

Investigating the history and evolution of plague in Eurasia

Maria Spyrou

University of Tübingen

Tübingen DE

Abstract

In the last decade, the growing field of ancient pathogen genomics has yielded chronological snapshots of microbial diversity, unravelling the evolutionary trajectories of various historically and presently significant infectious diseases. Notably, the zoonotic bacterium *Yersinia pestis*, the aetiological agent of plague, stands as the most extensively studied pathogen through ancient genomics. The history and evolution of *Y. pestis* are closely linked with its enduring presence and activity in sylvatic rodent populations across Central Asia, presently hosting the highest concentration of active plague reservoirs globally. This presentation will synthesize archaeological, historical, ecological, and genomic data from Central Asia to offer insights into various stages of plague evolution and history, both with regard to its prehistoric occurrences and historically recorded pandemics. Recent discoveries of basal *Y. pestis* lineages dating between 5,000 to 2,500 years ago, have shed light on the disease's widespread impact on prehistoric populations across Eurasia and has elucidated key genetic adaptations leading to its emergence as a highly virulent, flea-adapted, pathogen. Moreover, growing datasets of ancient *Y. pestis* genomes from historical periods have revealed Central Asia's role in the emergence of plague pandemic lineages, including those connected with Plague of Justinian (6th century CE) and the Black Death (14th century CE), as well as their contribution in the formation of present-day plague reservoirs in several regions across the world. The case of plague demonstrates how interdisciplinary research on past pandemics can contribute to our understanding of the processes that have shaped the contemporary infectious disease landscape.