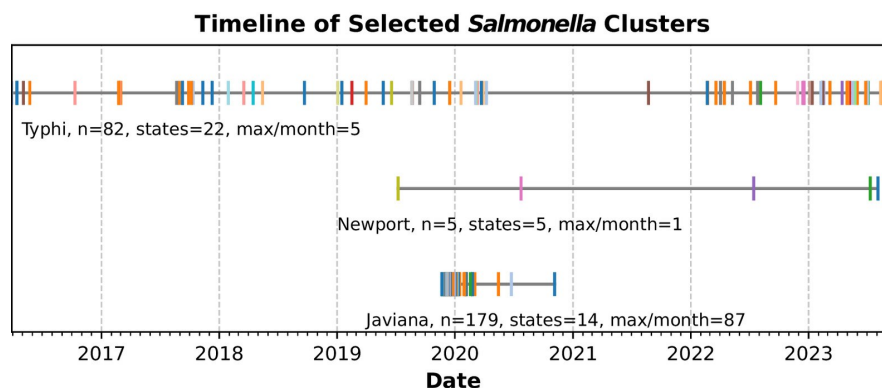


Genomic Perspectives on Foodborne Illness



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While outbreaks of foodborne illness receive much attention, they include only a small fraction of cases. To learn more about non outbreak cases, we use bacterial genomes generated for outbreak detection and identify clusters of closely related disease-causing isolates. Small clusters account for most cases. A high fraction have cases from multiple states, suggesting contamination at central food distribution sites. As previously observed, illness is especially common in the very young, at least partially due to greater susceptibility. Most cases in infants, who consume only breast milk and infant formula, cluster with cases from older people, implicating cross-contamination from noninfant food or early feeding of complementary foods. Analysis of such genetic clusters is a valuable tool for studying sporadic food poisoning.

Tuesday, December 3, 2024 @ 4:00PM ET in Glass Pavilion

Live Webcast:: <https://wse.zoom.us/j/93350879485>

Faculty Hosts: Prof. Steven Salzberg (CCB) and Prof. Joel Bader