

1000 Plagues in the Genomics Era

Exhibiting Biographies of Bacteria

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When used within a multi-disciplinary approach, genetic evidence provides an intriguing window into the disease experience of past populations. Ancient DNA techniques have been developed to identify bacterial and viral DNA in skeletal remains, and even affected artefacts. These methods have additionally been used to explore the patterns of spread and geographic origins of several high-profile diseases, including medieval plague. However, the ability to accurately reconstruct spatial patterns of an ancient disease requires robust comparative datasets. In order to produce such datasets, extensive sampling is required across both time and place, followed by careful curation. Fortunately, recent advances in DNA sequencing technology have facilitated efforts to conduct this extensive sampling on a Global scale, and data repositories continue to grow at unprecedented rates.

However, this technological progress has also placed a strain on our ability to effectively manage, curate, and present the avalanche of data effectively. Despite there being over 1000 publicly available plague genomes, only 200-300 are routinely used in comparative frameworks. We hypothesize this may be primarily attributed to the following three reasons, as the additional datasets are: 1) not known about, 2) known about, but difficult to access, or 3) accessible, but lack historically-meaningful metadata. To tackle these obstacles, this project aims to do the following. First, to design Database software to assist geneticists with the acquisition, organization, and discovery of infectious disease metadata. Second, to curate historically-meaningful metadata for the available plague genomes, both ancient and modern, and provide an accompanying bibliography. And third, to integrate these data into an updated global phylogeny, to broaden the scope of historical narratives present.

To facilitate curation and to promote engagement with the project, two digital exhibits are planned. The first exhibit is a Nextstrain phylogenetic presentation, which allows for an interactive display of disease relationships between regions and over time. The second [\[\[Digital Exhibit | digital exhibit\]\]](#) is an ArcGIS interactive StoryMap, where spatial distribution can be interrogated along with an accompanying presentation of relevant historical records and archaeologically artifacts. Overall, this project aims to contribute to our understanding of how and why epidemics of plague are related, with a particular focus on the Second Pandemic. Furthermore, by emphasizing the role that digital exhibits play, we hope to open up new avenues for the integration of multidisciplinary sources, collaborative, and pedagogical approaches to the study of medieval plague.