of lipoprotein QseG, which is likely involved in signal sensing.



Veer Vikram Singh

(Mentor: Stephan Krämer)

DNA from pre-historic humanoids, termed ancient DNA (aDNA), is widely used by anthropologists to study human evolution and migration. Traditionally, anthropologists obtain the aDNA from biological remains such as tissues, bone or teeth fragments. Long-term survival of these remains requires extremely well preservation conditions, which are very rare. Additionally, DNA is a fragile molecule that degrades rapidly once released in the environment from the cell.

This field was revolutionized by a recent discovery of aDNA preserved in sediments without identifiable bio-remains. The near-surface environment has a ubiquitous presence of diverse mineral groups, which provide various functional sites for the adsorption of DNA. The adsorption to the mineral surfaces has been shown to prevent or retard DNA degradation. However, the exact mechanisms of DNA preservation are poorly understood. My current project focuses on unraveling the molecular mechanisms of DNA preservation against degradation agents such as nucleases, reactive oxygen species and UV radiation when adsorbed onto mineral surfaces. This project will help identify the minerals providing the best preservation that can be targeted for high-yield aDNA recovery by anthropologists.





Sarah Al-Ajeel

(Mentor: Holger Daims)

Nitrification, the oxidation of ammonia to nitrate via nitrite, is an important process in engineered water treatment systems as it prevents high levels of ammonia from entering receiving waters. Nitrification is mediated by two guilds: ammonia-oxidizing bacteria (AOB) and ammonia-oxidizing archaea (AOA); both convert ammonia to nitrite, and nitrite oxidizers (NOB), that convert nitrite to nitrate. Alternatively, ammonia gets converted to nitrate (via nitrite) by comammox bacteria. Biofilms are the primary mode of existence for nitrifiers in the environment. Because nitrifiers co-exist in biofilms, they are often in direct competition for the same substrate. As such, ecological trade-offs between growth rate and yield arise. Essentially, an organism “decides” whether it grows quickly but inefficiently (growth strategy) or grow slowly but efficiently (yield strategy). Efficient organisms are selected for in biofilms, where the substrate influx is limited. My project examines the ecological strategies of nitrifiers in biofilms and attempts to disentangle the factors involved in their niche differentiation. Sarah will use a combination of in situ visualization (AMO-click, BONCAT, and FISH) and qPCR/metagenomics to study the abundance and distribution of nitrifiers in biofilms under varying environmental conditions.



Paul Jimenez

(Mentor: Martin Polz)

Microbes have an important role in regulating biogeochemical cycles, especially in marine environments, where they make up the majority of biomass. This is because microbes are the primary and secondary producers of the food chain in the oceans however, their role could change drastically in the coming years mainly because of global warming. Hence, it is important to understand how microbial communities are sustained in marine environments to find proper solutions to environmental problems. Phages have a great influence in shaping the ecological interactions within bacterial communities, primarily through lytic infections. The main purpose of this project is to determine the ecological interactions of *Vibrio* bacteria in a predatory environment mediated by phages. The cornerstone of the project is the determination of the mass-growth rate relationship of *Vibrio* populations by using suspended microchannel resonators (SMR), which can measure the mass of microorganisms at the single cell level with high precision and with high-throughput, this will provide a better insight into the effects of the environment in the bacteria population.

Anya Sherman

(Supervisor: Thilo Hofmann, TAC members: Thorsten Huffer / University of Vienna, Damian Helbing / Cornell University, Sara Rodríguez-Mozaz / Catalan Institute for Water Research)

Tire wear particles represent at least one third of microplastics entering the environment, with worldwide annual emissions estimated at 5.9 million tons. These particles contain many organic additives, some of which are highly toxic, which leach out of the particles into the environment. The overarching goal of my PhD is to investigate the fate of these tire additives in the environment, and specifically, how biotic phases can accumulate, and transform these additives. One of my projects is to investigate plant uptake and metabolism of tire additives in an agricultural context. At the same time, I am also investigating biofilm accumulation and transformation of tire additives in urban rivers.



Min Wen

(Mentor: Wolfgang Wanek)

High latitude and high altitude areas are more sensitive to the increases in temperature and nutrient inputs compared to low altitude areas. Soil temperature is a key factor controlling plant nutrient diffusive fluxes in soils. The amount of soil active nutrients is the key factor of soil nutrient release, but the effects of temperature and active nutrients on soil nutrient diffusive fluxes have rarely been reported. Moreover, a new technique based on passive microdialysis has been proposed as a possible tool for monitoring nitrogen (and other solute) dynamics in soils, which can better estimate plant available nitrogen in soil.

Aims: The purpose of this study is to reveal the characteristics of soil nitrogen flux and the effects of temperature on the uptake of ammonium nitrogen, nitrate nitrogen and organic nitrogen by plant roots using microdialysis.

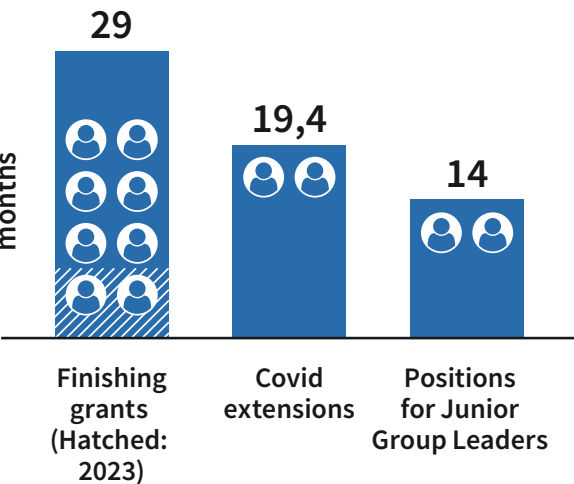
Approach: In order to better estimate the diffusion fluxes of organic and inorganic nitrogen, and to study the effects of nitrogen application and soil warming on nitrogen diffusion fluxes, temperature experiments, ¹⁵N tracer experiment, microdialysis experiment and nitrogen addition experiments will be carried out in an alpine meadow experimental area of the Austrian Alps.



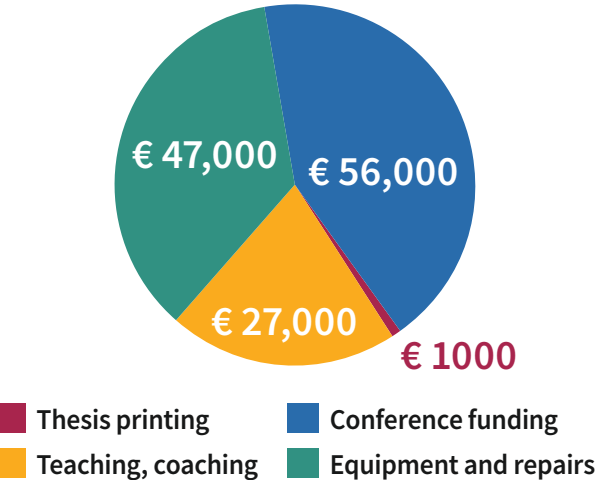
Budget and Services

PhD contracts

€ 212.000



Other services



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- Microbial symbiosis in nature
- Data management for ecologists

Outreach

Science to public



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