cytokinesis. Our results provide a detailed quantitative picture of in vivo Z-ring organization at the nanoscale.

2925-Pos Board B617

Role of Cell Wall Hydrolases in *Staphylococcus Aureus* Cell Division

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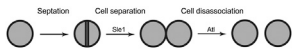
Most bacteria surround themselves with a tough cell wall made of peptidoglycan that preserves cellular integrity and maintains cell shape. Peptidoglycan must be dynamic to accommodate cell growth and division. Enzymes that hydrolyze peptidoglycan are crucial for these processes, but their activities can be lethal if not tightly controlled. In Gram-positive coccus *Staphylococcus aureus*, cell division can be classified into three stages: septation, daughter cell separation and finally disassociation. Previous Cryo-EM data has indicated that prior to cell separation the two daughter cells are only connected through the peripheral peptidoglycan. This result has led to the hypothesis that there are two classes of cell wall hydrolases: one class that splits the majority of the septum and the other class that resolves the final connecting ring to trigger cell separation. The identities of the hydrolases involved in these two stages and how the cell coordinates and regulates them are still not clear. We have examined the major cell wall hydrolases Atl and Sle1 in *S. aureus* and found that a *sle1* deletion mutant is delayed in cell separation while an *atl* mutant separated normally but was impaired in cell disassociation.



2926-Pos Board B618

Resolving a Function for Bacterial Cell Shape: Curvature Enhances Caulobacter Crescentus Surface Colonization

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Each bacterial species has evolved a characteristic shape that is stably maintained, indicating that specific shapes provide bacteria with selective advantages in nature. Much is known about the mechanisms by which bacteria acquire different shapes, but the benefits of specific morphologies are largely unknown. To understand the function of cell shape we focused on the curved bacterium Caulobacter crescentus. Paradoxically, C. crescentus curvature is robustly preserved in the wild but straight mutants have no known disadvantage in standard laboratory conditions. Here we demonstrate that cell curvature enhances C. crescentus surface colonization in flow, promoting the formation of larger and denser microcolonies. Leveraging microfluidics to mimic its natural environment and single-cell imaging, we also determined the mechanism by which curvature provides this benefit. Hydrodynamic forces cause curved cells to arc, optimally orienting polar pili, reducing their distance to the surface as the cell grows, and thereby enhancing surface attachment. C. crescentus thus repurposes pilus retraction, traditionally used for surface motility, for localized surface attachment. The benefit of curvature is modulated by flow intensity, potentially explaining why freshwater Caulobacter species that typically experience moderate flow are often curved while closely related marine species that experience stronger flows are often straight. Thus, our findings provide a mechanistic understanding of the potential benefit of bacterial curvature and highlight the importance of studying bacteria in conditions that reproduce their natural habitats.

2927-Pos Board B619

Spatiotemporal Evolution of Erythema Migrans, the Hallmark Rash of Lyme Disease

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To elucidate pathogen-host interactions during early Lyme disease, we developed a mathematical model that explains the spatiotemporal dynamics of the characteristic first sign of the disease, a large (5 cm diameter) rash, known as an erythema migrans (or EM). The model predicts that the bacterial replication and dissemination rates are the primary factors controlling the speed that the rash spreads, whereas the rate that active macrophages are cleared from the dermis is the principle determinant of rash morphology. In addition, the model supports the clinical observations that antibiotic treatment quickly clears spirochetes from the dermis and that the rash appearance is not indicative of the efficacy of the treatment. The quantitative agreement between our results and clinical data suggest that this model could be used to develop more efficient drug treatments and may form a basis for modelling pathogen-host interactions in other emerging infectious diseases.

2928-Pos Board B620

Chronic Wound Healing and Woundbed-Biofilm Interactions in Silico

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Chronic wound healing is very seriously hampered by a profound lack of basic understanding of the influence of bacteria and bacterial biofilms on the process. Treatment could greatly benefit from a longitudinal 3D assessment of spatial and biochemical properties of woundbed and fluid using molecular techniques. Inexpensive biosensor monitoring of a range of wound parameters and tissue cellular interactions would be beneficial, specially the profiling and early detection of multi-drug resistant organisms (MDROs).

Point-Of-Care (POC) wound assessment to monitor the healing process will benefit from digitization and automation of wound shape, size and volume determinations, wound color imaging including a simultaneously imaged calibration color card for digital processing, as well as imaging of pH, tissue oxygenation, vascularization and temperature distributions.

After initial haemostatis, a chronic wound develops when (a)biotic influences extend the inflammation period and hamper wound repair proliferation and remodeling. For healing to proceed the influence of the species and total number of bacteria present, the fraction of persister bacteria with reduced metabolic rates, the quantity of multiple drug resistance present in a (chronic) wound, disruption by wound dressings and the biochemistry of the woundbed - bacteria interaction eg. Extra Cellular Matrix (ECM) remodeling and bacterial motility has to be understood. To gain an understanding in chronic wound characteristics for theranostic purposes we present experiments in silico using Matlab and complement results with available open-source to simulate biofilms consisting of single and multiple species with species-specific properties under several of above described conditions. This may help to better understand the outcome of clinical trials and assist in the design of POC biosensors for monitoring and aiding chronic wound healing.

2929-Pos Board B621

Biochemical and Structural Characterization of an Archaeal Flagella

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Archaea cells possess a variety of motility and adhesion surface apparatus such as pili, hami, cannulae, and flagella which are genetically and biochemically unique to this domain of life. To explore the identity and properties of flagella from the model methanogenic archaean *Methanospirillum hungatei strain JF1*, we isolated the polar flagellar filaments by cell shearing and differential centrifugation. The flagella were visualized by negative stain electron microscopy revealing thin straight or gently curved filaments approximately 11 nm in diameter and up to 10 μm in length. This archaeal flagellum has a diameter significantly smaller than that of bacterial flagella. The *M. hungatei* flagellin components were separated by SDS PAGE, excised, tryptic digested and analyzed by LC/MS to identify the major flagellin proteins. Unlike the flagella of other described archaeal species, *M. hungatei* contains only one major flagellin protein, Mhun_3140, one of the three FlaB paralogs present in the genome. On SDS gel, this protein exhibited a molecular weight significantly higher than that predicted from its amino acid sequence, suggesting post-translational modifications. A glycostain and subsequent glycan analysis confirmed the presence of a glycan modification. We have determined a three-dimensional reconstruction of the archaeal flagellar filament at 7.5Å resolution by cryo electron microscopy (cryoEM). The structure reveals a core α helix in each subunit that contributes to the formation of the filament that is similar to that observed the bacterial type IV pili. Despite this similarity, the archaeal flagella structure exhibits many non-helical structural elements that bear little resemblance to the bacterial type IV pili.

2930-Pos Board B622

Escaping from Swarms

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Swarming behavior extends across multiple length scales in biology ranging from bacteria to whales. Swarms are affected differently by erratic, dissenting behavior, sometimes a swarm will follow an agent which changes directions, such as a school of fish when they are done feeding, while other times the swarm lets the individual leave the group while the swarm continues on its way, like a few birds leaving the flock to land in a tree. This research investigates the different universal swarm characteristics that can lead to these different kinds of behaviors. We model flocks with