Centre for Microbiology and Environmental Systems Science

UNIVERSITY OF VIENNA

VDS-MES

Annual Report 2024







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Imprint

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Preface

You are reading the third 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 2024 and highlight the graduates who left the school during that year.

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 PhD candidates. The supervisors contribute most to this training. The annual surveys among our students and supervisors demonstrated that PhD supervision works very well in our school and has even improved during the last years. The University of Vienna and our school support our PhD supervisors, e.g. by specific supervisor training workshops. Beyond the supervisors, the Thesis Advisory Committees (TAC) and the doctoral school engage in the training of our PhD students. In 2024, we have established a new “onboarding” curriculum for all students. Three modules introduce the PhD studies in our school and the writing of the expose, the design of experiments, and the management of research data. All three modules should be taken during the first year of the PhD, to prepare for the presentation of the PhD project on a New PhD Science Day. Also in 2024, our school has organised the first PhD student retreat. As the feedback was very positive, we plan to continue and extend the PhD student retreats in 2025.

In 2024, our school had the shortest time-to-degree in the University of Vienna. Although only a number, this measure is based on many successful PhD projects. The short time-to-degree has helped our students in starting a promising career in academia, industry or other sectors. Nevertheless, our school also will work on ambitious goals for 2025. We will extend the PhD student retreats to three per year, one for each main phase of PhD studies. We will improve our Alumni network, will develop new training opportunities and will invite our members to new social activities.

Our school could only be that successful in 2024 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. We thank Katharina Klaushofer very much for coordinating our school most of the year 2024, when Nadja Holzleitner was on maternity leave. It was a great pleasure, Kathi, to work with you! We wish you all the best for your next project, which will be a scientific one. Special thanks go also to all who have supported the school in 2024 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 2025 and look forward to another fruitful year for our school. Please enjoy reading this annual report!

Thomas Rattei
Head of the VDS-MES

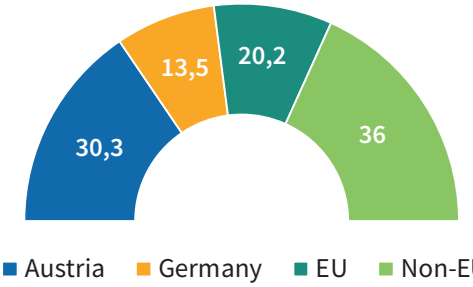
Facts and Figures

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 term 2024)



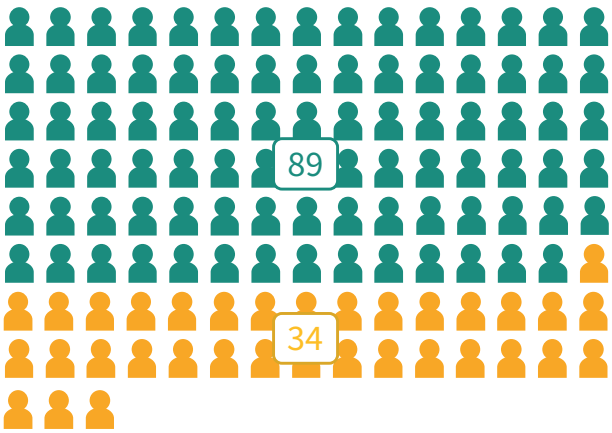
Sex ratio

60%
female students

38%
female faculty

Faculty-Student ratio

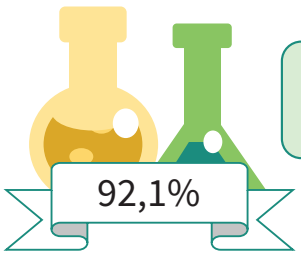
(Winter term 2024)



1:2,5

Financed students

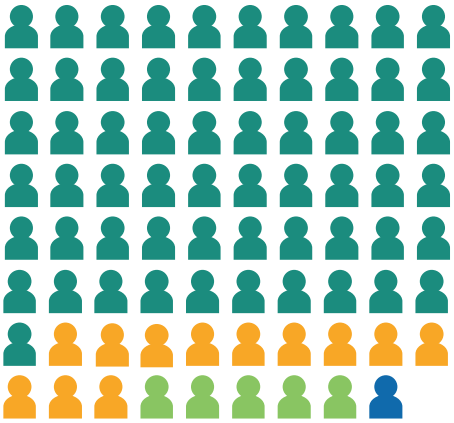
(Winter term 2024)



70,8% internal
14,6% external/industry
6,7% scholarship

Fields of study

(Winter term 2024)

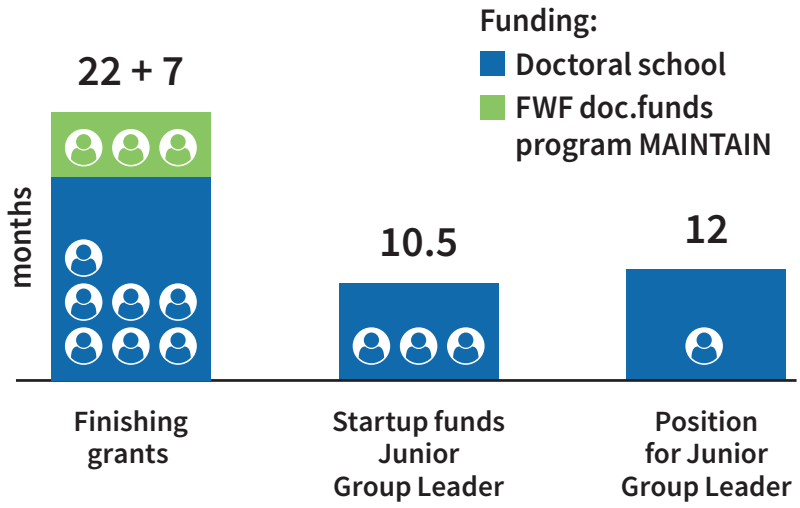


Biology
Molecular Biology
Environmental Science
Geosciences

Budget and Services

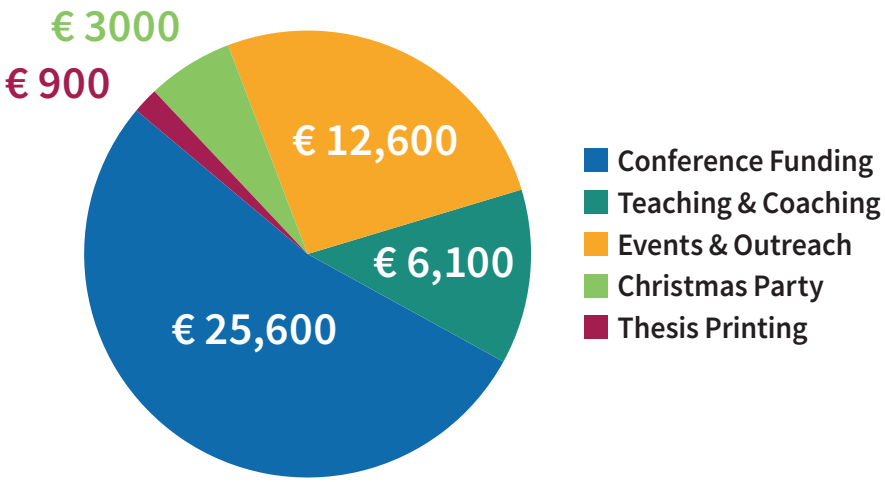
PhD contracts

€ 223.300



Other services

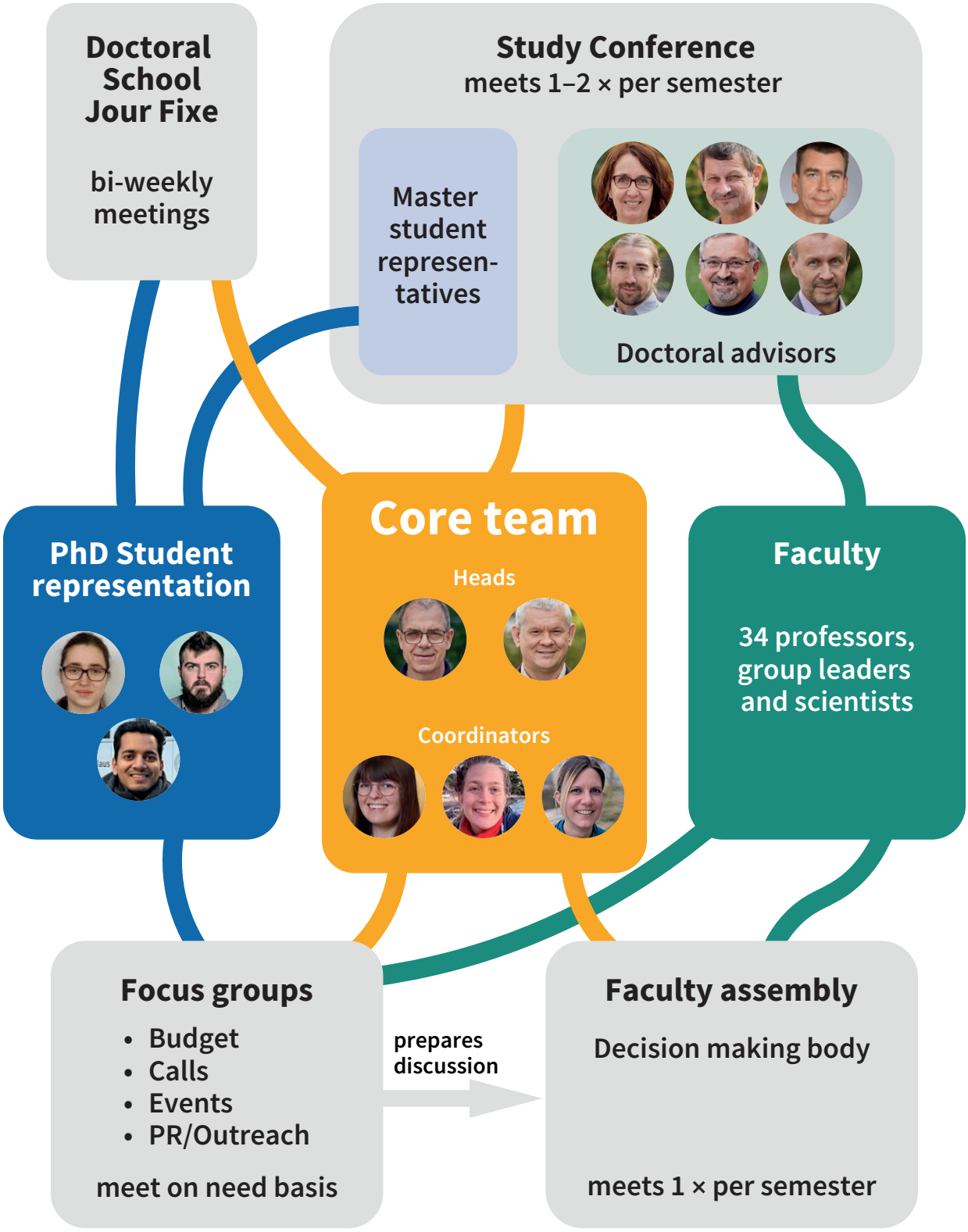
€ 48.200



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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** and **Franziska Bauchinger** serve as coordinators of the school. During Nadja's maternity leave, **Katharina Klaushofer** supported the school as coordinator.

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 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 – **Boris 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.



Marta Sudo

15.02.2024

HOST-MICROBE-ENVIRONMENT INTERACTIONS IN SULPHUR-OXIDISING SYMBIOSES

Supervisor: **Jill Petersen**

My PhD projects focus on studying the interactions between hosts and microbes in sulphur-oxidizing symbioses. I investigated the environmental factors that shape the ecology, physiology, and evolution of both hosts and symbionts. To achieve this, I used a diverse range of methods including in silico, experimental, and analytical techniques. I have focused on the most diverse family of symbiotic bivalves, the Lucinidae clams, and studied components of symbiotic systems of increasing complexity as units of ecological and evolutionary influence. These include symbiont sulphur metabolism, bipartite holobionts, and complex holobionts comprising animal hosts, symbiotic bacteria, and accessory microbiomes.

My thesis uncovered that sulphur-oxidizing symbioses employ a variety of ecological strategies, including specialist symbioses that are highly adapted to their symbiotic lifestyle, and generalist symbioses with more independent partners. In addition, my research introduced a new area of study in lucinid symbioses, which focused on accessory microbiome and organosulphur transformations.

Erika Kristel Salas Hernandez

13.03.2024

IDENTIFICATION AND QUANTIFICATION OF SOIL NECROMASS BIOMARKERS

Supervisors: **Christina Kaiser** and **Wolfgang Wanek**



Microbial necromass is a key contributor to soil organic matter (SOM, >50%) and biomarkers, particularly amino sugars (AS), are commonly used to trace microbial necromass C contributions to SOM. Most studies use these AS to trace fungal and bacterial C; however, the knowledge of other potential necromass biomarkers such as neutral sugars (NS) and amino acids (AA), as well as the contribution of other microbial groups such as archaea is still lacking. In this PhD thesis, I identified and quantified necromass biomarkers in archaeal, bacterial, fungal and plant species. I developed and used derivatization protocols, ultra-high performance liquid chromatography (UHPLC) and Orbitrap mass spectrometry to identify and quantify AS, NS and AA necromass biomarkers in these taxonomic groups. Results showed that AS were the best discriminant biomarkers to separate all taxa. I identified new specific biomarkers: talosaminuronic acid (TalA) for Euryarchaeota, hydroxyproline for plants, and L,L-diaminopimelic acid for bacteria. By combining AS, NS and AA biomarkers

we were able to extend the biomarker approach from separating bacterial and fungal necromass to separate microbes from plants. This PhD thesis expanded the repertoire of necromass biomarkers by including new specific biomarkers as well as combining AS, NS and AA biomarkers found in a wide variety of taxa.



Rouven Metz

26.03.2024

BIOGEOCHEMICAL MECHANISMS INFLUENCING THE BIOAVAILABILITY OF P AND FE FROM VIVIANITE

Supervisors: **Stephan Krämer** and **Walter Schenkeveld**

The global P cycle is caught between resource limitations and simultaneous surplus and pollution problems, requiring the development of a circular P economy. The natural mineral vivianite (Fe3(PO4)2*8H2O) may contribute by acting as a P sink in eutrophic waters and as a recyclable P source when recovered from wastewater treatment plants and used as a P fertiliser. Therefore, the (bio-)availability of P from vivianite with regard to dissolution mechanisms and kinetics was determined under environmentally relevant conditions.

Fast, proton promoted, defect driven dissolution rates were determined for vivianite dissolution under anoxic condition, which were controlled by solution saturation. However, the presence of oxygen resulted in rapid oxidation leading to the formation of a passivating Fe(III)-PO4 surface layer, decreasing strongly dissolution kinetics and further oxidation.

Isomorphic substitutions including several toxic metals are commonly observed for vivianite, and a continuous solid solution series between the endmembers of the vivianite group is suggested. However, besides morphological changes, little change in reactivity regarding solubility, dissolution and oxidation kinetics were observed for partially Co(II)- and AsO4-substituted vivianites and the incorporation and release was stoichiometric to the solution or solid phase respectively.

Considering the bioavailability of P from vivianite, the presence of biogenic Fe chelating ligands such as citrate and DFOB, could strongly enhance the solubility and dissolution kinetics of vivianite, even under oxic conditions due to a ligand-promoted dissolution of the oxidised Fe(III)-PO4 passivation layer; therefore increasing the mineral's effectiveness as an "on-demand" P fertiliser under environmental conditions.

Within the PhD project, we could show that vivianite represents a dynamic P source and sink due to its high redox reactivity.

Xiaofei Liu

21.06.2024

LONG-TERM SOIL WARMING EFFECTS ON ROOT TISSUE AND ROOT EXUDATE METABOLIC PROFILES AND MICROBIAL NECROMASS CARBON IN A TEMPERATE MOUNTAIN FOREST

Supervisor: **Wolfgang Wanek**



Climate warming significantly challenges temperate forests, impacting tree root metabolism and altering the release of primary metabolites in root exudates, essential for plant growth and rhizosphere interactions and highly sensitive to temperature variations. This warming may also affect the fate of microbial necromass carbon, but the resulting implications are not yet understood. We explored the effects of long-term soil warming on the metabolome of fine root tissues and root exudates in an old spruce forest. Additionally, we examined the dynamics of microbial necromass carbon in 0-10 cm and 10-20 cm soil layers.

Soil warming led to an increase in the concentration of amino acids (15%) and sugars (21%) in root tissue metabolites, but not organic acids. This suggests that trees under warming conditions sustain enhanced growth, respiration, and nutrient uptake without down-regulation of primary metabolism. Regarding root exudates, we observed seasonal variations, but no significant response to long-term soil warming. Root exudates profiles could be partly predicted by soil and root parameters, indicating a complex interaction between root tissue metabolism and environmental factors.

We found that soil warming resulted in a notable decrease in microbial necromass carbon. This reduction is primarily attributed to a decline in microbial biomass carbon and microbial carbon use efficiency, exacerbated by limited soil phosphorus availability. Additionally, warming increased the activity of specific soil extracellular enzymes, accelerating microbial necromass carbon decomposition. These results indicate a decoupling of microbial necromass carbon formation and decomposition under climate warming, potentially impacting soil organic carbon content in temperate forests.



Michael Predl

30.07.2024

PREDICTION OF CROSS-FEEDING INTERACTIONS IN MICROBIAL COMMUNITIES USING METABOLIC MODELLING

Supervisor: **Thomas Rattei**

This thesis explores the concept of cross-feeding interactions in microbial communities, where one organism produces a metabolite consumed by another. It focuses on leveraging metabolic modelling to predict these interactions and identify metabolites for experimental investigation. Firstly, the secondary metabolite production of Streptomyces venezuelae, particularly its response to ethanol stress, was examined and found to show changes in the production of antibiotics like chloramphenicol. Additionally, the effects of deleting regulatory genes related to ethanol stress were investigated, revealing significant gene expression changes and altered metabolite production.

The thesis additionally focuses on identifying limitations in existing metabolic modelling tools, particularly for generating community metabolic models and visualizing interactions. To address these challenges a Python package, PyCoMo, for community metabolic modelling, and ScyNet, a Cytoscape app for visualizing complex metabolic networks, were developed. These tools were applied to study gut archaea-bacteria co-cultures, predicting several cross-feeding interactions. Overall, the work demonstrates the potential of metabolic modelling in understanding and predicting cross-feeding interactions, with applications in microbial community engineering and experimental research.

Roko Šango

🎓 06.09.2024

COMPUTATIONAL METABOLIC MODELLING AND MULTI-OMICS ANALYSIS OF BONE-MARROW DERIVED AND TISSUE-RESIDENT MACROPHAGES

Supervisors: **Thomas Rattei** and **Thomas Weichhart**



Immunometabolism, the interaction between immunology and metabolism, influences immune cell behaviour in both health and disease. My thesis focuses on understanding the metabolic alterations in different macrophage populations using omics technologies and genome-scale metabolic models (GEMs). The research investigates how macrophages, crucial for immune responses, exhibit metabolic diversity depending on their origin (monocyte-derived or tissue-resident). I use transcriptomics and metabolomics data to constrain GEMs and predict metabolic fluxes in these macrophages.

First, I focus on the effects of gene deletions in bone marrow-derived macrophages, discovering a novel role for the Cyp27a1 gene in nucleotide metabolism. Second, I investigate the metabolic differences among tissue-resident macrophages (TRMs), analysing gene expression and enriched pathways. I identify both known and novel metabolic functions specific to TRM populations. This thesis presents a computational framework to explore macrophage metabolism and lays the groundwork for future studies on TRM metabolic functions, including secondary pathways, sex differences, and gene markers.



Lovro Trgovec-Greif

03.09.2024

VIRUS BIOINFORMATICS AND PHAGE-BACTERIA INTERACTIONS

Supervisors: **Thomas Rattei** and **Shawna McCallin**

The thesis is oriented towards developing viral bioinformatics and is divided into two distinct parts.

In the first part a new resource for viral genomics is introduced – VOGDB. VOGDB is a database where viral proteins from RefSeq are grouped into homologous groups of increasing evolutionary distance. First, challenges for detecting orthologs and homologs in viruses are discussed followed by the presentation of methodology for the creation of VOGDB. The results of the clustering are presented, and cluster quality metrics are compared with clusters from other databases grouping homologous proteins. Second, application of VOGDB in two scenarios is demonstrated. In the first scenario I analyse dental calculus of museum samples of great apes where I show it is possible to detect traces of past viral infections using automated pipeline based on VOGDB. Another example is an analysis of complex phage cocktails where VOGDB is used to assess their similarity and taxonomic composition.

The second part of the thesis is about understanding interactions between phages and their bacterial host with the aim of improving the phage selection procedure for phage therapy. The focus is placed on anti-phage defence systems. I analyse the defence systems present in a collection of clinically relevant E. coli strains isolated from human urine and compare the results with a published study on a bigger set of genomes. Later, I analyse interactions between bacterial strains and a collection of phages determined by spot tests and search for the defence systems that prevent individual phages from lysing certain strains.

Verónica Barrajón Santos

13.12.2024

IN THE TREE FARM OF *AZTECA* ANTS

Supervisors: **Dagmar Wöbken** and **Veronika Mayer**



Ants are found in nearly every terrestrial ecosystem, thriving through their eusocial organization and ability to adapt and shape their environment. Tropical arboreal ants, especially those in obligate plant associations, demonstrate this adaptive capacity through mutualistic relationships where they protect plants in exchange for nutrients and nesting spaces. These ants accumulate organic waste in dark-colored piles, known as "patches," which host a diverse community of bacteria, fungi, and nematodes. Although patch-making is crucial for ant colony survival, the significance of these patches within the ant-plant mutualism is not well understood. This thesis investigates the Azteca-Cecropia association, one of the most widespread ant-plant mutualisms in the tropics. Using metabarcoding analysis, this study reveals that fungal diversity in patches increases as ant colonies grow, while nematode diversity remains stable. The plant provides the environment for patches, but the ants are the primary drivers of community dynamics. The study also examines microbial activity, showing that patch communities can degrade polysaccharides like cellulose and chitin, with bacterial communities playing a key role. This research highlights how Azteca ants create a compost-like system, converting organic waste into more accessible nutrients. This thesis advances our understanding of the ecological functions of ant-made patches.



Stefan Gorka

19.12.2024

FROM PHOSPHOLIPIDS TO NEUTRAL LIPIDS: CHARACTERISING SOIL MICROBIAL COMMUNITIES AND THEIR FUNCTIONS

Supervisor: **Christina Kaiser**

Soil microbial communities are essential for ecosystem functioning but face frequent environmental perturbations that can cause lasting changes in their composition and activity. This thesis explores how such perturbations affect microbial resilience and nutrient dynamics, revealing persistent shifts rather than rapid recovery. It also expands on the analysis of microbial lipids, providing a deeper understanding of microbial community structure and functions. Additionally, bacterial neutral lipids are identified as indicators of carbon storage, offering new insights into microbial contributions to soil carbon dynamics. These findings enhance our understanding of soil microbial responses and improve tools for studying their ecological roles.



Giorgia Cantini

(Supervisor: Mark Anthony)

In my PhD, I will investigate the interactions between bacteria and ectomycorrhizal fungi and their impact on tree growth and resilience to climate change. Ectomycorrhizal fungi form symbiotic associations with tree roots, enhancing nutrient uptake and shaping microbial communities. However, the role of bacteria associated with these fungi remains poorly understood, particularly under realistic environmental conditions.

I will examine these interactions using a multi-scale experimental approach. First, I will use microfluidic systems to study how bacterial communities influence fungal growth and metabolism in an environment that simulates soil complexity. Then, I will conduct laboratory mesocosm experiments to assess the effects of bacterial inoculation on tree growth and drought resistance. Finally, I will leverage an already established multi-factor climate change field experiment in Switzerland to study soil bacterial community composition and diversity and explore how bacterial-ectomycorrhizal interactions respond to warming and drought. This research aims to establish a comprehensive framework for understanding how bacterial communities influence ectomycorrhizal fungi and, in turn, forest ecosystem function in a changing climate.



Edo Danilyan

(Supervisor: Martin Polz)

Microbial metabolism and growth underpin global biogeochemical cycles, yet the relationship between bacterial cell mass and metabolic rate remains poorly understood. My research focuses on modulating microbial mass in chemostats to probe the interplay of single-cell mass distribution and metabolism, specifically testing whether Kleiber's law (metabolic rate $\propto$ mass$^{3}/^{4}$) applies to bacteria. By systematically controlling bacterial growth rates in steady-state chemostat conditions, I investigate how cell mass scales with dilution rates and whether metabolic rate follows predictable allometric relationships. Using flow cytometry, microscopy, SMR, and metabolic assays, I further explore how nutrient limitations and predation influence these scaling laws. By integrating experiments across different bacterial species, this work aims to uncover fundamental principles governing microbial growth, resource allocation, and metabolic efficiency.

Maximilian Eiser



(Supervisor: Michael Zumstein)

The release of pharmaceutical compounds into the environment has been recognised as a global problem adversely affecting ecosystem functioning and human health. Microbiomes, which are present in all pharmaceutical-affected environments – from the human gut to wastewater and freshwater systems – harbour a highly diverse metabolic repertoire that has the potential to contribute to both the removal and the detoxification of many anthropogenic compounds. However, to fully leverage this metabolic potential, a detailed understanding of these processes and especially the enzymes catalysing them is necessary.

I am investigating how microbiomes and their enzymes contribute to the biotransformation of pharmaceuticals using high-resolution mass spectrometry based environmental bioanalytics. By studying the kinetics and pathways of these reactions and characterising the responsible enzymes, my work contributes to improving our understanding of the structural determinants and the underlying enzymatic basis of these biotransformations. Thereby, I aim to provide an avenue towards designing pharmaceuticals that are stable in-vivo, but quickly degradable in the environment.

Nir Shmuel Even



(Supervisor: Martin Polz)

Prophages – integrated viral elements within bacterial genomes – may play a crucial role in shaping the gut microbiome. However, the extent to which prophages and lytic bacteriophages contribute to microbial dynamics and host interactions remains unclear, particularly in the context of inflammation. My PhD research aims to explore the potential activity of prophages within gut-associated bacteria, investigate their possible effects on bacterial-host interactions, and examine how inflammation could influence phage activity and microbiome composition.



Florian Exler

(Supervisor: Stephan Krämer, Ron Pinhasi)

Ancient DNA (aDNA) extracted from sediments (sedaDNA) provides valuable genetic insights into past environments and biodiversity. However, its recovery is often challenged by modern DNA contamination and inhibitory substances that co-extract with the target DNA, reducing data quality and limiting analytical potential. This project explores separation techniques to fractionate sediment components prior to DNA extraction. By selectively isolating aDNA-enriched fractions, this method aims to minimize contamination and inhibitory effects, thereby improving the efficiency and reliability of sedaDNA analyses. Additionally, as the exact origin and preservation mechanisms of aDNA within sediments remain poorly understood, complementary analytical approaches are employed to investigate the distribution of aDNA within different sediment components. This integrated approach contributes to refining sedaDNA methodologies and broadening our understanding of aDNA preservation in archaeological and paleoenvironmental contexts. Furthermore, the method has the potential to be applied to other sample types facing similar challenges, expanding its relevance beyond sediments.



Rebecca Gallo

(Supervisor: Isabella Wagner)

The gut microbiota plays a crucial role in shaping brain and behaviour by producing metabolites, such as the neurotransmitter gamma-aminobutyric acid (GABA). GABA is the most abundant inhibitory neurotransmitter in the mammalian central nervous system, affecting cognition, mood, and mental health, but whether and how gut microbially-produced GABA directly influences brain and behaviour is still unclear. The project aims at answering whether gut microbial GABA production is causative in shaping the GABA-related brain processes that give rise to neural plasticity and hippocampus-dependent cognition. The murine gut microbiota will be manipulated, and the effects will be studied with behavioral assays and immunostaining of brain tissue. This work will thoroughly assess the role of microbially-produced GABA in hippocampal memory and its potential for ameliorating or preventing the progression of neurodegenerative disease.

Joana Luisa Góis Valério



(Supervisor: Shaul Pollak)

Community assembly and ecological invasion are fundamental processes, yet their genetics and eco-evolutionary constraints remain poorly understood. This project investigates genetic determinants of bacterial invasion into root-associated microbiomes using Variovorax, synthetic rhizosphere microbial communities (SynComs), and Arabidopsis thaliana. We focus on three questions: (1) how single-gene disruptions influence Variovorax invasion into SynComs, (2) how invasion changes SynCom composition, and (3) how A. thaliana genetic variation modulates outcomes. We'll generate transposon mutant libraries in Variovorax to profile fitness effects during invasion, complemented by targeted gene deletions and gain-of-function assays. High-throughput experiments will involve competition assays of Variovorax mutants across diverse SynComs to assess gene-gene and gene-environment interactions. Finally, we'll examine invasion of phylogenetically diverse Variovorax isolates into SynComs on genetically distinct A. thaliana hosts, probing potential co-evolutionary dynamics. These projects will integrate insights at host, bacterial community, and invader levels, allowing detailed study of ecological and co-evolutionary aspects at high resolution.

Nathalie Heldwein



(Supervisors: Wolfgang Wanek, Katharina Kitzinger)

Nitrous oxide (N_2O) is a potent greenhouse gas and a major ozone depleting agent. The most important source of N_2O are soils, especially fertilised soils. While many studies have measured net N_2O emissions under various agricultural practices, little is known about the underlying processes and microbial populations that shape this response. In this project we want to contribute to the study and understanding of these underlying processes and their response to fertilization. This shall be achieved by (1) developing a method to extract hydroxylamine (NH_2OH), an important intermediate in the nitrogen cycle and direct precursor for abiotic N_2O production, from soils and measure its concentration and turnover via ^{15}N-tracing, (2) studying the effect of denitrifying community composition on N_2O emissions under different NO_3- input levels in a synthetic soil approach and (3) investigating the legacy effect of different long-term fertilization treatments on the N_2O cycling pathways and populations.



Saee Joshi

(Supervisor: Jillian Petersen)

The spread of invasive species is a substantial challenge for ecosystems worldwide. Rapid climate change is not only shifting the habitats and distributions of native plants and animals but also intensifying the effects of invasive species, leading to profound ecological and economic repercussions. This doctoral research examines the relationships between invasive species and their microbiomes. The study will focus on a widely invasive plant *Impatiens glandulifera,* commonly known as Himalayan Balsam. It is a native western Himalayan species that has become invasive in Britain, North America and many parts of Europe, including Austria. *I. glandulifera* is an annual plant which colonises riverbanks and other damp places. It can be very damaging, causing erosion to riverbanks, and forming dense stands that increases likelihood of flooding and reduce or suppress native plants, as well as negatively impacting other biodiversity. While the ecological impacts of invasive species are well documented, research on the broader implications of invasive plants on microbial ecosystems is still emerging. *I. glandulifera* is particularly known for its aggressive growth patterns and production of naphthoquinones. By assessing the diversity and composition of microbial communities associated with *I. glandulifera* and isolating the microorganisms metabolising the allelopathic compounds; this project aims to provide insights about the effect of naphthoquinones on plant associated microbiome and to collect more data on the microbial communities and the correlations within them.

Vitalii Kovtunyk

(Supervisor: Matthias Horn)

The goal of my project is to investigate the impact of giant viruses on complex microbial communities and ecosystem processes within a variety of biotopes. We will develop a better understanding of host-virus interaction by isolating and investigating giant viruses from activated sludge of wastewater treatment plants and freshwater/soda lake communities using a variety of native protist hosts as bait. Major part of the project will be adaptation and development of research methods for description of novel organisms and their genomes, which may benefit wider scientific society working on protists, giant viruses and symbiotic organisms. Finally, the original biotopes will be replicated in the laboratory to allow for controlled investigation of complex interactions between the hosts, their symbionts, and the giant viruses from the microbial communities.

Zeynep Kurt



(Supervisor: Barbara Bayer)

Methane is a greenhouse gas produced biogenically and non-biogenically. Biogenic production accounts for over 70% of global emissions. Aquatic environments are the largest contributors (41-53% yearly). In these ecosystems, methane oxidising bacteria (MOBs) consume methane by oxidising it to carbon dioxide using oxygen, mitigating emissions.

Methane paradox is a phenomenon where methane accumulates at the surface of well-oxygenated water columns, suggesting inhibition of consumption or subsurface production. This research examines how environmental factors (light, oxygen depletion, ammonia) affect methane consumption by aerobic oxidising bacteria in aquatic ecosystems. Understanding methanotrophic communities and their environmental responses is crucial for mitigating atmospheric methane emissions. Exploring these dynamics will improve our understanding of microbial methane consumption in relation to environmental changes in coastal and lake ecosystems.

Margareta Andrea Mayer



(Supervisor: David Berry, Susan Lynch)

Preterm birth (PTB), defined as pregnancy termination before 37 weeks gestation, affects approximately 10% of pregnancies and remains the leading cause of perinatal morbidity and mortality. One challenge in studying PTB is that it's a common symptom of multiple pathologies, complicating identification of associated factors. Microbial dysbiosis and inflammation are more pronounced in women experiencing pregnancy complications. Microbiota-associated immunoglobulins, particularly maternal IgG that crosses the placenta, indicate previous microbial exposures and shape neonatal health. This thesis investigates the relationship between maternal microbial colonisation patterns and pregnancy pathologies resulting in PTB. We will map microbial communities in maternal vaginal swabs and infant meconium while tracking metabolites. Additionally, we'll use maternal and fetal serology to identify microbial antigens targeted by maternal IgG and its transfer to the fetus across clinical groups. This approach will provide insights into how microbial perturbations contribute to PTB etiology, potentially improving diagnostic and therapeutic strategies for maternal-fetal health.



Milena Nenadovic

(Supervisor: Isabella Moll)

Like other molecules, RNA nucleotides can undergo post-transcriptional modifications across various RNA types, including mRNA, tRNA, and rRNA, which are crucial for RNA function, stability, localization, and translation efficiency. While well-studied in eukaryotes, their role in bacterial biology is still relatively unexplored (Roundtree et al., 2017).

The tRNA^{1}Val family contains the cmo5U34 modification, allowing efficient decoding of all four valine codons (Näsvall et al., 2007). Additionally, the tRNA-specific methyltransferase TrmM introduces N^{6}-methyladenosine (m6A) at the A37 residue within the ACA motif of the anticodon loop. This modification has no effect under normal conditions, but benefits bacterial survival during stress (Golovina et al., 2009). In this project, we want to study the functional impact and biological significance of tRNA modification on translation dynamics in Escherichia coli, using m6A as an example of dynamic modification, and determine the environmental conditions upon which it is up- or downregulated.



Jessica Neubauer

(Supervisor: Thomas Böttcher)

Bacteriophages, the most abundant biological entities on Earth, significantly shape microbial community dynamics. A key event is the transition of lysogenic phages into the lytic cycle, triggered by environmental stressors or signalling molecules like pyocyanin, produced by *Pseudomonas aeruginosa.* Pyocyanin has been found to induce prophage activity in *Staphylococcus aureus,* specifically targeting prophage phiMBL3. Unlike other repressors, the cI*-like repressor of phiMBL3 lacks a RecA-cleavage site, suggesting alternative induction mechanisms. Research has proposed that oxidative stress may deactivate the repressor, but the precise molecular pathways remain unclear. My studies are focused on exploring these mechanisms, particularly through protein-protein or protein-nucleic acid interactions. Quantitative PCR and deletion libraries can also help identify key genes involved in prophage activation. Understanding pyocyanin's role in microbial ecology, bacterial population dynamics, and pathogenesis could have significant therapeutic implications, especially in combating bacterial resistance and virulence.

Florian Panhölzl



(Supervisor: Matthias Horn)

In 2003, the discovery of protist infecting giant viruses triggered exploration of a new zone of the virosphere, challenging our understanding of viruses. Some giant viruses exceed bacteria in virion and genome size and encode translational system components, previously considered exclusive to living cells. They show diverse morphologies and genome features. Metagenomic studies revealed numerous novel giant virus species across environments. As protists are important in microbial networks shaping organic matter flow and microbial community composition, understanding their relationships with microorganisms and viruses is crucial. With few giant virus isolates infecting only some amoeba species available, our knowledge of host interactions remains limited. The isolation of Catovirus naeglerienses with Naegleria clarki in our lab demonstrates the potential of using new protists for giant virus isolation. The genus Naegleria is known for the pathogen N. fowleri, causing primary amoebic meningoencephalitis, a rare but almost always fatal disease. After characterizing this giant virus, I'm exploring its ecological landscape across Naegleria species using transcriptomics, dPCR and microscopy techniques.

Elisabeth Prager



(Supervisor: Isabella Moll)

Bacteria, like Escherichia coli, frequently encounter fluctuating environmental conditions requiring proteome remodelling for survival. This adjustment occurs at transcriptional, post-transcriptional and translational levels, allowing swift response to changing conditions including antibiotic treatment. Beyond protein synthesis, protein localization is fundamental for functionality. A key player ensuring correct localization into the bacterial inner membrane is the signal recognition particle (SRP), consisting of Ffh protein and 4.5S RNA. The SRP function has been studied in detail, but less is known about its individual components. Evidence including interactions with translational machinery indicates moonlighting functions for 4.5S RNA in translation. Given its essential SRP role, these results suggest 4.5S RNA functions as a regulatory hub connecting membrane stress signals to protein synthesis. My project aims to validate and characterize these potential moonlighting functions by combining in vitro and in vivo approaches.



Clara Priemer

(Supervisor: Wolfgang Wanek)

Organic sulfur compounds play an important but understudied role in biogeochemical sulfur cycling. Abundant organosulfur compounds include amino acids cysteine and methionine, taurine, and dimethyl sulfide (DMS), but the most overlooked are sulfolipids. The prominent sulfoquinovosyl diacylglycerols (SQDGs) have an estimated 10 giga tons yearly production by photosynthetic organisms. Several microbial taxa employ one of 6 known catabolic pathways to metabolise SQDGs, but metabolic fluxes haven't been investigated in environmental or host-associated microbiomes. This study aims to understand mechanisms and fluxes of SQDG catabolism in soils and map the SQDG-based sulfur cycle using stable isotope tracing. Sulfur isotope labelled 34SQDGs will be produced in algal cultures and applied to soil microbiota from various habitats. Using anion-exchange-chromatography coupled to high resolution mass spectrometry, 34S labelled degradation products will be identified and quantified to calculate turn-over rates. This will provide understanding of sulfolipids' contribution to biogeochemical sulfur cycling in terrestrial habitats.



Cornelia Rottensteiner

(Supervisor: Andreas Richter)

Human activities have led to rapid climate change, affecting microbes and microbiome functioning. Climate extremes like heatwaves and drought are expected to increase in intensity and frequency, potentially altering the plant-soil system and influencing microbial ecosystem functioning even during non-stress periods. My project investigates effects of heatwaves and droughts on soil microbial communities, food webs, and functions using quantitative stable isotope probing. We'll explore how recurrent drought shapes ecological memory within microbial communities and affects soil and root microbiomes of tree species with different mycorrhizal partners. We'll assess how future climate conditions and drought impact microbial growth across seasons. Using microbial communities exposed to ten years of future climate conditions and drought, we'll test additional anthropogenic stressors on microbial functioning and investigate whether effects of agricultural pollutants on soil microbiomes change in future climate. This will provide assessment of soil microbiome resistance and resilience to global change.

Lior Jonathan Shachar



(Supervisor: Shaul Pollak)

Two major bottlenecks make it difficult to map bacterial community structure to their collective function: the decoupling of function from taxonomy, and the lack of bacterial gene annotations. We seek to develop statistical methods to associate combinations of genes to function at the community scale. The methodology developed in this project will be used to investigate how community function emerges from its individual constituents and serve as a tool to predict function from genomic data without relying on annotations or taxonomic classifications.

Philipp Spiegel



(Supervisor: Mark Anthony)

Biotrophic fungi affect plants in all ways, generating mutualistic and parasitic outcomes. However, these fungi co-inhabit plants and interactively shape plant fitness as part of a complex system. The emergent development of plants under changing environmental conditions will, in part, depend on the strength and direction of mycorrhizal, endophytic, and pathogenic fungal responses. How any one of these fungal groups responds to global change will ultimately influence the performance of host plants. For this reason, I hypothesise that the positive effects of endophytes on plant resistance will be enhanced by endophyte diversity. However, the probability of an endophyte to become pathogenic under future environmental conditions also increases with endophyte diversity. To disentangling this, I will conduct experiments that manipulate endophyte diversity under current and future environmental conditions. In addition, I also investigate endophyte diversity and their interaction between endophytes, mycorrhizae, and pathogens, their influence on plant growth and their response to global changes. Answering this will be essential in establishing robust techniques for inoculating plants with endophytes and mycorrhizae to promote resistance to global changes.



Senwei Tong

(Supervisor: Michael Wagner)

This project aims to investigate variations in hydroxylamine (NH_2OH) release among different ammonia-oxidizing microorganisms (AOB, AOA, and comammox) under various cultivation conditions. Specifically, we will examine the relationship between NH_3 and NH_2OH affinities and their influence on NH_2OH release. Additionally, we will explore the potential role of enzyme interactions between ammonia monooxygenase (AMO) and hydroxylamine oxidoreductase (HAO) in regulating NH_2OH release. Using CLSM-STED imaging and fluorescently labeled peptide antibodies, we will determine whether co-localization of these enzymes in the periplasm affects NH_2OH release. These findings will enhance our understanding of ammonia oxidation mechanisms and their implications for nitrogen cycling.



Dean Velikov

(Supervisor: Thilo Hofmann)

Biodegradable plastics such as PLA are a promising alternative to non-degradable, persistent plastics such as PS. The main reason for this is that they are able to degrade in a relatively short period of time in certain environments and conditions, like for example in compost. However, there is currently a big debate in Europe about whether biodegradable plastics are completely degraded in industrial composting plants. For this reason, during my PhD, I will analyze the final compost products for the presence of microplastics; not only focusing on persistent plastics, but also trying to see whether or not microplastics of biodegradable materials are present. This will help to resolve the current debate and provide factual evidence.

Jyothsna Pujar Venkataramaiah



(Supervisor: Shaul Pollak)

A fundamental question in ecology is to understand how diverse communities maintain their stability. Both experimental and observational evidence show that a community's stability increases with increase in diversity. However, theoretical models show that there is a limit to the stability of diverse communities, after which species go extinct. The dynamics of these communities can be explained using different mathematical models based on competition between species for common resources. One such model is a set of coupled ODEs called consumer-resource models (CRMs), where species-species interactions are mediated through resource dynamics. A good example of such dynamical system is decomposition of leaf litter, where diverse soil microbial communities are limited in growth by different resources (such as carbon, electron acceptors and donors, etc.) and experience more environmental variation than the bulk soil below. The goal is to understand interactions between different species (consumers) and its surrounding environment (resources) by studying how a particular function of a microbial community changes with different environmental conditions and model the data obtained using CRMs.

Berna de Vries



(Supervisor: Matthias Horn)

My project, "From Pipe to Policy," is all about uncovering the hidden microbial world within the sewer systems and wastewater treatment plant (WWTP) influent of Vienna and Wiener Neustadt. By tracking microbial diversity over time, we aim to establish a baseline that supports my research on how the sewer environment drives microbial adaptations. Most sewer microbiome studies focus mainly on bacteria and viruses, but we want to take a broader approach exploring protists, (giant) viruses, microeukaryotes, and fungi – key players that shape prokaryotic communities. Using comparative genomics, metabolic reconstruction, and genome-resolved metagenomics, I will dig into microbial interactions, screen for plasmids, hunt for antimicrobial resistance genes, and hopefully uncover novel microbial species. This work will deepen our understanding of sewer microbiomes and contribute to better environmental and public health policies.



Valerie Wilkeit

(Supervisor: Thilo Hofmann)

My research is about the fate of organic pollutants in the environment, mainly looking at their bioavailability from different perspectives. Therefore, I am looking at the sorption behaviour of different tire-derived compounds to a variety of soils, analyse their presence in environmental samples (e.g. Danube sediments) and look at remediation strategies such as biochar.



Zhiyuan Xu

(Supervisor: Mark Anthony)

I am a PhD student from Northwest A&F University, where my primary research focuses on the impact of reforestation using different tree species—particularly black locust (Robinia pseudoacacia) and Chinese pine (Pinus tabuliformis)—on deep soil microbial communities and their ecological functions. Since November 2024, I have been a visiting PhD student in the Fungal Ecology Group led by Mark Anthony at the University of Vienna. Here, my work centers on investigating the fungal communities associated with black locust in its non-native ranges, with an aim to understand how these fungi influence the tree's establishment, spread, and ecological interactions. Through integrating my previous experiences in reforestation ecology with cutting-edge fungal community research, I hope to provide new insights into plant–microbe interactions and their broader implications for ecosystem function.

VDSMES Offers

Activities

- Joint DocSchool Winter Party
- Annual PhD Retreat

Outreach

- Life Science Career Fair
- Long Night of Research

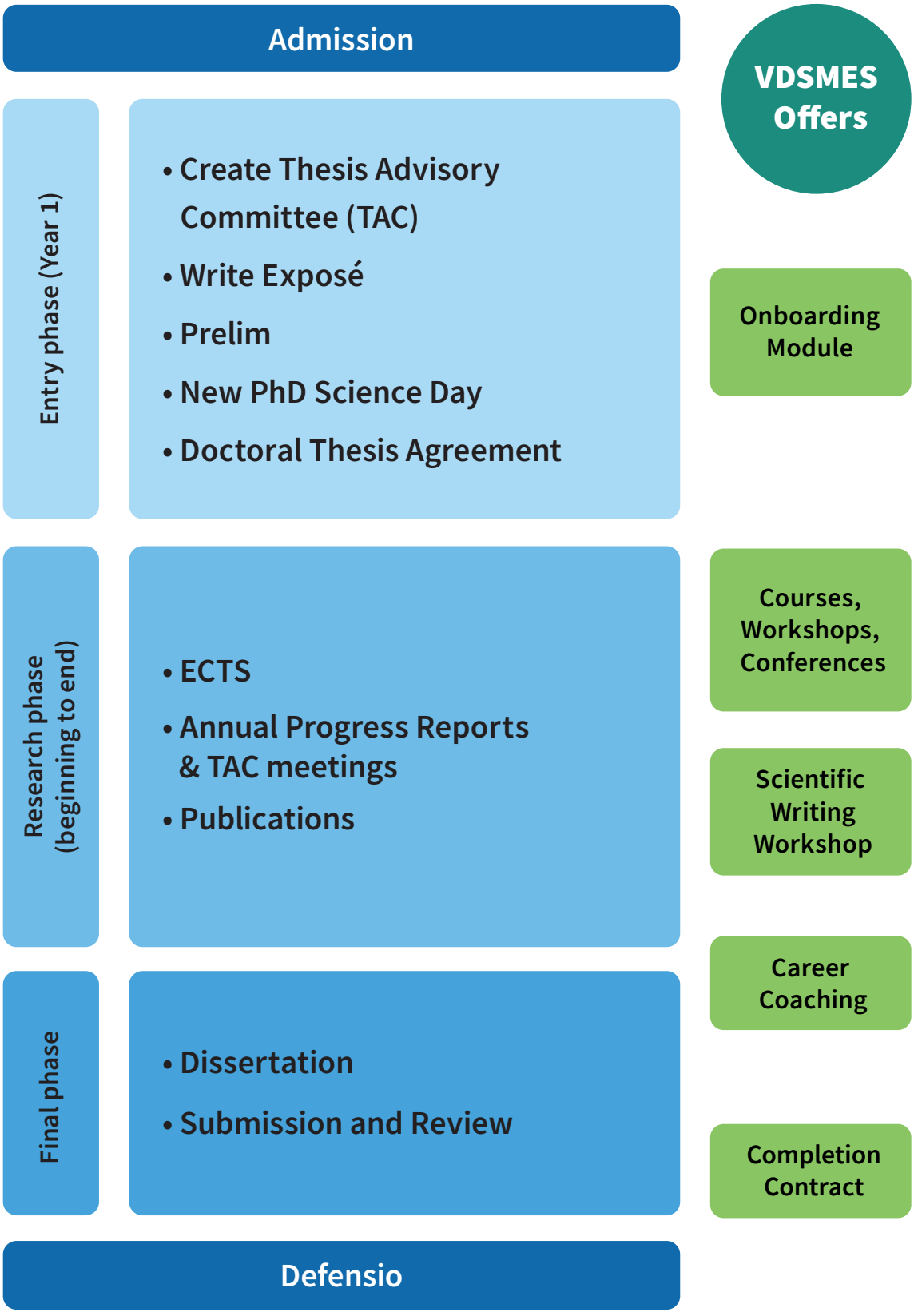




Support & Opportunities

- Onboarding module for new PhD students
- Individual career coaching
- Intensive paper writing courses
- 1-on-1 support for research data management and statistical analysis
- Visa and residence support for international PhD students
- Annual anonymous supervision surveys
- Conflict management
- Alumni network

PhD Timeline





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Doctoral School in Microbiology and Environmental Science