



MAX PLANCK INSTITUTE
FOR TERRESTRIAL MICROBIOLOGY

September
ScienceACADEMY
International Summer School for Postdocs

Monday, 09/01

09:00	Prof. Dr. Helge Bode Opening		
09:30	Dr. Nicole Paczia Organisation		
10:00	Workshop 1 (1/2) Making the most out of your postdoc	Workshop 2 (1/2) The Art of Communication for Leaders	Workshop 3 (1/2) Empowering you performance with presence
13:00	Lunch and Poster Session 1: Early Career Scientists		
14:00	Workshop 1 (2/2) Making the most out of your postdoc	Workshop 2 (2/2) The Art of Communication for Leaders	Workshop 3 (2/2) Empowering you performance with presence
17:10	Session 1: Mechanisms and Models of Microbial Evolution and Genomic Innovation		
18:10	Dinner		
19:10	Poster Session 2: Early Career Scientists		

Tuesday, 09/02

9:00	Dr. Martina Preiner Coenzymes as connection between mineral-based and enzymatic catalysis en route to protometabolism
09:20	Dr. Jing Yuan From small size to big influence: small proteins modulate bacterial virulence
09:40	Dr. Maren Nattermann Leveraging orthogonality to escape the limitations of bioproduction
10:00	Prof. Dr. Victor Sourjik Real-time dynamics of cellular processes in bacteria
10:20	Prof. Dr. Tobias Erb Fixing Carbon-fixation: Rebuilding photosynthesis with synthetic biology
10:40	Coffee Break
11:00	Session 2: Engineering Biology for a Sustainable Carbon Future
12:10	Coffee Break
12:20	Session 3: Discovery and Design of Bioactive Compounds
13:10	Lunch and Poster Session 3: Infrastructure at its best
14:10	Dr. Johannes Rebelein Decoding and Taming Nitrogenases for CO ₂ Conversion
14:30	Dr. Anke Treuner-Lange Structure analysis of the Type IV pilus machine from <i>Myxococcus xanthus</i> reveals a novel component
14:50	Prof. Dr. Gert Bange Decoding Microbial Stress: The Hidden Role of Adenosine Dinucleotides
15:10	Dr. Judith Klatt The secret nightlife of phototrophs
15:30	Prof. Dr. Helge Bode
15:50	Coffee Break
16:00	Session 4: Cooperation, Conflict, and Communication in Microbial Worlds
17:00	Coffee Break
17:10	Session 5: Microbiomes and Microbes in Agriculture and Plant Health
18:10	Dinner
19:10	Poster Session 4: Meet the Faculty

Wednesday, 09/03

09:00	Workshop 4 (1/2) Future perspectives and strategic career planning	Workshop 5 (1/2) Funding opportunities and key aspects of grant proposal writing
13:00	Lunch	
14:00	Workshop 4 (2/2) Future perspectives and strategic career planning	Workshop 5 (2/2) Funding opportunities and key aspects of grant proposal writing
16:00	Coffee Break	
16:10	Wrap-up and Goodbye	

Session 1

Mechanisms and Models of Microbial Evolution and Genomic Innovation

Chair: Dr. Delphina Pereira

Speakers

Natalia Mrnjavac

From LUCA to Life: Tracing the Metabolic Transitions to Bacteria and Archaea

Lavisha Parab

Tradeoffs in bacterial evolution: Prophage maintenance can be costlier than phage resistance via surface receptor modifications

Prachitha Nagendra

Gene Flow and Adaptive Evolution: Insights from Experimental Evolution in Yeast

Mamantia Constantinou

A Novel Role for the Histone Acetyltransferase Nat4 in the DNA Damage Response of *Saccharomyces cerevisiae*

Kayleigh Ellen Phillips

Uncovering and Characterizing Native Myxobacterial Plasmids for Genetic Tool Development

Yazhini Arangasamy

MAGmax: An Efficient Bin Merging and Dereplication Tool for High-Quality Metagenome-Assembled Genomes

Abstracts Session 1

Natalia Mrnjavac

From LUCA to Life: The assembly of ancestral metabolism

The last universal common ancestor (LUCA) marks a pivotal stage in life's evolution, linking prebiotic chemistry to modern cellular biology. While LUCA has long been studied through phylogenetic reconstructions, the nature of its metabolic network and its divergence into the last bacterial common ancestor (LBCA) and the last archaeal common ancestor (LACA) remain unresolved. In this study, we use a phylogeny-independent computational framework to investigate the metabolic transition from LUCA to LBCA and LACA. Analyzing 424 core metabolic reactions—responsible for synthesizing amino acids, cofactors, and nucleotides from simple inorganics such as CO₂, H₂, and NH₃—we assess gene distributions across modern bacteria and archaea. This approach offers new insights into the environmental and biochemical factors that may have shaped early metabolism and provides a glimpse into the primordial architecture underlying the divergence of life's major domains.

Lavisha Parab

Tradeoffs in bacterial evolution: Prophage maintenance can be costlier than phage resistance via surface receptor modifications

Temperate phage infections can drive bacterial populations along divergent evolutionary paths, each associated with distinct trade-offs. Lysogeny—the integration of prophages into the bacterial genome—confers immunity to superinfection but imposes costs such as genomic maintenance and the latent risk of lysis. Alternatively, resistance through receptor modification can prevent infection but may compromise receptor function, incurring fitness costs. In this study, we examined the evolutionary dynamics of naïve *Escherichia coli* K-12 populations exposed to one of four different temperate phages. Our results show consistent population diversification into lysogenic and non-lysogenic subpopulations, with non-lysogens typically gaining a competitive advantage over lysogens. These findings highlight the complex fitness landscape that shapes phage-bacteria co-evolution and provide insights into how microbial populations navigate infection-mediated selective pressures.

Prachitha Nagendra

Gene Flow and Adaptive Evolution: Insights from Experimental Evolution in Yeast

Gene flow is a fundamental evolutionary process influencing adaptation, divergence, and speciation. Defined as the integration of alleles into a non-native gene pool, gene flow can either facilitate or constrain adaptation depending on the fitness effects of the incoming alleles. Alongside natural selection, gene flow shapes evolutionary outcomes, yet its impacts are context-dependent and not fully understood. Both theoretical models and empirical studies using natural isolates have shown that gene flow can variably influence adaptive divergence and reproductive isolation. To dissect these dynamics, we employ experimental evolution in *Saccharomyces cerevisiae*—a simple eukaryotic model organism. By manipulating gene flow and selective pressures in controlled laboratory settings, we aim to uncover the mechanisms by which gene flow influences adaptation and the evolutionary trajectories of populations. This approach enhances our understanding of evolutionary predictability and the genetic architecture underlying complex evolutionary outcomes.

Mamantia Constantinou

A Novel Role for the Histone Acetyltransferase Nat4 in the DNA Damage Response of *Saccharomyces cerevisiae*

The DNA damage response (DDR) involves extensive chromatin remodeling, regulated in part by histone modifications. However, the roles of specific histone-modifying enzymes in this process are not fully defined. In my PhD research, I identified a previously unrecognized role for the histone N-terminal acetyltransferase Nat4 in the DDR of *Saccharomyces cerevisiae*. Loss of NAT4 leads to hypersensitivity to genotoxic agents, increased DNA break accumulation, and impaired checkpoint signaling. Upon DNA damage, NAT4 expression is upregulated and the protein is recruited to double-strand breaks (DSBs). Cells lacking Nat4 show reduced levels of H2AS129 phosphorylation (γ H2A) and diminished recruitment of Rad9, a key checkpoint adaptor protein, near DSBs. Additionally, Nat4 deficiency impairs localization of the Mec1 kinase at DSBs, leading to reduced Mec1-mediated

activation of Rad53, a critical checkpoint effector. These defects are dependent on Nat4's catalytic activity, specifically its acetylation of histone H4. Together, these findings highlight a novel function for Nat4 in coordinating chromatin modifications that support genome integrity under DNA damage stress.

Kayleigh Ellen Phillips

Uncovering and Characterizing Native Myxobacterial Plasmids for Genetic Tool Development

Myxobacteria are soil-dwelling predators known for their complex behaviors and rich secondary metabolism, yet many of their biosynthetic gene clusters (BGCs) remain silent or poorly characterized. To help address this, we are investigating natural plasmids identified through whole-genome sequencing of environmental myxobacterial isolates collected from diverse U.S. soils. We have discovered at least seven distinct plasmids across our isolates, several of which contain BGCs or replication-associated genes. One particular plasmid carries the tubulysin BGC and was identified in two geographically distinct strains, displaying near identical synteny and suggesting strong conservation. We are currently annotating these plasmids to better understand their gene content, replication systems, and potential for horizontal transfer. In parallel, we are functionally testing replication and partitioning genes, such as *repA* and *repB*, using GFP-tagged constructs to assess their ability to support plasmid maintenance in various myxobacterial hosts. This work aims to explore the role of natural plasmids in secondary metabolism and evaluate their potential as modular tools for gene expression in myxobacteria.

Yazhini Arangasamy

MAGmax: An Efficient Bin Merging and Dereplication Tool for High-Quality Metagenome-Assembled Genomes

Microorganisms are essential to ecosystem function, yet many remain uncultured and poorly understood. Advances in shotgun metagenomic sequencing have enabled the recovery of metagenome-assembled genomes (MAGs), offering key insights into microbial diversity and function. A standard MAG reconstruction workflow includes metagenomic read assembly, binning of contigs, and dereplication of near-identical genome bins across samples. To address the limitations of current dereplication methods, we developed MAGmax—an efficient tool that improves both the quantity and quality of MAGs. Unlike dRep, which selects a single representative bin per genome cluster, MAGmax merges multiple bins within a cluster and reassembles them to enhance coverage. This strategy results in more complete, higher-quality, and less redundant MAGs. Benchmarking shows that MAGmax outperforms dRep by producing superior MAGs 1.6 times faster and with one-third of the memory usage. MAGmax thus offers a robust solution for high-throughput, scalable MAG dereplication, supporting deeper exploration of microbial communities in complex environmental samples.

Session 2:

Engineering Biology for a Sustainable Carbon Future

Chair: Dr. Maren Nattermann

Speakers

Amelia Bergeson

Biological Strategies for Plastic Upcycling: From Whole-Cell Degradation to Enzyme Optimization

Anna Christina Ngo

Modular Enzymatic Cascades for Methanol Valorization: Toward a Circular C1 Bioeconomy

Antonia Ebert

Engineering *Hydrogenophaga pseudoflava* for Multi-C1 Substrate Assimilation from Waste Gases

Neha Bansal

Rewiring C1 metabolism for autotrophic CO₂ conversion

Laura Beth Quinto

A versatile approach to genome-scale rewriting in cyanobacteria

Emily Radley

De Novo Design of Metalloenzymes for Efficient and Selective CO₂-to-CO Conversion

Anna Kohn

Engineering photoenzymes for synthetically useful transformations

Abstracts Session 2

Amelia Bergeson

Biological Strategies for Plastic Upcycling: From Whole-Cell Degradation to Enzyme Optimization

The global proliferation of plastic waste presents an urgent environmental challenge, necessitating innovative and sustainable disposal methods. This research explores biological alternatives, leveraging both enzyme-based systems and whole-cell microbial platforms to convert plastic waste into value added chemicals or degrade it into monomeric building blocks. This research project works towards expanding biological plastic depolymerization by isolating and characterizing plastic-degrading microorganisms from a municipal composting environment. Through laboratory enrichment, strains which exhibit the capacity to degrade various plastics have been isolated. Notably, some isolates utilize plastic as a sole carbon source, presenting a promising foundation for metabolic engineering aimed at plastic valorization. These findings contribute to the development of integrated microbial solutions for plastic waste mitigation and circular biomanufacturing.

Anna Christina Ngo

Modular Enzymatic Cascades for Methanol Valorization: Toward a Circular C1 Bioeconomy

In response to the urgent need for sustainable alternatives to petrochemical-based production, C1 compounds such as methanol are gaining attention as renewable feedstocks in the emerging circular bioeconomy. This project aims to develop NAD⁺-dependent enzymatic cascades for the efficient biocatalytic conversion of methanol into high-value products. Key enzymes—including engineered variants of alcohol dehydrogenase and formaldehyde dehydrogenase—were optimized for activity, thermostability, and altered cofactor specificity. Additional enzymes such as formate oxidase, formate dehydrogenase, and lipases were also explored to enable in situ regeneration of NAD(P)H and production of formate esters. To further enhance process applicability, enzyme immobilization strategies on conductive mesh anodes were developed for integration into electrobiochemical systems. This work contributes to the design of modular, scalable biocatalytic platforms for C1-based bioproduction, advancing the transition toward a climate-resilient bioeconomy.

Antonia Ebert

Engineering *Hydrogenophaga pseudoflava* for Multi-C1 Substrate Assimilation from Waste Gases

Harnessing aerobic gas-fermenting bacteria for the sustainable conversion of one-carbon (C1) waste gases into valuable products offers a promising route toward a circular bioeconomy. My research focuses on *Hydrogenophaga pseudoflava*, an aerobic carboxydrotroph with a natural capacity to metabolize CO, CO₂, and H₂, as a versatile microbial chassis for C1 substrate bioconversion. To broaden its metabolic capabilities, I am engineering *H. pseudoflava* with synthetic modules, including a metal-dependent formate dehydrogenase and the reductive glycine pathway, aiming to enable the efficient assimilation of formate and methanol. The long-term objective is to develop a robust platform capable of converting mixed C1 gases, including methane. I have successfully demonstrated the assimilation of formate-derived CO₂ via the Calvin cycle through heterologous expression of a molybdenum-dependent formate dehydrogenase from *Cupriavidus necator* H16. This work lays the foundation for advanced multi-C1 bioprocessing strategies, contributing to the development of flexible microbial platforms for the valorization of industrial gas waste streams.

Neha Bansal

Rewiring C1 metabolism for autotrophic CO₂ conversion

The escalating climate crisis results from continuous emissions of CO₂ into the atmosphere, highlighting the urgent need for innovative carbon mitigation strategies. While plants naturally fix CO₂, recent research has shown growing interest in microbial alternatives, particularly autotrophic bacteria that use the Calvin-Benson-Bassham (CBB) cycle for carbon fixation. Although common, the CBB cycle is not highly efficient. The key enzyme, RuBisCO, converts inorganic CO₂ into biomass precursors like pyruvate but is equally reactive toward O₂, causing photorespiration—an energy-wasteful process that re-releases CO₂ and consumes more ATP, thereby lowering overall carbon fixation efficiency via CBB. My research focuses on designing and implementing energy-efficient and oxygen-tolerant CO₂

fixation strategies. Specifically, I aim to develop a synthetic pathway in *Cupriavidus necator*, formerly known as *Ralstonia eutropha* is an autotrophic bacterium. The pathway involves two novel, new to nature enzymes that offer a potential way to bypass RuBisCO-related limitations. By integrating this pathway with the previously demonstrated reductive glycine pathway¹ in *C. necator*, we aim to shift some cellular flux away from photorespiration toward more efficient autotrophic growth. This combined approach is promising, not only to increase biomass production in *C. necator*. But also, a successful demonstration would pave the way for future applications in plant systems to enhance yield and carbon assimilation.

Laura Beth Quinto

A versatile approach to genome-scale rewriting in cyanobacteria

Biological carbon fixation offers a powerful strategy for mitigating atmospheric CO₂ and enabling sustainable biomanufacturing. Yet, many of the most metabolically promising organisms—such as *Clostridium* spp., *Cupriavidus necator*, and cyanobacteria—remain genetically intractable due to limited engineering tools. In this work, we introduce a phylogenetically generalizable platform for large-scale genome rewriting, combining broad host range nuclease-based editing with recombinase-mediated integration. We demonstrate this approach in *Synechococcus elongatus* UTEX 2973 by recoding over 3% of the genome in three streamlined steps. Additionally, we show that these editing tools are compatible with targeted diversification strategies, facilitating exploration of broader genotypic and phenotypic space. This work supports the development of biocontained, genetically isolated microbial chassis capable of producing proteins with unnatural chemistries. Ultimately, our technology lays the groundwork for engineering robust microbial systems across diverse taxa, accelerating the deployment of synthetic biology solutions for carbon sequestration and climate-resilient manufacturing.

Emily Radley

De Novo Design of Metalloenzymes for Efficient and Selective CO₂-to-CO Conversion

To meet net-zero emission goals, robust and scalable methods for CO₂ conversion are urgently needed. While both chemical and enzymatic approaches exist, their practical application is often limited by stability and catalytic specificity. In this study, we explore de novo enzyme design as a strategy to overcome these challenges, focusing on the integration of non-natural cofactors to expand catalytic capabilities. Specifically, we designed and characterized novel metalloenzymes capable of binding cobalt porphyrin (CoPPiX), a cofactor known to reduce CO₂ to CO with high selectivity. Using RFdiffusion and ProteinMPNN design pipelines, we screened approximately 200 enzyme variants encompassing diverse topologies, active site geometries, axial ligand coordination schemes, and electrostatic environments. Several candidates demonstrated enhanced catalytic activity and selectivity for CO production over H₂. Structural and biophysical analyses confirmed strong concordance between computational models and experimental structures, as well as high thermostability. By identifying design features linked to superior performance, our work provides key insights into the next generation of CO₂ reductases for biocatalytic carbon capture and utilization.

Anna Kohn

Engineering photoenzymes for synthetically useful transformations.

Photocatalysis promotes a broad range of valuable chemical transformations, including cycloadditions, electrocyclic reactions, deracemizations, migrations and rearrangements, many of which are not accessible from the ground state. Enantioselective versions of photochemical reactions have been developed by employing chiral photosensitizers,¹ or through dual catalytic strategies that combine an achiral photosensitizer with a photochemically inactive chiral catalyst.² Although powerful, these approaches do not offer a general solution, and many desirable photochemical processes are not amenable to enantioselective catalysis. The incorporation of photosensitizing noncanonical amino acids (ncAAs) into protein scaffolds offers a versatile strategy for the engineering of novel photoenzymes for stereoselective catalysis. Aryl ketones such as benzophenone and (thio)xanthenes are widely employed in both photoredox and triplet energy transfer catalysis, making them attractive candidates for installation into proteins as ncAA side chains. Here we have demonstrated that new-to-nature photocatalytic activity can be introduced into protein scaffolds using such genetic code expansion methodology, through the generation of photoenzymes for [2+2]-cycloadditions³ and C-H insertions.⁴ These energy transfer biocatalysts exhibit triplet excited states that significantly outlive that of the small-molecule sensitizers that they harbor. Remarkably, in contrast to small molecule photocatalysis which typically necessitates low temperatures and an inert atmosphere, these photoenzymes retain catalytic efficiency under ambient conditions, and are not affected by the presence of oxygen.

Session 3:

Discovery and Design of Bioactive Compounds

Chair: Dr. Li Su

Speakers

Anitra Zīle

Isolation of Actinobacteria from Unique Biotopes in Latvia and Bioactivity-Guided Discovery of Natural Products

Chidoh Kootlole

NMR-Based Metabolomic Profiling and Anti-Leukemic Potential of *Maytenus senegalensis*

Kesi Kurnia

Engineering *Acinetobacter baylyi* ADP1 for production of flavonoids from lignin derived aromatics

Golsa Nayeb Ghanbar Hosseini

Uncovering the Ecological and Evolutionary Drivers of Chemical Diversity in *Streptomyces*

Sukanya Bhowmick

CglA: A Novel Glycopolymer Ligase Linking Cell Wall Biogenesis and Developmental Robustness in filamentous *Streptomyces*

Abstracts Session 3

Anitra Zīle

Isolation of Actinobacteria from Unique Biotopes in Latvia and Bioactivity-Guided Discovery of Natural Products

The rise of antimicrobial resistance (AMR) has become a serious threat to global health, requiring the discovery of novel bioactive compounds. Actinobacteria, historically responsible for over 75% of known antimicrobials, remain a promising yet underexplored source of potentially new antibiotics. To find new antimicrobial compounds, bioprospecting was done in five unique and largely untapped biotopes, in Latvia, and a small Actinobacteria library was created. The strains were isolated using traditional extinction-to-dilution method, as well as, an in situ device iChips. To activate more biosynthetic gene clusters, strains were cultivated in diverse conditions and multiple extracts were prepared. The extracts were screened for antimicrobial activity against a panel of Gram+, Gram-, and fungal human pathogens. The bioactivity screening revealed multiple candidates for novel natural product discovery.

Chidoh Kootlole

NMR-Based Metabolomic Profiling and Anti-Leukemic Potential of *Maytenus senegalensis*

Natural products (NPs) of plant origin have been an important source of bioactive molecules for centuries, playing a crucial role in drug discovery due to their vast chemical diversity and evolutionary optimization for biological activities. They serve as a rich source of lead compounds, inspiring the development of novel drugs to treat a wide range of diseases. Historically, natural products have yielded numerous pharmaceutical agents, including antibiotics, anticancer drugs, and cardiovascular medications. In the recent studies, cancer has been suggested as one of the major causes of mortality globally and burden for the health care systems including leukemia. The search for novel, effective, and less toxic cancer therapies continues to be a global priority, particularly in addressing drug resistance and side effects associated with current treatments for leukemia. Drawing on traditional medicinal knowledge in Botswana, this work investigated the anti-leukemic potential of natural products from several native plant species by employing Nuclear Magnetic Resonance spectroscopy and bioassays.

Kesi Kurnia

Engineering *Acinetobacter baylyi* ADP1 for production of flavonoids from lignin derived aromatics

Flavonoids are bioactive plant-derived compounds with wide-ranging applications in pharmaceuticals, nutraceuticals, and cosmetics. However, current production strategies—relying on plant extraction or chemical synthesis—face significant challenges, including limited scalability, environmental burden, and dependence on agricultural inputs. This project pioneers the use of *Acinetobacter baylyi* ADP1 as a synthetic microbial chassis for the sustainable biosynthesis of flavonoids from lignin-derived aromatics. Through the integration of a heterologous pathway and targeted deletion of a native catabolic gene, *p*-coumarate is converted into naringenin, with titers reaching up to 66.4 mg/L under fed-batch conditions. This work demonstrates the feasibility of flavonoid production in *A. baylyi*, establishing it as a promising chassis for lignin valorization and natural product biosynthesis.

Golsa Nayeb Ghanbar Hosseini

Uncovering the Ecological and Evolutionary Drivers of Chemical Diversity in Streptomyces

Streptomyces species are prolific producers of natural products and exhibit remarkable chemical and phenotypic diversity, even within individual populations. Soil-dwelling Streptomyces demonstrate extensive diversification not only in their secondary metabolite profiles but also in morphotype traits such as sporulation patterns, filamentous growth, and extracellular matrix production. This diversity is thought to be shaped by the dynamic and heterogeneous nature of microbial communities and their adaptation to environmental change. Importantly, these phenotypic traits are closely linked to variations in antibiotic biosynthesis—particularly of β -lactam and other clinically relevant compounds—making Streptomyces a focal point for natural product research. However, despite their significance, the ecological and evolutionary forces underlying the structural diversification of Streptomyces metabolites in soil ecosystems remain poorly understood. In this talk, I will explore the link between community-level heterogeneity, ecological adaptability, and metabolic innovation in Streptomyces, with a focus on how these factors drive natural product diversity.

Sukanya Bhowmick

CglA: A Novel Glycopolymer Ligase Linking Cell Wall Biogenesis and Developmental Robustness in filamentous Streptomyces

The complex life cycle of Streptomyces—renowned producers of antibiotics—relies on tightly regulated cell envelope biogenesis to maintain morphology, viability, and developmental transitions. The Gram-positive cell envelope consists of a thick peptidoglycan layer linked to glycopolymers, yet the spatial and regulatory coordination of this architecture remains poorly understood in filamentous bacteria. In this study, we identify the LCP-LytR_C domain protein CglA as a key glycopolymer ligase that localizes to active cell wall biosynthesis zones in Streptomyces venezuelae. Loss of CglA results in reduced glycopolymer deposition, abnormal hyphal morphology, mislocalized FtsZ rings, and defective septation and sporulation. Furthermore, we uncover a functional interaction between c-di-AMP signaling and cell wall homeostasis: deletion of *cglA* rescues the salt-sensitive growth defect of a *disA* mutant, linking second messenger signaling to glycopolymer deposition. These findings position CglA as a crucial regulator of cell wall construction, developmental robustness, and stress resilience in Streptomyces.

Session 4:

Cooperation, Conflict, and Communication in Microbial Worlds

Chair: Irina Kalita

Speakers

Anaïs Biquet-Bisquert

Dynamic Landscapes of the Proton Motive Force in Single Bacterial Cells

Cristina Palma

Spo0A~P oscillatory dynamics are the primary cause for biofilm matrix deactivation

Olajumoke Ajao Yewande

From Solitary Predators to Social Hunters: Exploring Microbial Cooperation in *Bdellovibrio* and *Myxococcus*

Rhian Marie Ford

Uncovering the Role of Polyamines in the Predatory Life Cycle of *Bdellovibrio bacteriovorus* HD100

Elizabeth Riana Dwi

Unraveling Respiratory Syncytial Virus Diversity in Laos Through Genomic Surveillance

Sara Šreibr

Investigating Host-Induced Activation and Protein Secretion in the Entomopathogenic Nematode *Heterorhabditis bacteriophora*

Abstracts Session 4

Anaïs Biquet-Bisquert

Dynamic Landscapes of the Proton Motive Force in Single Bacterial Cells

The proton motive force (PMF) is a fundamental electrochemical potential that drives a multitude of essential processes across biological membranes in bacteria, mitochondria, and chloroplasts. Traditionally viewed as a stable bioenergetic parameter, recent findings challenge this notion by revealing dynamic temporal and spatial fluctuations of the PMF at the single-cell level. In *Escherichia coli*, rapid membrane depolarizations and mechanosensing responses point to a temporally dynamic PMF, while polar clustering of respiratory complexes indicates potential spatial heterogeneity. Similar spatial structuring has been observed in mitochondrial membranes, suggesting a broader relevance of PMF heterogeneity. Despite these advances, our understanding of the spatiotemporal behavior of the PMF in bacteria remains limited. In this talk, I will present current insights into single-cell PMF dynamics, highlight recent experimental approaches, and discuss the implications of these findings for bacterial physiology and bioenergetics.

Cristina Palma

Spo0A~P oscillatory dynamics are the primary cause for biofilm matrix deactivation

In non-optimal conditions, *B. subtilis* survives by differentiating into one of two cell types: biofilm matrix-producing cells or sporulating cells. These two cell-differentiation pathways are activated by the same phosphorylated transcription factor - Spo0A~P. Despite sharing the activation mechanism, these cell fates are mutually exclusive at the single-cell level. This has been shown to be controlled by the effects of growth rate on gene dosage and protein dilution in the biofilm network. In this work, we explore an alternative mechanism on how growth rate controls the mutual exclusivity of this cell fates. Namely, using mathematical modeling, we investigate how the growth-dependent oscillatory dynamics of Spo0A~P affect biofilm deactivation. Specifically, we first show that the biofilm network is sensitive to the effects of growth rate on the period of Spo0A~P oscillations. Next, we show that for oscillatory Spo0A~P signals the biofilm network is more easily deactivated as growth rate decreases. Interestingly, we find that the effects of growth rate on gene dosage and protein dilution in the biofilm network only change the biofilm deactivation threshold by ~10%. Finally, we show that the increase in the DNA replication time is the determining factor to turn biofilm matrix production off. In summary, our findings elucidate the mechanism governing biofilm deactivation during the late stages of starvation, thereby advancing our understanding of how bacterial networks interpret dynamic signals to regulate stress-response pathways.

Olajumoke Ajao Yewande

From Solitary Predators to Social Hunters: Exploring Microbial Cooperation in *Bdellovibrio* and *Myxococcus*

Predatory bacteria exhibit a wide range of ecological strategies and behaviors, offering unique insights into microbial cooperation and developmental biology. My recent work has focused on *Bdellovibrio bacteriovorus*, a solitary bacterial predator studied for its potential as a biocontrol agent. Through bacterial isolation, culturing, genome analysis, and molecular investigations of host-prey dynamics, I have developed a strong foundation in microbial ecology and predator-prey interactions. This expertise now informs my interest in *Myxococcus xanthus*, a contrasting predator known for its complex social behaviors, multicellular development, and cooperative predation. While quorum sensing (QS) regulates collective behaviors such as swarming and fruiting body formation in *Myxococcus*, QS systems are notably absent in *Bdellovibrio*. Investigating the evolutionary and mechanistic differences between these organisms provides a compelling opportunity to understand the molecular basis of microbial sociality, signal transduction, and community coordination. These insights are relevant not only for evolutionary microbiology but also for advancing antimicrobial approaches and synthetic biology applications.

Rhian Marie Ford

Uncovering the Role of Polyamines in the Predatory Life Cycle of *Bdellovibrio bacteriovorus* HD100

Predatory bacteria like *Bdellovibrio bacteriovorus* HD100 offer promising avenues for antimicrobial applications due to their ability to kill and consume Gram-negative pathogens. These highly motile bacteria invade the periplasmic space of prey cells, degrade intracellular contents, and release progeny capable of repeating the predation cycle. Despite their therapeutic potential—especially against antibiotic-resistant strains—the molecular mechanisms governing *B. bacteriovorus* predation remain incompletely understood. This PhD project focused on the role of polyamines, small polycationic molecules, in regulating predatory behavior, inspired by early findings in related marine *Bdellovibrio* species. Specifically, we investigated how polyamine systems in both predator and prey influence predatory efficiency, life cycle progression, and host interaction dynamics. By shedding light on this largely unexplored regulatory layer, our work contributes to a deeper understanding of *B. bacteriovorus* biology and supports the development of effective biocontrol strategies using predatory bacteria.

Elizabeth Riana Dwi

Unraveling Respiratory Syncytial Virus Diversity in Laos Through Genomic Surveillance

Respiratory syncytial virus (RSV) is a leading cause of acute lower respiratory infections (ALRI), particularly among young children, with the potential to cause severe illnesses such as pneumonia and bronchiolitis. In Laos, RSV prevalence has reached alarming levels—up to 49%—across multiple age groups. RSV exists in two major antigenic groups, RSV A and B, which can co-circulate and are characterized by high variability in their glycoprotein and fusion protein genes. These genetic differences may influence disease severity, transmission dynamics, and antiviral susceptibility. Despite its public health importance, genomic surveillance of RSV in Laos remains limited, especially in comparison to influenza and COVID-19. To address this gap, our study performs whole genome sequencing of RSV isolates from diverse regions in Laos. We aim to elucidate RSV genetic diversity, uncover spatial and temporal circulation patterns, and characterize the dominant lineages. This work provides a foundation for enhanced RSV monitoring and informs future public health strategies in Southeast Asia.

Sara Šreibr

Investigating Host-Induced Activation and Protein Secretion in the Entomopathogenic Nematode *Heterorhabditis bacteriophora*

Entomopathogenic nematodes such as *Heterorhabditis bacteriophora*, have gained recognition as effective biocontrol agents against insect pests, offering an eco-friendly alternative to synthetic insecticides. A critical aspect of their pathogenicity is the transition of infective juveniles (IJs) from an arrested stage to an active parasitic state upon encountering a host—a process known as activation or recovery. It is a complex and not fully understood process, involving several characteristics, including cuticle shedding, morphological transformations, the release of symbiotic bacteria, expression of stage-specific genes, and the release of bioactive molecules known as excretory/secretory products (ESPs). In this study, we aimed to evaluate the protein spectrum of *Heterorhabditis bacteriophora* ESPs released in relation of different activation materials. We optimized the *in vitro* activation process of *H. bacteriophora* and selected three fractions of activation materials from *Galleria mellonella* larvae, each prepared differently, along with two control fractions: water or phosphate buffer. All tested materials induced IJ activation, although none achieved a maximal recovery rate. Protein analysis of ESPs revealed variations in the released products depending on the activation material used, with insect-derived stimuli resulting in fewer proteins compared to phosphate buffer activation. Notably, insect-derived stimuli induced ESPs enriched in virulence-related proteins such as alpha-2-macroglobulins, trypsin inhibitor-like proteins, and metalloendopeptidases, whereas non-biological controls yielded broader protein spectra, including stress response factors. These findings provide novel insight into the stimulus-specific activation pathways of *H. bacteriophora* and underscore the role of ESPs in nematode-host interactions. Understanding the regulatory dynamics of ESP release may contribute to the development of more effective nematode-based biocontrol strategies.

Session 5:

Microbiomes and Microbes in Agriculture and Plant Health

Chair: Dr. Anke Treuner-Lange

Speakers

Angélica Mariana Jara Servín

Exploring the Root Microbiome and Genomic Adaptation of Soil Bacteria

Daniela Ramirez-Sanchez

A Genome-Wide Association Study Reveals the Genetic Architecture of *Arabidopsis thaliana* in Response to Non-Pathogenic Bacterial Species

Jana Ordon

Chromosomal barcodes for simultaneous tracking of near-isogenic bacterial strains in plant microbiota

Vanessa Nya Dinango

Desert-Derived Endophytes as Biocontrol Agents Against *Fusarium verticillioides* in Maize

Helen Katharine Feord

Cellular Mechanisms of Algal Survival in the Terrestrial Cryosphere: Insights from Glacier Bloom Communities

Abstracts Session 5

Angélica Mariana Jara Servín

Exploring the Root Microbiome and Genomic Adaptation of Soil Bacteria

Plant-microbe interactions are essential for plant health, nutrient acquisition, and resilience to biotic and abiotic changes in the environment. In my PhD research, I investigated the diversity and structure of root-associated microbial communities and conducted comparative genomic analyses of *Solirubrobacter*, a dominant but understudied soil bacterium. Through a combination of metagenomics, phylogenomics, and pangenomics, I uncovered key microbial traits involved in community assembly, environmental adaptation, and potential functional contributions to the host, as well as a broader description of the genus *Solirubrobacter*. This work provides new insights into microbial ecology and the evolutionary mechanisms driving bacterial success in soil environments.

Daniela Ramirez-Sanchez

A Genome-Wide Association Study Reveals the Genetic Architecture of *Arabidopsis thaliana* in Response to Non-Pathogenic Bacterial Species

Microbiota can largely contribute to plant health by mobilizing and supplying nutrients and by providing protection from abiotic stresses and pathogens. Nonetheless, the number of genome-wide association studies (GWAS) reporting the genetic architecture of the response to individual members of the beneficial microbiota remains limited. Thus, we set up a GWAS under field conditions to

estimate the level of genetic variation and the genetic architecture among 162 *Arabidopsis thaliana* accessions originating from 54 natural populations located in the southwest of France, in response to 13 native strains of seven of the most abundant and prevalent non-pathogenic bacterial species isolated from the phyllosphere.

Jana Ordon

Chromosomal barcodes for simultaneous tracking of near-isogenic bacterial strains in plant microbiota

DNA-amplicon-based microbiota profiling can estimate species diversity and abundance but cannot resolve genetic differences within individuals of the same species. Here we report the development of modular bacterial tags (MoBacTags) encoding DNA barcodes that enable tracking of near-isogenic bacterial commensals in an array of complex microbiome communities. Chromosomally integrated DNA barcodes are co-amplified with endogenous marker genes of the community by integrating corresponding primer binding sites into the barcode. We use this approach to assess the contributions of individual bacterial genes to *Arabidopsis thaliana* root microbiota establishment with synthetic communities that include MoBacTag-labelled strains of *Pseudomonas capeferrum*. Results show reduced root colonization for certain mutant strains with defects in gluconic-acid-mediated host immunosuppression, which would not be detected with traditional amplicon sequencing. Our work illustrates how MoBacTags can be applied to assess scaling of individual bacterial genetic determinants in the plant microbiota.

Vanessa Nya Dinango

Desert-Derived Endophytes as Biocontrol Agents Against *Fusarium verticillioides* in Maize

Maize is a critical global food and feed crop, but its productivity is increasingly threatened by ear and root rot diseases caused by the fungal pathogen *Fusarium verticillioides*. This pathogen not only compromises yield but also produces fumonisins—mycotoxins harmful to humans and animals. In this study, we investigated the biocontrol potential of endophytic bacteria isolated from three desert plants, building on previous findings that endophytes from *Euphorbia antiquorum* can confer disease resistance and promote plant growth. We screened 27 bacterial strains for their ability to inhibit *F. verticillioides* both in vitro and in situ, and assessed the antifungal efficacy of their lipopeptide metabolites. Our results identified *Bacillus subtilis* RA15 and *Bacillus tequilensis* FC6 as promising candidates for the ecological management of *F. verticillioides*. Their lipopeptides significantly inhibited fungal growth and protected maize seeds from infection, highlighting their potential use in sustainable crop protection strategies.

Helen Katharine Feord

Cellular Mechanisms of Algal Survival in the Terrestrial Cryosphere: Insights from Glacier Bloom Communities

The terrestrial cryosphere, encompassing glaciers and semi-permanent snow patches, supports dynamic microbial ecosystems dominated by chlorophyte and streptophyte microalgae. These primary producers coexist with bacteria, fungi, protists, and viruses in extreme conditions characterized by freezing temperatures, intense light, nutrient scarcity, and prolonged darkness. Snow and glacier ice algae accumulate high levels of photoprotective pigments—red carotenoids and purpurogallin, respectively—that not only safeguard cellular function but also reduce surface albedo. This darkening effect enhances light absorption and accelerates ice/snow melt, creating a feedback loop that promotes microbial growth. Despite their ecological importance and influence on cryospheric melt dynamics, the cellular biology of these algae remains poorly understood. This project utilizes samples from the Greenland Ice Sheet, employing meta-transcriptomic and -proteomic techniques to investigate the molecular basis of algal survival and proliferation during glacier algal blooms. Our findings provide foundational insight into the adaptive strategies of cryophilic algae and their role in shaping polar ecosystem function and surface melt rates.

Marburg Minds

Tuesday, 2nd 09:00 am

Coenzymes as connection between mineral-based and enzymatic catalysis en route to protometabolism

The last universal common ancestor (LUCA) arose in an environment of rocks and water on the early Earth about 4 billion years ago. Top-down comparative bioinformatics reveal LUCA's carbon metabolism: the acetyl-CoA (or Wood-Ljungdahl) pathway, driven by CO₂ and H₂ gas [1,2]. Looking at abiotic, mineral-assisted organic syntheses occurring in hydrothermal vents today, we see how they resemble segments of the pathway [3], possibly revealing LUCA's geochemical roots. In order to connect undirected, mineral-assisted catalysis with the complex enzymatic catalysis in LUCA (and extant biochemistry), we are zooming in on central metabolic organic cofactors, so helper molecules employed by enzymes. Examples also found in the acetyl-CoA pathway are nicotinamide adenosine dinucleotide (NAD), C1 donors and acceptors such as tetrahydrofolate (H₄F) or, the namesake of the pathway, coenzyme A (CoA). Cofactors have been hypothesized to predate enzymes [4], so in other words: cofactors could be the missing link between abiotic and biotic (enzymatic) catalysis. Our group shows how cofactors employed in the acetyl-CoA pathway can function under conditions found in serpentinizing systems, where iron- and nickel-containing minerals transfer electrons to the protons of water, continuously producing hydrogen gas (H₂) – LUCA's main electron and energy source [5,6].

Dr. Martina Preiner leads the Geochemical Protoenzymes research group at the Max Planck Institute for Terrestrial Microbiology in Marburg. Her interdisciplinary research focuses on understanding how life emerged from non-life by exploring the transition from geochemistry to biochemistry. By integrating chemical, biochemical, and geochemical methods, her team investigates how mineral surfaces and organic cofactors could have facilitated early CO₂ fixation and metabolic processes. Dr. Preiner's work aims to bridge the gap between environmental reactions and genetically encoded metabolic functions, providing insights into the origin of life.



1. M. Weiss et al. (2016) Nat. Microbiol. 1, 16116.
2. Moody et al. (2024) Nat. Ecol. Evol. 8, 1654–1666
3. M. Preiner et al. (2020) Nat. Ecol. Evol. 4, 534–542.
4. J.C. Xavier et al. (2020) Proc. Biol. Sci. 287, 20192377
5. D. P. Pereira et al. (2022) FEBS J. 289, 3148–3162.
6. D. P. Pereira et al. (2024) BioRxiv. 10.1101/2024.10.11.617347

Tuesday, 2nd 09:20 am

From small size to big influence: small proteins modulate bacterial virulence

Small proteins are typically defined as proteins of less than 100 amino acids, which are directly synthesized from short mRNAs by ribosomes. Small proteins are found across all three domains of life and participate in various biological processes, including stress response, drug efflux, cell-cell communication, and immune surveillance. One medically relevant function of small proteins is regulating bacterial virulence by targeting two-component systems - the primary signaling pathways that enable bacteria to adapt to environmental changes. One such system, PhoQ/PhoP, detects certain host-associated stimuli and regulates virulence gene expression in *E. coli*, *Salmonella*, *Klebsiella*, and related enterobacteria. The small MgrB inhibits PhoQ function, thereby reducing the output of the pathway. In this talk, I will discuss our findings on MgrB inhibition, its natural physiological role, and how we are using it as a blueprint to design “Super-MgrBs.”

Dr. Jing Yuan is a Research Group Leader at the Max Planck Institute for Terrestrial Microbiology in Marburg, Germany. Her research focuses on the roles of small proteins in bacterial signaling networks, particularly their influence on two-component systems like PhoQ/PhoP that regulate virulence in enterobacteria. By integrating molecular biology, synthetic biology, and structural approaches, her team aims to elucidate the mechanisms by which these small proteins modulate bacterial pathogenicity and to explore their potential as targets for novel antimicrobial strategies.



Tuesday, 2nd 09:40 am

Leveraging orthogonality to escape the limitations of bioproduction

Engineered microbes offer exciting new opportunities for the sustainable production of value-added chemicals from cheap feedstocks without the need for high temperatures, pressure, or toxic solvents. However, the metabolic integration of synthetic pathways can be challenging. One major concern is the competition of natural and synthetic pathways for the same core metabolites. So far, these conflicts have been approached by spatial or temporal separation of synthetic metabolism. Orthogonal pathways offer a third possibility for metabolic separation – one on the biochemical level. Pathways proceeding via non-natural intermediates lower the cross-talk between synthetic and natural metabolism, and thus the overall burden on the cell. Here, we discuss the benefits of such systems, and propose the use of non-natural cofactors to achieve further separation of synthetic and natural metabolism.

Dr. Maren Nattermann leads the research group Synthetic Cofactors and Orthogonal Metabolism at the Max Planck Institute for Terrestrial Microbiology in Marburg. Her work focuses on engineering synthetic metabolic pathways and developing orthogonal cofactor systems to enhance the efficiency and sustainability of microbial production processes. Dr. Nattermann earned her Ph.D. in Biology from Philipps-Universität Marburg in 2023, following her M.Sc. in Biochemistry from Heidelberg University. She has been recognized with awards such as the VAAM Doctoral Prize and the MarBiNa Award for her contributions to synthetic metabolism and CO₂ utilization.



Tuesday, 2nd 10:00 am

Real-time dynamics of cellular processes in bacteria

Cellular processes are known to be highly dynamic, but how these dynamics are controlled and used by living cells remains only poorly understood. This is particularly true for the operation of many protein networks that cannot be directly monitored using gene expression reporters. One of the aims of our group is thus to investigate the dynamics of signaling, motility and metabolic networks, using a combination of FRET sensors of signaling molecules and metabolites with microfluidics and mathematical modeling, to obtain insights into the real-time operation of bacterial cells.

Prof. Dr. Victor Sourjik is Director at the Max Planck Institute for Terrestrial Microbiology in Marburg, Germany, where he leads the Department of Systems and Synthetic Microbiology. His research aims to understand the organization and dynamics of cellular networks in microorganisms, focusing on how cells sense, process, and respond to environmental signals. Using approaches from systems biology, biophysics, and synthetic biology, his group studies model organisms such as *Escherichia coli* and yeast. Victor Sourjik has received multiple honors, including an ERC Advanced Grant and election to the European Academy of Microbiology.



Tuesday, 2nd 10:20 am

Fixing Carbon-fixation: Rebuilding photosynthesis with synthetic biology

Microorganisms and plants capture billions of tons of CO₂ every year through photosynthesis. However, natural photosynthesis is not sufficient to mitigate anthropogenic climate change. My talk will discuss the evolution and limitation of biological photosynthesis and show how we can use synthetic biology to create alternatives that convert CO₂ more efficiently than those processes evolved by nature. I will present strategies of how to engineer novel enzymes and pathways for the fixation of CO₂ and talk about the transplantation of these solutions into natural and synthetic cells to create novel catalytic systems, cell factories and artificial chloroplasts for the capture and conversion of CO₂. My lecture will also take a broader look at the field of synthetic biology, through which humans can become an active part of evolution and initiate and realize new solutions that natural evolution has not invented (yet).

Prof. Dr. Tobias J. Erb is Director at the Max Planck Institute for Terrestrial Microbiology in Marburg, Germany, where he leads the Department of Biochemistry and Synthetic Metabolism. His research focuses on understanding and engineering carbon metabolism with the goal of developing novel synthetic pathways for carbon fixation. Combining tools from biochemistry, synthetic biology, and systems biology, his group explores how microbes can be harnessed or redesigned to address challenges in sustainability and climate change. Tobias Erb is a recipient of numerous awards, including the Gottfried Wilhelm Leibniz Prize and the EMBO Gold Medal.



Tuesday, 2nd 14:10 am

Decoding and Taming Nitrogenases for CO₂ Conversion

Nitrogenases are the only known enzymes that catalyze the reduction of molecular nitrogen (N₂) to ammonia (NH₃), driving the global nitrogen cycle. Besides the conversion of N₂, we recently showed that nitrogenases convert carbon dioxide (CO₂) to carbon monoxide, formate and hydrocarbons (1-5), suggesting CO₂ to be a competitor of N₂.

We have investigated the competing reduction of CO₂ and N₂ by the molybdenum (Mo)- and iron (Fe)-nitrogenase (6). We find the Fe-nitrogenase almost three-fold more efficient in CO₂ reduction than the Mo-isoform. The same effects translate in vivo, where *Rhodobacter capsulatus* strains relying on the Fe-nitrogenase reduce CO₂ physiologically to formate and methane, highlighting the potential of Fe-nitrogenases for the biotechnological conversion of CO₂ into value-added compounds. Furthermore, we use structural approaches (cryo-EM (7) and X-ray crystallography (8)) to obtain new insights of the nitrogenase mechanism to engineer nitrogenases towards CO₂ reduction.

Dr. Johannes Rebelein is the leader of the Emmy Noether Research Group Microbial Metalloenzymes at the Max Planck Institute for Terrestrial Microbiology in Marburg. His research focuses on understanding and engineering metalloenzymes, particularly nitrogenases, to convert carbon dioxide (CO₂) into valuable hydrocarbons. By combining structural biology, biochemistry, and synthetic biology, his group aims to develop sustainable biocatalytic processes for carbon capture and utilization. Dr. Rebelein earned his Ph.D. from the University of California, Irvine, and conducted postdoctoral research at the University of Basel. He has been recognized with the 2024 VAAM Research Prize and was selected as an EMBO Young Investigator in 2024.



References:

1. J. G. Rebelein, Y. Hu, M. W. Ribbe, *Angew. Chem. Int. Ed.* 53, 11543-11546 (2014).
2. J. G. Rebelein, Y. Hu, M. W. Ribbe, *ChemBioChem* 16, 1993-1996 (2015).
3. J. G. Rebelein, M. T. Stiebritz, C. C. Lee, Y. Hu, *Nat. Chem. Biol.* 13, 147-149 (2017).
4. N. N. Oehlmann, J. G. Rebelein, *ChemBioChem* 23, e202100453 (2022).
5. N. N. Oehlmann et al., *Sci. Adv.* 10, eado7729 (2024).
6. N. N. Oehlmann et al., *Sci. Adv.*, accepted (2024).
7. F. V. Schmidt et al., *Nat. Struct. Mol. Biol.* 31, 150-158 (2024).
8. M. Ren et al., *Nat. Commun.* 16, 5845 (2025).

Tuesday, 2nd 14:30 am

Structure analysis of the Type IV pilus machine from *Myxococcus xanthus* reveals a novel component

The most widespread form of surface-associated bacterial motility is mediated by Type IV pili (T4P), which undergo cycles of extension, surface attachment, and retraction to generate forces that pull the cell forward. This mode of motility has been extensively studied in Gram-negative bacteria such as *Pseudomonas*, *Neisseria*, and *Myxococcus*. In these organisms, T4P function is driven by a complex machinery comprising at least 15 proteins, present in multiple copies and spanning the outer membrane, periplasm, inner membrane, and cytoplasm.

The overall architecture of the type IV pilus machinery (T4PM) has been resolved in both pilated and non-piliated states at ~3–4 nm resolution. However, this level of detail does not yet reveal how the individual protein components are organized, how they assemble into a functional nanomachine, or how they have evolved to adapt to environmental changes.

Our goal is to obtain a high-resolution structure of the *M. xanthus* T4aPM in order to define the precise protein–protein interactions and stoichiometry of its 15 core components. In this process, we have identified a previously unrecognized component, which we have designated PilL. We are now pursuing structural and functional analyses of PilL.

Dr. Anke Treuner-Lange is a Project Group Leader in the Department of Ecophysiology at the Max Planck Institute for Terrestrial Microbiology in Marburg. Her research focuses on the structure, function, and regulation of the Type IVa pilus (T4aP) machinery in *Myxococcus xanthus*, utilizing a combination of genetics, cell biology, biochemistry, and transcriptome and proteome analyses.



Tuesday, 2nd 14:50 am

Decoding Microbial Stress: The Hidden Role of Adenosine Dinucleotides

Microorganisms frequently face environmental stress, requiring swift cellular responses. Diadenosine tetraphosphate (Ap₄A), once thought to be a metabolic byproduct, is now recognized as a conserved stress-signaling alarmone. Its levels surge under conditions like oxidative damage, heat shock, and nutrient limitation, influencing stress response pathways through protein interactions. Uncovering Ap₄A's role provides fresh insights into microbial resilience and offers potential for novel antimicrobial or bioengineering strategies.

Prof. Dr. Gert Bange is a structural biologist and biochemist at Philipps-Universität Marburg, where he serves as Vice President for Research and holds a professorship in Biochemistry. He is also a Max Planck Fellow at the Max Planck Institute for Terrestrial Microbiology. His research focuses on the molecular mechanisms of microbial adaptation to environmental stresses, utilizing structural biology, systems biology, and cell biology approaches. Prof. Bange's work has significantly advanced the understanding of macromolecular machines, bacterial stress responses, and microbe-host interactions. He has been recognized with numerous awards, including an ERC Advanced Grant, and actively contributes to scientific communities through editorial roles and mentorship programs.



Tuesday, 2nd 15:10 am

The secret nightlife of phototrophs

Phototrophs are defined by their ability to harvest light energy, yet they often experience extended darkness: night, polar winters, sinking in the water column, or burial in sediments. How do they cope? Diatoms, globally important eukaryotic primary producers and central to the carbon cycle, reveal surprising metabolic flexibility. They can store nitrate at concentrations orders of magnitude above ambient levels and use it as an electron acceptor under dark, anoxic conditions. In sediments, they migrate over centimeter scales, switching from photosynthesis in the light to nitrate respiration in the dark. Even more striking, their intracellular nitrate pool can fuel sulfide-dependent CO₂ fixation, uncovering a role in chemosynthetic productivity. These findings broaden the ecological niche of diatoms and highlight overlooked connections between their physiology and global biogeochemical cycles. With genetically tractable model systems, we can now begin to resolve the molecular basis of these metabolisms and their implications for ecosystem functioning.

Dr. Judith Klatt leads the Biogeochemistry Lab at the Microcosm Earth Center, a joint initiative of the Max Planck Institute for Terrestrial Microbiology and Philipps-Universität Marburg. Her interdisciplinary research explores how microbial processes influence elemental cycles in Earth's present and past humid environments. By integrating chemical, geological, and biological perspectives, her team investigates microbial interactions across molecular to ecosystem scales, with a particular focus on CO₂-fixing photosynthetic microorganisms. Dr. Klatt's work has contributed to understanding the links between microbial activity and global biogeochemical processes, including insights into Earth's oxygenation history.



In 2024, Dr. Klatt was awarded a European Research Council (ERC) Starting Grant for her project "RETRO-PUMP," which aims to reconstruct global redox transitions based on an evolving Precambrian biological carbon pump.

Tuesday, 2nd 15:30 am

Natural Products in Organismic Interactions

Prof. Dr. Helge B. Bode is Director of the Department of Natural Products in Organismic Interactions at the Max Planck Institute for Terrestrial Microbiology in Marburg, Germany, and holds a professorship in Chemical Biology at Philipps-Universität Marburg. His research focuses on understanding the roles of microbial natural products in inter-organismal interactions and engineering their biosynthetic pathways. Utilizing model systems such as entomopathogenic nematodes and their symbiotic bacteria, his team investigates how these metabolites function as chemical signals and explores the manipulation of biosynthetic gene clusters to produce novel compounds. Prof. Bode has been recognized with several prestigious awards, including multiple European Research Council (ERC) grants, for his contributions to natural product research and synthetic biology.



Poster Sessions

Session 1: Early Career Scientists 1

Monday, 1st 13:00 am (Poster Session includes a walking lunch)

Discover cutting-edge research from postdocs at the Max Planck Institute for Terrestrial Microbiology and selected guest researchers. This is your chance to explore diverse projects, ask questions, and learn firsthand what it's like to work as a postdoc at an MPI. Use this opportunity to connect with peers, gain insights into different research paths, and start building valuable professional relationships.

Session 2: Early Career Scientists 2

Monday, 1st 19:10 am (Poster Session includes a walking dinner)

You enjoyed exploring research over lunch—now it's time to do it again, but with dinner on the side! Join us for another round of poster presentations from postdocs and guest researchers, dive into new projects, and keep the conversations going. Great science, good food, and even better networking opportunities await.

Session 3: Infrastructure @MPIterMic

Tuesday, 2nd 13:10 am (Poster Session includes a walking lunch)

Science doesn't happen in isolation—it's supported by a whole network of people and resources. In this session, meet the non-scientific players who keep the institute running and thriving. Learn about our cutting-edge infrastructure in metabolomics, proteomics, and microscopy, and get to know the postdoc representatives, the works council, and other socially engaged groups. This is your chance to discover the broader community, explore the resources available, and see how science and support go hand in hand.

Session 4: Faculty Dinner

Tuesday, 2nd 13:10 am (Poster Session includes a walking dinner)

Over dinner, connect with the people who shape the institute's research vision. Faculty members, established PIs, and emeritus professors will be sharing posters, stories, and insights from their scientific journeys. Take this unique opportunity to ask questions, exchange ideas, and gain perspective from those who have built their careers in science—and are ready to share their experience with you.

Early Career Scientists 1

Poster 1 - Dr. Dana Piazza

Dual-approach enzyme engineering of feruloyl esterases for efficient polyphenol extraction in hydroalcoholic media

Agro-industrial by-products are a sustainable source of polyphenols, such as ferulic acid and other hydroxycinnamic acids. These high-value bioactive molecules are widely used as antioxidant, anti-inflammatory, and UV-protective agents, making them particularly attractive for applications in the cosmetic and food industries. Enzyme-assisted extraction offers a greener alternative to chemical or solvent-based methods but is often limited by low yields and poor enzyme performance. Here, we applied a dual-approach protein engineering strategy to enhance both the catalytic efficiency and solvent tolerance of FaeLam, a feruloyl esterase from *Lactobacillus amylovorus*. Through a semi-rational approach we first identified beneficial mutations, which were then further diversified through random mutagenesis. Using this strategy, we achieved a 2.5-fold increase in catalytic efficiency and nearly a threefold increase in enzyme activity in 10% v/v ethanol.

Poster 2 - Dr. Leanid Laganenka, Ananda Sanches Medeiros, Melissa Kivoloka, Timo Glatter, Victor Sourjik

Toolkit for investigating phenotypic heterogeneity in multidrug-resistant *Klebsiella pneumoniae*

Molecular studies of *Klebsiella pneumoniae* are hindered by the prevalence of multidrug-resistant (MDR) variants, which are resistant to most commonly used antibiotic selection markers, making standard molecular tools ineffective. We are developing a set of plasmids enabling simultaneous visualization and single-cell gene expression analysis in MDR *K. pneumoniae* using alternative antibiotic markers.

With this system, we observed pronounced phenotypic heterogeneity during *in vitro* biofilm formation, with two distinct cell populations: biofilm-associated cells at the base and large clonal microcolonies on the top. Proteomic analysis revealed that microcolony growth is linked to elevated expression of RpoS-regulated stress-response genes. Confocal microscopy with our dual-fluorophore system confirmed higher RpoS expression in microcolony cells compared to the rest of the biofilm.

Our toolkit offers a robust approach for studying phenotypic heterogeneity in MDR *K. pneumoniae* and will be further validated in *ex vivo* and *in vivo* models under physiologically relevant conditions.

Poster 3 - Dr. Ghada Yousif

Good vibes: Positive interactions are common in soil bacterial communities

The majority of soil bacteria resist cultivation in our labs, which limits our understanding of their ecological functions. One possible explanation is the metabolic dependencies among soil bacteria, yet we lack systematic studies of how prevalent these interactions are and how they shape the community structure. To fill this gap, I systematically screened 27 soil bacterial communities, isolating a large library of soil bacteria, and metabolically characterized them. The results showed that metabolite-dependent phenotypes (auxotrophs) are common, forming more than 50% of the cultivated bacteria. Whole genome sequencing of 60 representative isolates showed that gene loss and insertion sequences are key drivers of the evolution of metabolic dependencies. Genome-scale metabolic models, computational analyses, and cocultivation experiments demonstrated that co-occurring genotypes complemented the metabolic needs of auxotrophs. The genomic data revealed that a carbon source exchange drives the formation of mixed clusters, demonstrating that soil bacteria exist within integrated metabolic networks.

Poster 4 - Dr. Chanqing Liu

Lanthanide-dependent metabolism in a phyllosphere *Methylophilus* from oak leaves

Our study describes an obligate methylotrophic bacterium (*Methylophilus* oak M-7) isolated from the phyllosphere. For methanol oxidation, strain M-07 harbors two distinct types of PQQ-methanol dehydrogenase (MDH): one encoded by *mxafJG*, referred to as Ca-MDH, and four encoded by *xoxF*, known as La-MDH (Group 4). In addition, a small metallophore-Protochelin is found when strain M7 growing under lanthanides conditions, and this compound was produced in *Escherichia coli* via heterologous expression of a gene cluster derived from strain M7. A yield of 340 mg was achieved from a 12-liter culture, representing the highest reported yield to date. Protochelin was shown to bind lanthanides, however, it has a higher binding affinity for Fe³⁺ compared to La³⁺. Proteomics analysis of cells cultivated under low/high La and Ca concentrations further revealed significant changes in protein expression, suggesting the presence of a La utilization and transport system, which may provide valuable insights into microbial strategies for rare earth element acquisition.

Poster 5 - Dr. Daniela Vidaurre Barahona

Molecular regulation of the symbiosis between entomopathogenic nematodes and their bacterial symbionts

The bacteria *Photobacterium* and *Xenorhabdus*, members of the Enterobacteriaceae family, establish mutualistic associations with entomopathogenic nematodes (EPNs) belonging to the genera *Heterorhabditis* and *Steinernema*, respectively. The life cycle of EPNs involves a free-living stage known as infective juvenile (IJ). The primary function of the IJ is to locate and infect potential insect hosts, carrying the bacterial symbiont within its intestinal tract. Upon entering the insect through natural openings, the bacteria are released into the hemocoel, producing a diverse array of natural compounds, including toxins and enzymes. These compounds serve to digest insect tissues, providing a nutritional source that facilitates the optimal development and reproduction of the nematode. This maturation process is marked by an initial recovery phase during which IJs transition into the adult stage. Following 2-3 nematode generations and depletion of the food source, the offspring undergo a developmental shift, transforming into the next generation of IJs that retain the bacterial symbiont. Subsequently, these IJs emerge from the insect, actively seeking a new host. In the case of *P. luminescens*, signals associated with the nematode life cycle include isopropyl stilbene (IPS) and intermediates of its biosynthetic pathway. The aim of this project was to investigate the influence of natural products (NPs) synthesized by the bacterial symbiont on nematode development. Comparative experiments were conducted in *S. diaprepesi* using wild-type (WT) and mutant strains of *X. doucetiae* deficient in NP synthesis. These strains included those lacking the global post-transcriptional regulator protein Hfq, a phosphopantetheinyl transferase (PPTase), deletions and promoter exchange related to tryptophan/phenylalanine decarboxylase (DC) linked to acyl amide biosynthesis, and promoter exchange associated with gene clusters responsible for NP production. Based on the obtained results, it has been determined that amines/amides and proteogomycin are essential for the proper development of EPNs. Conversely, excessive production of GameXPeptide has a detrimental effect.

Early Career Scientists 2

Poster 6 - Dr. Yu Ping

Engineering of ferulic acid decarboxylase for 1,3-butadiene biosynthesis

As one of the most valuable building blocks applied in synthetic rubber and plastic production, over 95% of 1,3-butadiene is derived as a by-product of ethylene production via naphtha steam cracking at approximately 800 °C. The unstable price of petrochemicals and fluctuations in fossil-based feedstock availability increase the demand for alternative sustainable bioproduction from feedstocks such as glucose and lignin. One promising solution involves the use of engineered ferulic acid decarboxylase (FDC) to produce 1,3-butadiene. However, the low activity remains a major bottleneck for its practical application. Therefore, our goal is to enhance the activity of ferulic acid decarboxylase and develop a more efficient artificial biosynthetic pathway for the sustainable production of 1,3-butadiene.

Poster 7 - Dr. Nataliya Safronova

A genetic in vitro system to decipher the mechanisms of thylakoid protein import

Cell membranes are fascinating bioactive platforms that protect the cellular environment and support metabolism. As a striking example, thylakoid membranes encompass photosynthetic protein complexes and pigments, to serve as the central site for light-dependent processes. At the heart of these functions, membrane proteins mediate intricate interactions with surrounding lipids as well as a diverse array of inter- and intracellular signals. However, the amphipathic nature of membrane protein machinery presents a significant challenge to deciphering its functionality in shaping organelle identity, biogenesis and membrane traffic. Consequently, protein transport mechanisms across chloroplast membranes remain elusive, leaving a gap in our understanding of thylakoid biogenesis. The development of cell-free protein synthesis (CFPS) introduced a novel experimental framework for synthesizing and inserting membrane proteins into synthetic lipid membranes, enabling their functionalization in vitro. The most prominent successful example is the key E.coli inner membrane translocon SecYEG, which transports numerous proteins into the periplasmic space and facilitates their insertion into the membrane. Broad substrate range and functional versatility of Sec (and its chloroplast homolog SecYE) make it a promising foundation for studying the thylakoid proteome import in vitro and for investigating the molecular mechanisms underlying protein transport and insertion in thylakoid membranes.

Poster 8 – Dr. Delfina Patricia Henriques Pereira

NAD's dinucleotide structure enables specific reduction on mineral surfaces

Coenzymes may have played a central role in the origin of metabolism by bridging geochemical catalysis and early biochemistry, as they can function independently of enzymes in mineral-rich environments. Many share nucleotide-derived features, such as AMP moieties. Here we compare the universal redox cofactor Nicotinamide Adenine Dinucleotide (NAD), with its AMP-free fragment, Nicotinamide Mononucleotide (NMN). The differences between the two revealed that the AMP “tail” of the dinucleotide seems to be necessary to prevent overreduction of the nicotinamide-bearing nucleotide in our mineral-based setup, and attributes a competitive advantage when both molecules are present. These results support the theory that AMP is a prebiotic handle and that further experimentation should be done on NAD and other AMP-containing cofactors.

Poster 9 - Helena Schulz-Mirbach

Coupling growth of *Escherichia coli* to modules of synthetic CO₂ fixation cycles

Microbial one-carbon (C₁) assimilation is paving the way towards a more sustainable future based on a circular bioeconomy, with synthetic metabolic designs overcoming the limitations of natural metabolism. While a plethora of such designs have been proposed and multiple have been shown in vitro, their translation to in vivo systems has progressed much slower. Therefore, we followed a streamlined approach to identify bottleneck reactions of the most efficient CO₂ fixation cycles and design auxotrophic metabolic sensor strains that would rely on those reactions for growth. We constructed and characterized the relevant arrays of selection strains, namely selecting for 3-hydroxypropionate, pyruvate, acetate, succinate, glyoxylate or glycolate. To enhance the use of extant selection strains, we created a comprehensive overview of the *E. coli* selections which cover central, amino acid and energy metabolism and are already available to the metabolic engineering community. Using those sensors, we engineered growth via parts of the MOG cycle, the THETA cycle and the HOPAC cycles which were not yet part of the in vivo metabolism repertoire. Especially the development of a novel lactyl-CoA mutase activity as core element of the envisioned MOG cycle required interfacing in vitro characterisations tightly with in vivo mutagenesis and selection of improved enzyme variants. To more efficiently optimize entire reaction cascades in vivo, we designed a novel workflow for the machine-learning guided optimisation of expression levels and demonstrate it on a proof-of-principle basis using parts of the THETA cycle. Where needed, we evolved modules by adaptive laboratory evolution, so they can be combined with other cycle parts in a mix and match fashion for further engineering of synthetic CO₂ fixation in the future.

Poster 10 – Dr. Anna Papageorgiou

Evolution and functional diversity of archaeal Replication Protein A

Replication Protein A (RPA) is the primary single-stranded DNA-binding protein in Archaea and Eukaryotes; it is essential for genome integrity during DNA replication and repair. While canonical heterotrimeric RPAs are well-characterised, many Archaea encode atypical dimeric and/or monomeric variants whose structure and function remain largely unknown. This gap of knowledge limits our understanding of how essential protein complexes evolve and retain function despite architectural simplification. In my current study I take an integrative approach to uncover the functional and evolutionary diversity of archaeal RPAs. I combine biochemistry, biophysics, and structural biology to examine how three distinct atypical RPA variants from *Methanosarcina acetivorans* bind and protect ssDNA. Preliminary results reveal major structural differences; thus, this complex offers a unique opportunity to study François Jacob's concept of 'evolutionary tinkering' within an essential genome maintenance complex. The gained mechanistic insights will inform a large-scale phylogenomic analysis across thousands of archaeal genomes to reconstruct the evolutionary history of RPA, focusing on gene loss, domain reshuffling, and compensatory adaptations. By bridging structural and evolutionary biology, I expect to reveal how genome stability is maintained in Archaea with simplified forms of an essential replication factor.

Poster 11 – Dr. Victoria Anastasia Sajtovich

Making an IMPRINT on *Ideonella sakaiensis* Domestication: Combining Genomics, Proteomics, and Biochemistry to Advance the First Plastic-Degrading Microbe for Biotechnology

Waste streams such as polyethylene terephthalate (PET) are a unique carbon source for engineered microbes to produce value-added products for the circular bioeconomy. Several researchers have tackled the enzymology of the components of plastic degradation pathways, however little attention has been given to the microbe in which the complete PET degradation pathway was first elucidated: *Ideonella sakaiensis* (Yoshida, S. et al, 2016). While this reflects economic incentives to advance enzymatic recycling as well as the paucity of genetic tools for non-model microbes, my research aims to address this gap. I offer the first closed genome of *I. sakaiensis*, an electro-transformation method, as well as a functional origin-of-replication for building genetic tools for the microbe. Strides towards improving its poor transformation efficiency are also made through the construction of an IMPRINT system, although further optimization is necessary to obtain a clear boost in transformation efficiency. To complement these genomic investigations, proteomic characterization of microbial growth on terephthalic acid (TPA), one of the monomers of PET degradation, was undertaken alongside a thorough biochemical characterization of its TPA-dependent transcription factors. Together, these data advance our understanding of *I. sakaiensis* PET catabolism, offer new TPA-dependent transcription factors for biosensing, and provide a path forward for engineering other environmental isolates for biotechnological benefit.

Poster Session 3 - Infrastructure @MPIterMic

Poster 12 - Silvia Gonzalez

Know Your Works Council – Empowering Postdoctoral Women at MPI-TM

The Works Council at MPI Marburg is a democratically elected body that represents all employees, including postdocs, advocating for fair working conditions, equal treatment, and work–life balance. Through legal co-determination rights and close collaboration with institutional representatives, it actively supports a healthier and more inclusive workplace.

Poster 13 - Dr. Anke Treuner-Lange, Dr. Nicole Paczia, Dr. Martina Preiner

The Gender Equality Office - Mind the leaky pipeline: Gender equality officers at work & the Max Planck Society's Voluntary Self Commitment

The “leaky pipeline” refers to the steady decline in the proportion of women in science, technology, engineering, and mathematics (STEM) as they progress to more senior career stages. To address this issue, the Max Planck Society has committed to a Voluntary Self Commitment (SVP) with two clear goals: to increase the number of women in leadership roles by one percentage point each year until 2030, and to ensure every Max Planck Institute has at least one female director.

Approximately 200 Gender Equality Officers (GEOs), along with their deputies, actively contribute to creating an inclusive and gender-equal workplace within the Max Planck Society. At the Max Planck Institute for Terrestrial Microbiology (MPITM) in Marburg, we are a dedicated team of three GEOs and we will share insights into our voluntary work and invite your perspectives and ideas on strategies to fix the leaky pipeline. Your input is invaluable as we work together to foster lasting change.

Poster 14 - Postdoc Representatives at MPI Marburg

The Postdoctoral Representatives at the MPI-TM serve as a bridge between postdocs, institute leadership, and external networks. We organize professional development activities, foster community engagement, and ensure that Postdoc voices are represented in decision-making processes within and beyond the institute. We attend regular meetings with the directors and the scientific administration to represent the interests of the postdoc community and to raise and discuss various topics that concerns the community. Through collaboration with PostDocNet, we aim to strengthen community connections beyond the institute. Our overall goal is to support postdocs in career development, collaborations, networking and communication, thereby creating a supportive research environment for all.

Poster 15 - Dr. Georgia Angelidou, Dr. Inal Bakhytkyzy

Meatbolomics@MPIterMic

The Metabolomics Core Facility at the Max Planck Institute for Terrestrial Microbiology in Marburg provides comprehensive support for small molecule analysis using advanced LC MS platforms. Featuring four state of the art LC MS systems, the facility offers end to end services—including experimental design consultation, sample preparation, targeted and untargeted metabolite profiling, semi quantitative and absolute quantification across diverse sample types (e.g., bacterial and mammalian cells, yeast, body fluids, and tissues), and robust statistical data analysis pipelines

Poster 16 - Dr. Timo Glatter

The Proteomics Core Facility

The Proteomics Core Facility (PCF) provides state-of-the-art shotgun proteomics strategies to support the scientists in their research. The PCF staff members have broad experience in proteomics workflows and provide custom-tailored workflow solutions for the individual projects. We offer collaborative support for each step of the proteomics experiment including planning, execution as well as discussion of results and follow-up possibilities. The PCF is strongly involved in collaborative projects with a constantly growing number of clients. An update of the instrumentational and quantitative proteomics workflow infrastructure has been successfully installed, thereby supporting and advancing the research of the MPI scientists. The many different collaborative proteomics projects contributed to a number of publications. Intense teaching activities are continuously offered within the IMPRS course program.

Poster 17 - Dr. Gabriele Malengo

The Microscopy Core Facility

The Flow Cytometry & Imaging Facility at the Max Planck Institute for Terrestrial Microbiology provides state-of-the-art instrumentation and support for single-cell analysis. Our cytometry suite includes BD Fortessa analyzers with high-throughput multi-well sampling and a BD FACSAria Fusion cell sorter for advanced multi-color sorting. The imaging platform comprises confocal, super-resolution, and wide-field microscopes, enabling detailed studies of microbial structure, dynamics, and interactions. Together, these technologies support a wide range of applications from quantitative single-cell phenotyping to protein localization and live-cell imaging.

Poster Session 4 – Faculty Dinner

Poster 18 - Dr. Irina Kalita

Motility and chemotaxis of bacterial minicells

Bacterial minicells are submicron-sized spherical cells produced by bacteria as a result of aberrant cell division. While their cellular composition is similar to parental bacteria, minicells lack genomic DNA and therefore cannot reproduce. Because of their inability to proliferate and small size, bacteria-derived minicells have attracted attention of targeted drug delivery, where severe toxicity of drugs can be mitigated through more precise and efficient chemotaxis-based delivery methods. To develop an active delivery approach, we engineered *Escherichia coli* strains that generate motile minicells and further enhanced their swimming speed and chemotaxis response via genetic modifications targeting flagella number, length, and rotation speed. We further established a procedure for conjugating minicells with cargo particles and demonstrated that these minicell-driven biohybrids are chemotactic and capable of actively accumulating at the source of an attractant.

Poster 19 - Dr. David Adam

HAPPY: High-throughput APPLication for age determination in Yeast

The average human life expectancy has increased rapidly in the last decades. As people live longer and longer, the impact of age-related diseases becomes increasingly important. Despite great efforts in research, the scientific understanding of the aging process continues to be obscure.

The single-cell organism *Saccharomyces cerevisiae* has been and continues to be an important model for studying the molecular mechanisms of aging. It has played a pivotal role in the understanding of basic cellular processes and has some surprising similarities with mammalian (including human) cells, which makes it effective to model human diseases, e.g. in the context of drug repurposing. However, current yeast lifespan determination's laborious and low-throughput methods limit its usefulness in high-throughput experiments.

We have invented an innovative microfluidic technology to track the lifespan of yeast in a way that reduces the workload by more than 90 %. Thus, our technology makes it possible to utilize the full potential of yeast as a model organism in aging research and drug screening.

Poster 20 - Dr. Ilka Bischofs-Pfeifer

Complex adaptive traits in beneficial Bacilli

The μ CATs Lab studies beneficial, spore-forming and industrially relevant Bacilli. Our goal is to unravel the mechanisms that enabled these bacteria to spread in nature and survive in ever-changing environments. By understanding their complex adaptive traits (CATs), we aim to develop innovative solutions to better control and engineer these bacterial populations in applied settings. Much of our work focuses on the fascinating biology and biophysics of dormant and very resistant endospores, which serve in a wide range of spore-based applications ranging from green agriculture, health & material science to astro-biotechnology. We also study the ability of these bacteria to make special metabolites and act as cell factories to produce valuable compounds. Importantly, not all spores and cells behave identical. We investigate how this heterogeneity arises and study its consequences.

Poster 21 - Dr. Remy Colin, Silvia Espada Burriel, Giacomo Di Dio, Paula Siaucho Unriza, Andrea Alvarez Osorio

Physically emergent spatiotemporal structures in mixed bacterial communities

Physically emergent spatiotemporal structures in mixed bacterial communities

Abstract: Natural bacterial communities usually mix many phenotypically diverse species and often exhibit complex spatial structures that are thought to be important for their functioning. Our lab uses a simple model system, a mixture of motile and non-motile *Escherichia coli* bacteria, to investigate the roles of physical interactions, especially the ones arising from motility, in structuring the community in various conditions, and the physiological consequences of the emergent structures. In microfluidics systems, we found that the fluid flows generated by the swimmers near surfaces, combining with non-motile sedimentation, induce heterogeneous patterns of non-motile cell density. Additionally, externally imposed fluid flows and chemotactic motion stir the motile cell motion, leading to a complete reshaping of the bacterial community structure. All these patterns affect the aggregation dynamics and lead to original biofilm structures. We currently investigate how these emergent structures affect the ability of co-dependent bacterial strains to collaborate.

Poster 22 - Astrid Isabell Bendix

Supporting Female Entrepreneurship in Science – The Mafex Approach

Mafex, the technology transfer office of Philipps-Universität Marburg, actively promotes entrepreneurship among researchers with a particular focus on supporting women in science. Recognizing that female founders remain underrepresented in the start-up landscape, Mafex provides tailored guidance, mentoring, and networking opportunities to encourage and empower women to transform their research into business ideas. Through workshops, funding advice, and close collaboration with regional and national initiatives, Mafex helps reduce barriers to entrepreneurship and fosters a more inclusive innovation ecosystem. This poster presents current programs, success stories, and ongoing efforts to strengthen female entrepreneurship at the interface of academia and industry.

Poster 23 - Prof. Dr. Martin Thanbichler

Spatiotemporal organization of bacterial cells

Who will be joining for Dinner

The following pages introduce the experienced researchers who will be present and happy to connect with you during the dinner.

Some of our dinner guests have also shared their expertise in talks earlier today — you will find their full bios in the section with the talk abstracts. We encourage you to reach out to them as well, as they will be available for conversation and networking during the evening.

Speakers joining the dinner:

- Dr. Martina Preiner
- Dr. Jing Yuan
- Dr. Maren Nattermann
- Prof. Dr. Victor Sourjik
- Prof. Dr. Tobias Erb
- Dr. Johannes Rebelein
- Dr. Anke Treuner-Lange
- Prof. Dr. Gert Bange
- Dr. Judith Klath
- Prof. Dr. Helge Bode

Prof. Dr. Anke Becker is a German microbiologist and a W3-professor of Microbiology at the Philipps-Universität Marburg, where she has led the Centre for Synthetic Microbiology (SYNMIKRO) since 2016. She studied biology in Bielefeld, earning her PhD in microbial genetics in 1994 and completing her habilitation. After leading the microbial genetics groups at Bielefeld and serving as visiting researcher at MIT, she held a professorship at Freiburg prior to moving to Marburg in 2011. Her research focuses on microbial genomics, synthetic biology and genome engineering to design robust bacterial chassis for new biotechnological applications.



Prof. Dr. Verena Taudte heads the research group for Mass spectrometry-based metabolomics at the Philipps-Universität Marburg, where she develops and oversees advanced mass spectrometry-based workflows for targeted and untargeted metabolomics, including tracer-based flux analysis. Her research applies these techniques to biomedical challenges, investigating metabolic alterations in infections, fibrotic diseases, and immune responses.



In addition to her academic role, Prof. Taudte serves as President of the German Society for Metabolomics (DGMet), actively promoting the exchange of knowledge and collaboration within the metabolomics community

Prof. Dr. Martin Thanbichler is a microbiologist at Philipps-Universität Marburg and the Max Planck Institute for Terrestrial Microbiology. He studied in Munich and completed his postdoctoral work at the Stanford University before establishing his own research group in Marburg. His work focuses on the molecular mechanisms of bacterial cell organization, particularly how bacteria control growth, division, and shape through regulatory systems like cytoskeletal elements and C-switches. He is a Max Planck Fellow and has received several honors, including the VAAM Research Prize and an ERC Advanced Grant.



Prof. Dr. Georg Hochberg leads the "Evolutionary Biochemistry" research group at the Max Planck Institute for Terrestrial Microbiology in Marburg and holds a LOEWE top professorship at the Philipps-Universität Marburg. After completing his BA and DPhil at the University of Oxford, he conducted postdoctoral research in evolutionary biochemistry at the University of Chicago before establishing his own group in Marburg. His lab probes how complexity in life's molecular machinery arises. By reconstructing ancient proteins and combining molecular phylogenetics with biophysical experimentation, his team seeks to unravel how these vital assemblies formed and evolved



In recognition of his groundbreaking work, he received an ERC Starting Grant in 2022, was named an EMBO Young Investigator in 2023, and was awarded the Leopoldina 'Zukunftswissen' Nachwuchspreis in 2024.

Dr. Remy Colin received his PhD in Physics from University Paris 7 Diderot, following BSc and MSc degrees from University Paris-Sud 11. He completed his postdoctoral training at the Rowland Institute, Harvard University, before joining the Max Planck Institute in Marburg as a postdoc. Since December 2018, he has led the "Biophysics of Environment Sensing by Motile Microorganisms" project group, investigating how motility and chemotaxis drive bacterial population behaviors through microscopy, microfluidics, and modeling. His research combines quantitative biophysics with microbiology to uncover the principles of microbial decision-making and adaptation.



Dr. David Adam leads the project HAPPY at the Max Planck Institute for Terrestrial Microbiology in Marburg, developing a high-throughput microfluidic platform to measure the lifespan of individual yeast cells. This technology enables large-scale screening for compounds and genetic factors that influence cellular ageing and has strong potential for applications in drug discovery and biotechnology.

Beyond his scientific work, Dr. Adam has successfully translated his research into innovation, winning multiple national and international start-up prizes for HAPPY and its commercialisation concept. His career combines cutting-edge ageing research with entrepreneurial drive, aiming to bridge fundamental science and real-world applications.



Dr. Ilka Bischofs-Pfeifer leads the Complex Adaptive Traits (CATs) research group at the Max Planck Institute for Terrestrial Microbiology in Marburg. Her interdisciplinary work explores how beneficial Bacilli, such as *Bacillus subtilis*, adapt to environmental stress through coordinated behaviors and regulatory networks. By combining systems biology, fluorescence microscopy, and theoretical modeling, her team investigates phenomena like spore formation, peptide-based signaling, and microbial population dynamics. Dr. Bischofs-Pfeifer earned her Ph.D. in Theoretical Physics from the University of Potsdam and held research positions at UC Berkeley and Heidelberg University.



Astrid Isabell Bendix studied Physical Geography, Biology, Soil Science, and Forestry at Justus Liebig University Giessen and the University of Bonn, graduating as a Diplom-Geographer. She then worked for almost a decade as a research associate at the Academy of Sciences and Literature, Mainz, in the Geoecology Research Unit in Bonn, with extensive research stays in Ecuador, Peru, and Bolivia. After a family break, she returned to academia, teaching at the Department of Geography with a focus on climate ecology, applied methods, and practice-oriented learning. From 2015 to 2020, she headed the Quality Pact for Teaching office at Philipps University Marburg, overseeing the implementation of innovative teaching concepts and quality assurance. Since 2020, she has been with MAFEX, where she developed and manages a cross-disciplinary qualification program for entrepreneurs, with a strong commitment to supporting female founders. In recognition of her long-standing dedication to women in academia and entrepreneurship, she received the Women's Advancement Award 2024 from Philipps University Marburg.



Workshops



Workshop 1: Making the most out of your postdoc

Dr. Dagmar Sigurdardottir

In this workshop, participants will identify their future goals to determine the type of supervision that best supports their aspirations. With these goals in mind, they will explore key aspects of lab management, stress management, and effective communication with colleagues.



Workshop 2: The Art of Communication for Leaders

Kathrin Keune

This workshop enhances the communication and leadership of the participants. Participants will engage in interactive sessions to address workplace challenges, such as asserting oneself, managing conflicts, and leading diverse teams. Through real-life scenarios and simulations, attendees will practice effective communication strategies, explore body language nuances, and learn to deliver concise, impactful messages. By the end, participants will have practical skills to navigate their careers with confidence and authority.



Workshop 3: Empowering you performance with presence

Thomas Müller

This workshop empowers women in scientific fields by enhancing assertiveness and charisma. Participants will engage in activities to develop confident body language and vocal techniques, essential for effective leadership. The program addresses critical communication scenarios, such as presentations and meetings, focusing on body awareness and gestural communication to assert oneself and present compelling arguments. By exploring both inner attitudes and outward appearances, attendees will cultivate a convincing and authoritative presence in their professional environments.



Workshop 4: Future perspectives and strategic career planning

Dr.-Ing. Christian Baron

This interactive training supports participants exploring their values, strengths, and security needs, providing a foundation for clear career orientation and actionable planning. Through guided reflection, group activities, and practical tools, participants will leave with insights and a personalized action plan for their next professional steps.



Workshop 5: Funding opportunities and key aspects of grant proposal writing

Dr. Sabine Preusse

This workshop focuses on the essential skills needed for successful grant proposal writing, a key component in securing research funding. Participants will learn how to design attractive proposals from the funding agency's perspective, enhance the scientific quality of their research, and effectively communicate complex ideas to reviewers. Attendees will work on their own research projects, whether for a new grant proposal or ongoing work. The workshop also provides valuable insights into various funding programs, evaluation processes, and common pitfalls to avoid in proposal writing.