

Genetic study of 15th century samples shows adaptive changes in bacteria that cause relapsing fever

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The skeleton (right) excavated at the St. Nikolay Church in Oslo, which carried sequences for the pathogen of louse-borne relapsing fever. Credit: PNAS

A team of researchers with members from the University of Oslo and the Norwegian Institute for Cultural Heritage Research has conducted a genetic analysis of the bacteria that causes relapsing fever obtained from 15th century skeletons in Norway. In their paper published in *Proceedings of the National Academy of Sciences*, the group describes their study and what they found when they compared their results with the genome of modern bacteria.

Relapsing fever, as its name implies, is an ailment whereby an infected person experiences a fever several times following a single infection. If untreated, it is fatal in 10 out of 40 cases. It is transmitted by fleas and lice. Back in the 15th century, it was responsible for killing millions of people in Europe—today, it is mostly confined to several countries in Africa. In this new effort, the researchers conducted a [genetic analysis](#) of the bacteria that caused the disease 600 years ago and compared it to bacteria causing the same disease today. Samples of *Borrelia recurrentis* were retrieved from skeletons excavated from St. Nikolai Cemetery in Old Oslo—they have been dated to between 1430 and 1465.

After generating a genetic assembly, the researchers compared it with genetic assemblies created by prior researchers studying the genome of the modern form of the bacteria. This allowed them to see how the bacteria has evolved over time.

The researchers report that they were able to sequence approximately 17 percent of the bacterial genome from skeletal bones which they

bolstered by sequencing samples taken from teeth. Using data from both, they were able to sequence approximately 98.2 percent of the main chromosome. Comparing the findings with modern strains, they found that the earlier strains lacked three variable short protein genes and one plasmid found on modern strains. Prior research has shown that the proteins act as proinflammatory agents for the [bacteria](#), which, the researchers note, are key elements of the relapsing nature of the disease. They note further that such changes likely account for the differences in relapse rates—the disease tended to relapse just once or twice back in the 1400s, but is known to relapse up to five times in people afflicted today.

More information: Meriam Guellil et al. Genomic blueprint of a relapsing fever pathogen in 15th century Scandinavia, *Proceedings of the National Academy of Sciences* (2018). [DOI: 10.1073/pnas.1807266115](https://doi.org/10.1073/pnas.1807266115)

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