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Genomic and transcriptomic characterization of E. coli and Shigella

David A. Rasko University of Maryland School of Medicine, USA

Escherichia coli/Shigella exist as the major facultative anaerobe in the human gastrointestinal tract, but also can cause serious disease especially in young children, travelers and those that do not have access to clean water. *E. coli/Shigella* have been a model microbial system in use for decades, the advent of the genomic era has allowed unprecedented insight into the variation of this important species. Genome scale analysis has identified that approximately half of the *E. coli/Shigella* genome, ~2.2 Mbp, is highly conserved and represents an open genome structure that is constantly acquiring novel genetic material. Detailed studies have focused on the enterotoxigenic *E. coli* (ETEC) pathovar and the *Shigella* species. Genomic studies of each of these pathogens have revealed a complex and convoluted genomic evolution that is unique to each of the examples. Additionally, we have examined the ETEC transcriptional response to known virulence signals such as glucose concentration and intra-kingdom signals and have identified a number of candidate ETEC virulence factors. In addition to potential virulence factors, we have also identified novel genes that are conserved and may be involved in the regulation of virulence in this group of pathogens. Comparative genomics and transcriptomics has reached a new era where the number of strains that can be rapidly sequenced will begin to address epidemiological questions and become a more integrated component of the global health care system.

Biography

David A. Rasko is an Assistant Professor at the Institute for Genome Sciences at the University of Maryland, School of Medicine. He trained at the University of Alberta, completed post-doctoral studies at the University of Maryland, and held research positions at The Institute for Genome Research and University of Texas Southwestern Medical Center at Dallas. His laboratory focuses on the genome scale evolution, functional genomics and transcriptome analysis of enteric pathogens. Recent studies have focused on pathogen identification using high-throughput sequencing methodologies. He has published over 80 papers in reputed journals and serves on a number of Editorial Boards.

drasko@som.umaryland.edu