Genomic epidemiology of a major Mycobacterium tuberculosis outbreak: Retrospective cohort study in a low incidence setting using sparse time-series sampling

Since 1992, Denmark has documented the largest outbreak of tuberculosis in Scandinavia ascribed to a single genotype, termed ’C2/1112-15’. As of spring 2017, the International Reference Laboratory of Mycobacteriology in Copenhagen has collected and identified isolates from more than a thousand cases belonging to this outbreak via routine MIRU-VNTR typing. Here, we present a retrospective analysis of the C2/1112-15 dataset, based on whole-genome data from a sparse time-series consisting of five randomly selected isolates from each of the 23 years. Even if these data are derived from only 12% of the collected isolates, we have been able to extract important key information, such as mutation rate, conserved single-nucleotide polymorphisms to identify discrete transmission chains, as well as the possible historical origins of the outbreak.

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