

SCDS Project Proposal (2019-2020)

1000 Plagues in the Genomics Era: Databases and Digital Exhibit

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Authors

• Katherine Eaton

 [0000-0001-6862-7756](#) ·  [ktmeaton](#)

McMaster Ancient DNA Center, McMaster University

Project Overview

Background

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 present in skeletal remains, and even affected artifacts [1]. These methods have additionally been used to explore the patterns of spread and geographic origins of several high-profile diseases, including the plague (Bos et al., 2011). 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 (Stephens et al., 2015).

References

1. **17 th Century Variola Virus Reveals the Recent History of Smallpox**

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