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**DISSERTATION TITLE:** *Disease during the Second Plague Pandemic (14<sup>th</sup>-18<sup>th</sup> century CE): Genomic, Metagenomic and Phylogenetic Analysis of ancient DNA from putative plague victims.*

A new doctoral thesis from the University of Oslo reports the results of a research project investigating human pathogens circulating during the second plague pandemic (14<sup>th</sup> -18<sup>th</sup> century CE) in Europe. The aim of the project was to investigate the occurrence, origin, paths of transmission and dynamics of plague as well as gaining a better knowledge of the health of analysed individuals. Samples from more than 170 skeletons associated with the Second Plague Pandemic were studied via ancient DNA analysis. The samples analysed in this thesis span the entire Second Plague Pandemic, stem from all over Eurasia and include samples from the Caucasus region.

The isolated strains of the causative pathogen of plague *Yersinia pestis* shed light on the origin of plague during the Second Plague Pandemic and on the genomic and socio-political changes which could have led to its slow retreat out of Europe at the end of the 18<sup>th</sup> century.

A metagenomic analysis of ancient DNA extracted from plague victims of the city of Imola (1630--32), also illustrates the difficulties involved in the study of ancient plague genomes and the potential of multidisciplinary studies to gain a complex picture of a historical epidemiological event.

Lastly, this thesis aimed to detect signs of other pathogens and potential cases of co-infection. We also detail the findings of the first ancient *Borrelia recurrentis* genome, the causative pathogen of louse-borne relapsing fever, an epidemic fever specialised to human hosts. The isolated strain has a discrete genomic make-up, including the deletion of genes and pseudogenes directly involved in the complex immune evasion system, which causes the fever relapses the pathogen is known for.