

AN INTEGRATIVE GENETICS APPROACH FOR STUDYING DISEASE IN EARLY MEDIEVAL EUROPE

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In the fields of archaeology, anthropology, and history, the study of human health and diseases have always played an important role as they have a substantial impact on individuals and societies. However, this is often limited to diseases that either leave traces on the skeleton or are documented in historical sources. Applying genetic methods, the field of archaeogenetics could add to our understanding of numerous pathogens that do not leave visible lesions on the skeleton. However, meaningful interpretation of genetic results is only possible following an integrative approach by combining information from all disciplines. In the ERC funded project 'HistoGenes', researchers and scholars from various fields work together to study the population history of Early Medieval Eastern Central Europe to understand more about human migration and mobility, the structure of past societies, such as kinship, as well as health and diseases.

One pathogen that can be observed across sites and through time is the hepatitis B virus, the causative agent of chronic hepatitis, cirrhosis and hepatocellular carcinoma in humans, which can be transmitted vertically from mother to child and horizontally as a sexually transmitted disease. Combined with our knowledge about relatedness and kinship within these social groups, we can interpret infections in much more detail, potentially tracing back chains of transmission and gain insights about the impact this disease might have had on individuals in the past.

Here we present first genetic results about the hepatitis B virus in Early Medieval Europe that are discussed and interpreted in an interdisciplinary context.

Keywords

Carpian Basin, Early Medieval Eastern Central Europe, Diseases, Hepatitis B virus, Interdisciplinary study

Note/comment