

Surveillance of human and environmental drivers of cholera in Bangladesh

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The population of Bangladesh is largely rural and poor, highly mobile, and subject to repeated natural disasters - particularly cyclones and flooding - due to its position in the Bay of Bengal. Cholera remains a constant epidemic threat as a result. Surveillance for infectious diseases, including cholera, is virtually nonexistent outside the capital city Dhaka. This reflects the lack of distributed capacity for the reliable collection and reporting of epidemiological data in rural areas that are most vulnerable to disease.

Here we propose to build on a successful collaboration with partners in Bangladesh prior to, and during, the COVID-19 epidemic, to develop new approaches to cholera surveillance. We are currently building our capacity to conduct distributed genomic capacity using MinION nanopore sequencing approaches - which have successfully been deployed to analyze SARS-COV-2 genomes this year - to conduct surveillance of *Vibrio cholerae* and other water-borne pathogens in environmental samples. In parallel, we have been working with the major mobile phone operators to understand the human population dynamics that leads to the dissemination of outbreaks out of their environmental reservoir hotspots to other parts of the country.

We propose to hire a postdoctoral fellow to work on methods to integrate these two analytical approaches, since currently genomic surveillance and models parameterized using mobility data usually use separate analytic tools. In previous work (with collaborators including Prof Kwiatkowski) we have started to develop integrated models of this kind for malaria, but environmental samples represent a different challenge because they monitor complex environmental reservoirs for potentially outbreak-causing pathogens, rather than clinical samples. Spatial epidemiological models also tend to rely on one or other type of data, and in both cases these methods are relatively new, rather than leveraging both sources of information. The integration of this kind will require a researcher who is comfortable with dynamical modeling, bioinformatic and genomic analysis, and handling large data sets such as those from mobile phones.

This project will benefit from the expertise of other Associate Faculty members, since these analytical tools are generally applicable to other pathogens. In fact, the longer-term goal for this project is the integration of genomic data from multiple pathogens and mobility data, since - depending on the transmission route - these surveillance platforms should be relevant across infectious disease causing organisms. Bangladesh is an ideal place to start because it encompasses so many of the challenges facing LMICs globally, and we have long-standing collaborative networks across different pathogen systems, in industry, and in academia.