UC RIVERSIDE

BCH 252 Make-Up Seminar

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Seminar Title: "Determining the functional roles of novel RNA binding proteins in a human gut microbe"

Abstract: The anerobic environment of the human gastrointestinal tract is colonized by microbial communities that are dense (~10^{12} CFU/g luminal contents) and complex (100s of species). The genus *Bacteroides* represents one of the major constituents of the gut microbiota. These microbes have been linked to a variety of human health conditions (e.g., inflammatory bowel disease, celiac disease). One of the principle metabolic roles is the degradation of a diverse array of dietary fibers which is mediated by genomic gene clusters known as polysaccharide utilization loci (PUL). While transcriptional regulatory pathways for some PULs have been characterized, there is an increased interest in their post transcriptional regulation. In well-studied members of the phyla *Proteobacteria* and *Firmicutes*, post transcriptional regulation often occurs via the actions of sRNAs and helper RNA chaperones such as, Hfq, CsrA, and ProQ. However, these chaperones are not present in members of the phylum Bacteroidetes. Instead, the *Bacteroidetes* encode a conserved family of distinct RNA binding proteins (Rbps). Previously, we have established that these Rbps bind single-stranded RNAs *in vitro* and most Bacteroides species have three to four Rbp homologs. Our model organism, *Bacteroides thetaiotaomicron* VPI-5482, encodes three copies namely, *rbpA*, *rbpB*, and *rbpC*. *Bacteroides* mutants lacking these Rbps exhibit global changes to their transcriptomes, with PUL-associated genes and those belonging to capsular polysaccharide (CPS) loci being most dramatically regulated. This suggests that regulation by Rbps underly mechanisms critical for several metabolic pathways, such as carbohydrate utilization and production of cell surface capsular polysaccharides, and hence, characterizing the Rbps may provide insight into how *Bacteroides* colonize and persist in the human gut. To this end we are carrying out additional genetic deletions, phenotypic screens, gene complementation, immunoprecipitation assays and transcriptome analyses to understand the role(s) of this protein family in potentially supporting *Bacteroides* gene regulation.

Tuesday, January 30th, 2024 12:00 p.m. - 12:50 p.m. PST

In-Person: Genomics Auditorium 1102A

Host: Dr. Seán O'Leary