BP 22: Bacterial Biophysics II

Time: Wednesday 15:00–17:15 Location: H 0112

BP 22.1 Wed 15:00 H 0112

Heterogeneous distribution of the adhesion capability across the cell envelope of *Staphylococcus aureus* cells — •Hannah Heintz[1], Christian Spengler[1], Erik Maikranz[2], Michael Klatt[1,3], and Karin Jacobs[1] — [1]Department of Experimental Physics, Saarland University, Saarbrücken, Germany — [2]Department of Theoretical Physics, Saarland University, Saarbrücken, Germany — [3]Department of Physics, Princeton University, Jadwin Hall, Princeton, USA

Understanding how a bacterium attaches to a surface is particularly important for controlling biofilms. Bacterial adhesion is known to be mediated by thermally fluctuating cell wall macromolecules [1], but the distribution of these adhesive-supporting macromolecules across the cell envelope is still unknown. We apply single cell force spectroscopy to study the adhesion force of *Staphylococcus aureus*. As a new approach, a sinusoidal PDMS surface is used, and force-distance curves are recorded along a path perpendicular to the structured surface. This allows for probing contact points distributed over almost a hemisphere of an individual bacterium. The analysis of the adhesion strength data shows that some bacterial cells display particularly strong adhesion at certain locations [2]. To obtain a complementary picture, Monte Carlo simulations are used to interpret the resulting adhesion profiles. Simple geometric considerations couldn't explain the origin of all adhesion profiles. Therefore, angle-dependent molecule-substrate interactions must be considered. [1] Spengler, C, et al., Front. Mech. Eng., 7:661370 (2021). [2] Spengler, C., et al., Softmatter, D3SM01045G (2023).

BP 22.2 Wed 15:15 H 0112

Local decrease in cell wall mechanical stress as a possible trigger for cell splitting in *Staphylococcus aureus* — •Sheila Hoshyaripour[1,2,3], Marco Mauri[1,2], Abimbola F. Adedeji Olulana[4], David Owen[4], Jamie K. Hobbs[4], Simon J. Foster[4], and Rosalind J. Allen[1,2] — [1]Friedrich Schiller university, Jena, Germany — [2]Cluster of Excellence Balance of the Microverse, Jena, Germany — [3]Jena School of Microbial Communication, Jena, Germany — [4]University of Sheffield, Sheffield, UK

Staphylococcus aureus is a clinically important Gram-positive bacterium able to generate antibiotic-resistant strains. Cell division happens in few milliseconds without cell wall constriction and how the cell controls the initiation of division is not clear. Our observations using atomic force microscopy and fluorescence microscopy show that the mechanical and geometrical properties of the cell and the cell cycle timing change with genetic mutations and in the presence of antibiotics. In addition, it is observed that peptidoglycan hydrolase activity, which plays a key role in cell division, may be negatively stress dependent. Here, we created a theoretical model to show how mechanics and hydrolysis work together to regulate the cell cycle. Our modelling shows that, during the cell cycle, mechanical stress decreases around the division site. With the hypothesis of stress-dependent triggering of the enzymes, the model predicts the timing of the later phases of the cell cycle which is supported by microscopy data. The model provides new insights into the combined effects of mechanical forces and enzyme activity in cell cycle regulation and initiation of division in *S. aureus*.

BP 22.3 Wed 15:30 H 0112

How Does a Riboswitch Differentiate Between Mg^{2+} and its experimental mimic Mn^{2+} for Specific Binding? — Kushal Singh and •Govardhan Reddy Patluri — Indian Institute of Science, Bangalore, India

Metalloriboswitches regulate metal ion homeostasis in bacteria. The aptamer domain of the Mn-sensing riboswitch (Mn-AD) binds to Mn^{2+} with high specificity in the presence of Mg^{2+}. However, Mn^{2+} can substitute Mg^{2+} in the binding pockets of RNA structures and is exploited as an experimental probe. To understand the specificity of Mn-AD towards Mn^{2+} sensing in the presence of Mg^{2+}, we used computer simulations and RNA models with different resolutions. We find that the specificity of the binding pocket for Mn^{2+} binding is driven by kinetics as Mn^{2+} loses a water molecule from its first solvation shell and transitions to an inner-shell interaction with a phosphate oxygen in the binding pocket relatively faster compared to Mg^{2+}. The enhanced sampling simulations show that Mn^{2+} further consolidates its binding to the MB pocket via conformational rearrangements, facilitating hierarchical dehydration of the six water molecules from its solvation shell and transitions to inner-shell coordination. The free energy for Mn^{2+} to lose six water molecules for its solvation shell is downhill compared to Mg^{2+}. These results provide insight into how bacteria use RNA to sense specific metal ions from a pool of biologically relevant metal ions to maintain homeostasis.

BP 22.4 Wed 15:45 H 0112

Amyloid fibers in biofilms: structure adaptation to environmental cues — •Macarena Siri, Agustín Mangiarotti, Mónica Vázquez-Dávila, and Cécile Bidan — Max Planck Institute of Colloids and Interfaces, Potsdam, Germany

E. coli biofilms consist of bacteria embedded in a self-produced matrix mainly made of protein fibers and polysaccharides. Not only the extracellular matrix plays a major role in achieving biofilm stability under different environmental conditions, but also is sensitive to their surroundings. The curli amyloid fibers found in the E. coli matrix determine the architecture and stiffness of their biofilms. They are promising versatile building blocks to design sustainable bio-sourced materials. To exploit their potential, it is crucial to understand how environmental cues during biofilm growth influence the molecular structure of these amyloid fibers, and how this translates at higher length scales. We studied the effect of water and nutrient content in the substrate on both biofilm materials properties and the structure and properties of curli amyloid fibers extracted from the biofilms. We used micro-indentation to measure the rigidity of the biofilms grown under different conditions, followed by microscopy and spectroscopy to characterize the amyloid fibers purified from the respective biofilms. The purified curli amyloid fibers present differences in the structure and functional properties upon different biofilm growth conditions. Our study highlights how E. coli biofilm growth conditions impact curli structure and functions contributing to macroscopic materials properties.

BP 22.5 Wed 16:00 H 0112

Global instabilities in maturing gonococcal colonies mediated by local type 4 pili interactions — •Marc Hennes[1], Kai Zhou[3], Benedikt Sabass[2], and Berenike Maier[1] — [1]Institute for Biological Physics, University of Cologne, Germany — [2]Institute of Infection Medicine and Zoonoses, Ludwig-Maximilians-University Munich, Germany — [3]Institute of Biological Information Processing, Forschungszentrum Jülich, Germany

Mechanical forces and interactions play a pivotal role in the outdifferentiation process of biofilm maturation. Active stresses in the form of swimming, growth pressure, and shear forces shape the three dimensional structure of bacterial aggregates and are linked to the metabolic activity of cells via underlying nutrient and metabolite fields. In the case of the pathogen *Neisseria gonorrhoeae*, initial aggregation is mediated by the short-range interaction of bound Type 4 Pili (T4P), filamentous appendages which cover the cell surfaces. Under load, pili connections continuously break, conferring dynamical and liquid-like properties to the proliferating colonies. As we discovered, the establishing nutrient gradients inside these growing aggregates entrain outdifferentiation of the local interaction frequency of T4Ps, and induce at a certain aggregate size a global mechanical instability which restructures the complete colony. We discuss the physical nature of the instability, identify the underlying nutrient trigger, and present possible advantages for the colonies in the form of increased cell dispersion.

15 min. break

BP 22.6 Wed 16:30 H 0112

Reciprocity of flagellar polymorphism and cell-body motion during tumbling of an *E. coli* — •Derek Cyrus Gomes[1], Holger Stark[2], and Tapan Chandra Adhyapak[1] — [1]Indian Institute of Science Education and Research (IISER) Tirupati, Tirupati, India — [2]Institut für Theoretische Physik, Technische Universität Berlin

The study of the dynamics of *E. Coli* has proven to be an extremely challenging problem due to the complex mechanisms underlying its motion. One such aspect of the dynamics involves *E.Coli's* abrupt change of swimming direction during the tumbling events. The event results from the reverse rotation of one of the flagella, making it leave

the flagellar bundle and causing, at the same time, an overall change in the bacterium's motion. It has been shown experimentally that during the tumbling event, the reverse-rotated flagellum undergoes transitions among several of its stable structures known as the polymorphic forms. While polymorphic transitions accompany a tumbling event, their necessity and influence over the tumbling statistics are unknown. In this work, we numerically probe the interplay of the cell body dynamics and flagellar polymorphism during a tumbling event. We find a reciprocal response between the two: while the polymorphic transitions do affect the cell body's tumbling dynamics, in turn, the cell-body motion can arrest the growth of the polymorphic forms. We present our results in light of the observed tumbling statistics, revealing new insights to understand the experimental observations. We also investigate the role of hydrodynamic interactions and shear flow in the aforementioned phenomena.

BP 22.7 Wed 16:45 H 0112

Sensory adaptation in a continuum model of bacterial chemotaxis - working range, cost-accuracy relation, and coupled systems — •Vansh Kharbanda[1,2] and Benedikt Sabass[1,2] — [1]Department of Veterinary Sciences, LMU München — [2]Department of Physics, LMU München

Sensory adaptation enables organisms to adjust their perception in a changing environment. A paradigm is bacterial chemotaxis, where the output activity of chemoreceptors is adapted to distinct baseline concentrations via methylation. The range of internal receptor states limits the stimulus magnitude to which these systems can adapt. Here, we use a highly idealized, Langevin-equation based model to study how the finite range of state variables affects the adaptation accuracy and the energy dissipation in individual and coupled systems. Maintaining an adaptive state requires energy dissipation. We show that the steady-state dissipation rate increases approximately linearly with the adaptation accuracy for varying stimulus magnitudes in the so-called fully adaptative state. This result complements the well-known logarithmic cost-accuracy relationship for varying chemical driving. Next, we study linearly coupled pairs of sensory units. We find that the interaction reduces the dissipation rate per unit and affects the overall cost-accuracy relationship. A coupling of the slow methylation variables results in a better accuracy than a coupling of activities. Overall, the findings highlight the significance of both the working range and collective operation mode as crucial design factors that impact the accuracy and energy expenditure of molecular adaptation networks.

BP 22.8 Wed 17:00 H 0112

Photokinesis and phototaxis in light-driven E. coli — •Giacomo Frangipane[1,2], Claudio Maggi[2], Maria Cristina Cannarsa[1], and Roberto Di Leonardo[1,2] — [1]Department of Physics, Sapienza University of Rome, Italy — [2]NANOTEC-CNR, Soft and Living Matter Laboratory, Institute of Nanotechnology, Italy

Bacteria inherently possess signal-detection capabilities, altering their movement patterns accordingly. Today synthetic biology techniques allow us to engineer bacteria by introducing heterologous receptors so that they respond to new stimuli. In this work, we expressed the light-driven proton-pump proteorhodopsin in E. coli cells to control their flagellar motors with light. In this modified bacteria, light affects both speed (photokinesis) and tumbling rate (phototaxis). We study the phenomenology emerging from the interplay between these two effects and observe that, if we apply a sinusoidal light pattern, its spatial frequency affects the fate of the cells' density profile. For slowly changing patterns bacteria tend to behave as if photophilic, while for high spatial frequency modulation, the photokinetic mechanism is dominant and results in an higher concentration in dark regions. We develop a run-and-tumble model that includes both phototaxis and photokinesis and provides a robust description and aligns well with the observed experimental data. Furthermore, for small modulation of light, this organism behaves as microswimmer whose tumbling rate can be controlled with light. This represents a way to control the tumbling rate of microorganisms with light and thus a significant step forward in achieving comprehensive control over the motility of at the microscale.