
Paleogenomics of a French population, from the Neolithic to the Bronze Age.

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Résumé

Methodological and technical advances in ancient DNA studies make it possible to have an ever deeper look into the genomes of individuals who lived several thousands of years ago. Benefits from this are two-fold: on one hand, we can directly address questions about the genomic diversity of ancient populations, and on the other hand relate this information to modern patterns of variation. Despite a rich archaeological record, little is known about how the multiple migrations that punctuate the history of present-day France have shaped its modern population. To tackle this question, our current project uses targeted enrichment to study informative SNPs and alleles in a wide panel of individuals from periods ranging from the Neolithic to the Middle-Ages, sampled from various sites across France. In this talk, we will report both mitochondrial and nuclear data obtained from 215 individuals from Neolithic and Bronze Age France. Besides a comparison with contemporary populations from across Europe, these complete mitochondrial genomes revealed contrasting population dynamics between northern and southern France, as culture once again proved to be a major determinant of the genetic differentiation between populations. The study of 120 nuclear SNPs, covering both physical and physiological traits, allowed us to follow the evolution of the allelic frequency of several phenotypes that characterize modern Europeans. This project significantly increases the amount of genetic data available for Neolithic France, which contributes to clear up the complex picture of Europe before the onset of Bronze Age.

Mots-Clés: Ancient DNA, paleogenomics, Neolithic, Bronze Age, France

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