

March Meeting 2023 Featured Presentations Biophysics

[Findings Describe How Cell Wall Development and Shape Impact Antibiotic Efficacy in Gram-Positive Bacteria like MRSA Superbug](#)

March 6, 12:54 p.m. PST, Room 202

Gram-positive bacteria include harmful germs like those in the Staphylococcus family, which can cause strep or pneumonia. This taxonomic category is also home to Methicillin-resistant Staphylococcus aureus (MRSA) — the pathogen behind antibiotic resistant staph infections. It is thought that exploring how cell walls develop in the related rod-shaped bacterium, Bacillus subtilis, could yield useful information for optimizing therapeutics that fight MRSA. This talk by Felix Barber and colleagues will answer a 20-year-old question concerning Gram-positive bacteria's cell walls: how does one step of development, cell wall teichoic acid (WTA) synthesis, regulate cell shape? The group says their work may help explain why antibiotics that target WTA synthesis restore MRSA's susceptibility to more common treatments. They add that the results, [which will also be viewable during a poster session](#), could also help in the creation of novel antibiotics that deliberately cause this outcome.

[Non-Invasively Studying Infant Ants and Other Insects Underground](#)

March 9, 9:24 a.m. PST, Room 206

Researchers are interested in understanding the collective behaviors of social insects like ants and termites. But these insects spend much of their lives underground, making it challenging to monitor their behaviors. In this talk, Hosain Bagheri and colleagues will describe how a laser spectroscopy technique previously used for studying the behavior of granular media could be used to non-invasively study the movements of underground insects. They demonstrated the technique in detecting ants in multiple developmental stages, showing that they could study the frequency, length and intensity of the insects' movements.

[Scientists Present a Path for Modeling Microbes' Immune Memory](#)

March 9, 12:06 p.m. PST, Room 238

Vaccines seek to build “immune memory” by training the immune system to mount better, faster responses upon reexposure to past pathogens. But this type of adaptive immune memory doesn't only exist in animals. Microbes also possess similar elements of immune memory. This talk, by Sidhartha Goyal and colleagues, will provide [a framework for modeling the dynamics of immune memory on a microbial-scale](#). Using theoretical simulations and experimental CRISPR models of adaptive immunity, the team made a counterintuitive discovery: high levels of microbial diversity correlate to low overall immune memory. In addition to this finding, other [results](#) related to the evolution of coexisting bacteria and phage diversity could enhance knowledge about microbial communities and how manipulating their immunity can advance public health.

[Study Explains How Two Individual Nostrils Work With Neurons to Perceive One Smell](#)

March 9, 11:54 a.m. PST, Room 203

Each human nose has two nostrils that independently sense and compile data from external cues. But despite their independence, those nostrils somehow interact with the brain in a way that ultimately results in one unified smelling experience. Here, Bo Liu and colleagues will show how olfactory cortical neurons that operate separately to process cues from each nostril ultimately align through crosstalk by projection fibers that connect brain hemispheres. The insights, derived from experiments in mice and modeling, reveal an inverse scaling relationship which shows that the inter-hemispheric projections can be sparser apart if there are more cortical neurons. According to the team, the inverse scaling relation adds new information about bilateral alignment in olfactory neural processing.

[Analysis of Yellowstone Bacteria Genomes Shows How Bacterial Populations Evolve](#)

March 10, 8:48 a.m. PST, Room 131

Because bacteria reproduce asexually and exchange little genetic material, conventional thought was that bacteria would tend to evolve into increasingly specialized strains over time. However, new evidence from a bacterial population in Yellowstone may challenge this assumption. In this talk, Gabriel Birzu and colleagues will describe how they analyzed the genomes of cyanobacteria from Yellowstone hot springs to study the genomic evolution of a bacterial population over a long time period. They found that even if subpopulations of bacteria had different ecological traits, the genetic differences between them tended to

decrease over time. Despite the traditional idea of increasing specialization, it seems that when subpopulations of bacteria from distinct genomic clusters coevolve for a long time period, they can result in populations that are a genetic mix of their ancestors.

[Chloroplasts in Plant Cells Show Glass-Like Behavior in Dim Light](#)

March 10, 9 a.m. PST, Room 129

The chloroplasts in plant cells can move toward or away from light depending on the light intensity, organizing themselves into various configurations. In this talk, Maziyar Jalaal and colleagues will describe a study of the re-arrangements of chloroplasts in cells of a water plant often used in home aquariums. They found that when chloroplasts in a plant cell arrange themselves into a single layer to increase their light exposure in dim lighting conditions, their collective motions bear [similarities to the behavior of glassy materials](#) near the glass transition — the point where glass shifts between solid and fluid states between solid and fluid states. The researchers suggest that being in a state close to this glass transition may let the chloroplasts quickly ball up into a clump to avoid damage when suddenly exposed to intense light.

[Study Uses Marine Microbes to Challenge Keystone Species Concept](#)

March 21, 10:24 a.m. PDT, Virtual Room 8

Keystone species are organisms that perform vital roles in ecosystems. But it is hard to evaluate the number of any given keystone species in a habitat because these species' value is usually not well-understood until after they disappear. In this talk, Akshit Goyal and colleagues suggest keystone species may be much rarer than previously thought by ecologists. Their lab-based experiments, involving marine microbial communities, indicate that there are very few keystone species whose removal can dramatically affect a biodiverse environment. Instead, additional analyses through machine learning and mathematical modeling underscore the value of structured interspecies interactions in habitats. The team argues that interactions among communities are structured and that it is the structure of those interactions that challenges the incidence of keystone species as understood by classical literature.