Speaker presentation summaries

Dr. Michael Ibba, Translational Control of Antibiotic Resistance

In response to different environmental stresses, such as the presence of antibiotics, microbes direct resources away from translation to a variety of pathways that contribute to antibiotic resistance. This lecture describes recent advances in key examples of such pathways, ranging from tRNA-dependent lipid modification to the use of a tRNA mimic that allows post-transcriptional control of gene expression.

Pat Schlievert, Can Coconuts Kill Many Microbial Pathogens?

Coconut oil is a major source of broadly active antimicrobial and anti-inflammatory fatty acid monoesters, such as glycerol monolaurate (GML). Most pathogens cause disease by causing minor or major inflammation at mucosal and skin surfaces. GML is highly active in killing pathogens, including bacteria, enveloped viruses, fungi, and protozoa, while not killing normal flora lactobacilli and bifidobacteria. At the same time, GML reduces inflammation that is required for microbes on human surfaces to initiate disease. The chance for microbial resistance to GML is estimated to be $1/10^{-105}$ because of the large numbers of GML targets on microbes. The mechanism of action for GML killing of microbes depends on dissipation of potential difference across plasma membranes, and the mechanism of resistance depends on lactobacilli and bifidobacteria using GML as a quorum sensing molecule.

Elitza Theel, Zika Virus – A Perspective from the Clinical Laboratory

This talk will provide the most up-to-date information regarding the ongoing Zika virus outbreak, including the evolving epidemiology and clinical impact of infection. The discussion will also review the available diagnostic tests and their performance characteristics for detection of Zika virus in clinical specimens.

Kim Brogden, Creating computational simulation models containing patient mutational profiles predict drug responder status to anti-PD-1/PD-L1 immunotherapy

Immunotherapy has demonstrated significant response in certain cancer patients, but predicting these responses can be variable. Here, we created individual patient-specific computational simulation models to predict PD-1 (and PD-L1) immunotherapy drug responder status using genomic information from patients with non-small cell lung cancers.

John Bannantine, The wild goose chase in mycobacterial research: the need to question even repeated observations

I will briefly discuss some of the most interesting findings from the Mycobacterium avium subspecies paratuberculosis genome sequencing project and then zero in on the very interesting research path that led to the discovery of a novel and specific monoclonal antibody to detect this veterinary pathogen. There were many twists and turns in this path!

Elizabeth Rucks, Lessons learned in mapping the chlamydial inclusion membrane

In the U.S., chlamydial infections result in over $700 million in medical costs. Novel strategies aimed at preventing or limiting the primary infection are needed. Chlamydia grows within a pathogen-specified organelle within host cells. We are applying innovative approaches to examine binding partners for host proteins that localize to this membrane, as well as, identify binding partners for inclusion membrane proteins knowns as Incs. Defining the molecular composition of inclusion membrane is a necessary first step towards identifying novel targets for preventive therapeutics.