



BIWEEKLY COLLOQUIUM
Monday, October 21st, 5.00 pm

**ANCIENT PATHOGEN GENOMICS: INSIGHTS INTO THE
EVOLUTION OF INFECTIOUS DISEASES.**

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Studying ancient pathogens may help to identify the causative agents of past pandemics and provide new insights into host pathogen interactions throughout historical times. We reconstructed complete genomes of three pathogens that among others had a major impact on human history using a combination of next generation sequencing and targeted DNA enrichment: two human bacterial pathogens, *Yersinia pestis* from the Black Death pandemic and *Mycobacterium leprae* from the medieval era, and a plant eukaryotic pathogen, *Phytophthora infestans* from the Irish potato famine.

While the most recent common ancestors for both human pathogens, can be dated to around 4000 years ago, differences arise in phylogenetics and DNA preservation: A phylogenetic comparison of the medieval *Y. pestis* strain with modern strains reveals a close position of the Black Death strain to the root of most human pathogenic strains, indicating a rapid radiation of *Y. pestis* strains in the 14th century. The medieval *M. leprae* strains however can be placed on at least two main branches within the present genetic diversity, showing a rather constant rate of divergence events without evidence of major diversifications. Compared to *Y. pestis* and mammalian DNA the medieval *M. leprae* DNA showed a remarkable preservation that enabled the reconstruction of the first de novo assembled genome of an ancient organism and may open a perspective to trace back the prehistoric origins of *M. leprae*.

In contrast to both bacterial pathogens that show a high level of genetic conservation during the last 1000 years, the plant pathogen *P. infestans* evolved rapidly during the last 100 years displaying different strategies of host adaptation such as an increase in ploidy and the loss of effector genes.

Venue: Leibnizstraße 1, Seminar Room 204