Bayesian Modeling of Spatiotemporal patterns of TB-HIV co-infection risk in Kenya

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Abstract
Background Tuberculosis (TB) and Human Immunodeficiency Virus (HIV) diseases are globally acknowledged as a public health challenge that exhibits adverse bidirectional relations due to the co-epidemic overlap. To understand the co-infection burden we used the case notification data to generate spatiotemporal maps that described the distribution and exposure hypotheses for further epidemiologic investigations in areas with unusual case notification levels. Methods We analyzed the TB and TB-HIV case notification data from the Kenya national TB control program aggregated for forty-seven counties over a seven-year period (2012 - 2018). Using the Integrated Nested Laplace Approach (INLA), we modeled the risk of TB-HIV co-infection. Six competing models with varying space-time formulations were compared to determine the best fit model. We then assessed the geographic patterns and temporal trends of coinfection risk by mapping the posterior marginal from the best fit model. Results Of the total 608312 TB case notifications, 194129 were HIV co-infected. The proportion of TB-HIV co-infection was higher in females (39.7%) than in males (27.0%). A significant share of the co-infection was among adults aged 35 to 44 years (46.7%) and 45 to 54 years (42.1%). Based on the Bayesian Defiance Information (DIC) and the effective number of parameters comparisons, the spatiotemporal model 3b was the best in explaining the geographical variations in TB-HIV coinfection. The model results suggested that the risk of TB-HIV coinfection was influenced by infrastructure index (Relative risk (RR)=5.75, Credible Interval (Cr.I) = (1.65, 19.89)) and gender ratio . The lowest and highest temporal relative risks were in the years 2016 at 0.9 and 2012 at 1.07 respectively. The spatial pattern presented an increased co-infection risk in a number of counties. For the spatiotemporal interaction, only a few counties had a relative risk greater than 1 that varied in different years. Conclusions We identified elevated risk areas for TB/HIV co-infection and fluctuating temporal trends which could be because of improved TB case detection or surveillance bias caused by spatial heterogeneity in the co-infection dynamics. Focused interventions and continuous TB-HIV surveillance will ensure adequate resource allocation and significant reduction of HIV burden amongst TB patients.

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