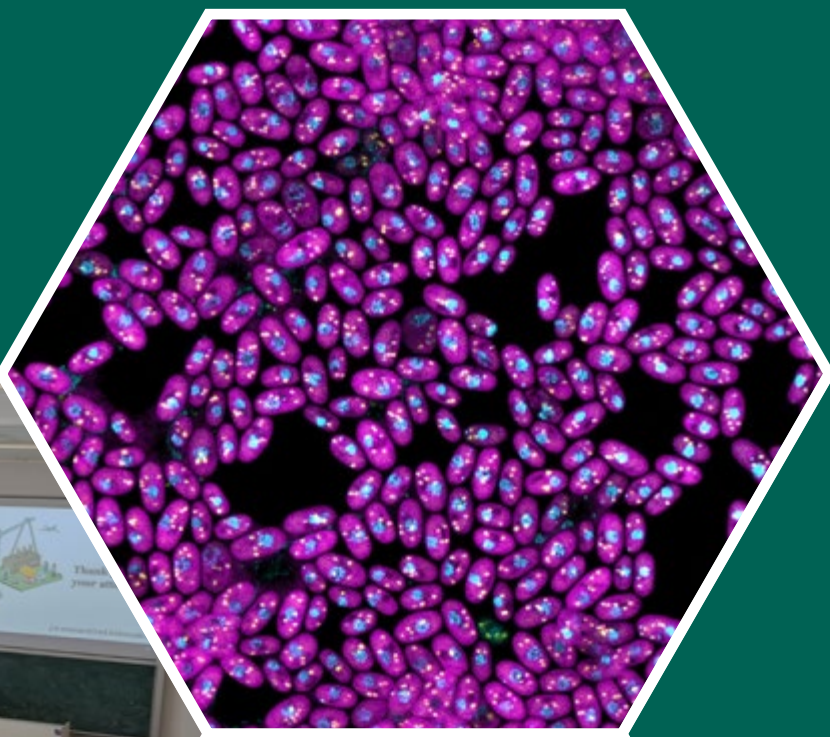
Centre for Microbiology and Environmental Systems Science
UNIVERSITY OF VIENNA

VDS-MES

Annual Report 2025







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Imprint

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Preface

You are reading the fourth 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 and highlight the graduates who finished the school in 2025.

Since its foundation in 2020, the mission of our school is the advancement of education and research in microbiology and environmental science. This mission requires excellent training of our students. Most of this training takes place in our research groups under the supervision of one or more of our PhD supervisors. From the yearly surveys among students and supervisors we could learn that the quality of supervision is constantly increasing. Periodic and frequent personal meetings, good supervision practices and careful preparation of meetings by students and supervisors seem to be most important for an efficient project-specific training. Based on excellent feedback from previous supervision trainings, we plan to offer further trainings for supervisors in 2026. In 2025, the University of Vienna has released the "Key Principles of Good Doctoral Supervision", to which Dagmar Woebken, PI from our school, has contributed. Thanks, Dagmar!

The research-focused training and supervision of our students is flanked by our "Thesis Advisory Committees" (TACs). Each student selects a TAC and meets at least once per year with the TAC members. The Thesis Advisory Committees have supported our students since the foundation of our school. In 2025, we released a digital platform that simplifies sharing and distribution of documents for TAC meetings. We expect that using this "DS Project Monitor" platform will improve the quality of TAC meetings. Sharing the Annual Reports of the students with TAC members before the meeting will allow the TAC members to better prepare for a meeting and to use the meeting time more specifically for relevant topics. Sharing the TAC meeting reports via the "DS Project Monitor" makes them a helpful element of the project-specific training, beyond a formal University document that needs to be submitted .

Our school could only be that successful in 2025 because it was broadly supported by the organizational units, by the students and by our faculty. We all enjoy an open culture of discussion, contribution and criticism – I hope we will keep this spirit also for the future. We thank Katharina Klaushofer very much for coordinating our school again in the end of 2024, when Nadja Holzleitner was on a partial maternity leave. It was a great pleasure, Kathi, to work with you! We wish you all the best for own PhD project, which is about to start. Special thanks to all who have supported the school in 2025 by taking 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 an interesting and successful 2026 and look forward to another fruitful year for our school. Please enjoy reading this annual report!

Thomas Rattei
Head of the VDS-MES

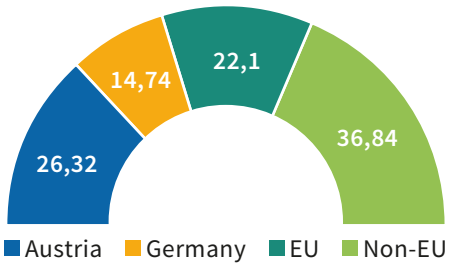
Facts and Figures

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 %

(Winter semester 2025/26)



Faculty-Student ratio

Winter semester 2025



1:2,8

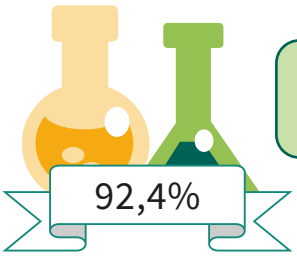
Sex ratio

59%
female students

39%
female faculty

Financed students

2025



72% internal
14% external/industry
6,4% scholarship

Fields of study

2025

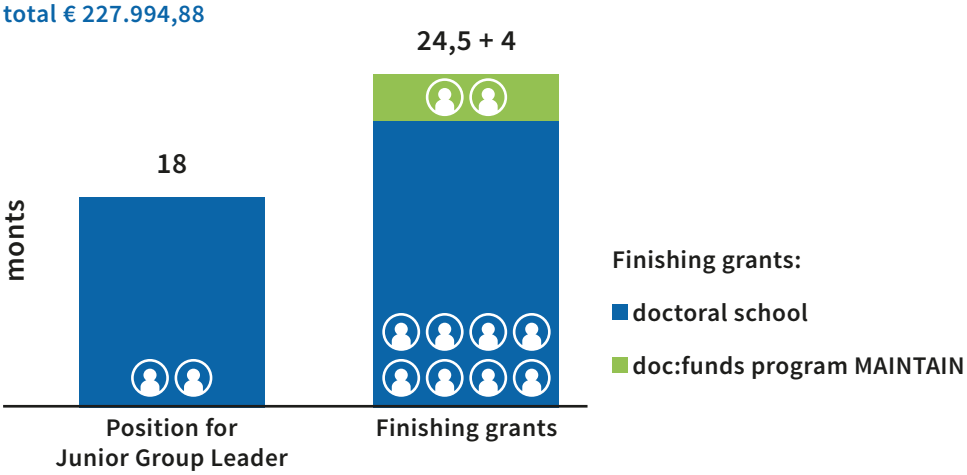


Biology
Environmental Sciences
Molecular Biology

Budget and Services

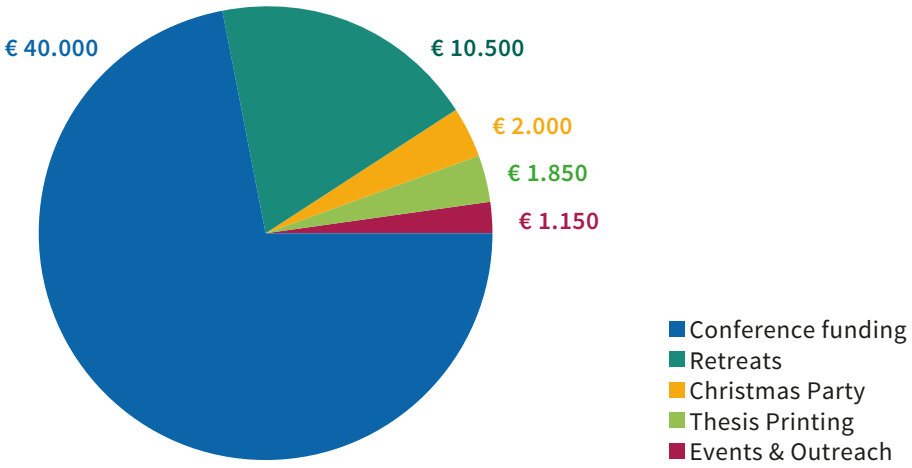
PhD contracts

total € 227.994,88



Other services

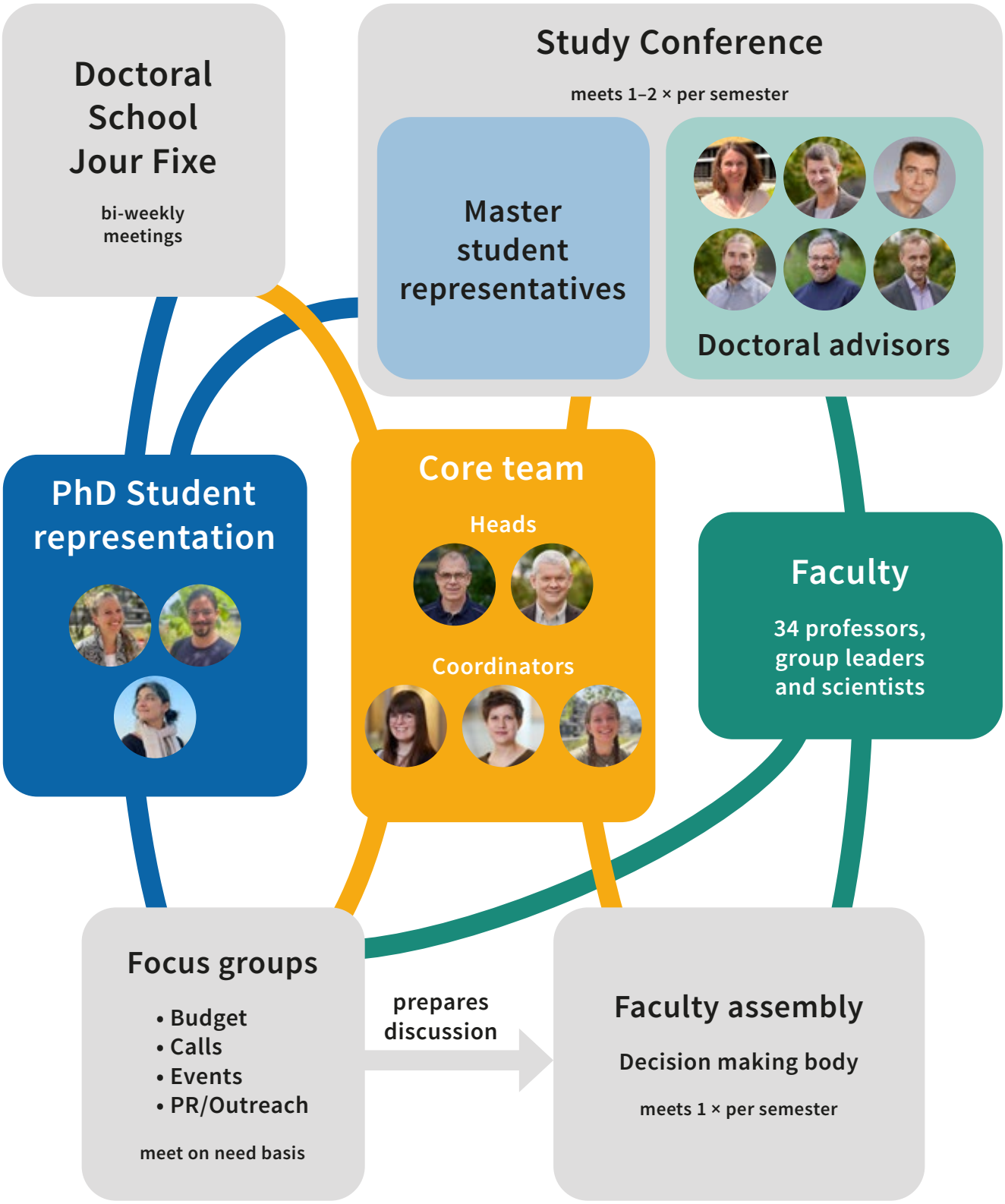
total € 55.500



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vds-mes.univie.ac.at

Team and Structure



CORE TEAM

The doctoral school is led by **Thomas Rattei** and **Stephan Krämer** as head and vice-head, respectively. **Nadja Holzleitner**, **Franziska Bauchinger** and **Katharina Klaushofer** serve as coordinators of the school.

PHD STUDENT REPRESENTATIVES

Our school's elected student representatives **Clara Priemer**, **Philipp Spiegel**, and **Laura Sánchez** 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 ÖH (Students' Union) representatives. 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 – **Christina Kaiser** and **Wolfgang Wanek**
Molecular Biology – B**oris Görke** and **David Berry**
Environmental Sciences and Geosciences – **Andreas Richter** and **Thilo Hofmann**

ÖH representatives – **Jakob Habitzl** and **Hayk Palabikyan**

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 finalize discussion points that have been prepared within the focus groups.



Philipp Ausserhofer

09.01.2025

Supervisors: **Reinhard Klein, Angela Witte**

Adenoviruses pose a significant risk for immunocompromised patients, while they simultaneously bear huge potential as therapeutic agents with an ever-increasing number of potential applications. This study investigated the interaction dynamics of adenoviruses with the human RNA interference (RNAi) system, aiming at generating data to support development of therapeutic solutions. In that context, this work already documents the development of bespoke, anti-adenoviral microRNAs to impair pathogenic adenoviruses' life cycle and steps taken to improve their performance by co-delivering RNAi effector proteins.

Anya Sherman

22.01.2025

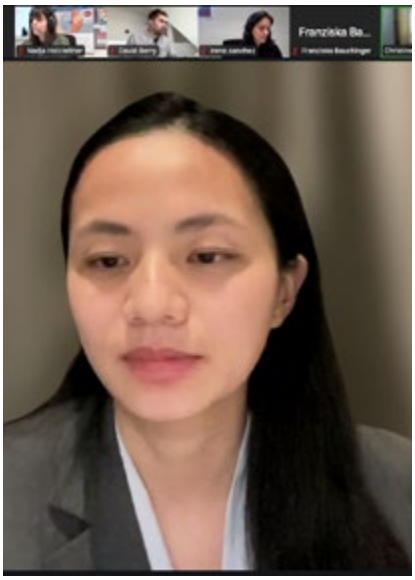
Supervisors: **Thilo Hofmann, Thorsten Hüffer**



Tire wear particles and associated rubber-derived compounds are a contaminant class of rapidly emerging concern due to their environmental ubiquity and demonstrated ecological toxicity. This PhD thesis focused on two routes of human exposure to rubber-derived compounds: food and air.

We first showed that five rubber-derived compounds could be taken up by lettuce plants in a hydroponic system and translocated to edible leaves, where compounds were metabolized, forming novel transformation products. We then showed that tire-derived compounds could also be taken up by lettuce grown in soil, although the formation of non-extractable residues in soil reduced the bio-accessibility of some compounds, especially in soil with a high clay content. Finally, we analyzed commercial leafy vegetables, and found low concentrations of rubber-derived compounds in 71% of samples, indicating that dietary exposure contributes to overall rubber-derived compound intake.

Although most rubber-derived compound research has focused on tires, rock climbing shoes are also made of specialized rubber, and generate particles due to friction with climbing holds in indoor facilities. We measured elevated concentrations of rubber-derived compounds in climbing shoes, and in air samples from indoor climbing facilities.



Huimin Ye

31.01.2025

Supervisors: **Alexander Loy**

My research explores the diversity and role of sulfite-reducing bacteria (SRB) in the mammalian gut, particularly in mice and common marmosets. While Desulfovibrio species and Bilophila wadsworthia are well-studied in the human gut, SRB in other mammals remain poorly understood. Using next-generation sequencing, microbial isolation, genome characterization, and functional analyses, I aimed to bridge this knowledge gap. I identified and characterized Taurinivorans muris, a novel taurine-respiring bacterium from the mouse gut, revealing its unique desulfonation pathway and potential protective effects against pathogens. In captive common marmosets, I assessed SRB diversity using 16S rRNA and dsrB gene sequencing, identifying an uncultured bacterium (dsrB OTU1) as the predominant SRB. Furthermore, I investigated microbiota variance in marmosets under controlled conditions, showing that beta diversity was influenced by age, gender, dominance status, and personality traits but not relatedness. These findings provide new insights into SRB diversity, their metabolic capabilities, and their potential roles in host health.

Peter Peneder

18.02.2025

Supervisors: **Thomas Rattei, Eleni Marina Tomazou**



My research focuses on developing machine learning models for analyzing complex multimodal biomedical datasets, particularly in cancer detection and single-cell biology. I have designed computational approaches to improve non-invasive tumor detection using cell-free DNA (cfDNA) analysis and to enhance data interpretation in single-cell transcriptomics.

For liquid biopsy-based cancer detection, I developed integrative machine learning methods that leverage epigenetic features rather than relying solely on mutations. I created LIQUORICE, a tool that quantifies sequencing coverage changes in open chromatin regions, and DEFT, a deep learning model that integrates cfDNA fragmentation and DNA methylation data. These approaches improve tumor detection sensitivity, especially for cancers with low mutational burden.

In single-cell transcriptomics, I co-developed CellWhisperer, a deep learning model that connects transcriptomics data with natural language annotations. Using contrastive learning, it enables intuitive visualization and chat-based interactions for exploring single-cell RNA-seq data.

Through my PhD research, I demonstrate the power of multimodal machine learning for advancing cancer diagnostics and deepening our understanding of cellular biology at the single-cell level.



Julia Hildegard Wiesenbauer

24.02.2025

Supervisors: **Christina Kaiser**

This doctoral thesis investigates the fine-scale spatiotemporal dynamics of microbial activity in response to simulated root exudation, exploring how different compositions of root exudates influence microbial processes and soil organic matter dynamics across different soil types. Employing a novel ‘reverse’ microdialysis technique, the study simulated root exudation, enabling the analysis of the resulting microbial metabolism and its impact on soil chemistry. Key findings demonstrate that organic acids significantly drive microbial respiration and nutrient cycling, markedly affecting soil chemistry and suggesting a nuanced influence of exudate composition on rhizosphere dynamics. Advanced imaging techniques, including confocal microscopy and nanoscale secondary ion mass spectrometry, provide a detailed visualization of microbial interactions and substrate assimilation at the microscale level. Collectively, the research highlights the complexity of microbial responses to root exudates, advancing our understanding of their pivotal roles in biogeochemical cycles and nutrient availability in soil ecosystems.

Cristina Alcaraz

27.02.2025

Supervisors: **Jillian Petersen**

Project description: Investigating host-microbe interactions in marine lucinid clams.



Symbiotic relationships with microorganisms play a crucial role in shaping host ecology, evolution, and health. While these interactions are often complex, lucinid clams offer an ideal system for studying these interactions due to their highly specific symbiosis with sulfur-oxidizing bacteria. Research has traditionally focused on the gills of lucinids as the primary symbiont-housing organ, but this study challenges that assumption. Using molecular techniques, microscopy, immunohistochemistry, and metaproteomics, I examined the distribution of symbionts and symbiont-derived proteins throughout the host body. My results revealed a much broader presence than previously recognized, with symbiont-associated proteins involved in nutrient exchange, detoxification, immune modulation, and stress resistance across the holobiont. These findings suggest that symbioses, including those in medically significant systems like the human gut, may have far-reaching, organism-wide effects. Understanding these dynamics provides valuable insights into host resilience and microbial contributions to adaptation in changing environments.



Eva Simon

28.03.2025

Supervisors: **Christina Kaiser**

My PhD thesis investigates the spatial organization of microbial communities in soil at the millimeter scale by analyzing individual soil aggregates and model substrate particles. The results show that soil aggregates exhibited greater variability in microbial composition compared to homogenized bulk soil samples and that their community structure was closely linked to sampling location and organic matter content. Observation scale impacted research findings and aggregates systematically differed from bulk soil in terms of microbial diversity and organic matter properties. In experiments with model organic particles, temporal changes of particle-associated communities were substrate-specific, with chitin particles showing more pronounced temporal changes than cellulose particles. Overall, this work highlights that microbial communities in soil are spatially structured and strongly influenced by organic matter characteristics and environmental conditions.

Kerrin Steensen

26.05.2025

Supervisors: **Martin Polz**



The exchange of mobile genetic elements (MGEs) drives bacterial evolution, yet despite ongoing discoveries, their full diversity and impact on bacterial hosts remain largely unknown. This dissertation explores the diversity and evolution of MGEs in a model system consisting of Vibrio bacteria sampled from a coastal ocean environment. Chapter I investigates the diversity and distribution of prophages in the collection using de novo prophage predictions, which are unaffected by database biases. These analyses reveal a predominance of tailless and filamentous prophages, in contrast to the dominance of tailed phages in current databases. Chapter II expands the scope beyond prophages, uncovering a large number and diversity of MGEs from a single environment, underscoring their key role in bacterial evolution.



Linnea Kop

27.06.2025

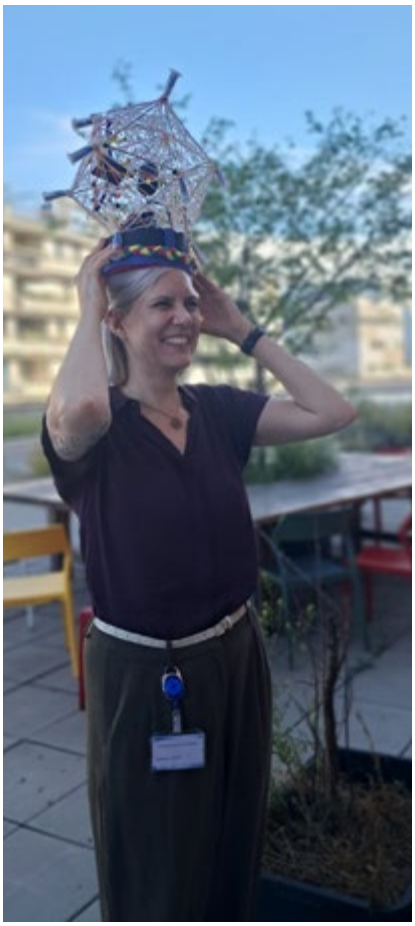
Supervisors: **Holger Daims, Mike Jetten**

Nitrification, the microbial oxidation of ammonia to nitrite and nitrate, is an important process in the nitrogen cycle with implications for greenhouse gas emissions, biotechnological applications and nitrogen availability, especially in marine oxygen deficient zones (OMZs). This thesis focused on investigating the habitat distribution, phylogeny and metabolic potential of NOB using genomic and metagenomic methods. New Ca. Nitromaritima species were discovered in marine OMZs, and novel unclassified NXR-like genes were identified. The work revealed a broad habitat range and unexpected metabolic diversity within the phylum Nitrospinota and the order Nitrospirales, suggesting broader ecological roles beyond nitrite oxidation. A study on biofilms on subsea concrete surfaces showed high nitrifier diversity, spatial variation, and possible cooperation with iron oxidizers.

Franziska Bauchinger

30.06.2025

Supervisors: **David Berry**



The human gut microbiome is a complex and dynamic microbial community crucial for various aspects of human health, including immune development and pathogen resistance, and is shaped by host-specific factors like diet and genetics. I explored this complex ecosystem using various data analysis techniques and focused on microbial community composition, function and structure in two research projects. In one project I investigated the concept of microbial keystone taxa. I found that their detection is highly sensitive to taxonomic resolution and that they act as stabilizing agents in sub-communities of the gut microbiome. In my second project I studied mucosal glycan degraders. I discovered that, even though many species have the genes to break down mucus, few species prevalently transcribe these genes. Analyzing associations between mucosal glycan degraders furthermore indicates that both competitive and opportunistic degraders co-exist in a given community.



Sarah Zauner

30.07.2025

Supervisors: **Matthias Horn, Jillian Petersen**

Intracellular chemosymbiosis between the gamma-proteobacterial symbiont Ca. Thiodiazotropha and lucinid bivalves drives sulfur cycling in seagrass sediments, yet the broader ecological networks linking hosts, their microbes, and higher trophic levels remain underexplored. In the intertidal seagrass meadows of Banc d'Arguin, Mauritania, the lucinid Loripes orbiculatus acquires its Ca. Thiodiazotropha symbionts horizontally - gelatinous egg masses and newly hatched juveniles lack these bacteria, which later colonize gill epithelial cells. Adults also harbor a novel intracellular Shewanella sp., with metaproteomics revealing high abundances of GroEL, GroES, and DnaK - hallmarks of host association. Detection of Shewanella DNA in fecal samples from molluscivorous shorebirds (Calidris canutus canutus) suggests migratory birds may vector these microbes across seagrass beds. By integrating reproductive strategy, microbial community dynamics, and unexpected trophic dispersal, this thesis reframes symbiont transmission and uncovers the complex biotic interactions structuring coastal holobionts.

Julia Krasenbrink

04.09.2025

Supervisors: **Alexander Loy**



The thesis investigated the role of sulfoquinovose (SQ) in the gut of humans, mice, and cows. In vivo and in vitro studies demonstrated that SQ is not degraded by human or mouse cells, but is a substrate exclusively to the gut microbiota, with distinct metabolic outcomes in humans and mice. To assess SQ degrader diversity across ecosystems, an amplicon sequencing approach targeting the sulfoquinovosidase gene yihQ was developed and applied. These analyses revealed very high diversity of SQ degraders in the cow rumen, highlighting the ecological relevance of SQ in ruminant microbial fermentation.



Calin Rares Lucaciu

14.10.2025

Supervisors: **Thomas Rattei**

This study addresses the challenges of analyzing complex plant genomes and transcriptomes, particularly in non-model species such as the red and white Euphorbia pulcherrima. It includes the development of a de novo transcriptome assembly from RNA-seq data, differential gene expression and homology analyses, and the creation of a standardized workflow for plant microbiome studies. The work also investigates microbial contamination in plant genome assemblies, proposing a rapid ORF-based method for detecting bacterial sequences.

Veer Vikram Singh

06.11.2025

Supervisors: **Stephan Krämer**

Despite being a fragile molecule, DNA can persist in the environment for thousands to millions of years, providing a unique window into ancient ecosystems and evolutionary processes. This thesis investigates how adsorption to mineral surfaces—such as clays, iron oxides, and biominerals—contribute to DNA preservation by protecting it from environmental degradation. Experiments reveal that the polymer length of DNA strongly affects both its adsorption and stability: shorter DNA fragments are more readily adsorbed on mineral surfaces and better protected from enzymatic hydrolysis. These findings help explain why ancient DNA is often recovered as short fragments (<100 base pairs) and highlight the role of minerals as long-term protectors and potential carriers of genetic material in nature. Overall, this work deepens our understanding of DNA adsorption and preservation, with implications for elemental cycling, microbial evolution, and the recovery of ancient genomes from environmental samples.





Hamid Rasoulimehrabani

21.11.2025

Supervisors: **David Berry**

This PhD project investigated how three prebiotics, xylooligosaccharides (XOS), lactulose and arabinogalactan, selectively shape the human gut microbiota. Using ex vivo fecal incubations, 16S rRNA gene sequencing and single cell approaches such as BONCAT FACS and Raman activated cell sorting, it identified which bacteria are functionally active on each substrate. The work highlights Bifidobacterium as a consistent key responder and shows that primary degraders such as Bifidobacterium longum support other beneficial taxa through metabolic cross feeding. These findings provide a mechanistic basis for designing targeted prebiotic interventions to improve gut and overall host health.

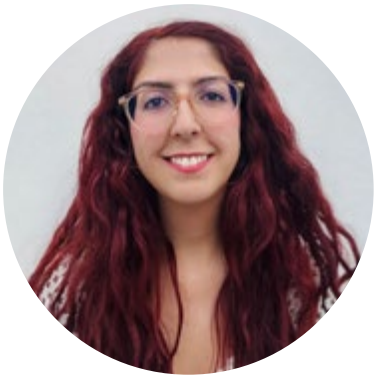
Incoming PhD students 2025



Araújo André

(Dagmar Woebken, DOME)

Biological activity in desert ecosystems is limited by water availability. I'm investigating how non-rainfall water sources, such as dew and fog, support the survival of biocrust microorganisms, enabling them to withstand the harsh conditions of drylands and sustain biogeochemical cycles.



Brites Ana

(David Berry, DOME)

I study the interactions between foodborne Alternaria mycotoxins and the human gut microbiota. My research looks at how these common fungal toxins affect the structure and function of gut microbial communities. I work with both individual toxins and realistic mixtures that reflect dietary exposure, with a particular focus on their antimicrobial mechanisms.

Dinis Gaehtgens Thomas

(Shaul Pollak, DOME)



My research investigates how microbial communities shape genomic variation and gene content across ecosystems. To address this, I develop computational methods for analysing microbial genome and metagenomic data, resolving strain-level diversity, and inferring the gene content of focal taxa conditional on community composition using statistical learning.

Elgin Resul Gökberk

(EMBL)



Patients can respond to drug therapies very differently. Some are treated efficiently while others suffer from side effects even when they are prescribed the same drug. We are interested in understanding the role of gut microbiome in these processes.



Felsberger Manuela

(Barbara Bayer, DOME)

I am fascinated by the hidden microbial drivers of ecosystem functioning and biogeochemical processes. My research focuses on the microbial pathways underlying oxic methane production in aquatic ecosystems and the environmental factors regulating methane cycling.



Folla Panagiota

(Matthias Horn, DOME)

"I have chlamydiae" is not a sentence many say with pride—but occasionally, I do. Chlamydiae inhabit a wide range of eukaryotic hosts, but lineages other than the known human pathogen are vastly underrepresented in research. My work explores diverse protists that host chlamydiae, hoping to uncover the metabolic capacities of the symbiont and the ecological impact of this relationship.

Giger Johanna

(Dagmar Woebken, DOME)

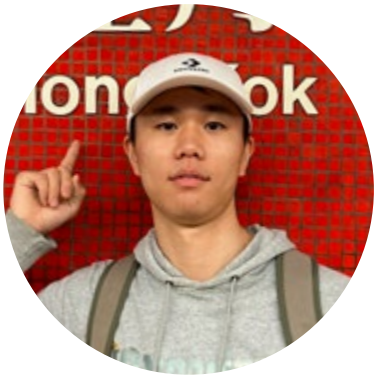
In my PhD project, I study the stress response of environmental bacteria to low oxygen, focusing on the regulation of low- and high-affinity terminal oxidases in Acidobacteriota and other ecologically relevant strains.



Guan Guoqing

(Alexander Loy, DOME)

Sulfur cycling in soil is complex and underexplored. My PhD focuses on investigating sulfoquinovose degradation and sulfur–iron coupling, aiming to provide new insights into microbial processes shaping soil sulfur dynamics.





Haque Faiz

(Sarah Pati, EDGE)

Originally from Karachi, Pakistan, and raised in Wigan, UK, I moved to Vienna for my doctoral studies investigating the sources and photochemical transformation pathways of organic sulphonates in aquatic systems.
My research focuses on developing LC-HRMS methods to quantify trace sulphonates and identify transformation products, combined with controlled sunlight experiments to determine reaction kinetics and mechanisms of direct and indirect photochemical processes.



Jezequel Gwen

(Thilo Hofmann, EDGE)

Originally from Brittany, France, I hold a Master's degree in Human and Environmental Toxicology. My research focuses on investigating the toxicological effects of tire additives on human health. Using various in vitro models, I aim to better understand the impact of these compounds within the human body and to characterize their potential adverse effects. A central objective of my work is to bridge analytical chemistry and bioassays by linking the physicochemical properties of these additives to their biological responses. This work will contribute to improving our understanding of emerging environmental contaminants and their impact on human health.

Kader Siraz



(Michael Zumstein, EDGE)

My research interests revolve around understanding the impact microorganisms have in mediating environmental processes. As a trained microbiologist and ecotoxicologist, I aim to bridge environmental microbiology with chemical risk assessment to support the sustainable use of chemicals in every-day applications. While the importance of wastewater microbiomes in the biological removal of contaminants is well recognized, the key microbial players responsible for the biodegradation of, for example, water-soluble polymers remain to be elucidated.

Kosier Andrea



(Katharina Kitzinger, DOME)

I'm looking into the nitrogen cycle in oceanic oxygen minimum zones (OMZs) with a focus on the physiology of nitrite oxidizing bacteria (NOB). Although nitrite oxidation has been considered an aerobic process, NOB are consistently found to be active even under (near-) anoxic conditions. My research explores the mechanisms that may allow them to survive and remain active under these conditions, including chlorite-supported nitrite oxidation and NXR equilibrium isotope effect.



Li Chen

(Thilo Hofmann, EDGE)

I study the interactions between per- and polyfluoroalkyl substances (PFAS) and iron-based materials in aquatic systems. My research investigates how these persistent contaminants are removed through adsorption and reductive processes, and how material properties influence their reactivity.



Mikes Anika

(Michael Zumstein, EDGE)

Water-soluble polymers (WSPs) are widely used in consumer products, including home and personal care formulations. After use, they can enter aquatic systems, primarily via wastewater treatment plant effluents. While the annual global production of WSPs is exceeding one million tonnes, sustainable end-of-life management of WSPs is a major challenge.

In my PhD project, I investigate how WSPs are biodegraded by freshwater microbial communities and how they are transported through wastewater treatments, aiming to better understand the key processes that govern their environmental fate.

O’Connor Madeline



(Michael Zumstein, EDGE)

Madeline O’Connor is a PhD student in EDGE. Her research, supervised by Michael Zumstein, focuses on the characterization of wastewater and freshwater extracellular enzymes linked to the biodegradation of selected water-soluble polymers.

Peter Anne



(Andreas Richter, TER)

My doctoral project focuses on the functional and taxonomic adaptation of soil microbial communities to long-term warming in a subarctic forest ecosystem. Drawing on a unique geothermal gradient near Takhini Hot Springs (Yukon, Canada), the research investigates how soil microbiomes change in their metabolic potential and community composition after over 100 years of warming.



Planat Laurine

(EMBL)

I am curious about the impact of marine heat waves on phytoplankton and their interactions. In particular, I am interested in the response of the microbiome associated with diatoms, across different scales from the lab to the natural environment. I am currently working in the lab of Flora Vincent at EMBL.



Schnaufer Franziska

(David Berry, DOME)

The human gut microbiota is a diverse microbial community that strongly influences human health through the production of metabolites such as short-chain fatty acids (SCFAs). My research explores how interactions between microbial species determine these metabolic outputs. Using experimental data together with computational and machine-learning approaches, we aim to understand and ultimately engineer microbial communities that enhance beneficial metabolite production.

Taft Thayer



(Christina Kaiser, TER)

Life as a soil microbe is never boring – there are drastic environmental changes like rain and drought, freezing and heat waves, rhizodeposition and starvation. I'm investigating how microbial communities respond to these perturbations, and how these responses shape soil function.

Tiis Elena



(Sarah Pati, EDGE)

Elena Tiis joined EDGE as a PhD candidate in January 2025. In the frame of the Cluster of Excellence "Microbiomes Drive Planetary Health" and with the supervision of Sarah Pati, she will study the degradation of emerging pollutants by oxygenase enzymes and the relevance of reactive oxygen species formation during such transformation processes.

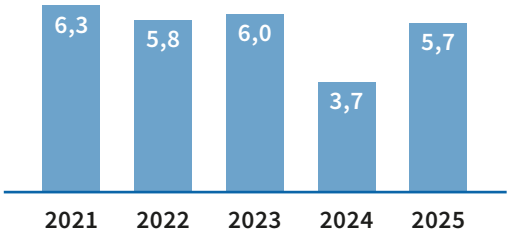
Elena received her MSc in Ecotoxicology and Environmental Management from University of Applied Sciences Technikum Vienna in 2024. Her Master thesis project was supported by the Austrian Marshall Plan Foundation and included a research stay at the University of North Carolina at Chapel Hill, USA, during which she was engaged in developing a method for quantifying cortisol residues in wastewater samples.

VDS-MES in 2025

Basic Data

- 95 active students, of which 21 started in 2025
  - 93 regular, 2 visiting students
- 122 supervisors and TAC members

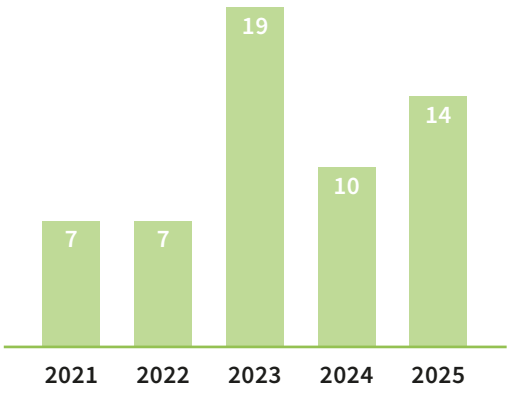
Time-to-degree in years



Events and Outreach

- Three VDS-MES student retreats
  - First year: project, time and self-management, introduction to the school
  - Second year: presentation and communication skills
  - Third year+: finishing the PhD, career planning in and outside of academia
- Three New PhD Science Days
- Connecting DocSchools: Winter Party with VDSEE & CoBeNe
- Life Sciences Career Fair 2025

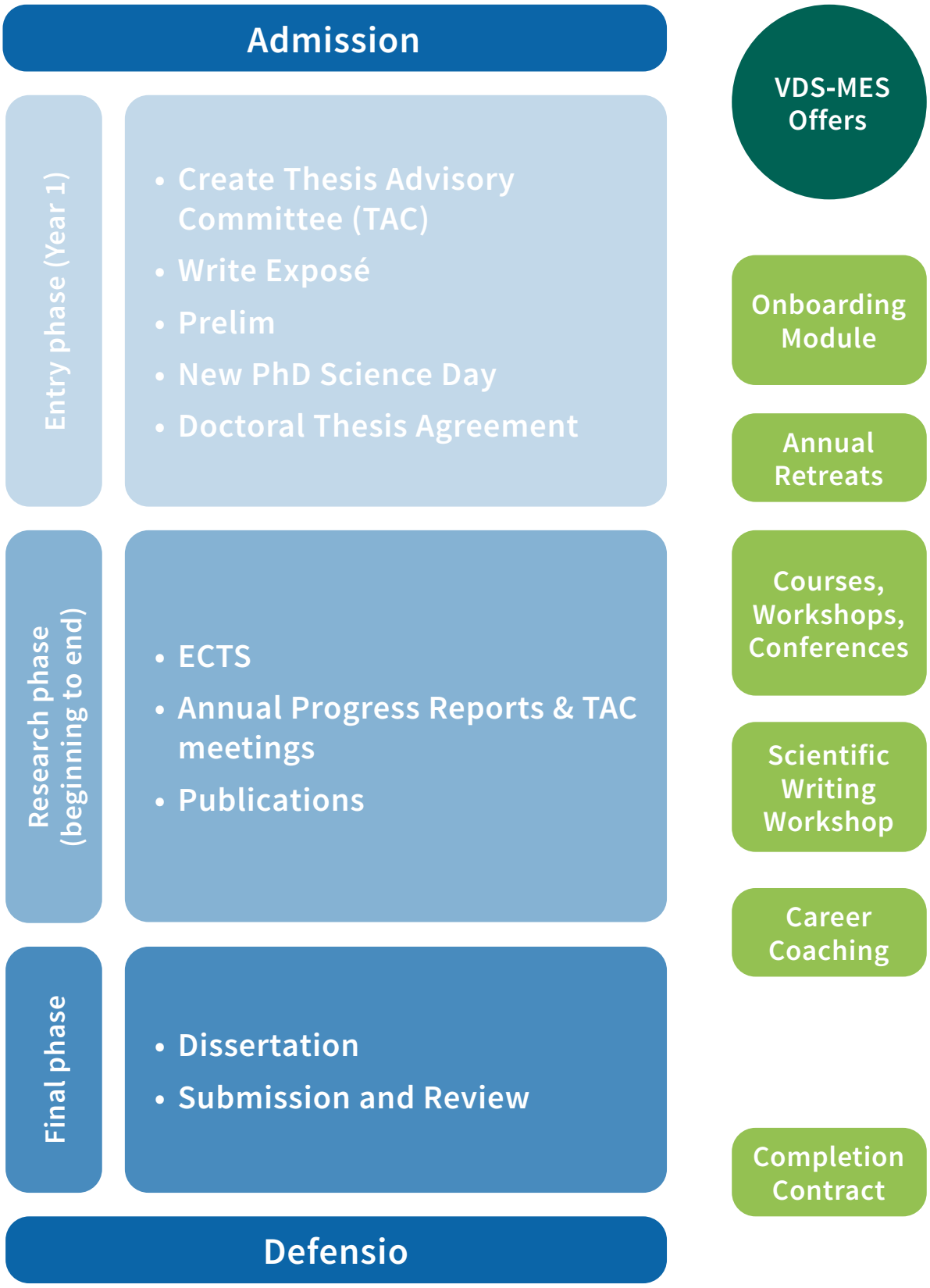
Graduations per year



Student benefits

- 10 completion contracts (3-4 months of employment)
- €40.000 to support travel to conferences and field trips

PhD Timeline





universität wien

Doctoral School in Microbiology and Environmental Science