Symposium

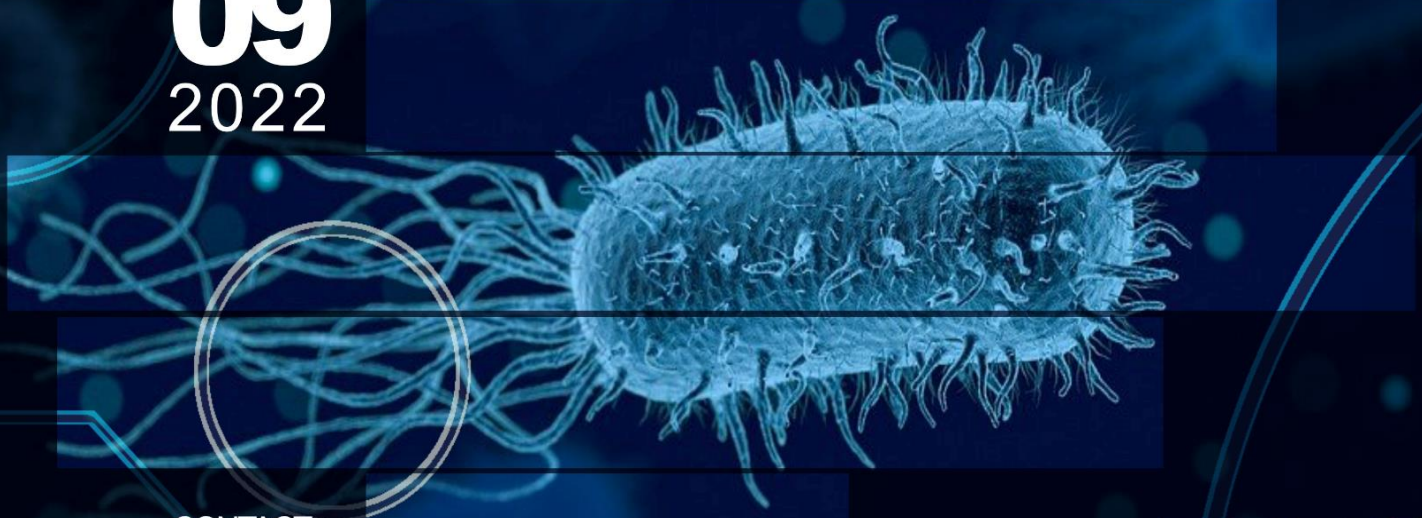
MICROFLUENCERS

– From small organisms to global impact –

on the occasion of the 50th anniversary of the Institute of Microbiology and Biotechnology, Bonn University

9:30AM – 6PM

JUN **09** 2022



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UNIVERSITÄT BONN

TRA MODELLING

Symposium „Microfluencers: From small organisms to global impact”

on the occasion of the Institute's 50th anniversary

Institute of Microbiology and Biotechnology, Bonn University

June 9th 2022, 9:30 am – 6 pm, Alfred-Philippson lecture hall

From 6:30 pm Network evening

	TIME	PROGRAM
ARRIVAL	9:00 – 9:30	Registration & Coffee
MORNING SESSION 9:30 – 12:00	9:30 – 9:45	Welcome, general information Managing director IfMB, Ulrike Endesfelder
	9:45 – 10:30	Keynote by Ruth Schmitz-Streit *Small but effective, Newly Identified Players in Nitrogen Regulation in Methanosarcina mazei*
	10:30 – 11:00	Berenike Maier *How mechanical forces shape bacterial biofilms*
	11:00 – 11:30	Tanja Schneider *Breaking down the wall - Cell wall biosynthesis as a target for antibiotics*
	11:30 – 12:00	Tobias Bollenbach *Drug interactions between translation-inhibiting antibiotics*
LUNCH & POSTERS	12:00 – 13:30	Group picture, Lunch and Posters (even numbers)
AFTERNOON SESSION 13:30 – 15:45	13:30 – 13:45	Festive greetings, Dean Faculty of Science, Walter Witke
	13:45 – 14:15	Ulrike Endesfelder *Visualizing cellular life: From single cell imaging to in vivo single-molecule biochemistry and (micro-)biology*
	14:15 – 14:45	Cornelia Welte *Climate change microbiology: novel insights into methane cycling archaea*
	14:45 – 15:15	Uwe Deppenmeier *Biotechnological potential of prokaryotes: A journey from biochemistry to application*
	15:15 – 15:45	Christiane Dahl *A biochemical view on prokaryotes shaping the natural sulfur cycle*
COFFEE & POSTERS	15:45 – 16:45	Coffee and Posters (odd numbers)
FAREWELL	16:45 – 17:00	Greetings & Farewell, Speaker Biology, Ute Vothknecht
	17:00 – 18:00	Erwin Galinski, Emeritus IfMB, Managing director 2001-2020 *The Story of Ectoine*
	18:00	Closing words
GET TOGETHER	from 18:30	Network evening

2 - General Information

Registration
Registration begins at 9 am, where you will receive a name badge. The program will not be printed.

Venues
Registration (from 9 am): Entrance hall, Geography, Meckenheimer Allee 166
Symposium: Alfred-Philippson lecture hall, Geography, Meckenheimer Allee 166
Lunch & Coffee: Tent outside IfMB, Meckenheimer Allee 168
Poster sessions: IfMB ground floor (hallway, lecture hall, historical entrance)
Network evening: Tent outside IfMB, Meckenheimer Allee 168

Posters
Please hang your posters according to your poster numbers after you arrive. The posters can be displayed for the whole day, including the network evening. They have to be taken down by Friday 8 am. Even numbers are presented during the 1st poster session, odd numbers during the 2nd poster session.

Internet
EDUROAM is available at all venues.

Covid-19 regulations
Masks are mandatory in all buildings. Speakers are allowed to take them down.

First Aid
Our first aid station can be found in room 0.01, IfMB. In case of an emergency, please ask for help and inform the organizers.

Photographs
Photos will be taken throughout the event. Please inform the registration desk if you do not want them to be published.

Organizers
Prof. Dr. Ulrike Endesfelder, IfMB, University of Bonn, microfluencers@uni-bonn.de
We gratefully acknowledge the support of TRA Modelling.

Morning Session - 9:30 – 12:00

Small but effective, Newly Identified Players in Nitrogen Regulation in *Methanosarcina mazei*

Ruth Schmitz-Streit (University of Kiel, Germany)

Co-authors Tim Habenicht (University Kiel, Germany), Miriam Gutt (University Kiel, Germany), Harald Schwalbe (University Frankfurt, Germany), Cynthia Sharma (University Würzburg, Germany), Andreas Tholey (University Kiel, Germany)

In recent years, increasing numbers of small regulatory RNAs (sRNAs) and small proteins (coding for proteins less than 70 amino acids in length) have moved into the focus of science. Small proteins, which have been overlooked for a long time due to challenges in detection and prediction, have been recently identified in all three domains of life. However, the majority still remains functionally uncharacterized, lack secondary structure, and exhibit limited evolutionary conservation. While several small proteins and their function have already been described for bacteria and eukaryotic organisms, the amount of known and functionally analyzed archaeal small proteins is still very limited. The talk documents the genome-wide identification of small proteins in the methanogenic archaeon *Methanosarcina mazei*, as well as exemplarily provides detailed inside into the physiological role of selected small proteins and sRNAs.

How mechanical forces shape bacterial biofilms

Berenike Maier (Institute for Biological Physics, University of Cologne, Germany)

Biofilms are structured communities formed by a single or multiple microbial species. Within biofilms, bacteria are embedded into extracellular matrix allowing them to build macroscopic objects. Biofilm structure can respond to environmental changes such as the presence of antibiotics or predators. By adjusting expression levels of surface and extracellular matrix components, bacteria tune cell-to-cell interactions. One major challenge in the field is the fact that these components are very diverse between different species. Deciphering how physical interactions within biofilms are affected by changes in gene expression is a promising approach to obtain a more unified picture of how bacteria modulate biofilms. In this talk, I will discuss how mechanical interactions between bacteria affect structure, dynamics, and antibiotic tolerance of bacterial biofilms.

Breaking down the wall - Cell wall biosynthesis as a target for antibiotics

Tanja Schneider (Institute for Pharmaceutical Microbiology, University of Bonn, Germany)

TBA

Drug interactions between translation-inhibiting antibiotics

Tobias Bollenbach (Institute for Biological Physics, University of Cologne)

Antibiotic combinations are increasingly important for treating infections. Drug interactions – determined by the potency of the antibiotic combination – can reveal fundamental couplings in cell physiology. Despite their relevance, the underlying mechanisms of drug interactions remain poorly understood. To improve this situation, we focus on pairwise interactions between antibiotics targeting translation. Combinations of translation inhibitors show surprisingly diverse interactions: The combined effects range from synergistic (the combined effect on growth is stronger than expected) to suppressive (one of the drugs loses potency). We use a combination of targeted experiments using inducible expression of various translation factors and mathematical modeling to elucidate the origins of these interactions. Our results support that traffic jams of ribosomes on transcripts are at the heart of suppressive drug interactions between antibiotics that target translation. We have started to extend this general approach to antibiotics with other modes of action than translation inhibition.

POSTER Session 1

Even numbers present between 12:30 and 13.30 pm.

Afternoon Session - 13:30 – 15:45

Festive greetings

Dean Faculty of Science, Walter Witke

Visualizing cellular life: From single cell imaging to in vivo single-molecule biochemistry and (micro-)biology

Ulrike Endesfelder (Institute for Microbiology and Biotechnology, University of Bonn, Germany)

Microbes as unicellular organisms are important model systems for studying cellular mechanisms and functions. In the last decade, immense progress has been made in our understanding of the life and inner workings of bacteria with the help of modern fluorescence microscopy techniques. By visualising single molecules and the molecular architecture of subcellular structures in living cells, we can now look at bacteria based on their molecular interactions and assemblies with molecular resolution. In particular, we can generate detailed, quantitative, spatially and temporally resolved molecular maps and decipher dynamic heterogeneity and subpopulations at the subcellular level. Here, we will present some examples of applications from our work and give an insight into our visions for the future.

Climate change microbiology: novel insights into methane cycling archaea

Cornelia Welte (Alumna IfMB, VAAM-Award 2022, Radbaud University, Nijmegen, The Netherlands)

Methane is a potent greenhouse gas that is produced by microorganisms living in the absence of oxygen, the methanogenic archaea. The amount of emitted methane is controlled by a powerful biological filter where aerobic and anaerobic methane oxidizing microorganisms thrive. In our work, we aim to understand the biochemistry and physiology of methanogens as well as anaerobic methanotrophic (ANME) archaea that are both key to understanding and eventually mitigating methane emissions into the atmosphere.

In this presentation, I will introduce the discovery and characterization of a novel methanogenic pathway, where methyl groups from methoxylated aromatic compounds that occur in oil and coal are used. With a combination of physiological, biochemical and crystallographic experiments we elucidate the metabolic pathway leading to methane generation. In addition, I will provide a glimpse on the exciting ability of anaerobic methanotrophic archaea to make electricity from methane.

This work is part of the SIAM Gravitation Excellence Cluster in which Dutch scientists investigate anaerobic microorganisms with key functions in health and the environment.

Biotechnological potential of prokaryots: A journey from biochemistry to application

Uwe Deppenmeier (Institute for Microbiology and Biotechnology, University of Bonn, Germany)

On the occasion of our 50th anniversary, I would like to take this opportunity to talk about the work that has been done in my group and I will mention the corresponding Ph.D. students and Postdocs who have been involved in these projects. The research areas include and included: Biochemistry and genetics of methanogenic archaea (energy conservation, respiratory chain, enzymology, utilization of acetate, methane production in biogas plants), whole-cell catalysis with *Gluconobacter oxydans* (production of fine chemicals and chiral building blocks, extension of the substrate spectrum, ketofructose production, synthesis of levan), microbial production of prebiotics and low-calorie

sweeteners (inulin and levan-FOS, lactosucrose, etc.), metabolism and physiology of intestinal bacteria (genetic system, growth parameters, synthesis of succinate). The work has and had links to basic and applied research up to the elaboration of industrially applicable biotransformations. Some focal points of the projects will be described in more detail and will be filled with content in the presentation.

A biochemical view on prokaryotes shaping the natural sulfur cycle

Christiane Dahl (Institute for Microbiology and Biotechnology, University of Bonn, Germany)

Sulfur is one of the most important and above all most versatile elements in biology. Not only does it play an immensely important role in all living beings as a component of amino acids such as cysteine or cofactors such as lipoic acid, but inorganic sulfur compounds such as sulfide, thiosulfate or sulfate serve a very large group of prokaryotes as the basis of their energy metabolism. Together, these organisms perform mass conversions that form the central basis for the biogeochemical cycling of the element. Dissimilatory sulfate-reducing prokaryotes respire sulfate instead of oxygen and, especially in the marine environment, release large amounts of malodorous hydrogen sulfide, which in turn serves as electron donor for sulfur-oxidizing chemotrophic and phototrophic sulfur bacteria. In these organisms, the oxidation of inorganic sulfur compounds is directly linked to energy conservation via photosynthesis or respiratory processes. Sulfur-dominated habitats range from tidal flats to Siberian soda lakes and from hydrothermal vents to the common garden pond. Less well known is that inorganic sulfur compounds also play an important role in the microbial flora of the human gut. The sulfur-oxidizing prokaryotes are just as diverse as the sites they inhabit and comprise Bacteria and Archaea. The diversity of these organisms is further reflected in the fact that there is no universal pathway of sulfur oxidation. We are attempting to elucidate the different pathways in detail and apply a broad battery of molecular genetic and biochemical methods to model organisms accessible to manipulative genetics. Some of our results will be presented during the talk.

POSTER Session 2

Odd numbers present between 15:45 and 16:45 pm.

Farewell

Greetings & Farewell

Speaker Biology, Ute Vothknecht

The Story of Ectoine

Erwin Galinski (Institute for Microbiology and Biotechnology, University of Bonn, Germany)

The novel amino acid derivative ectoine was discovered in 1985 in this institute as a minor compatible solute in the bacterial genus *Ectothiorhodospira*. It has since been found in an ever-growing number of procaryotic species and even in some eucaryotic protists. Ectoine (and its hydroxylated variant) can therefore be regarded as wide-spread common natural osmolytes which – surprisingly - remained undetected for so long. Due to its apparently unique stabilizing and protecting properties, ectoine has since found numerous applications as a medical product in the skin and health care sector and is at present produced industrially at several tons p.a. with the halophilic *Halomonas elongata*.

My talk recalls the story of ectoine from an exotic find to a sought-after medical device. I will explain the molecular features which make this molecule special in its interaction with proteins, DNA and membranes and address current and potential future medical applications. We will also learn about the importance of analytical coincidences (the application of NMR in microbiology), the problems encountered by “novices” with patent applications and the industrial adaptation of laboratory–scale production techniques (bacterial “milking”) – and last but not least the people behind this success story.

Poster Abstracts

1 - High-yield production of prebiotic inulin-type fructooligosaccharides using crude inulosucrase from *L. gasseri* DSM 20604

Franziska Wienberg (Institute of Microbiology and Biotechnology, University of Bonn, Germany)

Co-authors Uwe Deppenmeier (Institute of Microbiology and Biotechnology, University of Bonn, Germany)

Inulin-type fructooligosaccharides (I-FOS) stimulate the growth and activity of beneficial gut microbes. The global market for I-FOS is constantly growing due to their health-promoting effects and functional properties. Hence there is a continuing demand for new, efficient biotechnological approaches for I-FOS production. The aim of this work was the high-yield production of I-FOS from sucrose using a crude inulosucrase from *Lactobacillus gasseri* DSM 20604. To this end, the optimal process conditions were determined and employed in bioconversion reactions. Heterologous enzyme production of the inulosucrase InuGB-V3 was performed in *Escherichia coli* BL21. Cleared cell lysate (crude inulosucrase) was then applied in I-FOS synthesis reactions. Supplementation with 1 mM CaCl2, a pH of 3.5 - 5.5, and an incubation temperature of 40 °C were found to be optimal production parameters at which crude inulosucrase showed high conversion rates, low sucrose hydrolysis, and excellent stability over 4 days. Bioconversion of 800 g L-1 sucrose resulted in very high product titers of 400 g L-1 I-FOS within 20 hours of incubation. In summary, more than 8 kg I-FOS can be obtained when cell extract from 1 L *E. coli* culture (expressing InuGB-V3) is used for bioconversion. The predominant product was 1,1 kestotetraose (degree of polymerization (DP) 4) with 125.6 ± 8.1 g L-1 followed by 1,1,1 kestopentaose (DP5), which amounted to 97.9 ± 1.9 g L-1. Products with a DP > 6 were present in only small amounts. Increasing the reaction volume from 1 mL to 10 mL and 10 L confirmed the consistent performance of the enzyme at a larger scale. Thus, the crude inulosucrase exhibited excellent properties that make it suitable for biotechnological I-FOS production. The product titer obtained is the highest reported to date for a bacterial inulosucrase. The use of crude enzyme bypasses expensive enzyme purification steps, reducing production costs and improving the economics of the process.

2 - Genetic tools for the redirection of the central carbon flow towards the production of lactate in the human gut bacterium *Phocaeicola* (*Bacteroides*) *vulgatus*

Rebecca Lück (Institute of Microbiology and Biotechnology, University of Bonn, Germany)

Co-authors Uwe Deppenmeier (Institute of Microbiology and Biotechnology, University of Bonn, Germany)

Species of the genera *Bacteroides* and *Phocaeicola* play an important role in the human colon. The organisms contribute to the degradation of complex heteropolysaccharides to small chain fatty acids, which are in part utilized by the human body. Furthermore, these organisms are involved in the synthesis of vitamins and other bioactive compounds. Of special interest is *Phocaeicola vulgatus*, originally classified as a *Bacteroides* species, due to its abundance in the human intestinal tract and its ability to degrade many plant-derived heteropolysaccharides. We analyzed different tools for the genetic modification of this microorganism, with respect to homologous gene expression of the *ldh* gene encoding a D-lactate dehydrogenase (LDH). Therefore, the *ldh* gene was cloned into the integration vector pMM656 and the shuttle vector pG106 for homologous gene expression in *P. vulgatus*. We determined the *ldh* copy number, transcript abundance, and the enzyme activity of the wild type and the mutants. The strain containing the shuttle vector showed an approx. 1500-fold increase in the *ldh* transcript concentration and an enhanced LDH activity that was about 200-fold higher compared to the parental strain. Overall, the proportion of lactate in the general catabolic carbon flow increased from 2.9% (wild type) to 28.5% in the LDH-overproducing mutant. This approach is a proof of concept, verifying the genetic accessibility of *P. vulgatus* and could form the basis for targeted genetic optimization.

3 - A metabolic puzzle: chemo(litho)heterotrophy in *Hyphomicrobium denitrificans*

Jingjing Li (Institute of Microbiology and Biotechnology, University of Bonn, Germany)

Co-authors Julian Koch (Institute of Microbiology and Biotechnology, University of Bonn, Germany); Wanda Flegler (Institute of Microbiology and Biotechnology, University of Bonn, Germany); Leon Garcia Ruiz (Institute of Microbiology and Biotechnology, University of Bonn, Germany); Natalie Hager (Institute of Microbiology and Biotechnology, University of Bonn, Germany); Alina Ballas (Institute of Microbiology and Biotechnology, University of Bonn, Germany); Tomohisa S. Tanabe (Institute of Microbiology and Biotechnology, University of Bonn, Germany) and Christiane Dahl (Institute of Microbiology and Biotechnology, University of Bonn, Germany)

Many obligately heterotrophic methylotrophs oxidize thiosulfate as an additional electron source during growth on C1 compounds. Although two different pathways of thiosulfate oxidation are implemented in *Hyphomicrobium denitrificans* X^T, a pronounced negative effect on growth rate is observed when it is cultured in the simultaneous presence of methanol and thiosulfate. In this model organism, periplasmic thiosulfate dehydrogenase catalyzes formation of the dead-end product tetrathionate. By reverse genetics we verified the second pathway that also starts in the periplasm where SoxXA catalyzes the oxidative fusion of thiosulfate to SoxYZ, from which sulfate is released by SoxB. Sulfane sulfur is then further oxidized in the cytoplasm by the sulfur-oxidizing heterodisulfide reductase-like system (sHdr) which is produced constitutively in a strain lacking the transcriptional repressor sHdrR. When exposed to thiosulfate, the Δ*shdrR* strain exhibited a strongly reduced growth rate even without induction of pre-cultures. In accordance, the negative effect of thiosulfate on growth rate is released in strains lacking a functional sHdr system and thus being unable to consume thiosulfate. We propose that the effect is due to an over-reduction of the cellular nicotinamide dinucleotide and cytochrome c pools caused by thiosulfate oxidation. This over-reduction prevents effective assimilation of methanol into biomass, because in *H. denitrificans* methanol must first be oxidized all the way to formate before it can be hooked up to tetrahydofolate, re-reduced up to the level of formaldehyde and delivered into the serine pathway for assimilation. Fully in line with this interpretation, biomass production from formate is not negatively influenced by thiosulfate.

4 - A novel protein lipoylation pathway in sulfur oxidizers involves radical SAM proteins with unusual iron-sulfur cluster-binding regions

Martina Grosser (Institute of Microbiology and Biotechnology, University of Bonn, Germany)

Co-authors Rünz, Tom Leon (Institute of Microbiology and Biotechnology, University of Bonn, Germany), Kümpel, Carolin (Institute of Microbiology and Biotechnology, University of Bonn, Germany), Dahl, Christiane (Institute of Microbiology and Biotechnology, University of Bonn, Germany)

Many sulfur-oxidizing bacteria and archaea pursue a sulfur oxidation pathway involving a heterodisulfide-reductase like enzyme system including a lipoylated protein LbpA [1]. The LbpA proteins from sulfur oxidizers do not serve as substrates for the canonical lipoate-binding protein biosynthetic machineries of *B. subtilis* and *E. coli* [1]. Instead, a set of potential lipoylation proteins is encoded in immediate vicinity of shdr-lbpA clusters. Among these is a lipoate ligase and a geranylgeranyl reductase-like flavoprotein. The other encoded proteins include two unusual radical SAM proteins resembling LipS1 and LipS2 from the archaeon *Thermococcus kodakarensis*, which have recently been shown to act together as lipoyl synthase in vitro [2]. We produced the flavoprotein as well as LipS1 and LipS2 from the Alphaproteobacterium *Hyphomicrobium denitrificans* heterologously in *E. coli*. Lipoate synthases perform one of the most chemically challenging reactions known in enzymology by activating C-H bonds in a reaction mechanism involving the formation of a radical. All canonical lipoate synthases share the typical [4Fe-4S] cluster of radical SAM enzymes (RS cluster) bound by a CX3CX2C motif and are also known for harboring a second essential auxiliary FeS cluster ligated by an N-terminal CX4CX5C motif. In contrast, LipS1 and LipS2 contain cysteine arrangements suited for RS cluster binding but no signature sequence for binding an auxiliary FeS cluster. Instead, other cysteines in unprecedented arrangements are conserved in LipS1 and LipS2. We purified the recombinant proteins under anoxic conditions and reconstituted their iron-sulfur clusters. In both cases, brown proteins exhibiting UV-vis spectra characteristic for FeS clusters were obtained. Quantification of iron and sulfur indicated the presence of two FeS clusters in both proteins one of which must be coordinated in a novel fashion.

[1] Cao et al. 2018 eLife 7, e37439, [2] Jin et al 2020 Appl Environ Microbiol 86, e01359

5 - A sequence-based predictor for sulfur metabolism-related genes discloses a novel pathway for protein lipoylation in Bacteria and Archaea

Tomohisa Sebastian Tanabe (Institute of Microbiology and Biotechnology, University of Bonn, Germany)

Co-authors Christiane Dahl (Institute of Microbiology and Biotechnology, University of Bonn, Germany)

Lipoate-binding proteins (LbpA) resembling classical glycine cleavage system H proteins are indispensable components of the sulfur-oxidizing heterodisulfide reductase-like enzyme system (sHdr) that occurs in many chemolithotrophic sulfur-oxidizing prokaryotes [1,2]. In the most organisms the shdr-lbpA genes are linked with genes for enzymes involved in maturation of the lipoate-binding proteins. These include lipoate-protein ligase(s) and two radical SAM proteins although these organisms contain at least one of the established lipoate maturation pathways, i.e. lipoate scavenging or de novo synthesis [1]. Indeed, we showed that LbpAs are not modified by the canonical lipoyl attachment machineries but that the LplA-like lipoate-protein ligases encoded in immediate vicinity of shdr-lbpA gene clusters act specifically on these protein substrates [1]. Here, we posed the question whether the novel maturation pathway for lipoate-binding proteins is confined to sulfur-oxidizing Bacteria and Archaea pursuing the sHdr pathway or whether it is of more general importance. However, publicly available annotation pipelines are not able to reliably distinguish between genes encoding the novel versus the canonical lipoylation pathways. Thus, we developed HMS-S-S a tool for the identification of sulfur metabolism-related genes based on Hidden Markov Models (HMMs) [3]. When applied to the NCBI Genbank, the tool revealed an unexpectedly broad distribution of the novel lipoate biosynthesis pathway. Among the Bacteria it is not only present in sulfur oxidizers but also in several other bacterial phyla with diverse metabolic capacities. In Archaea, the novel pathway appears to be even more widespread, coinciding with recently published biochemical analyses [4].

[1] Cao et al. 2018 eLife 7, e37439, [2] Koch and Dahl 2018 ISME J 10, 2479, [3] Tanabe and Dahl 2022 Mol Ecol Resour, Epub ahead of print, [4] Jin et al 2020 Appl Environ Microbiol 86, e01359

6 - Regulation and Dynamics of the bacterial injectisome (Type-III secretion system (T3SS)) at the molecular level

Alexander Balinovic (Institute for Microbiology and Biotechnology, University of Bonn, Germany)

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Yersinia enterocolitica is a gastrointestinal human pathogen that uses a type III secretion system (T3SS), also called injectisome, as a major virulence factor to manipulate host cell behavior to its benefits. Upon host cell contact, effector proteins from the bacterial cytoplasm are secreted into the host cytoplasm via the T3SS, which establishes a direct connection between the bacteria and the host cell. Although the structure of the T3SS is well understood and can be divided into membrane-bound and cytosolic components, it is remarkably less known about the molecular regulation and dynamics of the T3SS components. In this project, we investigated the molecular regulation of the T3SS activity using live cell fluorescence microscopy, single particle tracking photoactivated localization microscopy (sptPALM) and functional assays. We found that the different external pH environments *Y. enterocolitica* encounters during its infection route through the gastrointestinal tract have a strong influence on the mobility of the cytosolic components

of the T3SS. We could show that at low external pH, effector secretion is inhibited by temporarily release of the cytosolic components. The membrane component SctD was shown to be responsible for sensing the drop in external pH and partially dissociating from the membrane. This process was shown to be reversible upon restoration of neutral pH. These results strongly indicate a regulatory mechanism, which controls T3SS activity in response to changes in environmental conditions. In a second project, we aimed to understand the recruitment of effector proteins by the sorting platform, a conserved complex consisting of cytosolically diffusing proteins, and the dynamics of these effector-sorting platform complexes, using sptPALM. Our results show that effector proteins bind to the sorting platform components SctQ and SctL and that the composition and dynamics of the sorting platform changes upon binding of effector proteins.

7 - Methods in microbial single-molecule microscopy

Laura Weber (Institute for Microbiology and Biotechnology, University of Bonn, Germany)

Co-authors Koen Martens (Institute for Microbiology and Biotechnology, University of Bonn, Germany), Marc Endesfelder (Institute for Assyriology and Hittitology, Ludwig-Maximillians-Universität München, Germany), Ulrike Endesfelder (Institute for Microbiology and Biotechnology, University of Bonn, Germany)

Super-resolution microscopy, and especially single-molecule localization microscopy (SMLM), is a powerful tool to gain insights in the inner life of microbes. It can both be used to obtain high-resolution structural (~10-30 nanometer precision) and to acquire detailed dynamic (~10 milliseconds temporal resolution) information in living micro-organisms. The methods underlying SMLM are, however, still an active and ongoing field of research. In this poster, we present the current methodology used in SMLM – both from the biochemical and instrumental point-of-view – and discuss their potential for research, specifically in living microbes. Furthermore, we present two active methods-oriented fields of research in our group. Firstly, SMLM is currently a heavily user-curated methodology, because the operator needs to expertly decide, set, and curate data acquisition parameters. We propose a high-throughput, artificial intelligence (AI)-powered, autonomous single-molecule microscope, where the instrument can make smart choices about the ongoing experiment. Secondly, we want to empower this 'self-driving' microscope by a very realistic simulation software. This software incorporates physical, biological, optical, and instrumental factors to generate data sets that are indistinguishable from real data, but where the ground-truth is known. This combination of ground-truth with realistic data can then be used as input for advanced deep-learning-based microscopy.

8 - The fission yeast kinetochore at the nanoscale: building a quantitative structural map with SMLM

Jannik Winkelmeier (Institute for Microbiology & Biotechnology, University of Bonn, Department of Physics, Carnegie Mellon University, USA, Department of Systems and Synthetic Microbiology, Max Planck Institute for Terrestrial Microbiology and LOEWE Center for Synthetic Microbiology (SYNMIKRO), Marburg, Germany)

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Bonn, Department of Physics, Carnegie Mellon University, USA, Department of Systems and Synthetic Microbiology, Max Planck Institute for Terrestrial Microbiology and LOEWE Center for Synthetic Microbiology (SYNMIKRO), Marburg, Germany)

The kinetochore is a multi-protein complex acting as a linker between microtubules from the spindle pole body and the centromeric DNA during mitosis. Misregulation can lead to erroneous segregation of chromosomes (aneuploidy) and because of that to diseases such as cancer, birth defects and cell death (Pfau et al. 2012). Here, we present a recently in our group developed multi-color SMLM imaging strategy, using primed photoconversion and UV-photoactivation (Virant et al. 2017), to visualize key structural proteins of the *S. pombe* kinetochore in reference to the SPB and the centromere. We established a dedicated imaging and post-processing pipeline that performs drift correction and channel alignment using fiducial markers (Balinovic et al. 2019), identifies individual cells and kinetochore clusters within the cells, performs protein counting of clusters calibrated by FtnA standards (Virant et al. 2018) and measures protein distances within individual kinetochores using Bayesian inference (Virant et al. 2021). From this quantitative workflow, we were able to frame earlier work (Lando et al. 2012) in a multi-protein context and construct a nanoscale map of the *S. pombe* kinetochore. We could confirm sub-complex positioning and stoichiometry as determined by in vitro studies of partially reconstituted kinetochores in the native environment of intact *S. pombe* cells and fully assembled kinetochores. Importantly, the exact kinetochore composition and the details of the linkage strategy vary between organisms. We could acquire new details of the *S. pombe* kinetochore, e.g. the *S. pombe*-specific variation in the prevalence and importance of the different inner kinetochore substructures for the assembly of the inner kinetochore and the *S. pombe*-specific positioning of the outer kinetochore protein Dam1. Furthermore, we established the combination of PALM and Expansion Microscopy in *S. Pombe*, allowing us to image the kinetochore at 5x higher resolution than PALM itself.

9 - THCz: Synthetic small molecules that target the bacterial cell wall precursor lipid II

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Tackling emerging antibiotic resistance requires the identification of novel resistance breaking compound classes. A bacterial whole-cell screen based on pneumococcal autolysin-mediated lysis induction was developed to identify potential bacterial cell wall synthesis inhibitors. A hit class comprising a 1-amino substituted tetrahydrocarbazole (THCz) scaffold, containing two essential amine groups, displayed potent activity against a broad spectrum of Gram-positive and selected Gram-negative pathogens and was prone to resistance development in vitro. Mode of action studies comprising comprehensive whole cell analysis and selected in vitro test systems revealed that THCz inhibit cell wall biosynthesis by simultaneously targeting undecaprenyl pyrophosphate-containing lipid intermediates of peptidoglycan, wall teichoic acid and capsule biosynthetic pathways. THCz represent the first chemically synthesized lipid II binding antibiotic amenable to derivatization.

10 - Mechanistic analysis of tripartite ATP-independent periplasmic (TRAP) transporters by TIRF microscopy

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Tripartite ATP-independent periplasmic transporters (TRAP) are found in bacteria and archaea and are responsible for the uptake of carboxylate- and sulfonate-containing substrates across the cell membrane into the cytoplasm. They consist of three components, a mobile periplasmic substrate-binding protein (SBP or P-domain) and two integral membrane proteins, a Q- and an M-domain. One of the most intensively studied TRAP transporters is HiSiaPQM from the pathogen *Haemophilus influenza*. HiSiaPQM represents the only pathway for the uptake of the sugar sialic acid, which is critical for the bacteria to evade the immune response of the host. Here, the interaction of the soluble substrate-binding P-domain with the QM transporter membrane domains was analysed to validate the structural model of the transporter [1]. To study this process in vitro, the purified QM domains were inserted into solid-supported lipid bilayers. In these, the formation of the tripartite complex was visualized at the single-molecule level by total internal reflection fluorescence (TIRF) microscopy. Using fluorescently labelled P-domains – with and without their cargo – and a range of mutants exhibiting specific modifications in the interaction region between P and QM domains we tested the predictions of the transport model, which was created on the basis of the QM domain and P domain structure as obtained by cryo-EM and AlphaFold.

[1] Peter, M.F., P. Depping, N. Schneberger, E. Severi, K. Gatterdam, S. Tindall, A. Durand, V. Heinz, P.-A. Koenig, M. Geyer, C. Ziegler, G.H. Thomas, and G. Hagelueken. 2021. The structure of HiSiaQM defines the architecture of tripartite ATP-independent periplasmic (TRAP) transporters. bioRxiv. 2021.12.03.471092.

11 - The Lipopeptide Antibiotic Corallorazine A interferes with Bacterial Transcription

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To overcome rising antibiotic resistance, new antibiotics with novel mechanisms of action are urgently needed. The newly discovered corallorazines are lipopeptides produced by *Corallococcus coralloides*, a myxobacterium isolated from a Belgian soil sample. Three members of the corallorazine family could be identified so far, namely corallorazine A, B & C. While corallorazine B & C differ in the presence of a methoxyl group, corallorazine A is the only compound having a cyclic dipeptide core. It is the most complex and abundantly extracted family member and thus thought to be the final product of the corallorazine biosynthesis pathway. Corallorazine A displays potent antimicrobial activity against selected Gram-positive and Gram-negative bacteria. Mode of action studies comprising comprehensive whole cell analysis and in vitro test systems revealed that corallorazine A inhibits bacterial transcription by targeting the DNA-dependent RNA polymerase.

12 - Development of an in vitro gut model as preclinical test system for decolonization strategies

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The human gut is densely populated with thousands of different microbial species that coexist in this environment in an antagonistic, mutualistic or even symbiotic manner. While co-evolution has predominantly resulted in a commensal and rather beneficial relationship between microbes and their host, also pathogenic bacteria are able to reside within the intestinal community, increasing the risk for subsequent life-threatening infections. A strategy to prevent pathogens inducing an infection is to decolonize them priorly. But so far experimental decolonization strategies are often based on broad-spectrum antibiotics, which not only affect the pathogenic targets but also the commensal bacteria. The associated risks of dysbiosis and antibiotic resistance can also lead to serious long-term problems, making the search for highly specific decolonization strategies essential. Within the DZIF research group 'Bacterial Interference', we are not only exploiting the intestinal microbiota for novel decolonizing agents, but have also developed a dedicated in vitro gut system for the evaluation of decolonization strategies. Using advanced cultivation techniques for growing strict anaerobes and conditions mimicking the intestinal environment, we were already successful in co-cultivating the core group of our in vitro model, which consists of seven important and very abundant members of the gut microbiota (called 'DeMiCo7'). For each run 16S metagenomic analyses were done to resolve the DeMiCo7 composition over time. Compared to data taken from literature the stable DeMiCo7 already resembles a simplified average human gut community but with an intentionally increased abundance of *E. faecium*, chosen as first target pathogen included in the in vitro gut system. Therefore, the in vitro gut model is ready to assess different decolonizing agents and their impact on target pathogens and the surrounding microbial community.

13 - MraY from *Pseudomonas aeruginosa* is inhibited by uridyl-peptide antibiotics

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Antibiotic resistance is one of the most serious health threats and the therapeutic options to treat infections caused by multidrug-resistant strains are seriously compromised. Especially for infections caused by *Pseudomonas aeruginosa* isolates which have emerged resistance towards all carbapenems, aminoglycosides, and fluoroquinolones, novel antibiotics with new targets or unprecedented mechanisms of action are urgently needed. Integral components of the drug development process are analysis of the mechanism of action and resistance of an antibiotic, as well as identification of the molecular target. Without this detailed knowledge, rational drug design is strongly hampered. Uridyl-peptide antibiotics (UPA) are a promising group of nucleoside natural products, which show potent activity against *P. aeruginosa*. An important molecular target of this compound class is the phospho-N-acetylmuramoyl-pentapeptide-transferase MraY, which catalyses the transfer of phospho-MurNAc pentapeptide to the membrane-standing lipid carrier undecaprenyl phosphate (C55-P) resulting in the formation of lipid I. Previous studies have shown that mutations in the transmembrane helix 9 of MraY from *E. coli* (F288L and E287A) confer resistance against UPAs (Rodolis et al., 2014). The MraY proteins from *E. coli* and *P. aeruginosa* share significant sequence similarity but differ in position 288. MraY from *P. aeruginosa*, as well as the respective mutants (E287A, I288L) were heterologously expressed in *E. coli* C43. The native MraY substrate UDP-MurNAc pentapeptide was purified and labelled with dansyl chloride to set up a fluorometric assay. In order to measure the IC50 of several UPAs, kinetic parameters were

determined and for nearly all compounds tested, the selected mutations/amino acid exchanges impacted on the inhibitory activity.

14 - Antimicrobial Potential of Bacteria Associated with Marine Sea Slugs from North Sulawesi, Indonesia

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Nudibranchia, marine soft-bodied organisms, developed, due to the absence of a protective shell, different strategies to protect themselves against putative predators and fouling organisms. One strategy is to use chemical weapons to distract predators, as well as pathogenic microorganisms. Hence, these gastropods take advantage of the incorporation of chemical molecules. Thereby the original source of these natural products varies; it might be the food source, de novo synthesis from the sea slug, or biosynthesis by associated bacteria. These bioactive molecules applied by the slugs can become important drug leads for future medicinal drugs. To test the potential of the associated bacteria, the latter were isolated from their hosts, brought into culture and extracts were prepared and tested for antimicrobial activities. From 49 isolated bacterial strains 35 showed antibiotic activity. The most promising extracts were chosen for further testing against relevant pathogens. In that way three strains showing activity against methicillin resistant *Staphylococcus aureus* and one strain with activity against enterohemorrhagic *Escherichia coli*, respectively, were identified. The obtained results indicate that the sea slug associated microbiome is a promising source for bacterial strains, which hold the potential for the biotechnological production of antibiotics.

15 - Coordination of capsule assembly and cell wall biosynthesis in *Staphylococcus aureus*

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The Gram-positive cell wall consists of peptidoglycan functionalized with anionic glycopolymers, such as wall teichoic acid and capsular polysaccharide (CP). How the different cell wall polymers are assembled in a coordinated fashion is not fully understood. Here, we reconstitute *Staphylococcus aureus* CP biosynthesis and elucidate its interplay with the cell wall biosynthetic machinery. We show that the CapAB tyrosine kinase complex controls multiple enzymatic checkpoints through reversible phosphorylation to modulate the consumption of essential precursors that are also used in peptidoglycan biosynthesis. In addition, the CapA1 activator protein interacts with and cleaves lipid-linked CP precursors, releasing the essential lipid carrier undecaprenyl-phosphate. We further provide biochemical evidence that the subsequent attachment of CP is achieved by LcpC, a member of the LytR-CpsA-Psr protein family, using the peptidoglycan precursor native lipid II as acceptor substrate. The Ser/Thr kinase PknB, which can sense cellular lipid II levels, negatively controls CP synthesis. Our work sheds light on the integration of CP biosynthesis into the multi-component Gram-positive cell wall.

Rausch, M. et al. Integration of Capsule Assembly Modules into Cell Wall Biosynthetic and Regulatory Networks. Nature Commun. 10(1):1404. doi: 10.1038/s41467-019-09356-x. (2019).

16 - In situ modification of FR900359 biosynthesis in *Chromobacterium vaccinii* MWU205

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FR900359 (FR) is an eight-membered, cyclic depsipeptide, which belongs to a small and specialized group of natural products named chromodepsins. So far, FR production has been reported from two different bacteria, the obligate plant symbiont "Candidatus Burkholderia crenata" and the free-living *Chromobacterium vaccinii* MWU205. In both cases a non-ribosomal peptide synthetase (NRPS) machinery is responsible for its assembly (Ref. 1 & 2). FR has proven to be an excellent tool for the investigation of Gq protein-coupled signaling pathways, that regulate important cellular processes in diverse organisms (Ref. 3). This activity also makes it a potential drug lead for the treatment of diseases, such as asthma or cancer (Ref. 1). Due to these interesting features there is a strong desire for new FR derivatives with altered activities. This includes the targeting of signaling pathways regulated by other G protein family members as well as the installation of chemical groups for the selective modification of the FR scaffold. Here we report our first results on the *in situ* modification of FR biosynthesis by *C. vaccinii* to generate altered FR molecules.

[1] C. Hermes et al, Nat. Prod. Rep., 2021, 38, 2276-2292. [2] C. Hermes et al., Nat. Commun., 2021, 12, 144. 3. R. Schrage et al. Nat. Commun., 2015, 6, 10156.

17 - Beyond predator-prey: Phages in bacterial communities

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Co-cultures of a bacteriophage and its host are a powerful model system for predator-prey co-evolution. However, in nature the phage-bacterium relationship is far more complex. Most phages can integrate their DNA into the bacterial host, linking their evolutionary success. Moreover, specific bacterial genetic actively hijack the phage machinery for horizontal gene transfer. However, we lack systematic experimental studies, as such events do not occur in mono-cultures and it is notoriously difficult to obtain stable multi-species co-existence due to resource competition. We have developed an assay consisting of separately cultured bacteria, but with phages periodically surging through the entire bacterial metapopulation. We have used this assay to evolve hundreds of clinically relevant bacteria and roughly equally many phages. We use this assay in combination with high throughput sequencing and phenotypic assays to map phage-host networks and track gene flow between bacteria. Our work reveals how phages govern evolution in bacterial communities, such as the spread of antibiotic resistance genes.

18 - Multiplication of the intracellular pathogen *Rhodococcus equi* depends on host ESCRT complexes

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Professional phagocytic cells such as macrophages ingest and kill microorganisms within microbicidal phagolysosomes. Gram-positive *Rhodococcus equi* evades killing, replicates in host macrophages and causes pneumonia in foals and immunocompromised humans. Intra-macrophage replication of *R. equi* is promoted by the secreted bacterial Virulence associated protein A (VapA). During infection, VapA permeabilizes the phagosomes for protons, leading to

pH-neutral, spacious *Rhodococcus* containing vacuoles (RCVs) containing many intraluminal vesicles. Morphology and function of RCVs can be mimicked by adding recombinant VapA to the macrophage growth medium. We purified VapA-induced vacuoles, analyzed them by mass spectrometry and observed enrichment of the host Endosome Sorting Complex Required for Transport (ESCRT). As the ESCRT complex can be involved in lysosome membrane repair, we hypothesized that it might repair VapA-permeabilized membranes. Intraluminal vesicles, which are formed ESCRT-dependently during repair might function in nutrient supply for intravacuolar *R. equi*. To test these hypotheses, we analyzed bacterial multiplication in macrophages treated with siRNAs against ESCRT-I or ESCRT-III and in macrophages overexpressing dominant-negative ESCRT-I/-III proteins. *R. equi* depended on ESCRT-III function for intracellular multiplication but surprisingly not on ESCRT-I. Transmission electron microscopy, macroautophagy experiments and analysis of type I immune response validated that the RCV stays intact during *R. equi* infection which made a role for ESCRT in phagosome repair unlikely. Therefore, ESCRT may rather functions in degradation of lysosome membrane proteins via microautophagy. In summary, our observations suggest that *R. equi* requires ESCRT-III (not ESCRT-I) for intraluminal vesicle formation from the phagolysosome membrane in a process which likely supplies *R. equi* (barely metabolizing sugars or peptides) with fatty acid-like nutrients.

19 - Nonspecific effect of amphiphilic antiviral rugs on the cell membrane as a possible strategy for viral diseases treatment

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The nonspecific influence of various amphiphilic and hydrophobic drugs on lipid composition can lead to changes in the fluidity of the plasma membrane, which in turn affects the membrane receptors. Nowadays, it is widely known that specific areas of the membrane called lipid rafts are involved in different signaling events and intracellular trafficking of proteins and are preferential sites for host-pathogen interactions. Our research studied how antiviral drug remdesivir triggers lipid raft domains of the membrane.
To determine the effect of remdesivir on the cell membrane, the liposomes of two types have been prepared. The first type included DOPC, SM, CHOL (1:1:0,7) liquid-ordered phases and liquid-crystalline ordered phases (ternary mixture), while the second one represented the lipid rafts (CHOL and SM).
Marker regions for lipid rafts can be defined as follows: 1670-1640 (C = O), 1570-1520 (C-NH_3 +), region 1400-1364 (CH_2 strain oscillations). For the formation of ordered structures, the defining characteristic peaks are 1400, 1644 and peak 1548 cm^{-1} . It was shown that remdesivir is able to disrupt the structure of lipid rafts, which accumulate different receptors for viral disease, which in turn prevents the penetration of the virus into healthy cells.

20 - Elucidation of the pathway of the glycine-glucolipid in *Alcanivorax borkumensis*

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Microorganisms produce a large variety of surface-active compounds. These biosurfactants enable the attachment to surfaces and subsequent biofilm formation and facilitate the utilization of hydrophobic substrates. In biotechnological applications, biosurfactants are employed in numerous processes such as petroleum recovery and agriculture. The marine bacterium *Alcanivorax borkumensis* produces a surface-active glycine-glucolipid for the attachment to long-chain alkanes as e.g. found in petroleum spills in the ocean. The core structure of this lipid consists of four 3-hydroxy fatty acids (mainly 10:0) esterified to each other (tetra-hydroxy-alcanoate), with a glycyl residue bound to the free carboxy group and a glucosyl moiety at the free 3-hydroxy group. We developed an HPLC method for the absolute quantification of this glycine-glucolipid based on its conversion into phenacyl esters and the use of undecanoic acid

(11:0) as internal standard. The measurements revealed that *A. borkumensis* cells grown on hexadecane accumulated higher amounts of the glycine-glucolipid compared with growth on pyruvate. Furthermore, we found that the glycine-glucolipid of is resident to the cell surface and enables the bacterium to bind alkanes at the lipid-water interface. *A. borkumensis* contains an open reading frame which codes for a protein with sequence similarity to non-ribosomal peptide synthetases (NRPSs) which are multi-modular enzymes that catalyze the synthesis of highly diverse natural products of bacterial or fungal origin. Mutant analyses and expression studies revealed that this gene catalyzes the synthesis of the glycyl-tetra-hydroxyalcanoate, and in a second step a glucosyltransferase transfers the sugar to the lipid molecule. A third open reading frame codes for a putative phosphopantetheinyl transferase which may play a role for the activation of the NRPS.

21 - A Below Ground Chemical Fight for Phosphate and Habitat - Interactions of Plants with Fungal and Bacterial Microorganisms

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Some soil microorganisms can solubilize insoluble phosphate which is available for plants. Inoculation of false flax (*Camelina sativa*) with the fungus *Trichoderma viride* and bacterium *Pseudomonas laurentiana* did not improve phosphate uptake by the plant as verified by rhizotron experiments with 33P-labeled apatite. Microorganisms adapted to the P-deficient soil, such as fungus *Penicillium aurantiogriseum*) and bacterial species, but also those colonizing the root surface, solubilize phosphate as determined by ICP-MS. A bacterial consortium with *Cytobacillus firmus*, forming biofilms on *Camelina* roots, can solubilize phosphate efficiently. Consequently, a competitive behavior between bulk soil microorganisms, root colonizing microorganisms and the plant is established. In pot experiments with P-deficient soil, *P. aurantiogriseum* killed older *Camelina* seedlings, whereas the fungus was harmless when a P-containing fertilizer was added. In turn, breakdown products of *Camelina* glucosinolates were inhibitory to *P. aurantiogriseum*. Several soil bacteria, but not root colonizing ones, are able to degrade glucosinolates, releasing fungitoxic isothiocyanates. *Camelina* glucosinolates, combined with cyclo(Leu-Pro), a bioactive peptide released by *P. aurantiogriseum*, selectively inhibited the root colonizing bacterial consortium synergistically, while other bacteria, e.g. *Paenibacillus polymyxa* and the fungus *Penicillium olsonii* were not affected. *P. aurantiogriseum* produces additional phytotoxic compounds, which are inhibitory for *Camelina*. Thus, secondary metabolites are used by all of the organisms for suppression of competitive ones to improve their own life conditions under phosphate deficiency. The results may contribute to explain the contradictory effects of phosphate solubilizing microorganisms when used as biofertilizers in agriculture. The study broadens the knowledge of the molecular communication between interacting organisms including their secondary metabolites.

22 - Spatiotemporal localization of proteins in time-resolved Fluorescence Microscopy of *Staphylococcus aureus*

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Staphylococcus aures is an appealing organism to study the working principle and effects of antibiotics on the cell wall and its biosynthetic machinery because of its thick cell wall and basic cell wall biosynthesis machinery. In vivo fluorescence microscopic wide-field studies offer a flexible way to learn about protein and antibiotic drug responses in their localization, in connection to one another, or in delocalization over time. However, these studies are associated with major hurdles like fluorescent growth media, loss of focus and other stumbling blocks alike. Here, we demonstrate a variety of remedies and strategies to overcome the detrimental impacts of those typical stumbling blocks in time-resolved microscopy. Two illustrative experiments of *S. aureus* with fluorescently labeled FtsZ and PBP2, proteins involved in divisome formation and cell wall synthesis machinery, are presented for antibiotic-treated and untreated samples, along with exemplary methods for evaluation of time-resolved datasets.

23 - Novel methanogenic methyl transferase systems

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Methoxylated aromatic compounds are components of lignin and coal and are very abundant on Earth. However, the conversion of these compounds has previously only been described for bacteria and not for archaea. The methanogenic archaeon *Methermicoccus shengliensis* was the first archaeon shown to be capable to convert methoxylated aromatic compounds, also called methoxydotrophic growth [1]. In a recent study we showed that *M. shengliensis* uses an O-demethylation/methyl transfer (Mto) system that is more related to that of acetogenic bacteria than the methyl transferase system of methylotrophic archaea [2]. We were able to elucidate the respective methyl transfer reactions by activity assays and protein crystallization highlighting that tetrahydromethanopterin instead of coenzyme M is the final methyl acceptor, which differs from the conventional methanogenic methyl-transfer systems. Next to the transfer of the methyl group deriving from methoxylated compounds also the methyl transfer from tetramethylammonium, a compound that is present in marine environments, is an intriguing topic and has not been studied in detail. We found that a member of the Methanococcoides is able to grow on tetramethylammonium and aim on characterizing the respective methyl transferase system by heterologous expression and protein activity assays.

[1] doi: 10.1126/science.aaf8821, [2] doi: 10.1038/s41396-021-01025-6

24 - "Novel points of attack" – Exploiting capsule biosynthesis in *Streptococcus pneumoniae* for antibacterial treatment

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Synthesis of a polysaccharide capsule is crucial for pneumococci to resist the immune system during infection. Whereas capsules have been successful targets for vaccines, biosynthetic reactions and mechanisms regulating capsule expression have not been investigated as potential therapeutic targets so far. Most *S. pneumoniae* serotypes produce capsular polysaccharides (CP) via the Wzx/Wzydependent pathway. In this case, CP building blocks are assembled on C55-P at the inner side of the cytoplasmic membrane, translocated and polymerized in a non-processive manner on the exterior of the cell. Enzymes of the LytR-CpsA-Psr (LCP) family are presumed to catalyze transfer and covalent linkage of CP to peptidoglycan under release of the lipid carrier. However, biochemical evidence and molecular details for these reactions are mostly lacking. Streptococcal capsular biosynthesis reactions are functionally

reconstituted in vitro using purified recombinant enzymes and substrates. Furthermore, post-translational regulatory mechanisms, particularly phosphorylation, which allow the orchestration of CP and PGN reactions are investigated.

25 - Recognition mechanisms of guanidine-containing lipopeptide antibiotics for cell wall precursor targets

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Infections with drug-resistant gram-positive pathogens have become a major global health burden worldwide, making new antibacterial substances with novel mechanisms of action urgently needed. One compound class with promising antimicrobial activity are guanidine-containing cyclic lipopeptide antibiotics (CLPs). The CLP Empedopeptin has been shown to interfere with membrane bound steps of cell wall biosynthesis in a calcium-dependent manner, by binding to lipid-linked intermediates, in particular the peptidoglycan precursor lipid II. Due to structural similarity of different CLPs, a similar mode of action is proposed for the whole compound class and lipid II is hypothesized to be the primary target of CLPs. However, the specific targets of other CLPs remain mostly elusive and multi-modality of the mechanisms of action has not been studied.

Using a combination of in vitro and in vivo experiments, we could show that CLPs target the cell wall precursor lipid II as well as related bactoprenol containing intermediates, leading to the inhibition of cell wall biosynthesis. Whole cell assays and fluorescence microscopy provided further insight into drug-target interactions and the antibiotic effects triggered in the bacterial cells.

26 - Identification, Isolation, and characterization of a novel epilancin produced by *Staphylococcus epidermidis* A37

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Drug and multidrug resistances are major factors contributing to growing numbers of bacterial infections that are increasingly difficult to treat with classic antibiotics. Antimicrobial peptides (AMPs) have emerged as promising alternatives to conventional antibiotics as they often show high antimicrobial activity against numerous pathogens and are potentially able to circumvent established mechanisms of resistance. We identified Staphylococcus epidermidis A37 as the natural producer of a novel AMP, which we named A37 accordingly. It was classified as an epilancins, a class of type A lantibiotics, which are elongated, flexible, and cationic peptides. The two previously described eiplancins K7 and 15X are structurally highly similar to A37 but their amino acid sequences differ in several positions. We established production and purification process for epilancin A37. Isolated from S. epidermidis A37 culture supernatant via hydrophobic interaction chromatography is followed by anion exchange and reversed phase chromatography. The identity of A37 was confirmed by mass spectrometry after purification. Although it has been shown that lantibiotics frequently act by disintegration of the bacterial membrane, the way epilancins interact with these membranes has not been studied in detail and remains largely unknown. We performed in vivo and in vitro experiments to investigate A37's antimicrobial potential and its mode of action. Activity studies revealed potent

antimicrobial activity of A37 against a wide range of bacteria. Corynebacterium glutamicum was chosen as a model organism for our studies due to its high susceptibility toward A37. Based on our findings, we postulate a multifaceted mode of action for A37 and related peptides. This model adds to the fundamental understanding and may provide a basis for further investigations of the antimicrobial activity of AMPs.

27 - The novel epilancin A37 disrupts bacterial and artificial membranes

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Epilancins are a group of type A lantibiotics consisting of two previously discovered specimen (K7 and 15X) and the novel epilancin A37, produced by *Staphylococcus epidermidis*. A37 shows potent antibacterial activity against a variety of gram-positive bacteria, e.g. coagulase-negative staphylococci and in particular corynebacteria, correlating with the ecological niche of the producer strain. We used fluorescence microscopy to visualize cellular effects of the fluorescently labelled derivative A37FL on the model organism *Corynebacterium glutamicum*. The compound localized in the cytoplasm, along with formation of fluorescence foci associated to the cytoplasmic membrane. Colocalization studies with a membrane dye and superresolution Airyscan microscopy revealed that A37FL forms intracellular lipid vesicles heavily loaded with the compound, thereby causing massive membrane deformations. In vitro experiments on Giant Unilamellar Vesicles (GUV) showed that A37 binds to and penetrates artificial lipid membranes, allowing for fluid exchange with the surrounding medium and causing GUV instability. In summary, the novel Epilancin A37 causes massive damage on both bacterial and artificial membranes, resulting in potent in vivo antimicrobial activity.

28 - Mechanism of Action of the Cell Wall Targeting Antibiotic Hypeptin

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Hypeptin (HYP) shares structural features with teixobactin (TEIX). It is a cyclodepsipeptide antibiotic produced by previously uncultured *Lysobacter* sp. K5869, isolated from an environmental sample by the iChip technology. Via systematic in vivo and in vitro analyses, we showed that HYP exhibits potent activity against a broad spectrum of gram-positive bacteria and binds to multiple undecaprenyl pyrophosphate-containing biosynthesis intermediates, blocking bacterial cell wall biosynthesis without affecting membrane integrity. In addition, HYP triggers secondary effects, such as increased autolysis likely contributing to limited resistance development, as observed with TEIX.

29 - The multifaceted role of the pilotin protein in assembly and function of the Yersinia enterocolitica type III secretion system

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The type III secretion system injectisome resembles a molecular syringe and is used by a wide range of pathogens to translocate effector proteins directly into eukaryotic host cells. To assemble this multi-protein nanomachinery, the presence of a so-called pilotin, a small lipoprotein that assists the formation of the secretin ring in the outer membrane is needed. In this study, we assess the role of the *Yersinia enterocolitica* pilotin by using functional assays, interaction studies, proteomics and live-cell microscopy. In the absence of the pilotin, the injectisome assembly is disrupted. Nevertheless, *Yersinia* remains able to secrete its virulence effectors, whereas the export of early substrates required to establish the needle and pore in the host cell is heavily reduced. The pilotin itself localizes in the membrane where it froms transient mobile clusters. Although it interacts with the secretin and the T3SS export apparatus in the inner membrane, the pilotin does not colocalize with the rest of the injectisome, but co-purifies with specific non-T3SS components. Based on these findings, we speculate that pilotins do not only aid in the assembly process of the T3SS, but fulfill additional downstream roles in type III secretion and feed into the bacterial cell biology.

30 - Modulation of cell envelope biosynthesis processes by glycopeptide antibiotics

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Glycopeptide antibiotics (GPA) are drugs of last resort for the treatment of infections caused by resistant Gram-positive bacteria. Despite intensive research on the molecular mechanisms of action, the cellular effects of GPA leading to cell death are not fully understood. In this context, mechanisms underlying the mode of action and resistance of teicoplanin (TEIC) are of major interest. TEIC is characterized by increased potency and bactericidality compared to vancomycin (VAN), but in contrast to other GPA does not self-associate and dimerize. It is presumed that the cellular mechanisms induced by TEIC and further (semi-synthetic) lipoglycopeptides significantly differ from VAN-triggered effects and may include binding to additional targets. While resistance to all GPAs is mediated by incorporation of modified lipid II into the peptidoglycan network, additional TEIC resistance is conferred by accessory Van proteins. The enzymatic activity and precise function of the proteins VanJ from *S. coelicor* and VanZ from *E. faecalis*/ *E. faecium* in TEIC resistance remain elusive and will be identified by in depth biochemical analyses.

31 - DeepBacs for multitask bacterial image analysis using open-source deep learning approaches

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Deep learning (DL) approaches change and shape the world around in almost every aspect. This is also true for biological and biomedical imaging, where DL opens up new avenues for advanced and content-rich image analysis. Some networks allow for efficient image segmentation from organelles in EM images to cell nuclei in entire organisms [1-2], other networks increase resolution or the signal-to-noise ratio in images, which improves performance in live-cell imaging [3-4]. As establishing DL from scratch requires coding experience and specific hardware, several studies were dedicated to the democratization of DL. ZeroCostDL4Mic is one example, representing a platform for cloud-

based DL with a large collection of streamlined notebooks that allow also non-experts to experience and use DL for their research [5]. Unfortunately, DL applications in microbiology are less widespread than for research in eukaryotes. In DeepBacs, we demonstrate how cloud-based DL approaches can be employed to analyze bacterial bioimages [6]. To show the potential and educate bacteriologists in DL technology, we created datasets for various image analysis tasks. This includes segmentation of rod- and cocci-shaped bacteria, object detection for cell classification or antibiotic phenotyping and image denoising for improved live-cell imaging. Resolution enhancement and artificial labeling are further tasks that can contribute to study bacterial cell biology or antibiotic action at greater detail. We hope that DeepBacs inspires bacteriologists to apply DL in their research and provides useful information that helps to make this application a success.

[1] Heinrich et al., Nature (599), 141–146 (2021), [2] Weigert et al., arXiv:1908.03636v2 (2020), [3] Weigert et al., Nat. Meth. (15), 1090–1097 (2018), [4] Krull, Buchholz and Jug, arXiv:1811.10980v2 (2018), [5] von Chamier et al., Nat. Commun. (12), 2276 (2021), [6] Spahn et al., bioRxiv:2021.11.03.467152 (2021)

4 - History of the IfMB

The Institute of Microbiology at the University of Bonn was founded in 1972 after Hans G. Trüper accepted the Chair of Microbiology at the Faculty of Mathematics and Natural Sciences and was housed in a small, temporary building (Kurfürstenstraße 74). In 1973, Jobst-Heinrich Klemme was appointed to the newly established professorship of Applied Microbiology. In 1975, the Institute moved to the historic building at Meckenheimer Allee 168, the former Chemical Institute ("Alte Chemie") facing Meckenheimer Allee, which had been built between 1865 and 1868 for August Kekulé, whose monument still adorns the facade of the building. With the move, the name was also changed to "Institute of Microbiology and Biotechnology" and the Department of Agricultural and Food Microbiology of the Faculty of Agricultural Sciences, headed by Bernd Stille, also moved into the new building. Between 1982 and 1992, the building was completely renovated, extended into the left courtyard and historically restored in the entrance areas. It was also modernized in terms of security, room layout and technical equipment. In 1991, the Department of Pharmaceutical Microbiology of the Faculty of Medicine, headed by Bernd Wiedemann, moved into the extended parts of the building, so that the institute now included working groups from three different faculties.

Bernd Stille, who became emeritus in 1978, was followed by Johannes Krämer, Hans G. Trüper, who became emeritus in 2001, was followed by Erwin Galinski, and Bernd Wiedemann, who became emeritus in 2004, was followed by Hans G. Sahl. After the retirement of Jobst-Heinrich Klemme in 2007, Uwe Deppenmeier took over the Department of Applied Microbiology and André Lipski succeeded Johannes Krämer.

With the acquisition of a “Forschergruppenprofessur” and the appointment of Tanja Schneider in 2015, Pharmaceutical Microbiology became an independent, interfaculty institution at the Faculty of Medicine and the Faculty of Mathematics and Natural Sciences. In the meantime, the Institute of Nutrition and Food Sciences (IEL) was given a new building at the Poppelsdorf campus and the Department of Agricultural and Food Microbiology, headed by André Lipski, was relocated. The freed space was used to create an adequate workspace for Pharmaceutical Microbiology. In 2021, Ulrike Endesfelder succeeded Erwin Galinski.

Today, on its 50th birthday, the institute is again undergoing extensive renovations and infrastructure renewal. Its research focus today is on Cellular Microbiology, Applied Microbiology/Biotechnology and Pharmaceutical Microbiology.