

Factors related to being a “transmitter” or a “transmittee”: a spatial Bayesian modeling analysis of *M. tuberculosis* whole genome sequence data

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Recent advances in molecular sequencing tools and analytical methods offer new opportunities for using pathogen whole genome sequencing (WGS) to infer who-infects-whom in infectious disease outbreaks. Here we use data from a WGS study of *M. tuberculosis* transmission in a city in Malawi with a high burden of tuberculosis (TB) and HIV to identify factors related to transmission. Specifically, we aim to use directed pairwise transmission probability estimates to identify TB cases that with high probability were source cases for other TB cases (“transmitters”), and to identify TB cases that were likely directly infected by other TB (“transmittees”). We assume that each transmitter could be the source case for several other cases, but that each case could have been infected by only one source. In total, we analyzed WGS data from 847 TB cases; we found that 307 transmitters were likely source cases for 395 cases and that 164 cases were direct transmittees of other cases. Our preliminary results show that TB cases with infection of lineage 4 *M. tuberculosis* strains have 1.3 times the expected number of secondary cases from “transmitters” (95% CIs: 1.02-1.67) and 1.57 times the odds of being “transmittees” (95% CIs: 1.13-2.18), compared with cases infected with other lineages. For every year increase in age, the odds of being a “transmittee” decrease by 2% (95% CIs: 0.97-0.99). We also located geographic areas of increased risk of cases being “transmittees” or “transmitters” using kernel density estimation. We are currently fitting a spatial Bayesian modeling to explore the relationship between location and environmental factors in transmission.

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