



10 PhD positions at the Max Planck Institute for the Science of Human History, Jena, Germany.

The **Archaeogenetics** department at the **Max Planck Institute for the Science of Human History in Jena**, Germany, is offering up to 10 PhD positions beginning June 2018. The overarching research topic at the institute is the use of novel scientific approaches from high throughput sequencing of **ancient DNA from human populations** and their **pathogens** to explore research questions related to **human history, gene-culture coevolution, microbiome evolution, and adaptation to infectious disease**. The main foci are the relationships between humans and pathogens, microbial evolution, and population expansions through time.

The institute hosts a multi-disciplinary research team and is looking for students from a variety of backgrounds including, but not restricted to, **molecular biology, bioinformatics, microbiology, chemistry, biochemistry, mathematics, physics, computer science, anthropology and archaeology**. Students holding a Master's degree (or equivalent) with a proven record of success in their discipline and a genuine interest in examining questions related to human history are encouraged to apply.

Deadline for applications is the 15th of March 2018.

The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply.

Please apply online at

https://s-lotus.gwdg.de/mpg/mjws/perso/shh_d007.nsf/application

The students will be part of the newly founded International Max Planck Research School (IMPRS) for Human history. The Max Planck Institute is not a faculty, but is affiliated to the Friedrich Schiller University, in Jena Germany. Doctoral degrees will be granted by the affiliated university.

Doctoral candidates enrol in a 3-year fully-funded graduate program that provides excellent research conditions. Graduate courses and all other degree requirements necessitate proficiency in English only.



Projects offered in 2018

Please find below a list of topics we offer for this year's recruitment. All projects are highly integrative and require collaboration between different research groups. Applicants should choose up to three topics of interest. If you are invited to Jena for a recruitment event/interview it is possible to change your preferences after talking to the supervisors.

Topic 1: Historical Human Population Genetics

Main supervisor: [Dr. Stephan Schiffels](#), MPI-SHH

Co-supervisors: [Dr. Wolfgang Haak](#), [Prof. Johannes Krause](#), MPI-SHH

Description: Human history leaves its traces in genomes, through changes in population size and structure. By analysing the genomes of living and ancient populations, we can therefore directly learn about historical events, such as migrations. In recent years, this approach has led to many new insights, mainly in prehistoric time periods. In this project, we want to develop advanced analytical methodology and analyse new data to investigate events in more recent, historical, time periods, as has been done for example in the case of the Anglo-Saxon migrations into England (Schiffels et al. 2016). Applicants for this topic should have a Master's degree in some field of the Sciences, technical/analytical skills (some programming experience), and an interest in human history.

Topic 2: Pleistocene Human Population Genetics

Main supervisor: [Prof. Johannes Krause](#), [Dr. Wolfgang Haak](#), MPI-SHH

Co-supervisor(s): [Dr. Stephan Schiffels](#), Dr. Choongwon Jeong, MPI-SHH

Description: Recent years have seen the emergence of the first genome wide data from Pleistocene Eurasia, painting a complex picture of genetic interactions and turnovers, likely often caused by major climatic events such as glaciation cycles and volcanic eruptions. In this project we want to establish a more detailed time transect through Pleistocene Eurasia, starting with genome wide data from the first modern humans that left Africa to the early Holocene hunter gatherers that were often absorbed or replaced by farming populations in the early Holocene. Specific questions include, the Pleistocene genetic connections of Eastern and Western Eurasians. The genetic origin of the Beringian population that gave rise to Native Americans. The genetic relationships that connect Northern-Africa and Pleistocene Europe.

Topic 3: Eastern Mediterranean Population Genetics

Main supervisor: [Prof. Johannes Krause](#), Dr. Choongwon Jeong, MPI-SHH

Co-supervisor(s): Prof. Philipp Stockhammer, Dr. Wolfgang Haak, MPI-SHH

Description: The Near East connects Africa and Eurasia and presents a crossroad for human interactions throughout human history. The Near East presents furthermore one of the centers of origin for agriculture in the world. In this project we are planning to analyze a time transect through the Eastern Mediterranean from the Late Pleistocene to the Late Bronze Age in order to understand the the complex genetic interactions between human populations in this region.

Topic 4: Neolithic and Bronze Age Population and Immunogenetics in Western Eurasia

Main supervisor: [Dr. Wolfgang Haak](#), [Prof. Johannes Krause](#)

Co-supervisor(s): Dr. Choongwon Jeong, [Dr. Stephan Schiffels](#), Dr Adam Powell

Description: This project continues to fill the temporal and spatial gaps in the three-dimensional grid of ancient human genome data. The main aim is to understand the processes that underlie main the demographic turnover events in Europe that were uncovered by ancient DNA studies in recent years. In the light of recent findings that lend weight to past epidemics being one of the potential driving force in human movements in prehistory, we would also like to focus on the immunogenetics of past populations. More generally we aim to characterise the interplay of human genetics and immunogenetics, human-pathogen interactions, and aspects of gene-culture co-evolution through time. This topic will form part of



the 5-year ERC-funded project *PALEoRIDER - Human health and migration in prehistory*. Applicants should have a combined broad interest in human genetics, archaeology, and bioinformatics.

Topic 5: Detection and Analysis of Human Pathogens from Metagenomic data

Main supervisor: Dr. Alexander Herbig

Co-supervisors: Dr. Kirsten Bos, Prof. Johannes Krause

Description: The Department of Archaeogenetics is producing thousands of DNA sequencing datasets from ancient human remains. These datasets are of metagenomic nature, which means that they not only contain the DNA of the human but also of other organisms, e.g. from the soil. In some cases we can even retrieve genetic material from bacteria or viruses that have infected the individual whose remains we are studying.

We have developed experimental and computational techniques to reconstruct the genomes of these pathogenic organisms in order to comparatively analyse them together with their modern relatives.

Furthermore, we are developing automated screening and authentication techniques for the detection of pathogens from metagenomic data.

In the context of this topic we want to apply these techniques to a wide range of sequence data in order to detect pathogens in different human populations, study their genome evolution in comparison to modern forms and identify the cause of past epidemics.

Topic 6: The prehistory of the Pacific

Main supervisor: Dr. Adam Powell

Co-supervisor(s): Prof. Johannes Krause

Description: The prehistory of the Pacific is relatively short yet incredibly complex. Uncovering the genetic, cultural and linguistic interactions between the indigenous Papuan peoples in Near Oceania and the incoming Austronesians is key to understanding the population history of the wider Pacific. This project will combine analyses of new modern and ancient genetic data from across the region with methods from archaeology and computational historical linguistics to provide an integrated account of Pacific demographic history. This topic will form part of the 5-year ERC-funded project *Waves: Waves of history in the South Pacific: A gene-culture coevolutionary approach*. Applicants should have an interest in human population genetics and archaeology, and ideally have bioinformatics or computational methods training.