Centre for Microbiology and Environmental Systems Science

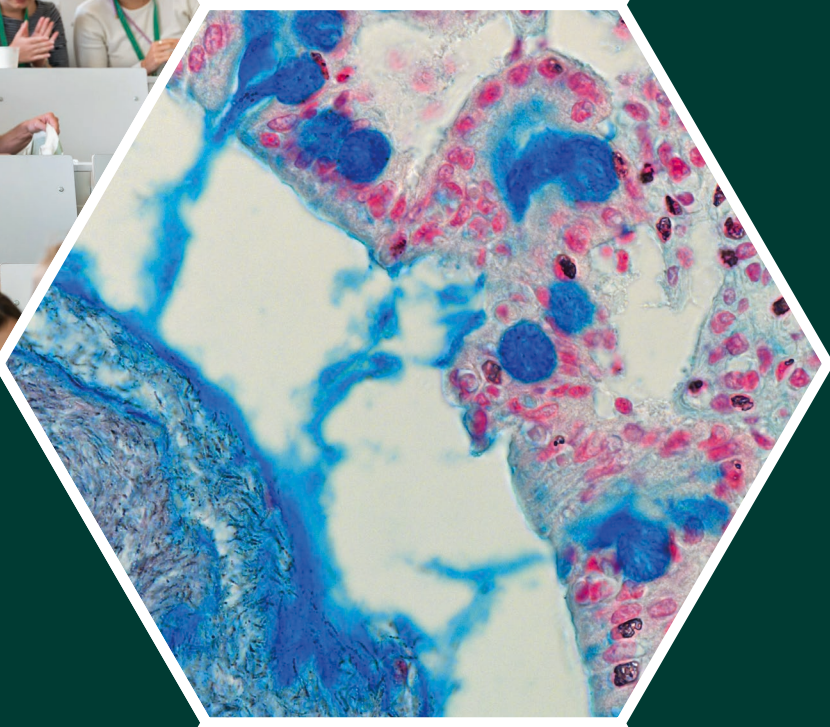
UNIVERSITY OF VIENNA

VDS-MES

Annual Report 2023







Contents

Contents 2
Preface 3
Facts and Figures 4
Budget and Services 5
Team and Structure 6
Graduates 2023 8
Incoming 2023 22
VDSMES Offers 30
PhD Timeline 31

Imprint

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

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Preface

You are reading the second 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 2023 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 funding of our school in mid-2021.In 2023 we have mainly focused on the admission standards to the school, the initial phase of the PhD, and have introduced group and individual coaching sessions for scientific writing, as well as data management courses. As we move into 2024, we have ambitious plans. For instance, we aim to implement a comprehensive “onboarding” curriculum for new students entering our school, increase opportunities for student and peer exchange, and establish an Alumni network.

Our school could only be that successful in 2023 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 2024 and look forward to another fruitful year for our school. Enjoy reading this annual report!

Thomas Rattei
Head of the VDS-MES

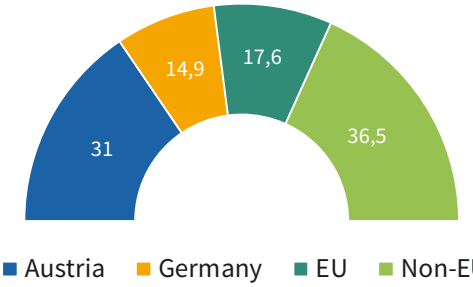
Facts and Figures

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

Student nationalities %

(WiSe 2023/2024)



Sex ratio



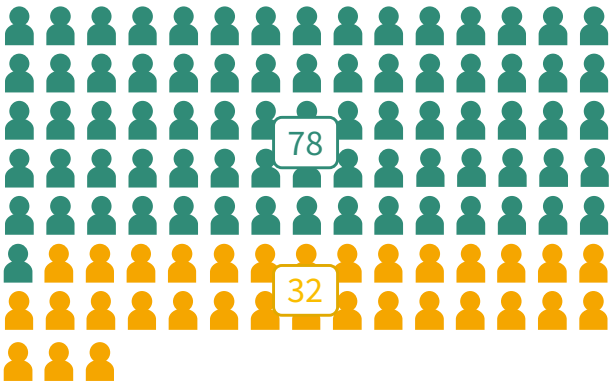
54%
female students



38%
female faculty

Faculty-Student ratio

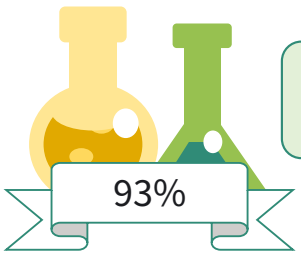
(WiSe 2023)



1:2,4

Financed students

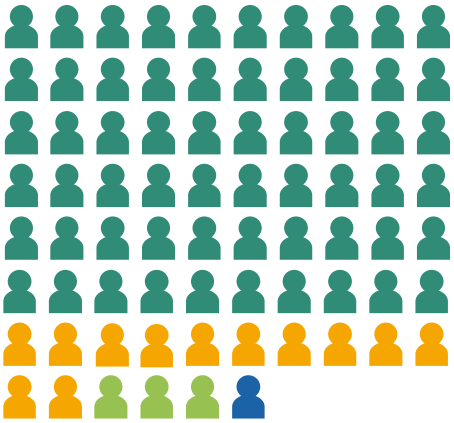
(Study year 2022/23)



75% internal
13% external/industry
5% scholarship

Fields of study

(WiSe 2023)

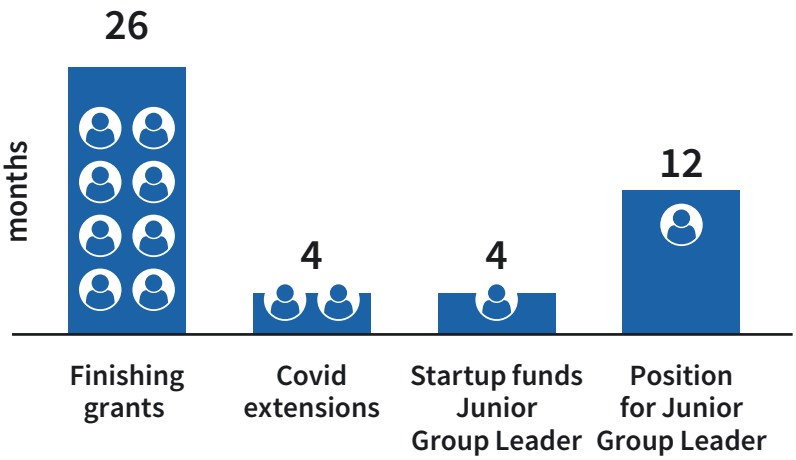


- Biology
- Molecular Biology
- Environmental Science
- Geosciences

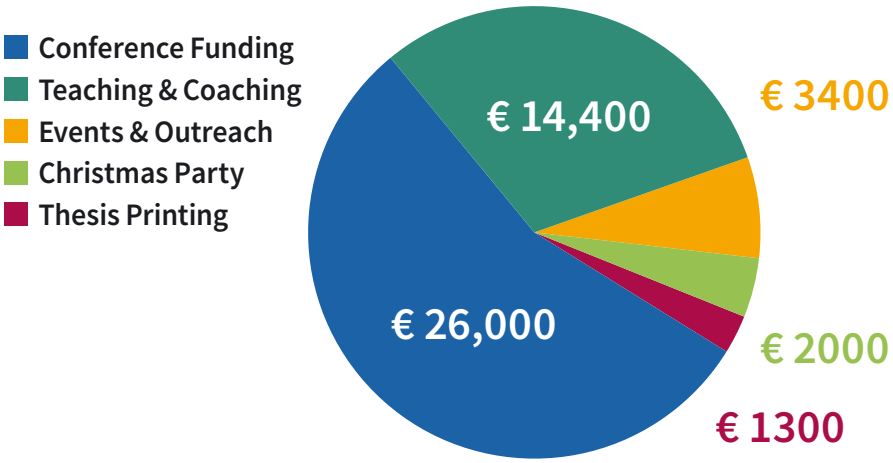
Budget and Services

PhD contracts

€ 235.000



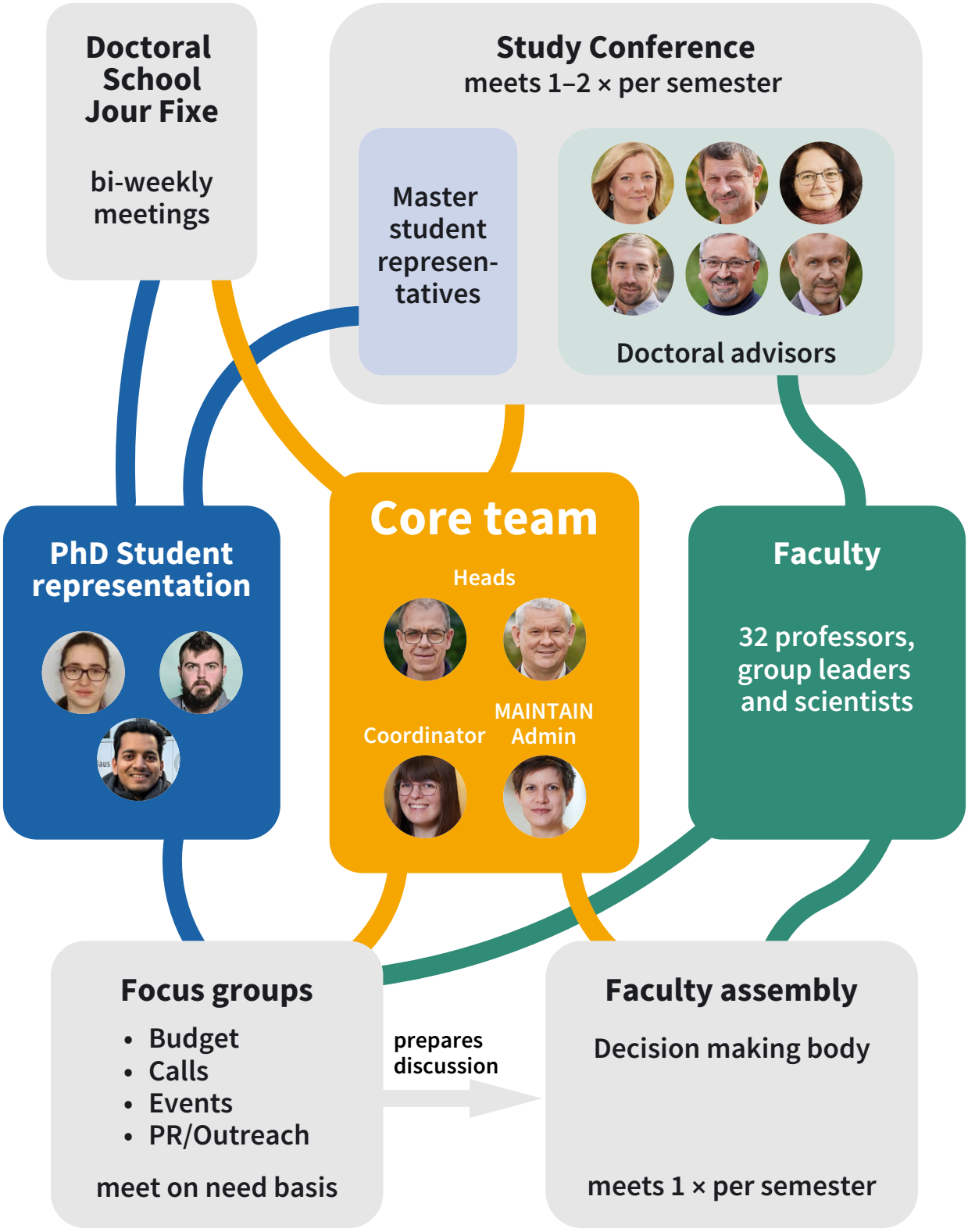
Other services



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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 10 of the students in our school.

PHD STUDENT REPRESENTATIVES

Our school's elected student representatives **Nataliia Solntseva, Sean Darcy** and **Veer Vikram Singh** support the team by taking part in our regular meetings as the voice of the student body.

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.

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**

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.

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.



Sampriti Chaudhuri

04.12.2023

THE ROLE OF WATER CHEMISTRY AND MINERAL AMENDMENTS IN THE IMMOBILIZATION OF METALS AND METALLOIDS BY BIOCHARS

Supervisors: **Thilo Hofmann** and **Gabriel Sigmund**

Biochars, produced from wood or crop waste, can be an eco-friendly alternative to traditional fossil-based and chemically-activated carbon in contaminant remediation practices. However, the mechanisms of metal and metalloid retention by biochars vary and can change depending on the surrounding water chemistry. Certain solution and soil chemical conditions can render biochars ineffective, and remediation can be improved by using other locally-sourced amendments with biochars. This thesis aims to broaden our understanding of the efficacy of using biochars in metal(loid) remediation. Road run-off is a major pathway for pollution of waterbodies by toxic metals like lead, copper, zinc, and cadmium. The first study compared the sorption performance of pristine wood-based biochar with wood-ash obtained from a biomass power plant and found that co-sintered wood ash-biochars performed significantly better in metal removal. The efficacy of biochar use for mercury immobilization in water matrices of varying chemical composition remains poorly understood. The second study explored the role of co-existing natural organic matter (NOM), chloride (Cl), Ca, and Hg(II) in biochar containing solutions. It found that sulfur-containing sites were the primary drivers for Hg(II) immobilization in biochar. The third study demonstrated the need to consider diverse water composition when evaluating the effectiveness of using biochar in metal(loid) remediation.

Alexandra Schilder



01.12.2023

ROLE OF THE BACTERIAL SMALL RNA 5'-PHOSPHORYLATION STATE FOR TARGET RNA REGULATION IN VIVO & FUNCTIONAL CHARACTERIZATION OF THE QSEEGF THREECOMPONENT REGULATORY SYSTEM IN E. COLI

Supervisor: **Boris Görke**

In the first part of the study, the role of the sRNA 5´P state for target RNA silencing by RNase E was investigated in Enterobacteriaceae. Therefore, a genetic tool was engineered, generating 5´P sRNAs on demand, which can support various applications in future RNA research. The results show that a 5´P has no major impact on target RNA destabilization, but rather on sRNA stability and highlight the importance of the RNase E C-terminal scaffolding domain for sRNA-mediated target decay. II. Functional characterization of the QseEGF three-component regulatory system in E. coli. In the second part of the study, a time-resolved RNA-sequencing approach was established and performed to clarify the regulon and physiological role of the potential novel stress response system QseEGF. The results confirm that sRNA GlmY is controlled by QseEGF and suggest that the system might control other genes under specific (stress) conditions at the transcriptional level. Moreover, the data indicates that QseEGF might interact with certain proteins to perform additional regulatory functions.

Patrick Arthofer

13.10.2023

INTERACTIONS OF GIANT VIRUSES WITH THEIR HOSTS AND SYMBIOTIC BACTERIA

Supervisor: **Matthias Horn**

Giant viruses, the most complex viruses in the world, have genomes and particle sizes comparable to bacteria. However, metagenomics provides limited insights into the interactions between hosts and giant viruses and their ecological roles. This dissertation investigates the biology of a novel giant virus isolate infecting Naegleria, reveals that bacterial symbionts can block viral replication, and demonstrates the adaptations of a giant virus to an alternative host in an evolution experiment.

The study characterizes Naegleriavirus (NiV), revealing its unique adaptations to Naegleria, including an unusually high number of translation genes and acquired genes via horizontal gene transfer from host organisms. NiV infection was lethal for all tested Naegleria species, expanding our knowledge of giant viruses and offering potential for controlling the deadly human pathogen Naegleria fowleri.

The dissertation also investigates interactions between bacterial symbionts and giant viruses in free-living amoebae, showing that protists are essential regulators of microbial communities. The study isolates a giant virus Marseillevirus viennavirus and its bacterial symbiont-infected Acanthamoeba host, finding that the symbiont represses Viennavirus replication and suppresses the replication of Acanthamoeba polyphaga mimivirus and Tupanvirus deep ocean (Tupanvirus).

The study also reports on an evolution experiment observing viral adaptation to diverse amoeba hosts, demonstrating the rapid adaptation of giant viruses to novel hosts.

Anna Mueller

11.10.2023

NOVEL, CULTIVATED MARINE NITRITE OXIDIZERS - CHARACTERIZATION OF THEIR GENOMES, PHYSIOLOGY AND MICROBE-MICROBE INTERACTIONS

Supervisor: **Holger Daims**



As a key element in all major biomolecules, nitrogen is central to life. In the ocean, nitrate, the primary fixed nitrogen species, is mainly produced by chemolithoautotrophic nitrite-oxidizing bacteria (NOB), with Nitrospinales and, to a lesser extent, Nitrospirales, being the dominant NOB in marine ecosystems. Despite their central role in the nitrogen cycle, relatively little is known about these organisms owing to their recalcitrance to cultivation. In this PhD, six novel marine Nitrospinales and Nitrospirales, including representatives of three novel genera, were successfully cultivated and characterized. This was facilitated by a novel cell sorting and activity screening approach, and the resulting strains and their genomes enabled phylogenetic analyses, genome comparisons, metabolic function predictions, and physiological characterizations. Finally, two native Nitrospinales-Alphaproteobacterial co-cultures were chosen as a model system to test hypotheses about microbe-microbe interactions and nitrification-denitrification dynamics. The data revealed numerous interactions, including vitamin exchange, and demonstrated how specific nitrogen cycling dynamics depend heavily on the specific heterotroph partner and oxygen concentration. This research establishes a foundation for studying elusive marine NOB and enhances our understanding of their role in the nitrogen cycle.



Marlies Dietrich

29.09.2023

THE IMPACT OF ENVIRONMENTAL FACTORS AND SMALL-SCALE INTERACTIONS ON THE STRUCTURE AND ACTIVITY OF ROOT-ASSOCIATED MICROBIAL COMMUNITIES

Supervisors: **Andreas Richter** and **Dagmar Wöbken**

The interface between plant roots and the surrounding soil represents a dynamic, nutrient-rich habitat that attracts highly specialized soil microbial communities and facilitates complex small-scale interactions. Soil conditions and plants critically impact root-associated microbial communities, yet human-induced alterations, such as fertilizer addition or global warming and their reciprocal effects on the root-microbiome are poorly understood.

This thesis aimed to assess community structures, diversity and activity of important microbial players in the soil-root continuum.

Determining fungal-bacterial colonization patterns of individual ectomycorrhizal root-tips of Fagus sylvatica demonstrated that distinct fungal communities are associated with unique bacterial/archaeal communities and highlighted the importance of the rare fungal community to contribute to new assemblages of bacteria/archaea. Investigating single and interactive effects shaping root-associated free-living diazotroph communities in temperate grasslands revealed that plant roots strongly influence associated microbial communities despite decades-long fertilization. Moreover, the successful application of NanoSIMS microarray imaging (Chip-SIP) on grassland soil microorganisms from a multifactorial climate change experiment linked microbial identity to their activity and demonstrated that predicted future climate conditions stimulate the activity of the investigated soil microbial taxa.

Taken together, this thesis highlights the complexity and importance of microbes thriving in the plant belowground habitat and disentangles small-scale interaction patterns and the effects of environmental factors on specialized root-associated microbial communities.

Charlotte Henkel

05.09.2023

THE LEACHING OF PHTHALATES FROM POLYVINYL CHLORIDE MICROPLASTICS INTO AQUATIC ENVIRONMENTS – FROM LABORATORY EXPERIMENTS TO MODELING

Supervisors: **Thilo Hofmann** and **Thorsten Hüffer**



Phthalic acid esters (phthalates) are commonly used additives (more precisely, plasticizers) and important for the stability and flexibility of polyvinyl chloride (PVC). However, phthalates can cause adverse health effects like endocrine disruptions. Phthalates have been detected everywhere in the environment but data on leaching kinetics and the governing mass transfer process remain largely unknown. The main aim of this doctoral thesis is to elucidate the leaching kinetics and leaching process of phthalates from PVC microplastics into aquatic environments. An infinite sink method - using activated carbon powder as sorbent - was developed enabling the quantification of phthalate leaching from PVC microplastics into aqueous media. Leaching curves were analyzed using models for intraparticle diffusion (IPD) and aqueous boundary layer diffusion (ABLD). ABLD was identified as the governing diffusion process for the continuous leaching of phthalates because phthalates are very hydrophobic slowing down the diffusion through the ABL.

The influence of environmental factor such as salinity, flow conditions and photoaging on phthalate leaching was investigated experimentally using DEHP as a model phthalate. By additionally including the influence of the water temperature and the concentration of dissolved organic carbon, specific desorption times, that is, desorption half-lives for the leaching of DEHP from PVC microplastics into different aquatic environments such as rivers and the ocean were calculated. Overall, this doctoral thesis shows that environmental factors strongly influence the leaching of phthalates from PVC microplastics. Combining leaching experiments and modeling revealed that PVC microplastics are a long-term source of phthalates in the aquatic environment.



Lukas Lüftinger

03.08.2023

ANTIBIOTIC RESISTANCE PREDICTION FROM SEQUENCING DATA BY MACHINE LEARNING

Supervisor: **Thomas Rattei**

Antimicrobial resistance (AMR) is a major global health concern, with up to one million deaths in 2019 due to AMR. The number is expected to rise by mid-century, with over 10 million preventable deaths in 2050. To combat this, improved diagnostic methods for antimicrobial susceptibility testing (AST) are being sought. Current AST techniques rely on observing bacterial cultures in the presence of antimicrobial compounds, which are dependent on their ability to isolate and cultivate pathogens and their growth rate. As bacterial genome sequencing enters clinical practice, inferring AST results directly from bacterial genomes is being investigated to reduce time-to-result (TTR) for slow-growing pathogens and obtain insight for unculturable pathogens. Machine learning (ML) is proving to be an increasingly effective paradigm for tackling this task. This thesis investigates the application of ML towards genomic AST, focusing on the reliability and applicability of ML models for epidemiological surveillance and diagnostic applications. It investigates possible algorithmic improvements to the state of the art of genomic AST, such as designing improved algorithms for training and validation of genomic AST ML classifiers, expanding data representations used in ML model training with biological prior knowledge, and evaluating specific settings and use cases where genomic AST ML models could be used to improve patient care in clinical practice.

We continued to explore the application of genomic AST techniques to native patient samples, specifically metagenomic AST. The research confirms the applicability of genomic AST to direct sample sequencing data, finding comparable predictive accuracy to standard AST methods. It also applies to complicated urinary tract infections (cUTIs) with a single pathogen. For infections by multiple taxa or significant bacterial background, performance metrics can be improved by adjusting in silico data preprocessing steps. The findings provide a solid foundation for genomic AST's continued advancement in clinical practice.

Yě Tián

26.06.2023

LONG-TERM SOIL WARMING EFFECTS ON SOIL CARBON, NITROGEN, AND PHOSPHORUS CYCLING AND SOIL ORGANIC MATTER DYNAMICS

Supervisor: **Wolfgang Wanek**



Climate warming can significantly affect biogeochemical cycles in terrestrial ecosystems, feeding back to climate warming itself. However, it has largely remained elusive how the simultaneous cycling of carbon (C), nitrogen (N), and phosphorus (P) in soils could be affected over long-term warming. During my Ph.D., I investigated the long-term (>14 years) soil warming (+4 °C) effects on soil organic matter (SOM) formation and decomposition as well as C, N, and P cycling and their interactions in a temperate mountain forest in Austria. The results showed that, although higher temperatures favored SOM formation via in vivo microbial pathway (of increased plant inputs), soil total C, N, and P contents uniformly decreased after long-term warming. This is because warming intrinsically stimulated SOM decomposition (by 37 %) more than formation, due to amplified microbial respiration and extracellular enzyme activities. Noteworthily, long-term warming caused more than doubled losses in soil P (-23%) compared to losses of soil organic C (-11%) and N (-11%). Combined with increased abiotic P sorption, warming reduced bioavailable P in soil solution, triggering microbial P limitation, and thus potentially changing microbial C and N allocation. Microbes allocated more C (energy) and N (nutrients) to produce exoenzymes to acquire restricted soil P. This is consistent with results of lower microbial C and N use efficiencies in the warming treatment, indicating decreased microbial C and N assimilation and greater C and N catabolism and losses to the environment. Overall, my work highlights that long-term warming negatively affected on soil C, N, and P stocks, and decoupled the soil P cycle from the soil C and N cycles, which had negative effects on soil C storage and fertility under climate warming.



Helene Walch

22.06.2023

HETEROAGGLOMERATION OF PARTICULATE CONTAMINANTS WITH NATURAL SUSPENDED PARTICULATE MATTER IN SURFACE WATERS

Supervisors: **Thilo Hofmann** and **Frank von der Kammer**

Anthropogenic particles such as engineered nanomaterials, nano- and microplastics, tire and brake wear, or soot receive increasing scientific as well as public attention as emerging contaminants of concern. Understanding the environmental fate of these contaminants is key to assessing potential related risks. In aquatic systems, interaction with natural suspended particulate matter (i.e., heteroagglomeration) is a crucial fate process because it affects the transport behavior and bioavailability of particulate contaminants. The inclusion of heteroagglomeration into fate models and exposure assessment requires parametrization and a harmonized test system.

There is scientific consensus that the heteroagglomeration attachment efficiency (α_het) is the most suitable parameter. It is defined as the probability of attachment upon collision between a contaminant particle and natural suspended particulate matter (SPM) and reflects the physicochemical affinity between their surfaces. A harmonized test system to determine α_het needs to consider those surface properties of SPM that govern particle interactions, as well as the relevant hydrochemical parameters affecting heteroagglomeration. The latter have been operationalized for homoagglomeration within the OECD test guideline No. 318, and the rationale beyond the parameter selection is equally applicable to heteroagglomeration. The selection of a suitable standardizable SPM material thus remains a major gap to fill, next to the development of a method to determine α_het under environmentally relevant conditions.

The present work comprises (1) a literature review on freshwater SPM, with a focus on rivers, to understand the relevant SPM properties and components governing agglomeration processes, (2) the generation of reproducible freshwater SPM analog flocs representing properties of natural SPM relevant to study interactions with particulate contaminants, (3) a versatile test matrix that combines the developed SPM analogs with the model hydrochemistry from OECD TG 318, validated against a natural water sample, as well as a robust experimental setup to determine α_het values under environmentally relevant conditions.

Florian Reithofer

22.06.2023

THE POTENTIAL OF CRISPR/CAS SYSTEMS IN TREATMENT OF ADENOVIRUS INFECTION

Supervisors: **Reinhard Klein** and **Angela Witte**



Human adenoviruses are pathogenic DNA viruses that pose a significant challenge to the immune system, especially in immunocompromised patients or closely packed environments. The risk of disseminated diseases and high mortality rates make new treatment options a clear medical need. RNAi and CRISPR/Cas based methods are increasingly being explored as antiviral treatment platforms. This thesis investigates the application of CRISPR/Cas based methods and their combination with RNAi to treat adenovirus infection. The first focus is on the RNA targeting effector CasRx, which has been developed to target human adenovirus (HAdV-5) replication in vitro. Inhibition rates of up to 2 orders of magnitude were achieved in assays. The second topic explores different ways of combining RNAi and CRISPR/CasRx, generating multiple plasmids using different approaches of multiplexing. The third topic focuses on DNA targeting Cas9, achieving inhibition rates of up 2 orders of magnitude using a single gRNA and up to three orders of magnitude when using Cidofovir in combination or a vector expressing four gRNAs. The results demonstrate the promising potential of CRISPR/CasRx and CRISPR/Cas9, alone or in combination with RNAi or concurrent medication against adenovirus infection and their application as means of antiviral defense in general.



Florian Moeller

16.06.2023

ECOPHYSIOLOGY OF THE SYMBIONT MICROBIOME IN THE SPONGE IANTHELLA BASTA

Supervisor: **Michael Wagner**

Sponge-microbe holobionts, being the oldest extant examples of microbial-metazoan symbiosis, are among the most complex and diverse holobionts in the marine environment with over 8000 globally distributed sponge species. Their microbial symbionts can constitute up to 35% of total sponge biomass. Microbiome communities within sponges are species-specific and stably associated across various prokaryotic taxonomic levels. Sponges, through their filter feeding capabilities, mediate critical biogeochemical processes, which have been attributed to the actions of their microbial symbionts.

The use of next-generation sequencing technologies and state-of-the-art techniques has provided a glut of sponge microbiome data, enabling the identification of specific microbial symbiont(s) and likely genes and metabolic pathways active in mediating crucial biogeochemical functions and potential symbiotic or environmental interactions. However, examples of clear-cut functional assignments to specific symbionts have been rather rare due to the length of potential symbiotic activities and the difficulty in cultivating dominant sponge holobiont members and experimentally manipulating sponge holobionts in targeted, meaningful ways.

This dissertation aims to investigate the ecophysiology of the dominant sponge microbiome residing in the marine sponge Ianthella basta through a combination of metaproteogenomics, fluorescence in situ hybridization, qPCR, and hypothesis-driven laboratory incubations coupled with isotope-based functional assays. The study demonstrates that sponges possess a complex and diverse microbial-metazoan symbiosis, with sponges playing a significant role in marine environments.

Zrinka Didara

24.03.2023

STRATEGIES FOR THE KNOCKOUT OF THE KEY ADENOVIRUS GENES DURING INFECTION

Supervisors: **Reinhard Klein** and **Angela Witte**



Since their discovery adenoviruses have been studied firstly for their pathogenic properties. The most studied member of the family, Adenovirus Type C5 (HAdV-C5), causes mostly non-harmful upper respiratory tract infections and majority of population develops immunity by the age of five. Nonetheless, it can cause life threatening systemic infections in immunocompromised and until now, there is no effective therapy used in clinic for treatment of severe adenovirus infections. Hence, in this study we explore gene editing tools as anti-adenoviral therapies in vitro. Accordingly, we employed two different state-of-the-art CRISPR methods to target essential genes of HAdV-C5. In the first part of this thesis, we aimed to inhibit adenoviral replication by using the CRISPR/Cas9 system. The early protein 1A (E1A), primarily responsible for the activation and regulation of the adenoviral replication, was chosen as main target due to its essential role in virulence. In the second part of this thesis, we aimed to target HAdV-C5 on RNA level therefore we tested novel CRISPR RNA interference (CRISPRi) method in which gRNA leads CasRx, a Cas13 type RNA targeting effector to the target. The targets were two main effectors of the adenoviral DNA replication, DNA polymerase (Pol) and pre-terminal protein pTP, or more precisely their mRNAs. Both CRISPR strategies, either targeting RNA or DNA of adenoviral early gene regions, have shown significant inhibition of viral progeny and great potential for anti-adenoviral therapy. In my dissertation, we proposed the application of either method with some adjustments for in vivo use.



Lorenz Schwab

23.03.2023

GEOCHEMICAL BEHAVIOR OF MERCURY IN CONTAMINATED ENVIRONMENTS – APPLICATION OF MERCURY STABLE ISOTOPES FOR SOURCE AND PROCESS TRACING

Supervisors: **Stephan Krämer** and **Jan Georg Wiederhold**

The overarching goal of the PhD project “MIRACOSA” was to achieve a better understanding of the geochemical behavior of mercury concerning risk assessment and remediation of contaminated sites, as well as the transfer of acquired process understanding to non-contaminated natural environmental systems. The focus was on the application of stable mercury isotopes for tracing sources and geochemical transformation processes.

In the first part of the project, mercury transformation processes were investigated at two contaminated field sites in Southwest Germany in collaboration with the Technical University of Braunschweig (TUBS). The results of the field studies provided insights into the applicability of mercury isotope ratios as process tracers in soil and groundwater as well as in river sediments.

In a further step, the applicability of tree rings as an archive for historical mercury emissions into the atmosphere at the selected field sites was examined, and insights into the distribution of mercury within the trees were obtained based on isotope ratios.

In the second part, laboratory experiments were conducted to define the isotopic fractionation of specific processes, focusing on the reduction of divalent mercury to elemental mercury. These fractionation factors form the basis by which processes in environmental systems can be identified and distinguished using isotope ratios.

Patrizia Pfohl

31.01.2023

AGING OF INTENTIONALLY PRODUCED MICROPLASTIC PARTICLES FOR INNOVATIVE APPLICATIONS

Supervisor: **Thilo Hofmann**



Microplastics are ubiquitous in the environment, but their fragmentation and degradation mechanisms are not fully understood, although essential to estimate their fate and impacts. This PhD thesis aimed to fill knowledge gaps regarding degradation and fragmentation processes of microplastics in different environmental compartments with the aid of appropriate laboratory set-ups for experimental reproducibility and environmental relevance. To investigate partially biodegraded microplastics occurring in complex environmental matrices, non-destructive extraction protocols with extensive controls are needed to assure particle and polymer stability, homogeneous sampling and appropriate recovery. We did biodegradation tests in combination with the developed extraction protocol for polyurethane (PU) microplastics to reveal which chemical design is needed to improve biodegradability of PU microplastics in the environment. In addition to that we developed an adapted NanoRelease protocol to investigate dry UV aging of polyamide and PU microplastics, as well as the release of micro- and nanoplastic fragments and water-soluble organics. In both studies, microplastic degradation resulted in fragmentation, but degradation strongly depends on the polymer composition and the environmental stresses. Overall, this thesis strongly underlines the importance of quality control by reference materials used for spiking, extraction efficiency, and systematic comparison against blank controls for microplastic aging, extraction, harmonized data report and analysis.

Incoming 2023

Summer semester 2023



Wajdi Allagui

(Mentor: Wolfgang Wanek)

The Tozeur oases in southern Tunisia, home to 10% of the population, are facing deterioration due to economic disparities. With over 200 oases spread across four governorates, the rehabilitation of these oases is crucial for preserving natural resources and ensuring subsistence for local inhabitants. Tozeur, located in the Sahara, is characterized by palm groves, oases, and Chot El Jerid. The geological and climatic context in southern Tunisia influences geosystem oases, particularly soil salinization and degradation. The study aims to identify pedogenesis factors influencing carbon sequestration in arid desert soils, understand the impact of soil salinity, irrigation, and climate change on soil microbial communities, and examine the effect of organic matter, C and N isotopes, and land use changes on pedogenesis.



Sobia Bibi

(Mentor: Wolfgang Wanek)

Climate change (CC) is one of the most critical issues today because it affects the balance of ecosystems. The negative impacts of climate change include an increase in temperature, intensive storms and floods, land degradation, drought, and food insecurity. Agriculture accounts for more than 25% of total GHG emissions. At the same time, agriculture offers the best solution to combat CC by sequestering carbon in soil. There is more carbon in soil (45%) than in the atmosphere (15%), which indicates that soil has the highest potential for storing carbon. Carbon has several benefits for soil, such as improving soil structure, reducing compaction, and increasing water and nutrient holding capacity, thereby improving soil fertility and productivity. This research will focus on identifying the sources of GHGs by using isotopic and related techniques in order to mitigate their emissions. In addition, carbon will be sequestered in the soil by applying more stable forms of carbon, such as biochar. Therefore, it will be a win-win situation to not only mitigate GHG emissions but also improve soil properties.

Richard Johannes Gruseck



(Mentor: Michael Zumstein)

Biopesticides are promising alternatives to synthetic pesticides – among other reasons also because they are expected to be biodegraded and thus of limited persistence in soils and other receiving environments. However, the current knowledge on the biodegradation and biotransformation of biopesticides is sparse. Therefore, I study the kinetics and pathways of the biotransformation of selected promising biopesticides by soil enzymes – with a focus on linking chemical structure to biodegradability.

Barira Shoukat Hafiza



(Mentor: Wolfgang Wanek)

Nitrous oxide (N_2O) stands out among greenhouse gases, surpassing carbon dioxide (CO_2) by 310 times and methane (CH_4) by 16 times in terms of global warming potential over a 100-year period. Its predominant source is application of nitrogenous fertilizers to agricultural soils. Despite its environmental significance, conventional methods for understanding the intricate relationships within gross nitrogen (N) transformation processes are limited in their analytical depth.

Current research increasingly focuses on the $N_2O/(N_2O+N_2)$ product ratio, offering valuable insights into the efficiency of N transformations and the potential for N2O and N2 emissions. Quantification of both gases, however, poses challenges that require specialized techniques. Leveraging isotopic methods, particularly the introduction of enriched ammonium (NH_{4+}) and nitrate (NO_{3-}), and monitoring 15N labelled denitrification products, proves instrumental in unravelling N_2O sources and facilitating emission mitigation strategies.

This study aims to contribute to the existing knowledge by employing a ^{15}N tracer to measure N_2O and N_2 and identify their sources. Integration with N tracing models provided crucial insights into the intricate connections between substrates and N transformation products. This approach sheds light on the impacts of synthetic fertilizer application, enabling the quantification of transformation rates and offering valuable information for sustainable agricultural practices.



Tao Li

(Mentor: Wolfgang Wanek)

Soil microbes assimilate plant carbon inputs for growth and release carbon as extracellular products (soil enzymes and extracellular polymeric substances, EPS) and respiratory CO2. However, after soil microbes die and undergo subsequent lysis and fragmentation, organic cellular compounds, EPS, and cell walls persist, contributing to the pool of microbial necromass. The balance between the formation and decomposition of microbial necromass significantly influences its contribution to the soil organic matter cycle. Therefore, investigating microbial necromass dynamics is crucial for understanding carbon sequestration and microbial community changes.

My project focuses on the effects of long-term warming on the turnover process of soil microbial necromass using double-labelled (13C and 15N) isotope tracing. I will analyze amino sugars and amino acids in soil samples after acidic hydrolysis, then separate them by C18-reversed phase chromatography followed by high-resolution orbitrap mass spectrometry. The latter, with its unique mass resolution, allows the distinction between 13C- and 15N-labelled isotopologues of amino sugars and amino acids, enabling me to determine the concurrent processes of microbial necromass formation and recycling.



Christian Ranits

(Supervisor: Andreas Richter)

In my PhD project I investigate an ecosystem of which we know little about: tropical deep soils. Tropical soils often run tens of metres deep and harbour considerable amounts of carbon in deeper soil layers. Yet, there is little information on deep soil microbial communities as a whole and no information on the actively growing parts of this community. This is, however, an important prerequisite in predicting consequences of anthropogenic changes such as land-use or climate change on biogeochemical cycling in deeper soil layers. Hence, the main goal of my PhD project is to characterize the active microbial community in tropical soils. Furthermore, I am interested in the effects of land-use change on microbial activity and the underlying reason for deep soil carbon persistence.

Daniela Schwarz



(Supervisor: Anouk Willemsen)

Giant viruses are ubiquitous in most ecosystems, particularly in aquatic environments, where their abundance and diversity can profoundly impact ecological processes. These unusual viruses form a diverse group within the phylum Nucleocytoviricota. They infect mainly unicellular eukaryotes and markedly differ from other viruses in both particle and genome size with some representatives reaching over 2 µm and up to 2.5 Mb. Giant virus genomes are highly complex and contain numerous genes that have been previously considered hallmarks of cellular life, including genes associated with translation (e.g. tRNAs, aminoacyl t-RNA synthetases, translation factors). While tRNAs in phages are not unusual, the high numbers of tRNA genes found in some giant viruses, and especially in Tupanviruses are presently unparalleled. This suggests selective pressure on these genes and an important function for Tupanvirus tRNAs, potentially in host adaptation, codon compensation, or the evasion of host defense mechanisms.

My research revolves around ecological interactions of giant viruses of the Mimiviridae and Marseilleviridae families. Within my first project, I will investigate giant virus-virus interactions by studying co-infections in a range of amoeba hosts and conditions. My second project focuses on our mechanistic understanding of giant virus-host interactions. Here, I want to elucidate the role of viral tRNAs by studying Tupanvirus translation dynamics and the abundance and modifications of viral tRNAs throughout the infection in different amoeba hosts. Novel insights into interactions of giant viruses will facilitate a better understanding of the role that these viruses play in natural environments and the factors that govern the distribution of viral populations. In turn, predictions about viral population dynamics are relevant to microbial community compositions and carbon flux in ecosystems.



Jan-Philipp Wittlinger

(Supervisor: David Berry)

The chronic skin disease atopic dermatitis (AD) has various pathophysiological characteristics. Besides inflammatory skin lesions and chronic pruritus, which is a major symptom that is often resistant to standard therapeutic medication, the altered skin microbiome of AD patients plays an important role in disease development and severity. Coagulase-positive Staphylococcus aureus is detectable in 70% of AD patients where it accounts for 65% in relative abundance while a healthy microbiome consists of less than 2%, if present at all. Due to its pathogenic properties, S. aureus is an important bacterium to study in context with atopic dermatitis and pruritus. Therefore, the goal of the project is to not only isolate and identify microorganisms, including S. aureus, from patients with AD and characterize secreted metabolites that might be directly involved in pruritus-generating mechanisms, but also commensal microorganisms which will be isolated and whose metabolites will be tested for antipruritic effects.



Soraya Marie Zwahlen

(Supervisor: Flora Vincent and Jillian Petersen)

Diatoms are single-celled photosynthetic eukaryotes that form the basis of the marine food web and are responsible for 20% of global primary production. Similar to land plants, diatom survival and growth is dependent on tight interactions with bacteria. Those interactions are faced with a plethora of anthropogenic marine pollutants whose impact on diatom-bacteria interactions remains completely unexplored. It is further unclear whether the diatom microbiome (bacteria consistently associated with diatoms) conveys a specific advantage or disadvantage to diatoms when faced with pollutant stress. The goal of my PhD project is to understand how diatom-associated bacteria may mediate diatom resilience under pollutant stress, combining lab-based and field-based experiments.In the lab, I will explore how the microbiome of Chaetoceros diatoms affects its resilience when faced with 250 commonly occurring marine pollutants, and study the mechanistic underpinnings of specific pollutant-diatom-microbe interactions in which the presence of the microbiome affects diatom resilience. In the field, I will and investigate the diversity of the Chaetoceros microbiome across the Euroepan coast, and how it is affected by marine pollutants in the natural environment. Overall, my project will further our understanding of the impact of human activity on the survival and growth of critical marine phytoplankton.

Incoming 2023

Winter semester 2023/24

Anita J Brijit



(Supervisor: Stephan Krämer)

The interaction of nucleic acids (NAs), particularly DNA, with mineral surfaces allows for their preservation for millions of years, providing insights into human evolution and migration history. Although the exact mechanism of this preservation is elusive, the discovery of the adsorption and long-term preservation of NAs on mineral surfaces could provide new insights into the origin of life and human history. Metal ions and organic matter (OM) are often present on environmental mineral surfaces, impacting the adsorption and protection of NAs. Common mineral surfaces in sediments and soils include iron oxides (goethite) and clay minerals (imogolite). Bone, a major source of ancient DNA, is also a major source of ancient DNA. This doctoral thesis aims to understand the role of metal ions and OM in the adsorption and protection of NAs against enzymatic degradation on selected mineral surfaces.

Anna-Celine Danklmaier



(Supervisor: David Berry)

The project aims to study gut bacteria's ability to colonize niches in premature infants. Growth assays will be conducted to determine growth rates under different conditions, similar to infant gut physiology. Whole genome sequencing will be performed on all bacterial isolates to characterize genomic and metabolic attributes. Deterministic factors of community assembly, such as niche preference and construction, will be resolved. A bioreactor system will simulate a multispecies neonatal gut microbiome, establishing minimal microbial communities and monitoring metabolic interactions. The effect of antibiotic and probiotic administration will also be investigated. The focus will be on Klebsiella pneumoniae, determining its elimination conditions.



Yuhua Li

(Supervisor: Wolfgang Wanek)

Research shows that global warming alters soil microbial communities, but little is known about the trade-offs between these activities and their impact on soil biogeochemistry. The Achenkirch warming experiment aims to study the metabolism and environmental effects on the core microbiome's metabolome/interactome in control and warmed soils. The study will focus on dominant and active microorganisms under both conditions. A high-throughput methodology will be developed to measure growth, respiration, and extracellular enzyme activity in pure cultures of various bacterial isolates. This will help understand the causes of changes in biogeochemical processes under global warming and predict potential effects on mountain forest soils under long-term warming conditions.



Marie Rutsch

(Supervisor: Michael Wagner)

The main aim of the project is to construct the host-symbiont dynamics in marine sponges at a single cell level. Overall, this project will help to understand the spatial distribution of microbial symbionts in relation to host cell types and chemical gradients and how host intrinsic factors shape the microbial community. A multifaceted view of the complex sponge-microbe interplay will be accomplished by three research objectives combining 'state-of-the-art' omic approaches and single-cell analyses of the Mediterranean Adria sponge species and the tropical sponge Ianthella basta. Firstly, the Adria sponges will be target of a metagenomic-based approach to identify and correlate host-intrinsic factors that modulate the microbial composition and metabolic potential within the holobiont. Secondly, the sponge-microbial landscape will be visualized on a single-cell level to link individual symbionts with specific microenvironments provided by the sponge host (i.e., different cell types ad tissue areas). Lastly, the role of brominated secondary metabolites will be investigated within the sponge holobiont and how their production shapes the relationship between sponge host and microbial symbionts within the of the two sponge species Ianthella basta and Aplysina aerophoba.

Laura Sánchez Lara



(Supervisor: Anouk Willemsen)

This doctoral project aims to deepen our understanding of the intricate arms race mechanisms between hosts and viruses. It focuses on giant viruses, large DNA viruses that infect unicellular eukaryotes and possess complex genomes with many orphan genes, challenging traditional views of viruses as small entities dependent on hosts. The project's first sub-project aims to explore how mobile genetic elements (MGEs) impact giant viruses' fitness and adaptation. CRISPR-Cas technology will be used to modify viral genomes and assess MGE effects on community dynamics. The second sub-project investigates extracellular vesicles (EVs) in virus-host interactions. It examines how giant viruses may exploit EVs produced by hosts, affecting viral transmission and infectivity, and employs diverse methodologies, including fluorescence labeling, electron microscopy, and EV analysis. These investigations aim to uncover the complex interplay between giant viruses, hosts, MGEs, and EVs, contributing to evolutionary biology, ecology, and virology.

VDSMES Offers

Activities

- Creating a VDS-MES promo video
- Diversity Symposium
- Doctoral Insights Symposium
- Joint Docschool Winter Party

Outreach

- European Researchers Night in Graz
- Life Science Career Fair (ÖGMBT)

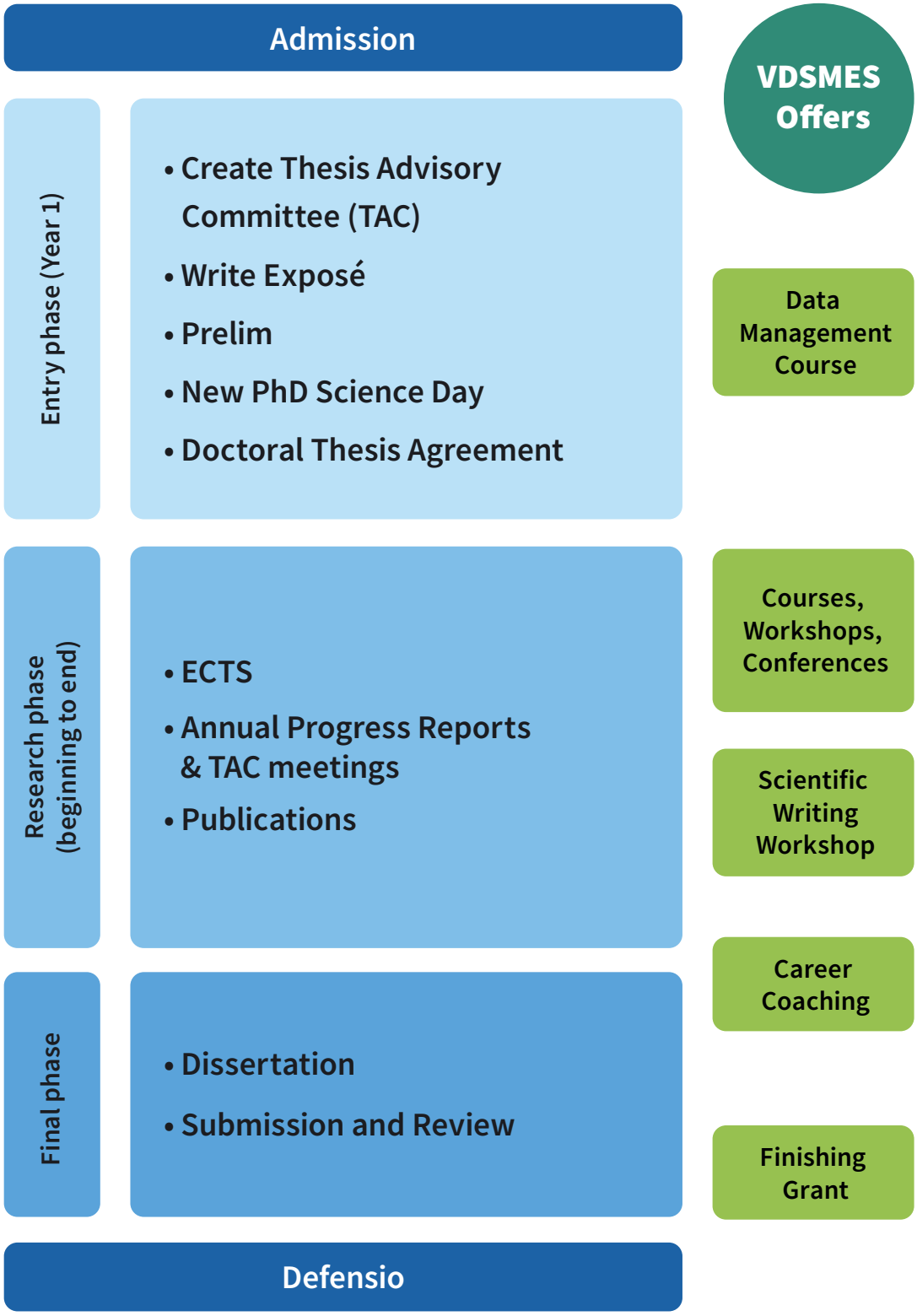
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- Alumni network

PhD Timeline





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Doctoral School in Microbiology and Environmental Science