

Reconstructing the sixth century plague from a victim

August 30 2016



Adult woman AE1175 (left) and adult man AE1176 (right) excavated

at Altenerding and found positive for presence of *Y. pestis* (© State Collection of Anthropology and Palaeoanatomy Munich). The arrow shows the third Molar sampled from individual AE1175 from which the Altenerding high coverage genome was obtained. Grave goods of individual AE1175 and AE1176 typical of the middle of the 6th century (© Archaeological State Collection Munich), Grave goods not shown true to scale). Credit: State Collection of Anthropology and Palaeoanatomy Munich

Before the infamous Black Death, the first great plague epidemic was the Justinian plague, which, over the course of two centuries, wiped out up to an estimated 50 million (15 percent) of the world's population throughout the Byzantine Empire—and may have helped speed the decline of the eastern Roman Empire.

No one knows why it disappeared.

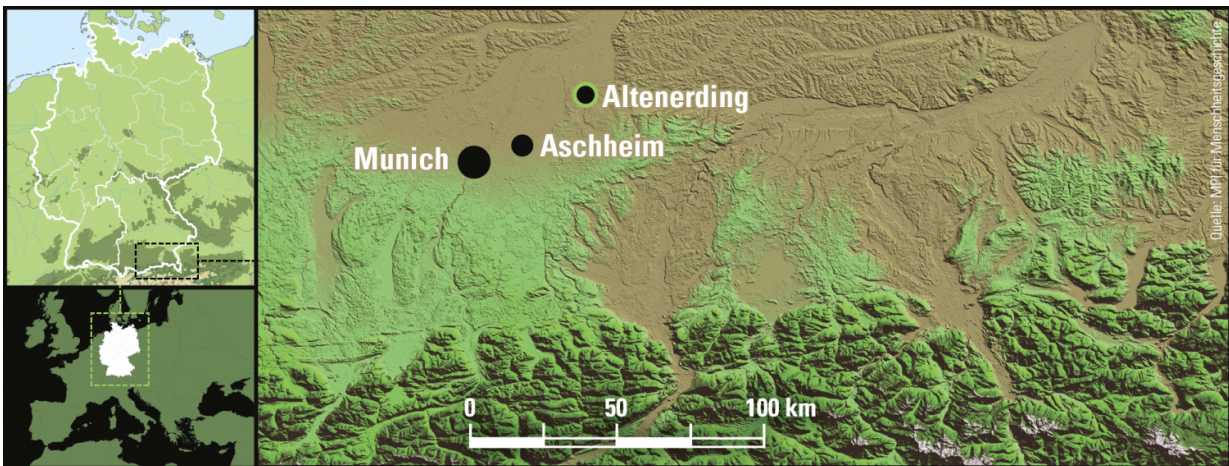
Recent molecular clues from ancient plague victims have suggested that plague may have been caused by the same bacterium, *Yersinia pestis*, which was responsible for the Black Death. But the geographic reach, mortality and impact of the Justinian pandemic are not fully known.

Both information from ancient hosts and bacteria could shed light on the role of plague, which has afflicted mankind for more than 5,000 years.

Now, scientists based in Germany, including Michal Feldman, Johannes Krause, Michaela Harbeck and colleagues have confirmed this by recovering the bacterial culprit from sixth century skeletons found in Altenerding, an ancient southern German burial site near Munich. The Altenerding genome dates back to the beginning of the plague.

They have generated the first high-coverage genome of the bacterial agent responsible for the Justinian plague. In addition to revealing new

insights in the molecular evolution of *Yersinia pestis* since the Byzantine times, the new sequence shows features that could not be detected due to the limitations in the coverage of a [draft genome](#) previously reported by Wagner, including 30 newly identified mutations and structural rearrangements unique to the Justinianic strain., as well as correcting 19 false positive mutations.



Geographical map specifying the location of the archaeological site "Altenerding". The other site, where *Y. pestis* has been identified, and its genome has been previously reconstructed (Wagner et al. 2014), is the cemetery of Aschheim, which is located approximately 20 km southwest of Altenerding.*Wagner DM, Klunk J, Harbeck M, Devault A, Waglechner N, Sahl JW, Enk J, Birdsell DN, Kuch M, Lumibao C. 2014. *Yersinia pestis* and the Plague of Justinian 541-543 AD: A genomic analysis. *The Lancet Infectious Diseases* 14(4):319-26. Credit: State Collection of Anthropology and Palaeoanatomy Munich

"The fact that the archeological skeletons which gave these exciting insights were excavated over 50 years ago underscores the importance of maintaining well curated anthropological collections," said author

Michaela Harbeck. "We were very fortunate to find another plague victim with very good DNA preservation in a graveyard just a few kilometers from where the individual analyzed in Wagner et al. was found. It provided us with the great opportunity to reconstruct the first high quality genome in addition to the previously published draft genome."

Three are located in genes critical to plague virulence: *nrdE*, *fadJ* and *pcp* genes. Their data also suggested that the strain was more genetically diverse than previously thought. How and why the pathogen reached Germany remains a mystery.

This new findings allow the authors to develop guidelines that could help improve the quality and authenticity of genomic data recovered from candidate ancient pathogens. And with plague classified as a re-emerging infectious disease in certain regions, an important historic, high-quality reference resource has been generated to offer insights into key the evolutionary changes, adaptation and human impact of plague.



Skulls of both plague victims buried together in one grave at the Altenerding cemetery. Right: Individual 1175 (female, 25-30 years old) left: individual 1176, (male, 20 to 25 years old). The *Yersinia pestis* genome was extracted from individual 1175. Credit: State Collection of Anthropology and Palaeoanatomy Munich

"Our research confirms that the Justinianic [plague](#) reached far beyond the historically documented affected region and provides new insights into the evolutionary history of *Yersinia pestis*, illustrating the potential of ancient genomic reconstructions to broaden our understanding of pathogen evolution and of historical events," said research colleague Michal Feldman. "Our reanalysis of previous datasets stresses the

importance of following strict criteria to avoid errors in the reconstruction of ancient pathogen genomes."

More information: *Molecular Biology and Evolution*, [DOI: 10.1093/molbev/msw1](https://doi.org/10.1093/molbev/msw1)

Provided by Oxford University Press

Citation: Reconstructing the sixth century plague from a victim (2016, August 30) retrieved 4 April 2024 from <https://phys.org/news/2016-08-reconstructing-sixth-century-plague-victim.html>

<p>This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.</p>
--