S8-03

Computational analysis of prokaryotic genomes: 250 bugs later

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In my talk I will review recent developments in genome-scale sequence analysis. The current state of the PEDANT genome database will be described and possible strategies for more efficient protein sequence annotation presented. I will also present novel protein function prediction tools based on genomic context, focusing on the analysis of conserved protein interactions.

S8-04

Seeing spots: Understanding *H. pylori* Pathogenesis in the Age of Genomics

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Helicobacter pylori chronically colonizes over half of the world's human population and causes maladies that range in severity from gastritis, to ulcer disease, to gastric carcinoma or mucosa-associated lymphoid tissue (MALT) lymphoma. Once infected, the human host is typically colonized for the lifetime of the individual unless they receive specific antibiotic treatment. Remarkably, *H. pylori* colonizes within the stomach, a site that is inhospitable for virtually all other microbes. Within the confines of the stomach, the bacterium encounters large fluctuations in pH and iron availability. Because of this and due to its high success rate at establishing persistent infections, *H. pylori*must be adept at regulating gene expression to facilitate survival in this dynamic environment. In support of this, we have utilized DNA microarrays to show that *H. pylori* modulates gene expression in response to a myriad of different environmental stresses *in vitro*. The degree of modulation is varied, depending on the stress encountered but reveals that *H. pylori* has a profound ability to adapt to environmental fluctuations. Additionally, we have investigated the process of host/pathogen interaction by elucidation of host cell signaling networks affected by *H. pylori*upon interaction with host cells. It is known that *H. pylori* forms intimate interactions with host cells during the process of infection. This interaction results in the delivery of CagA to the host cell via a Type IV secretion apparatus. Once in the cell, CagA is tyrosine phosphorylated by members of the Src family of tyrosine kinases and subsequently binds to and deregulates the SHP2 phosphatase. Affected host cell signaling pathways past these are poorly understood, but it is known that phosphorylation of CagA and subsequent deregulation of host cell signaling results in the induction of actin cytoskeletal rearrangements and morphological changes in infected gastric epithelial cells (AGS). We have used transcriptional profiling in conjunction with *in vitro* and *in vivo* models of infection to define previously unrecognized host signaling pathways that are affected by *H. pylori*.