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A functional genomics approach to the identification of virulence genes involved in *Edwardsiella tarda* pathogenesis

Edwardsiella tarda is an important cause of hemorrhagic septicemia in animals and also gastro- and extra-intestinal infections in humans. A comparison of extracellular proteins of virulent and avirulent *E. tarda* strains reveals several major, virulent-specific proteins such as SseB, SseC and SseD. They are the homologs of the *Salmonella* secretion system effectors of the type III secretion system (TTSS). At the same time, we also identified 14 virulence genes of pathogenic *E. tarda* that are essential for disseminated infection, via a genome-wide analysis. We screened 490 alkaline phosphatase fusion mutants from a library of 450,000 *TnphoA* transconjugants derived from strain PPD130/91, using gourami fish as an infection model. As compared to the wild type, 15 mutants showed significant decrease in virulence. They were divided into three groups: highly, moderately, and slightly attenuated mutants, depending on the level of attenuation. Proteomic analysis of bacterial proteins produced by the wild type, highly and slightly attenuated mutants identified additional putative virulence factors such as EtpA, EtpC, and the discovery of a TTSS in *E. tarda*. The present study showed that proteins involved in temperature-dependent protein secretion systems are the major determinants of *E. tarda* virulence, and the use of functional genomics is a powerful approach to study bacterial pathogenesis.

Date: 12 Sept 2003, Fri
Time: 4 pm
Venue: LT20
Host: A/P RM Kini



All are welcome