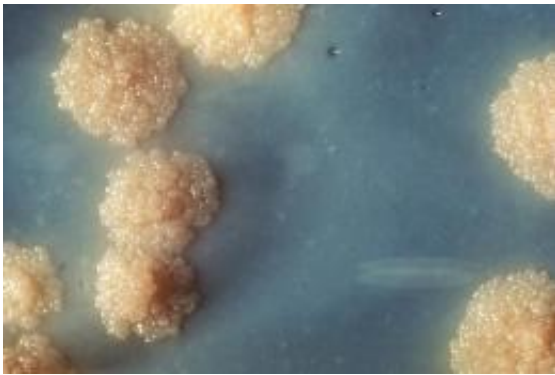


Mycobacterium tuberculosis: Our African follower for over 70,000 years

September 1 2013



M. tuberculosis bacterial colonies. Credit: Centers for Disease Control and Prevention.

Tuberculosis (TB) remains one of deadliest infectious diseases of humans, killing 50% of individuals when left untreated. Even today, TB causes 1-2 million deaths every year mainly in developing countries. Multidrug-resistance is a growing threat in the fight against the disease.

An international group of researchers led by Sebastien Gagneux from the Swiss Tropical and Public Health Institute (Swiss TPH) has now identified the origin in time and space of the disease. Using whole-genome sequencing of 259 *Mycobacterium tuberculosis* strains collected from different parts of the world, they determined the genetic pedigree of the deadly bugs. This genome comparison to be published September 1st in the journal *Nature Genetics* indicates that TB mycobacteria

originated at least 70,000 years ago in Africa.

Stunningly close relationship between humans and *M. tuberculosis*

The researchers compared the genetic evolutionary trees of mycobacteria and humans side-by-side. And to the researcher's surprise, the phylogenetic trees of humans and the TB bacteria showed a very close match. "The evolutionary path of humans and the TB bacteria shows striking similarities," says Sebastien Gagneux.

This strongly points to a close relationship between the two, lasting tens of thousands of years. Humans and TB bacteria not only have emerged in the same region of the world, but have also migrated out of Africa together and expanded all over the globe.

The migratory behaviour of modern humans accompanied with changes in lifestyle has created favourable conditions for an increasingly deadly disease to evolve. "We see that the diversity of tuberculosis bacteria has increased markedly when human populations expanded," says evolutionary biologist Sebastien Gagneux.

Human expansion in the so called Neolithic Demographic Transition (NDT) period combined with new human lifestyles living in larger groups and in village-like structures may have created conditions for the efficient human-to-human transmission of the disease, Gagneux suggests. This may also have increased the virulence of the bacteria over time.

The results indicate further that TB is unlikely to have jumped from domesticated animals to humans, as seen for other infectious diseases. "Simply, because *Mycobacteria tuberculosis* emerged long before humans started to domesticate animals," says Swiss TPH's Sebastien Gagneux.

New strategies to defeat tuberculosis

Tuberculosis remains a global threat. New drugs and vaccines are urgently needed to fight this poverty-related disease. Multidrug-resistance against first-line treatments is a growing threat in many countries. Therefore, the exploration of the evolutionary patterns of TB bacteria may help predicting future patterns of the disease. This may contribute to future drug discovery and to the design of improved strategies for disease control.

More information: Out-of-Africa migration and Neolithic coexpansion of Mycobacterium tuberculosis with modern humans. Iñaki Comas, Mireia Coscolla, Tao Luo, Sonia Borrell, Kathryn E Holt, Midori Kato-Maeda, Julian Parkhill, Bijaya Malla, Stefan Berg, Guy Thwaites, Dorothy Yeboah-Manu, Graham Bothamley, Jian Mei, Lanhai Wei, Stephen Bentley, Simon R Harris, Stefan Niemann, Roland Diel, Abraham Aseffa, Qian Gao, Douglas Young & Sebastien Gagneux. *Nature Genetics*, AOP, Sept 1 2013. 10.1038/ng.2744
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