BP 11: Franco-German Session: Bacterial Biophysics I

Time: Tuesday 9:30–12:45 Location: BAR/0106

BP 11.1 Tue 9:30 BAR/0106

Monitoring of biofilms formation using a QCM-D — •Philipp Sievers[1], Andreas Böttcher[1], Günther Räcker[2], Felix Bosch[2], and Diethelm Johannsmann[1] — [1]Institute of Physical Chemistry, Clausthal University of Technology, Arnold-Sommerfeld-Str. 4, 38678 Clausthal-Zellerfeld, Germany — [2]Feindrahtwerk Adolf Edelhoff GmbH & Co. KG, Am großen Teich 33, 58640 Iserlohn, Germany

Biofilms formed by bacteria are a severe problem in many industries. Biofilm formation leads to biofouling, which limits the heat transfer (e.g. in heat exchangers) or contaminates process water. Regular biofilm removal often is necessary. In order to reduce cost, an online detection of biofilm formation is highly desirable.

An instrument is described, which monitors biofilm formation based on a quartz crystal microbalance with dissipation monitoring (QCM-D). In contrast to a conventional gravimetric QCM, which would rely on the shift in the resonance frequency, the most useful parameter to quantify biofouling was found to be the increase in the resonance bandwidth. This is due to the fact that biofilms consist of soft material loosely attached to the resonator, mostly leading to the dissipation of energy. This behavior is recognized based on a specific overtone dependence of the bandwidth, namely increased bandwidth (**) being the same on the different overtones. This feature is best explained with a mechanical equivalent circuit containing a single dashpot coupled to the resonator surface.

BP 11.2 Tue 9:45 BAR/0106

Following bacterial biofilm formation with X-rays: From scanning gradients towards real-life studies. — •Matthias Schwartzkopf[1], Joanne Neumann[1], Edina Klein[1,2], and Holger Sondermann[1,2] — [1]Deutsches Elektronen-Synchrotron (DESY), Notkestr. 85, D-22607 Hamburg, Germany — [2]Centre for Structural Systems Biology (CSSB), Notkestr. 85, D-22607 Hamburg, Germany

Bacterial biofilm formation is a complex multi-step process yielding microbial communities encapsulated in an extracellular matrix of polymeric substances. Biofilms are a significant problem in treating bacterial infections and are one of the main reasons for the persistence of infections. Their increased resistance to classical antibiotics poses a severe threat to global health issues. Therefore, following and understanding the process of biofilm formation are essential for early detection and suppressing biofilm-associated infections. In this context, surface-sensitive X-ray scattering (GI-SAXS) is successfully applied to observe initial thin film growth morphologies and kinetics at various metal/organic interfaces [Schwartzkopf and Roth, Nanomaterials, 6, 239 (2016)]. In this contribution, we present the capabilities and first results of our combinatorial X-ray study on *Pseudomonas aeruginosa* biofilms aiming to provide nanoscale insight into the structure and dynamics of growing biofilms.

BP 11.3 Tue 10:00 BAR/0106

Nonlinear rheology of biofilm streamers: An eDNA-driven stress-hardening mechanism — Giovanni Savorana[1,2] and •Eleonora Secchi[1] — [1]ETH Zurich, Switzerland — [2]Princeton University, US

Biofilms are aggregates of microorganisms embedded in a self-secreted polymeric matrix that protects the community from physicochemical insults, enhancing their resilience across environmental, industrial, and medical settings. Because most biofilms develop in moist, flowing environments, they are constantly exposed to hydrodynamic forces. Yet how biofilms withstand strong or fluctuating flow conditions remains poorly understood.

Our work investigates how biofilms assemble under flow and how their morphology and rheology adapt across different flow regimes. Using a microfluidic platform enabling reproducible formation and in situ rheological testing, we show that biofilm streamers-filamentous assemblies that develop within the bulk of the flow-display stress-hardening: under flow-induced axial stress, both the differential elastic modulus and the effective viscosity increase linearly. This non-linear rheological response is conserved across several bacterial species. We develop a physical model showing that extracellular DNA (eDNA) is the key component enabling this stress-hardening behavior, allowing streamers to withstand both rapid and sustained variations in hydrodynamic load. Our work advances the physical understanding of biofilm development, reveals the molecular drivers of their mechanical resilience, and informs strategies for preventing biofilm-induced clogging.

BP 11.4 Tue 10:15 BAR/0106

Matrix-Microbe-Metabolite: Re-thinking transport phenomena in microbially-active soft matrices — •Juan Pablo Carmona Almazán[1] and Anupam Sengupta[1,2] — [1]Physics of Living Matter, Department of Physics and Materials Science, University of Luxembourg, Luxembourg — [2]Institute for Advanced Studies, University of Luxembourg, Luxembourg

The diffusion of biological metabolites through soft matrices is central to microbial biophysics, mediating healthy microbe-host interactions as well as diverse infections and biodegradation. An interplay of mechano-chemical cues, together with the microbe-induced remodeling of the local environments, impacts the metabolite transport in these settings. Yet, currently, we lack a mechanistic model of the Matrix-Microbe-Metabolite interactions. Here, we use a combination of high resolution imaging and quantitative image analysis techniques to study metabolite transport in diverse synthetic matrices with varying mechanical stiffness, composition, and biochemical complexity. Using suitable fluorescent probes as proxies, we quantify the transport kinetics in agarose as well as Matrigel, a model mammalian extracellular matrix. By interfacing atomic force microscopy, we map the results to the matrix structure, focusing on two key metabolites, formate and citrate. Finally, we embed bacterial cells to capture microbe-mediated impact on the diffusion kinetics, which together with the mechano-chemical datasets, provide a biophysical framework for active metabolite distribution in soft environments.

BP 11.5 Tue 10:30 BAR/0106

Differential pili interactions trigger colony eversion and dissemination of bacteria — Stephan Wimmi[1], •Isabelle Wielert[1], Kai Zhou[2], Marc Hennes[1], Benedikt Sabass[2], and Berenike Maier[1] — [1]Institute for Biological Physics, and Center for Molecular Medicine Cologne, University of Cologne, Germany — [2]Institute for Infectious Diseases and Zoonoses, Ludwig-Maximilians-Universitaet Munich, Germany

Attractive forces between cells determine the shape and sorting behaviour of bacterial colonies. During colony development, chemical gradients form within the colony but it is unclear how they affect cohesion. Here, we discover global eversion of colonies formed by Neisseria gonorrhoeae. Like a jet, the inner core flows towards the periphery where it is partially dispersed and partially spreads around the core of the colony. Living dispersed cells leading to fast dissemination. The eversion depends on local oxygen depletion that reduces cellular attraction: prior to eversion the colony consists of a weakly cohesive spherical core surrounded by a strongly cohesive shell. A computational model reveals when the thickness of the strongly interacting shell falls below a critical value a non-linear instability initiates colony-wide eversion. Simulations predict that an increase of cohesion forces among the bacteria suppresses colony eversion. This was confirmed experimentally by a genetic modification that increases attractive forces among bacteria. Overall, we conclude that a gradient of oxygen pushes the colony out of its equilibrium state and that non-linear instabilities trigger cellular fluxes during relaxation to a new stationary state.

BP 11.6 Tue 10:45 BAR/0106

How substrate stiffness and roughness tune early biofilm development: designing platforms for in situ observation of bacterial behavior — •Mathieu Letrou[1], Sofia Gomes[1], Kennedy Chagua Encarnacion[2], Rebecca Matthias[1], Yeraldinne Carrasco Salas[1], Elena Murillo Vilella[1], Lionel Bureau[1], Karin John[1], Delphine Débarre[1], and Sigolène Lecuyer[2] — [1]Université Grenoble Alpes, CNRS, LIPhy, Grenoble, France — [2]Laboratoire de Physique, ENS de Lyon, CNRS, Lyon, France

Biofilm formation begins with bacterial colonization of substrates, a process that occurs across diverse living tissues and abiotic surfaces. Early bacterial exploration of solid-liquid interfaces, governed by adhesion and individual motility, is a known determinant of the subsequent development and persistence of bacterial colonies. Yet, how bacteria integrate environmental cues at these interfaces and adapt their behav-

ior accordingly remains poorly understood. In this talk, I will present recent experimental approaches to generate microenvironments with precisely controlled properties, that also enable the in situ imaging of bacterial behavior within microfluidic channels. Using the pathogen Pseudomonas aeruginosa, I will show how substrate stiffness, rigidity gradients, and the presence of dispersed obstacles can alter surface exploration, thus modifying the onset of colony formation [1]. These results highlight how physical properties of solid-liquid interfaces can regulate early biofilm development and suggest new avenues for controlling surface colonization.

[1] Letrou et al., Eur Phys J E Soft Matter, 48(10-12):70 (2025)

15 min. break

Invited Talk BP 11.7 Tue 11:15 BAR/0106

Physics of bacterial adhesion: heterogeneity, patchiness, and surface interactions — •Karin Jacobs — Saarland University, Experimental Physics & Center for Biophysics, Saarbrücken, Germany

Bacterial cells interact with solid interfaces through a heterogeneous cell envelope, giving rise to rich physical behavior at solid-liquid boundaries. From a physics perspective, bacteria can be regarded as soft objects whose adhesion is governed by collective interactions of many fluctuating macromolecules. In this talk, I summarize recent experimental and theoretical work on bacterial adhesion using concepts from soft matter and surface physics.

Using atomic force microscopy-based single-cell force spectroscopy, we determine interaction forces between individual microbial cells and well-defined substrata. These experiments reveal heterogeneity of adhesion across the surface of single bacteria [1,2]. In particular, Gram-positive bacteria such as S. aureus exhibit a patchy adhesion landscape, reminiscent of patchy colloids, where a small number of adhesive regions dominate surface interactions.

We further show how surface properties such as wettability and protein coatings control bacterial adhesion by modulating the accessibility of tethering macromolecules [3]. Overall, these results place bacterial adhesion in the framework of condensed matter physics and illustrate how physical principles can guide the design of bio-interactive materials, ranging from simple functional interfaces to artificial cells. [1] C. Spengler et al., Soft Matter 20 (2024) 484; [2] E. Maikranz et al., Nanoscale 12 (2020) 19267; [3] F. Nolle et al., ACS Omega 10 (2025).

BP 11.8 Tue 11:45 BAR/0106

Bacterial motility and chemotaxis in porous media: lophotrichously flagellated *Pseudomonas putida* exhibits run motility with mechanical trapping and active turning events that enable chemotaxis based on a turn-angle bias — •Sönke Beier[1], Agniva Datta[1], Veronika Pfeifer[1], Robert Grossmann[1], and Carsten Beta[1,2] — [1]University of Potsdam, Institute of Physics, Germany — [2]Kanazawa University, Nano Life Science Institute, Japan

Chemotaxis has been extensively studied in bulk liquid, particularly for the peritrichously flagellated *Escherichia coli* with its run-and-tumble motility, where navigation toward chemoattractants relies on a run-time bias, which extends runs when cells swim up nutrient gradients. Less is known about chemotaxis in environments, where confinement limits free swimming and reduces the effectiveness of a run-time bias. Previous studies suggest that *E. coli* also bias its turning angle, adjusting reorientations to favor subsequent runs toward the chemoattractant. By analyzing the soil bacterium *P. putida* in porous media, we identify run phases and active turning events -known from bulk liquid- and additional mechanical trappings caused by the environment[1]. We provide evidence that the bacterium performs chemotaxis by employing a turn-angle bias and show that the resulting directional preference of runs arises from the active, motor-induced turning events, while passive mechanical trapping in the porous matrix weakens the preference[2]. Agent-based simulations indicate that the turn-angle bias is the predominant chemotactic strategy[2]. [1] Datta et al.:Sci Rep 15, 20320 (2025), [2] Beier et al.:arXiv:2503.05286 (2025)

BP 11.9 Tue 12:00 BAR/0106

Patchy Adhesion of Staphylococcus aureus on Structured Surfaces Uncovered via Single Cell Force Spectroscopy — •Samer Alokaidi[1], Hannah Heintz[1], Michael A. Klatt[1], Markus Bischoff[2], and Karin Jacobs[1] — [1]Saarland University, Saarbrücken, Germany — [2]Institute for Microbiologie, Homburg/Saar, Germany

Investigating bacterial adhesion at the single-cell level provides critical insights into bio-film formation and the influence of surface properties on microbial attachment. This study examines the adhesion behavior of Stapylococcus aureus on wrinkled polydimethylsiloxane (PDMS) surfaces using single cell force spectroscopy (SCFS) [1]. While conventional SCFS typically evaluates a single contact point, our approach-utilizing structured surfaces-enables mapping of adhesion across the lower portion of the bacterial cell envelope. This method reveals considerable variation in adhesion strength at different points on the cell surface, supporting the "patchy colloid" model originally proposed for Escherichia coli. Simulations, incorporating angle-dependent molecule-substrate interactions, suggest that localized adhesive "hotspots" on S. aureus may arise from surface roughness, chemical composition, and the clustering of specific adhesive proteins. These findings emphasize the significance of surface structuring in bacterial attachment and provide insights that inform the design of antimicrobial materials.

[1] C. Spengler, E. Maikranz, et. al: "The adhesion capability of Staphylococcus aureus cells is heterogeneously distributed over the cell envelope", Soft Matter, 20 (2024) 484

BP 11.10 Tue 12:15 BAR/0106

Drug interactions between translation and transcription-targeting antibiotics result from differences in ribosome regulation — •Natawan Gadjisade and Tobias Bollenbach — Institute for Biological Physics, Cologne, Germany

Combining antibiotics has the potential to improve treatment efficacy and slow the evolution of resistance. When two antibiotics are combined, their effect on bacterial growth may be stronger or weaker than expected. Recent work has shown that such interactions between ribosome-targeting antibiotics can often be predicted using a biophysical model based on bacterial growth laws. Here, we aim to understand the interplay between translation and transcription inhibitors. We identified different types of drug interactions by measuring E. coli growth in two-dimensional concentration gradients of the transcription inhibitor rifampicin and several translation inhibitors. We systematically quantify proteome allocation and individual protein regulation using mass spectrometry-based proteomics measurements. Notably, some translation inhibitors, such as kasugamycin, exhibit signs of disrupted coordination between the two ribosomal subunits. The ribosome concentration does not increase in response, thus violating the usual growth law. The way ribosomes respond to each translation inhibitor influences drug interactions with rifampicin, which itself causes a decrease in ribosome concentration. Based on the quantification of these different responses, we aim to build a biophysical model of antibiotic action that can explain the interaction patterns. Our work has the potential to facilitate quantitative predictions of drug interactions.

BP 11.11 Tue 12:30 BAR/0106

How transformation affects evolution in changing environments — •Ariana Leu, Mona Förster, Melih Yüksel, and Berenike Maier — Institute for Biological Physics, Cologne

Horizontal gene transfer (HGT) is known to play a critical role in bacterial evolution. However, it is still poorly understood under which exact conditions it can confer a fitness advantage and how it affects the dynamics of an evolving bacterial population. We study the effect of transformation on the adaptation of a bacterial population to a new environment depending on cell history.

First, the laboratory strain is adapted to two different environments, exponential growth in liquid and to growth in a structured environment. The pre-adaptation is driven purely by mutation. By selecting one of the two environments for further evolution we compare the adaptation pathways of a well adapted and a poorly adapted strain. We evaluate the fitness of the evolved populations relative to their ancestor, taking into account the effect of HGT. For well-adapted strains growing exponentially in a liquid environment, we see that the distribution of fitness effects broadens for hybrid populations. In a structured environment the adaptation of a poorly adapted strain is accelerated by transformation. We also find that transformation opens up a new genotypic pathway for adaptation that is not available through mutation. In addition, each cell is labeled with a unique genetic barcode at the beginning of evolution. By analyzing the ratio of barcodes at different time points, we gain insight into the evolutionary dynamics within the population.