

Using population dynamics and transposon-directed insertion site sequencing (TraDIS) to identify bacterial factors essential for the egress from the neonate epithelial cell

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Non-typhoidal *Salmonella* (NTS) are a global health problem in human and veterinary medicine. Low hygiene conditions and young age the risk for systemic dissemination. We applied our previously established neonatal mouse model to examine *S. Typhimurium* pathogenesis and systemic distribution. Within host cells, NTS typically reside in a specialized membrane-bound compartment, the *Salmonella* containing vacuole (SCV). To overcome the epithelial barrier, NTS use effector proteins encoded by *Salmonella* Pathogenicity Islands (SPIs). We recently demonstrated that SPI2 effector proteins play an important role in transmigration of the SCV across intestinal enterocytes. In the present study, our aim is to further identify essential genes for breaching the intestinal barrier, enterocyte egress and subsequent systemic spread. We created a mutant library with random Tn5 transposon integrations and will orally administer it to newborn mice (input pool). We will subsequently compare it to populations isolated from different tissues (output pool). The results of this study will contribute to a better comprehension of the process of egress and systemic spread and potentially assist in development of new treatment and prevention strategies for NTS infections in the newborn.

Keywords

Salmonella Typhimurium, Tn5 library, TraDIS, Egress

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Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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