MedicalXpress

Whole genome sequencing better at tracing TB outbreaks than standard test

February 19 2013

A new form of genetic testing of the bacteria that causes tuberculosis can provide better information on TB transmission and also trace TB outbreaks more accurately than the current standard test, according to a study from Germany published in this week's *PLOS Medicine*.

A team of researchers led by Stefan Niemann from Forschungszentrum Borstel, Molecular Mycobacteriology, compared the results of the two types of tests on 86 M. tuberculosis isolates from a TB outbreak in the German states of Hamburg and Schleswig-Holstein between 1997 and 2010, in which 2301 people were diseased in the study period.

They found that the new test (whole genome sequencing) provided more accurate information on clustering and longitudinal spread of the pathogen than the standard test (classical genotyping). Importantly, whole genome sequencing revealed that first outbreak isolates were falsely clustered by classical genotyping and do not belong to one recent transmission chain.

By using whole genome sequencing, the authors estimated that the genetic material of M. tuberculosis evolved at a rate at 0.4 mutations per genome per year, suggesting that the bacterium grows in its natural host (infected people) with a doubling time of 22 hours, or 400 generations per year. This finding about the evolution of M. tuberculosis indicates how information from whole genome sequencing can be used to help trace future outbreaks.

Importantly, as the costs of whole genome sequencing are declining, this test could soon become the standard method for identifying transmission patterns and rates of infectious disease outbreaks.

The authors say: "Our study demonstrates that whole genome sequencing-based typing provides epidemiologically relevant resolution of large, longitudinal [Mycobacterium tuberculosis] outbreaks much more efficiently than classical genotyping."

They continue: "We envision that [whole genome sequencing] progressive effective implementation will be accelerated by the continuously decreasing sequencing costs, broader distribution of so-called bench top genome sequencers, and upcoming bioinformatics developments to facilitate quick and relevant interpretation of the resulting data in public health and medical contexts."

More information: *PLoS Med* 10(2): e1001387. doi:10.1371/journal.pmed.1001387

Provided by Public Library of Science