# Ancient DNA Computational Genomics: Tracing Human Origins and Mobility in Prehistoric Europe

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Ancient DNA (aDNA) research has been at the forefront of prehistory studies for the past decade. It has shed light on various aspects of human history, from the formation of our species and interactions with other members of the genus Homo, to the spread of Paleolithic hunter-gatherer populations. Additionally, aDNA has provided insights into the advent and expansion of agriculture, the development of metal processing technologies, the rise and fall of empires, and the life stories of significant individuals. Furthermore, aDNA has revealed patterns of human migrations and the expansion of steppe populations, enriching our understanding of how these movements shaped societies. Through aDNA, we can now tell these stories with greater accuracy and detail.

In my talk, I will briefly summarize the topic aDNA sampling, processing, and the challenges in interpreting the results, along with the main findings of aDNA research. I will focus on Central Europe, particularly the Late Bronze Age and Early Iron Age. During this period, the widespread practice of cremation—characterized by the Urnfield phenomenon—created significant gaps in our understanding of the genetic history of the Lusatian, Knovíz-Štítary, and Hallstatt cultures. Our research project has assembled a unique collection of over 150 human skeletal samples from archaeological sites in Upper Silesia (Poland), and the Moravia and Bohemia regions (Czech Republic). These samples are being sequenced using the Illumina NovaSeq X platform. Our aim is to assess the genetic backgrounds of populations associated with these cultures and the gene flow between populations favoring inhumation practices. Kinship analysis among densely sampled archaeological sites will provide further insights into marriage patterns, social structures, and inheritance practices. To achieve these objectives, we employ a multidisciplinary approach, integrating aDNA analysis, radiocarbon dating, and isotopic measurements (δ15N, 87Sr/86Sr, δ18O, and δ13C). I will present the initial results from sequencing screening of our sample set and discuss our bioinformatics approach, including authenticity and contamination measurement of the aDNA samples, and insights into planned population genomics analyses.

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