

## PATHOGEN ANALYSIS IN ANCIENT INDIVIDUALS FROM THE CENTRAL EURASIAN REGION

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**Background:** Kazakhstan, situated at the crossroads of Eurasia, preserves rich archaeological materials that provide unique opportunities to study the evolution of infectious diseases. Paleogenomic research has recently identified ancient pathogens in human remains from Bronze and Iron Age contexts, offering new insights into the region's epidemiological history.

**Materials and methods:** Skeletal remains from East and Central Kazakhstan, spanning the Bronze Age to the Middle Ages, were analyzed using ancient DNA extraction and next-generation sequencing. Pathogen screening was performed through metagenomic approaches, followed by phylogenetic reconstruction.

**Results:** Genome-wide analyses revealed *Yersinia pestis* in several individuals. Early Bronze Age genomes represented basal lineages predating flea-adapted strains (Andrades Valtueña et al., 2022), while fourteenth-century samples from the Tian Shan region corresponded to the source of the Black Death pandemic (Spyrou et al., 2022). An-

cient hepatitis B virus (HBV) genomes were also recovered from Iron Age individuals, contributing to reconstruction of more than 10,000 years of HBV evolution (Kocher et al., 2021). Additional evidence of *Salmonella enterica* and parvovirus B19 suggests a broader spectrum of infections in ancient populations of Kazakhstan. **Conclusion:** These findings demonstrate that Kazakhstan played a central role in the long-term history of major human pathogens. The identification of early *Y. pestis* lineages and HBV genomes highlights the region's significance in tracing the evolutionary trajectories of epidemic diseases. Integration of genomic, archaeological, and epidemiological data will further advance reconstructions of ancient disease dynamics across Eurasia.

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**Key words:** archeogenetics, ancient pathogens