Institute for Universal Biology (IUB)

BCXT-IUB Seminar Lecture

Friday, October 3, 2014
12 noon – 1 pm
Lecture Hall 612
Institute for Genomic Biology
Directions: http://www.igb.illinois.edu/about/directions

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"Investigating the impact of sRNAs and phage in the dynamics of human gut microbes"

Abstract

Human gut microbes play critical roles in human health and disease, however our understanding the mechanisms responsible for these important roles remains elusive. Our lab is interested in exploring two areas: RNA-based gene regulation and the interactions and dynamics of mobile genetic elements in gut microbes. In the last decade, study of microbial pathogens has revealed the important functions RNA regulators are responsible for, particularly the ability of RNAs to turn 'on' and 'off' genes essential for causing disease in hosts. We hypothesize that these types of RNA regulators (RNA riboswitches, small RNAs, and antisense RNAs) play equally important roles in beneficial gut microbes and structuring healthy gut communities. Furthermore gut microbial communities are inundated with mobile genetic elements such as bacteriophage, plasmids, and transposons, which play an important role in both community structure (e.g., predation) and acquisition of new traits (e.g., horizontal gene transfer). Presently we are evaluating the importance of the predicted RNA riboswitches involved in vitamin B_1 biosynthesis and transport in *Bacteroides thetaiotaomicron*. Like the many gut microbes *B. thetaiotaomicron* encodes thiamine pyrophosphate (TPP) riboswitches which regulate not only the core enzymes involved in synthesizing thiamine, but also its import. We are also using directional RNAseq to empirically identify novel RNAs in *B. thetaiotaomicron* and possible RNA binding proteins. In addition we are leveraging recent advances in sequencing and automation approaches that make it possible to identify and cultivate ~70% of the genera from the mammalian gut and combine that with microbial virus isolation techniques to identify and dissect novel mobile genetic element/microbe interactions. Together, our findings will help elucidate the roles of RNA regulators and mobile genetic elements in shaping genome evolution and community dynamics during health, disease and other perturbations.