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Targeted omics to understand pathogen evolution

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Abstract:

Diseases affecting vulnerable populations share the same obstacles: sparse surveillance, sparse genomic data, and limited mechanistic understanding of virulence. My work addresses leishmaniasis, a neglected tropical disease; cholera in Bangladesh; and *Bartonella quintana* infection across Canada and Europe among persons experiencing homelessness. These diseases can cause fatal visceral or disfiguring cutaneous lesions, acute dehydrating diarrhoea, and endocarditis, respectively.

By lowering the cost and increasing the accessibility of sequencing technologies, particularly long-read sequencing, my work provides a broader view of circulating populations and, more importantly, a more complete view of their genomes. These genomic data can then guide bench and field experiments, which in turn refine the computational analyses, and are extended through targeted transcriptomics, proteomics, and metabolomics. Two examples illustrating this cycle will be presented: the role of genome hybridization in *Leishmania* tissue tropism, and the functional consequences of chromosomal fusion in *Vibrio cholerae*.