

Dr. Eppinger is an Assistant Professor of Microbial Genomics and Co-Director of the Genomics Core at the University of Texas at San Antonio. His laboratory is also affiliated to the South Texas Center for Emerging Infectious Diseases (STCEID). He obtained a MS and Ph.D degree from the University of Tuebingen - Max Planck Institute for Developmental Biology in Germany and received Postdoctoral training at the Pennsylvania State University and The Institute for Genomic Research (TIGR).

One research focus is on Shiga toxin (Stx) producing *E. coli* (STEC) by applying whole genome sequencing and typing strategies following genomic epidemiology principles. To exploit the information content of whole genome sequence data his laboratory has developed high-resolution whole genome sequencing and typing strategies (WGST) to retrace the evolutionary history of pathogenic bacteria and study outbreak dynamics. This approach provides the necessary phylogenetic accuracy and resolution power to distinguish “near clonal” outbreak isolates for strain attribution, and ultimately track outbreaks to their contaminated source.

Among circulating STEC pathogen populations we have identified hypervirulent clones and are particularly interested how the genotype of both the STEC core- and accessory Stx prophage genome, independently or in combination, contributes to amplifying or dampening toxin production in STEC pathogens. Data from this research can provide crucial insights into the make-up of bacterial pathogens and how genomic variants relate to differences in evolutionary and ecological niches that underlie human transmissibility, infectivity and disease outcome.