



Press Release

Medieval Leprosy Genomes Shed Light on Disease's History

Tübingen-led scientists reconstruct the complete historical genome of medieval and ancient scourge

Tübingen, 13.06.2013

An international team of scientists reconstructed a dozen medieval and modern leprosy genomes – suggesting a European origin for the North American leprosy strains found in armadillos and humans, and a common ancestor of all leprosy bacteria within the last 4000 years.

It is the first time scientists have reconstructed an ancient genome without a reference sequence (de novo) due to the extraordinary preservation of the medieval pathogen's DNA. This finding indicates that ancient bacterial DNA may survive in some cases much beyond the one million year boundary suggested for vertebrate DNA.

Leprosy, a devastating chronic disease caused by the bacterial pathogen *Mycobacterium leprae*, was prevalent in Europe until the late Middle Ages. Today, the disease is found in 91 countries worldwide with about 200,000 new infections reported annually.

To retrace the history of the disease, an international team of scientists, led by Johannes Krause from Tübingen and Stewart Cole from EPFL Lausanne, have reconstructed entire genome sequences of *M. leprae* bacteria from five medieval skeletons that were excavated in Denmark, Sweden and the United Kingdom as well as seven biopsy samples from modern patients.

The researchers compared the medieval European *M. leprae* genomes with 11 worldwide modern strains, including the seven biopsy strains, revealing that all *M. leprae* strains share a common ancestor that existed within the last 4000 years. This is congruent with the earliest osteological evidence for the disease in the archaeological records dated to 2000 BC from India. The genome comparisons indicate a remarkable genomic conservation of the bacteria during the past 1,000 years. The team of scientists could furthermore show that *M. leprae* genotypes in medieval Europe are today found in the Middle East, whereas other medieval strains show a striking similarity to modern strains found today in North American armadillos and leprosy patients suggesting a European origin of leprosy in the Americas.

One skeleton from Denmark (Jorgen 625) showed extraordinary

Myriam Hönig
Director

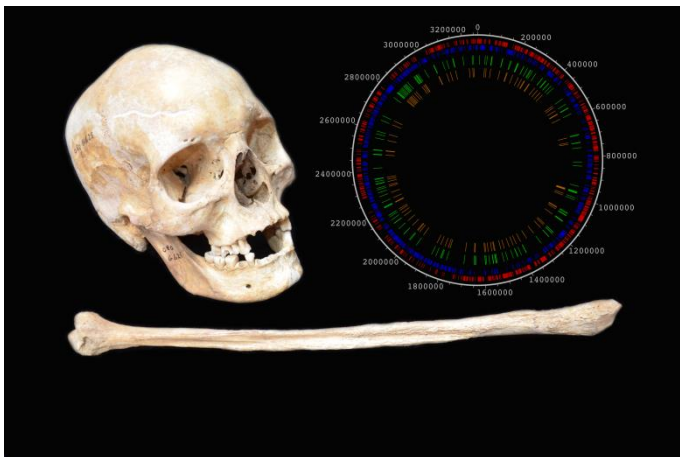
Antje Karbe
Phone +49 7071 29-76788
+49 7071 29-76789
Fax +49 7071 29-5566
myriam.hoenig@uni-tuebingen.de
antje.karbe@uni-tuebingen.de
www.uni-tuebingen.de/aktuell

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preservation of the pathogen DNA, allowing a genome reconstruction without using a modern reference sequence, which was never done before for an ancient organism's genome. The scientists found that almost half of the DNA recovered from that particular specimen derived from *M. leprae* bacteria; this is orders of magnitude higher than the amount of pathogen DNA usually observed in skeletons and modern patients. They furthermore found that the *M. leprae* DNA was far better preserved compared to the human DNA, which may explain this unusually high amounts of bacterial DNA in these skeleton samples. According to the authors this may be due to the extremely thick and impervious waxy cell wall of the leprosy bacillus that protects their DNA from degradation. Therefore, the authors speculate that some bacterial DNA may be preserved much longer than any vertebrate DNA, which is usually less protected. "This opens the possibility that certain types of bacterial DNA may survive well beyond the maximum age for mammalian DNA of around one million years," says Krause and adds, "This gives us a real perspective to trace back the pre-historic origins of a disease."

Source:

Verena J. Schuenemann et al. 2013. Genome-wide comparison of medieval and modern *Mycobacterium leprae*. *Science*, in press, 1238286



Skull and femur of a medieval leprosy sufferer from Denmark. In the background, a *de novo* reconstructed leprosy genome.

Photo: Ben Kyora-Krause

Excavations of the St. Mary Magdalen leper hospital in Winchester. One set of remains examined in the study was found here.

Photo: University of Winchester



More photos at: <http://www.eurekalert.org/jrnls/sci/>

Contacts:

Johannes Krause

University of Tübingen
Institute for Archaeological Sciences
Rümelinstr. 23 · 72070 Tübingen
Germany
Phone: +49 7071 29-74089
Johannes.krause@uni-tuebingen.de

Kay Nieselt
University of Tübingen
Center for Bioinformatics Tübingen
Sand 14, 72076 Tübingen
Germany
Phone: +49(0)7071 / 29-78981
kay.nieselt@uni-tuebingen.de

Stewart Cole
EPFL/SV/GHI/UPCOL
Station 19,
CH-1015 Lausanne, Switzerland.
Tel: +41 21 693 18 51
stewart.cole@epfl.ch

The following authors contributed to the publication: Verena J. Schuenemann, Günter Jäger, Kirsten I. Bos, Alexander Herbig, Peter Bauer, Kay Nieselt and Johannes Krause of the University of Tübingen (Germany); Pushpendra Singh, Andrej Benjak, Philippe Busso and Stewart T. Cole of the Ecole Polytechnique Fédérale de Lausanne (Switzerland); Thomas A. Mendum, Huihai Wu, Graham R. Stewart and G. Michael Taylor of the University of Surrey (UK); Ben Krause-Kyora and Almut Nebel of the University of Kiel (Germany); Christos Economou and Anna Kjellström of the University of Stockholm (Sweden); Jesper L. Boldsen of the Medicine University of Southern Denmark (Denmark); Oona Y.-C. Lee, Houdini H.T. Wu, David E. Minnikin and Gurdyal S. Besra of the University of Birmingham (UK); Katie Tucker and Simon Roffey of the University of Winchester (UK); Samba O. Sow of the Center for Vaccine Development-Mali (Mali).

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