

## References

### Anthropologie

CURRY 2023

Andrew Curry, *Ancient DNA upends European prehistory*. [science](#) **379** (2023), 865–866.

ORLANDO 2023

Ludovic Orlando, *The genomic history of ice-age Europeans*. [nature](#) **615** (2023), 41–42.

An extensive genomic time series has been produced for 356 humans from across ice-age Europe. The data reveal how climate change affected the ranges of hunter-gatherer populations as they developed diverse cultures.

POSTH 2023

Cosimo Posth, He Yu, Thomas Terberger, Eveline Altena, Wolfgang Haak & Johannes Krause et al., *Palaeogenomics of Upper Palaeolithic to Neolithic European hunter-gatherers*. [nature](#) **615** (2023), 117–126. [n615-0117-Supplement.pdf](#)

Modern humans have populated Europe for more than 45,000 years<sup>1,2</sup>. Our knowledge of the genetic relatedness and structure of ancient hunter-gatherers is however limited, owing to the scarceness and poor molecular preservation of human remains from that period<sup>3</sup>. Here we analyse 356 ancient hunter-gatherer genomes, including new genomic data for 116 individuals from 14 countries in western and central Eurasia, spanning between 35,000 and 5,000 years ago. We identify a genetic ancestry profile in individuals associated with Upper Palaeolithic Gravettian assemblages from western Europe that is distinct from contemporaneous groups related to this archaeological culture in central and southern Europe<sup>4</sup>, but resembles that of preceding individuals associated with the Aurignacian culture. This ancestry profile survived during the Last Glacial Maximum (25,000 to 19,000 years ago) in human populations from southwestern Europe associated with the Solutrean culture, and with the following Magdalenian culture that re-expanded northeastward after the Last Glacial Maximum. Conversely, we reveal a genetic turnover in southern Europe suggesting a local replacement of human groups around the time of the Last Glacial Maximum, accompanied by a north-to-south dispersal of populations associated with the Epigravettian culture. From at least 14,000 years ago, an ancestry related to this culture spread from the south across the rest of Europe, largely replacing the Magdalenian-associated gene pool. After a period of limited admixture that spanned the beginning of the Mesolithic, we find genetic interactions between western and eastern European hunter-gatherers, who were also characterized by marked differences in phenotypically relevant variants.

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## SCHMID 2023

Clemens Schmid & Stephan Schiffels, *Estimating human mobility in Holocene Western Eurasia with large-scale ancient genomic data*. [PNAS 120 \(2023\), e2218375120](#).

[pnas120-e2218375120-Supplement.pdf](#)

The recent increase in openly available ancient human DNA samples allows for large-scale meta-analysis applications. Trans-generational past human mobility is one of the key aspects that ancient genomics can contribute to since changes in genetic ancestry—unlike cultural changes seen in the archaeological record—necessarily reflect movements of people. Here, we present an algorithm for spatiotemporal mapping of genetic profiles, which allow for direct estimates of past human mobility from large ancient genomic datasets. The key idea of the method is to derive a spatial probability surface of genetic similarity for each individual in its respective past. This is achieved by first creating an interpolated ancestry field through space and time based on multivariate statistics and Gaussian process regression and then using this field to map the ancient individuals into space according to their genetic profile. We apply this algorithm to a dataset of 3138 aDNA samples with genome-wide data from Western Eurasia in the last 10,000 y. Finally, we condense this sample-wise record with a simple summary statistic into a diachronic measure of mobility for subregions in Western, Central, and Southern Europe. For regions and periods with sufficient data coverage, our similarity surfaces and mobility estimates show general concordance with previous results and provide a meta-perspective of genetic changes and human mobility.

**Keywords:** aDNA | prehistory | mobility estimation | Gaussian process regression

**Significance:** Ancient human DNA (aDNA) extracted from archaeological contexts allows reconstructing past population movements. Previous methods work by calculating proportions of shared ancestry among individuals or groups in order to answer specific, regional research questions. Here, we propose a large-scale algorithm to quantify human mobility through time and space using bulk aDNA data. The algorithm has two core components: i) interpolation of the spatiotem-

poral distribution of genetic ancestry to obtain a continuous ancestry information field and ii) probabilistic estimation of a spatial genetic similarity surface for each input sample by projecting its ancestry profile into this field. We apply this to thousands of published genomic samples in the last 10,000 y to trace diachronic mobility patterns in Western Eurasia.

## Biologie

### ALLABY 2017

Robin G. Allaby, Chris Stevens, Leilani Lucas, Osamu Maeda & Dorian Q. Fuller, *Geographic mosaics and changing rates of cereal domestication*. [Phil. Trans. Royal Society B 372 \(2017\), 20160429](#).

Domestication is the process by which plants or animals evolved to fit a human-managed environment, and it is marked by innovations in plant morphology and anatomy that are in turn correlated with new human behaviours and technologies for harvesting, storage and field preparation. Archaeobotanical evidence has revealed that domestication was a protracted process taking thousands of plant generations. Within this protracted process there were changes in the selection pressures for domestication traits as well as variation across a geographic mosaic of wild and cultivated populations. Quantitative data allow us to estimate the changing selection coefficients for the evolution of non-shattering (domestic-type seed dispersal) in Asian rice (*Oryza sativa* L.), barley (*Hordeum vulgare* L.), emmer wheat (*Triticum dicoccon* (Shrank) Schuj. bl.) and einkorn wheat (*Triticum monococcum* L.). These data indicate that selection coefficients tended to be low, but also that there were inflection points at which selection increased considerably. For rice, selection coefficients of the order of 0.001 prior to 5500 BC shifted to greater than 0.003 between 5000 and 4500 BC, before falling again as the domestication process ended 4000–3500 BC. In barley and the two wheats selection was strongest between 8500 and 7500 BC. The slow start of domestication may indicate that initial selection began in the Pleistocene glacial era.

This article is part of the themed issue ‘Process and pattern in innovations from cells to societies’.

Keywords: archaeology | archaeobotany | niche construction | origins of agriculture | Near East | China

### ALLABY 2023

Robin G. Allaby, *Two domestications for grapes*. [science 379 \(2023\), 880–881](#).

Glacial cycles and wild adaptations shaped grape domestication and the rise of wine.

### DONG 2023

Yang Dong, Shengchang Duan, Qiuju Xia, Xiao Dong & Wei Chen et al., *Dual domestications and origin of traits in grapevine evolution*. [science 379 \(2023\), 892–901](#).

[s379-0892-Supplement.pdf](#)

We elucidate grapevine evolution and domestication histories with 3525 cultivated and wild accessions worldwide. In the Pleistocene, harsh climate drove the separation of wild grape ecotypes caused by continuous habitat fragmentation. Then, domestication occurred concurrently about 11,000 years ago in Western Asia and the Caucasus to yield table and wine grapevines. The Western Asia domesticates dispersed into Europe with early farmers, introgressed with ancient wild

western ecotypes, and subsequently diversified along human migration trails into muscat and unique western wine grape ancestries by the late Neolithic. Analyses of domestication traits also reveal new insights into selection for berry palatability, hermaphroditism, muscat flavor, and berry skin color. These data demonstrate the role of the grapevines in the early inception of agriculture across Eurasia.

Yang Dong, Shengchang Duan, Qiuju Xia, Zhenchang Liang, Xiao Dong, Kristine Margaryan, Mirza Musayev, Svitlana Goryslavets, Goran Zduniæ, Pierre-François Bert, Thierry Lacombe, Erika Maul, Peter Nick, Kakha Bitskinashvili, György Dénes Bisztray, Elyashiv Drori, Gabriella De Lorenzis, Jorge Cunha, Carmen Florentina Popescu, Rosa Arroyo-Garcia, Claire Arnold, Ali Ergül, Yifan Zhu, Chao Ma, Shufen Wang, Siqi Liu, Liu Tang, Chunping Wang, Dawei Li, Yunbing Pan, Jingxian Li, Ling Yang, Xuzhen Li, Guisheng Xiang, Zijiang Yang, Baozheng Chen, Zhanwu Dai, Yi Wang, Arsen Arakelyan, Varis Kuliyeu, Genady Spotar, Nabil Girollet, Serge Delrot, Nathalie Ollat, Patrice This, Cécile Marchal, Gautier Sarah, Valérie Laucou, Roberto Bacilieri, Franco Röckel, Pingyin Guan, Andreas Jung, Michael Riemann, Levan Ujmajuridze, Tekle Zakalashvili, David Maghradze, Maria Höhn, Gizella Jahnke, Erzsébet Kiss, Tamás Deák, Oshrit Rahimi, Sariel Hübner, Fabrizio Grassi, Francesco Mercati, Francesco Sunseri, José Eiras-Dias, Anamaria Mirabela Dumitru, David Carrasco, Alberto Rodriguez-Izquierdo, Gregorio Munoz, Tamer Uysal, Cengiz Özer, Kemal Kazan, Meilong Xu, Yunyue Wang, Shusheng Zhu, Jiang Lu, Maoxiang Zhao, Lei Wang, Songtao Jiu, Ying Zhang, Lei Sun, Huanming Yang, Ehud Weiss, Shiping Wang, Youyong Zhu, Shaohua Li, Jun Sheng & Wei Chen

#### PENNISI 2023

Elizabeth Pennisi, *Wild mammals add up to a ‘shockingly tiny’ total biomass.* [science](#) **379** (2023), 868.