



Maria Spyrou in the clean lab of the Max Planck Institute for the Science of Human History in Jena. Credit: Lyazzat Musralina

Persistence of *Y. pestis* within Europe

Although the researchers found that the European-wide Black Death was likely caused by a single strain, analysis of genomes from later in the pandemic shows the emergence of a lineage displaying a higher genetic diversity. "In the later phase of the second pandemic, we see the development of multiple branches within Europe, which suggests that plague was maintained in different local foci," says Marcel Keller, co-first author of the Max Planck Institute for the Science of Human History. "No modern descendants of this lineage have been found to date, possibly indicating the extinction of these reservoirs."



Mass grave dating to the Black Death period, identified in

the '16 rue des Trente Six Ponts' archaeological site in Toulouse, France. Credit: Archeodunum SAS, Gourvenec Michaël

The researchers also identified a deletion including two virulence-related genes from genomes within this second lineage. Interestingly, genomes from the late stages of the first plague pandemic have shown a deletion in the same region. "Given that this deletion occurred in lineages from the first and second pandemic, both now extinct, determining how these genes impact maintenance in human and flea hosts would be an important area for future study," comments Kirsten Bos, research group leader of the Max Planck Institute for the Science of Human History.

The current study provides new perspectives into the initiation and progression of the second plague pandemic and adds significantly to the database of published ancient *Y. pestis* genomes. "We have shown that extensive analysis of ancient *Y. pestis* genomes can provide unique insights into the microevolution of a pathogen over a period of several hundred years," says senior author Johannes Krause, Director of the Department of Archaeogenetics at the Max Planck Institute for the Science of Human History. In the future, integrating this data into disease modelling efforts, in conjunction with data from other areas such as climate science, epidemiology and history, will be important for better understanding the second plague pandemic.

More information: Maria A. Spyrou et al. Phylogeography of the second plague pandemic revealed through analysis of historical *Yersinia pestis* genomes, *Nature Communications* (2019). DOI: [10.1038/s41467-019-12154-0](https://doi.org/10.1038/s41467-019-12154-0)

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