Sequence Based Approaches To Mechanisms Of Infectious Disease

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My lab is interested in new methods for understanding host-pathogen interactions in general and in understanding urinary tract infections (UTI) caused by Escherichia coli in particular. UTI is an extremely common disease, affecting billions, and we are unable to treat certain subtypes. In addition, UTI has an outstanding mouse model system and we have full molecular control of E. coli on the pathogen side. Therefore, UTI is a perfect system for combining immediate relevance with model convenience as we develop and validate new methods for studying infectious diseases.

I will discuss how evolutionary analysis of DNA sequence has led to novel and nontrivial insights into the function of FimH, a key virulence factor for E. coli to cause UTI. This has demonstrated that FimH has a second function that is not apparent from previous biochemical, genetic, or structural analysis. This second function is important for an intracellular infection mode that is not targeted by current therapy and may explain our inability to treat certain types of UTI. Finally, I will present preliminary data on additional genomic technologies and approaches to study this intracellular infection in earnest, with a focus on human infections and the search for new therapies.

Selected Publications
