QUANTITATIVE AND SYSTEMS BIOLOGY COLLOQUIUM:

Managing your multitudes: multicellular bacteria from symbiosis and immunity to biofilms and novel materials

Lizzy Wilbanks
UC Santa Barbara

Date:
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Time:
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Location:
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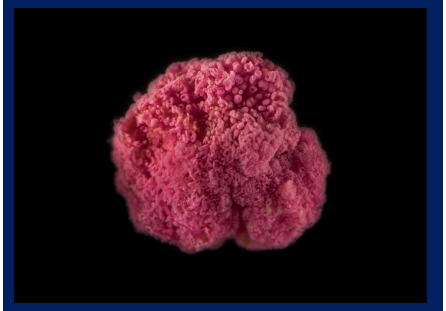

About the Speaker:

Wilbanks received her B.A. in Chemistry and Biology from Swarthmore College, where she conducted undergraduate research in synthetic organic chemistry (and discovered that microbes are marvelous chemists!). She completed her Ph.D. in Microbiology from the University of California, Davis, where she was co-advised by Jonathan Eisen and Marc Facciotti. Her dissertation research was inspired by projects at the Marine Biological Laboratory's Microbial Diversity summer course in Woods Hole, and focused on the metabolism and metagenomics of sulfur cycling bacterial consortia. Following NASA and Agouron postdoctoral fellowships at Caltech with Victoria Orphan, Wilbanks served as a visiting professor at Swarthmore College in the Biology Department. Wilbanks joined the University of California, Santa Barbara's Ecology, Evolution and Marine Biology department in 2016. Beyond the microbes in her life, Lizzy has 2 children, 2 dogs, 3 cats, a turtle, a snake, a parrot, and a wonderful (and very patient) wife.

Abstract:

From their earliest origins, multicellular hosts have been bathed in microbes. To survive, they have evolved to select and support populations of beneficial symbionts and fend off infectious pathogens. There is a rich literature on the physiological mechanisms mediating hosts' delicate balance with microbial friends and foes. This body of work on host-microbiome symbioses focuses almost exclusively on multicellular eukaryotic hosts (e.g., animals and plants). Yet, simple forms of multicellularity abound amongst bacteria and indeed, pre-date the emergence of multicellularity in eukaryotes likely by about a billion years. This gap in knowledge reflects our microbial myopia: until quite recently, we simply could not interrogate ecologically relevant partnerships between these often uncultivated bacteria. Recent work by us and others reveal unexpected complexity in multicellular bacteria's novel defense systems, many homologous to key components of innate immunity in plants and metazoans. These discoveries hint at remarkable sophistication for modulating their microbiomes, and more broadly, beg the question: what fundamentals can we learn about host-microbiome interactions from studying multicellular bacterial "hosts"? My research focuses on uncultivated, millimeter-sized bacterial consortia ("pink berries") formed by a multicellular, phototrophic bacterial species (purple sulfur bacteria, PSB) and its stable, low diversity microbiome. These consortia form granular biofilms, composed of microcolonies of PSB and their sulfate reducing symbionts encased in matrix composed of exopolysaccharides, extracellular DNA, and unusual crystalline protein sheets similar to a detached bacterial S-layer. Micro- and nano-indentation measurements indicate the granular biofilm matrix is a soft, gel-like, poroelastic material with adhesive properties and remarkable resilience. With extensive long read metagenomic sequencing, we have recovered a comprehensive genomes library for ~100 consortia members, which, for the core 14 members of the consortia, are present as single circular contigs or megabase sized contigs. These genomes reveal some unusual properties, such as an abundance of transposons and novel defense systems, that are enriched in other multicellular bacterial species. We discovered that numerous multicellular bacteria, including those in the pink berries, use dedicated systems for targeted hypermutation (diversity generating retroelements, DGRs) to diversify what we believe to be novel conflict systems for phage defense. In ongoing work, we characterized the bacterial populations, phage populations, and plasmid reservoirs by generating 88 PacBio HiFi metagenomes with paired viromes, capturing daily, weekly, and monthly time scales. Using this data, we are exploring the community and population dynamics of CRISPR-Cas immunity, and find that the acquisition of novel CRISPR spacers operates on a far longer timescale than anticipated, with many CRISPR genotypes preserved over decadal timescales.

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