

Literatur

2014-01-30 aDNA

BALTER 2013

Michael Balter, *Farming's Tangled European Roots*. [science 342 \(2013\), 181–182](#).

In the second event, beginning about 6000 years ago, central European farmers spread to Scandinavia, where they mixed with hunter-gatherers to give rise to the Funnel Beaker culture. These people were talented animal herders, but also continued to hunt and fish. And in a plot twist typical of the farming story, farmers carrying this mixture of farmer and hunter-gatherer genes then migrated from Scandinavia back into central Europe about a thousand years later, further complicating the genetic picture. Researchers are now busy on the next wave of studies: using ancient nuclear DNA to get an even crisper picture of what both men and women were doing during a revolution that apparently came in fits and starts.

BRAMANTI 2009

B. Bramanti et al., *Genetic Discontinuity Between Local Hunter-Gatherers and Central Europe's First Farmers*. [science 326 \(2009\), 137–140](#).

s326-0137-Supplement.pdf

B. Bramanti, M. G. Thomas, W. Haak, M. Unterlaender, P. Jores, K. Tambets, I. Antanaitis-Jacobs, M. N. Haidle, R. Jancauskas, C.-J. Kind, F. Lueth, T. Terberger, J. Hiller, S. Matsumura, P. Forster & J. Burger

After the domestication of animals and crops in the Near East some 11,000 years ago, farming had reached much of central Europe by 7500 years before the present. The extent to which these early European farmers were immigrants or descendants of resident hunter-gatherers who had adopted farming has been widely debated. We compared new mitochondrial DNA (mtDNA) sequences from late European hunter-gatherer skeletons with those from early farmers and from modern Europeans. We find large genetic differences between all three groups that cannot be explained by population continuity alone. Most (82%) of the ancient hunter-gatherers share mtDNA types that are relatively rare in central Europeans today. Together, these analyses provide persuasive evidence that the first farmers were not the descendants of local hunter-gatherers but immigrated into central Europe at the onset of the Neolithic.

BRANDT 2013

Guido Brandt et al., *Ancient DNA Reveals Key Stages in the Formation of Central European Mitochondrial Genetic Diversity*. [science 342 \(2013\), 257–261](#).

s342-0257-Supplement1.pdf, s342-0257-Supplement2.xls, s342-0257-Supplement3.mov

Guido Brandt, Wolfgang Haak, Christina J. Adler, Christina Roth, Anna Szécsényi-Nagy, Sarah Karimnia, Sabine Möller-Rieker, Harald Meller, Robert Ganslmeier, Susanne Friederich, Veit Dresely, Nicole Nicklisch, Joseph K. Pickrell, Frank Sirocko, David Reich, Alan Cooper, Kurt W. Alt & The Genographic Consortium

The processes that shaped modern European mitochondrial DNA (mtDNA) variation remain unclear. The initial peopling by Palaeolithic hunter-gatherers $\approx 42,000$ years ago and the immigration of Neolithic farmers into Europe ≈ 8000 years ago appear to have played important roles but do not explain present-day mtDNA diversity. We generated mtDNA profiles of 364 individuals from prehistoric cultures in Central Europe to perform a chronological study, spanning the Early Neolithic to the Early Bronze Age (5500 to 1550 calibrated years before the common era). We used this transect through time to identify four marked shifts in genetic composition during the Neolithic period, revealing a key role for Late Neolithic cultures in shaping modern Central European genetic diversity.

BURGER 2007

J. Burger, M. Kirchner, B. Bramanti, W. Haak & M. G. Thomas, *Absence of the lactase-persistence-associated allele in early Neolithic Europeans*. [PNAS 104 \(2007\), 3736–3741](#).

Lactase persistence (LP), the dominant Mendelian trait conferring the ability to digest the milk sugar lactose in adults, has risen to high frequency in central and northern Europeans in the last 20,000 years. This trait is likely to have conferred a selective advantage in individuals who consume appreciable amounts of unfermented milk. Some have argued for the “culture-historical hypothesis,” whereby LP alleles were rare until the advent of dairying early in the Neolithic but then rose rapidly in frequency under natural selection. Others favor the “reverse cause hypothesis,” whereby dairying was adopted in populations with preadaptive high LP allele frequencies. Analysis based on the conservation of lactase gene haplotypes indicates a recent origin and high selection coefficients for LP, although it has not been possible to say whether early Neolithic European populations were lactase persistent at appreciable frequencies. We developed a stepwise strategy for obtaining reliable nuclear ancient DNA from ancient skeletons, based on (i) the selection of skeletons from archaeological sites that showed excellent biomolecular preservation, (ii) obtaining highly reproducible human mitochondrial DNA sequences, and (iii) reliable short tandem repeat (STR) genotypes from the same specimens. By applying this experimental strategy, we have obtained high-confidence LP-associated genotypes from eight Neolithic and one Mesolithic human remains, using a range of strict criteria for ancient DNA work. We did not observe the allele most commonly associated with LP in Europeans, thus providing evidence for the culture-historical hypothesis, and indicating that LP was rare in early European farmers.

ancient DNA | dairying | selection

CAI 2014

Dawei Cai, Yang Sun, Zhuowei Tang, Songmei Hu, Wenying Li, Xingbo Zhao, Hai Xiang & Hui Zhou, *The origins of Chinese domestic cattle as revealed by ancient DNA analysis*. [Journal of Archaeological Science 41 \(2014\), 423–434](#).

JArchSci41-0423-Supplement1.xls, JArchSci41-0423-Supplement2.xlsx

Recent ancient DNA analyses have revealed the origins of European and Near Eastern domestic cattle. In East Asia, however, only a few ancient cattle remains from Korea have been studied. The origins of East Asian domestic cattle and the genetic contribution by ancient cattle to modern cattle are still unclear. To provide new insight into the early history of East Asian domestic cattle, we analyzed mitochondrial DNA (mtDNA) from 53 cattle remains, aged between 4500 and 2300 years, excavated from five archaeological sites in Northern China. All

ancient Chinese cattle were identified as belonging to taurine cattle. On the one hand, the results support the previous hypothesis that taurine cattle spread into Northern China between 3000 and 2000 BC; on the other hand, the results suggest that zebu cattle did not spread into the Central Plains until at least 1500 BC. Three haplogroups T2, T3, and T4 were present in the ancient Chinese cattle, of which T3 was predominant (79.3%), while T2 and T4 were less common (9.4% and 11.3% respectively). Considering the geographic origin and estimated age of mtDNA haplogroups and the archaeological record of cattle remains in China, our results suggest that Chinese domestic cattle originated from the Near East and were already introduced into the Central Plains around 2500–1900 BC. Furthermore, phylogenetic network analysis indicates that the haplogroup distribution pattern of ancient Chinese cattle is similar to that of modern East Asian taurine cattle, suggesting a genetic continuity from the Bronze Age to present day. Lastly, population pairwise F_{ST} distance analysis and multidimensional scaling analysis also support close genetic relationship between ancient Chinese cattle and modern East Asian taurine cattle. All these results suggest that ancient Chinese cattle made an important contribution to the gene pool of modern East Asian taurine cattle.

Keywords: Domestic cattle | *Bos taurus* | Ancient DNA | Mitochondrial DNA | Haplogroup

CAVALLI-SFORZA 1996

L. Luca Cavalli-Sforza, *The spread of agriculture and nomadic pastoralism: insights from genetics, linguistics and archaeology*. In: DAVID R. HARRIS (Hrsg.), *The Origins and Spread of Agriculture and Pastoralism in Eurasia*. ([Washington 1996](#)), 51–69.

CHIKHI 2002

Lounès Chikhi, Richard A. Nichols, Guido Barbujani & Mark A. Beaumont, *Y genetic data support the Neolithic demic diffusion model*. [PNAS 99 \(2002\), 11008–11013](#).

There still is no general agreement on the origins of the European gene pool, even though Europe has been more thoroughly investigated than any other continent. In particular, there is continuing controversy about the relative contributions of European Palaeolithic hunter-gatherers and of migrant Near Eastern Neolithic farmers, who brought agriculture to Europe. Here, we apply a statistical framework that we have developed to obtain direct estimates of the contribution of these two groups at the time they met. We analyze a large dataset of 22 binary markers from the non-recombining region of the Y chromosome (NRY), by using a genealogical likelihood-based approach. The results reveal a significantly larger genetic contribution from Neolithic farmers than did previous indirect approaches based on the distribution of haplotypes selected by using post hoc criteria. We detect a significant decrease in admixture across the entire range between the Near East and Western Europe. We also argue that local huntergatherers contributed less than 30% This finding leads us to reject a predominantly cultural transmission of agriculture. Instead, we argue that the demic diffusion model introduced by Ammerman and Cavalli-Sforza [Ammerman, A. J. & Cavalli-Sforza, L. L. (1984) *The Neolithic Transition and the Genetics of Populations in Europe* (Princeton Univ. Press, Princeton)] captures the major features of this dramatic episode in European prehistory.

GILBERT 2008

M. Thomas P. Gilbert et al., *DNA from Pre-Clovis Human Coprolites in Oregon, North America*. [science](#) **320** (2008), 786–789.

[s320-0786-Supplement1.pdf](#), [s320-0786-Comment1.pdf](#), [s320-0786-Reply1.pdf](#), [s320-0786-Comment2.pdf](#), [s320-0786-Supplement2.pdf](#), [s320-0786-Reply2.pdf](#), [s320-0786-Supplement3.pdf](#)

M. Thomas P. Gilbert, Dennis L. Jenkins, Anders Götherstrom, Nuria Naveran, Juan J. Sanchez, Michael Hofreiter, Philip Francis Thomsen, Jonas Binladen, Thomas F. G. Higham, Robert M. Yohe II, Robert Parr, Linda Scott Cummings, Eske Willerslev

The timing of the first human migration into the Americas and its relation to the appearance of the Clovis technological complex in North America at about 11,000 to 10,800 radiocarbon years before the present (14C years B.P.) remains contentious. We establish that humans were present at Paisley 5 Mile Point Caves, in south-central Oregon, by 12,300 14C years B.P., through the recovery of human mitochondrial DNA (mtDNA) from coprolites, directly dated by accelerator mass spectrometry. The mtDNA corresponds to Native American founding haplogroups A2 and B2. The dates of the coprolites are >1000 14C years earlier than currently accepted dates for the Clovis complex.

HAAK 2010

Wolfgang Haak et al., *Ancient DNA from European Early Neolithic Farmers Reveals Their Near Eastern Affinities*. [PLoS Biology](#) **8** (2010), [xi](#), [e1000536](#).

[PLoSBio08.11-e1000536-Supplement.ZIP](#)

Wolfgang Haak, Oleg Balanovsky, Juan J. Sanchez, Sergey Koshel, Valery Zaporozhchenko, Christina J. Adler, Clio S. I. Der Sarkissian, Guido Brandt, Carolin Schwarz, Nicole Nicklisch, Veit Dresely, Barbara Fritsch, Elena Balanovska, Richard Villems, Harald Meller, Kurt W. Alt, Alan Cooper & the Genographic Consortium

In Europe, the Neolithic transition (8,000-4,000 B.C.) from hunting and gathering to agricultural communities was one of the most important demographic events since the initial peopling of Europe by anatomically modern humans in the Upper Paleolithic (40,000 B.C.). However, the nature and speed of this transition is a matter of continuing scientific debate in archaeology, anthropology, and human population genetics. To date, inferences about the genetic make up of past populations have mostly been drawn from studies of modern-day Eurasian populations, but increasingly ancient DNA studies offer a direct view of the genetic past. We genetically characterized a population of the earliest farming culture in Central Europe, the Linear Pottery Culture (LBK; 5,500-4,900 calibrated B.C.) and used comprehensive phylogeographic and population genetic analyses to locate its origins within the broader Eurasian region, and to trace potential dispersal routes into Europe. We cloned and sequenced the mitochondrial hypervariable segment I and designed two powerful SNP multiplex PCR systems to generate new mitochondrial and Y-chromosomal data from 21 individuals from a complete LBK graveyard at Derenburg Meerenstieg II in Germany. These results considerably extend the available genetic dataset for the LBK ($n = 42$) and permit the first detailed genetic analysis of the earliest Neolithic culture in Central Europe (5,500-4,900 calibrated B.C.). We characterized the Neolithic mitochondrial DNA sequence diversity and geographical affinities of the early farmers using a large database of extant Western Eurasian populations ($n = 23,394$) and a wide range of population genetic analyses including shared haplotype analyses, principal component analyses, multi-dimensional scaling, geographic mapping of genetic distances, and Bayesian Serial

Simcoal analyses. The results reveal that the LBK population shared an affinity with the modern-day Near East and Anatolia, supporting a major genetic input from this area during the advent of farming in Europe. However, the LBK population also showed unique genetic features including a clearly distinct distribution of mitochondrial haplogroup frequencies, confirming that major demographic events continued to take place in Europe after the early Neolithic.

Author Summary

The transition from a hunter-gatherer existence to a sedentary farming-based lifestyle has had key consequences for human groups around the world and has profoundly shaped human societies. Originating in the Near East around 11,000 y ago, an agricultural lifestyle subsequently spread across Europe during the New Stone Age (Neolithic). Whether it was mediated by incoming farmers or driven by the transmission of innovative ideas and techniques remains a subject of continuing debate in archaeology, anthropology, and human population genetics. Ancient DNA from the earliest farmers can provide a direct view of the genetic diversity of these populations in the earliest Neolithic. Here, we compare Neolithic haplogroups and their diversity to a large database of extant European and Eurasian populations. We identified Neolithic haplotypes that left clear traces in modern populations, and the data suggest a route for the migrating farmers that extends from the Near East and Anatolia into Central Europe. When compared to indigenous hunter-gatherer populations, the unique and characteristic genetic signature of the early farmers suggests a significant demographic input from the Near East during the onset of farming in Europe.

JENKINS 2012

Dennis L. Jenkins et al., *Clovis Age Western Stemmed Projectile Points and Human Coprolites at the Paisley Caves*. [science](#) **337** (2012), 223–228.

s337-0223-Supplement.pdf

Dennis L. Jenkins, Loren G. Davis, Thomas W. Stafford Jr., Paula F. Campos, Bryan Hockett, George T. Jones, Linda Scott Cummings, Chad Yost, Thomas J. Connolly, Robert M. Yohe II, Summer C. Gibbons, Maanasa Raghavan, Morten Rasmussen, Johanna L. A. Paijmans, Michael Hofreiter, Brian M. Kemp, Jodi Lynn Barta, Cara Monroe, M. Thomas P. Gilbert & Eske Willerslev

The Paisley Caves in Oregon record the oldest directly dated human remains (DNA) in the Western Hemisphere. More than 100 high-precision radiocarbon dates show that deposits containing artifacts and coprolites ranging in age from 12,450 to 2295 14C years ago are well stratified. Western Stemmed projectile points were recovered in deposits dated to 11,070 to 11,340 14C years ago, a time contemporaneous with or preceding the Clovis technology. There is no evidence of diagnostic Clovis technology at the site. These two distinct technologies were parallel developments, not the product of a unilinear technological evolution. “Blind testing” analysis of coprolites by an independent laboratory confirms the presence of human DNA in specimens of pre-Clovis age. The colonization of the Americas involved multiple technologically divergent, and possibly genetically divergent, founding groups.

KAISER 2004

Jocelyn Kaiser, *Ural Farmers Got Milk Gene First?* [science](#) **306** (2004), 1284–1285.

The populations having the greatest DNA sequence diversity around the lactase gene mutations-suggesting that lactose tolerance first appeared in them-include the Udmurts, Mokshas, Ezras, and other groups that originally lived between the

Ural mountains and the Volga River. The trait most likely developed 4800 to 6600 years ago, Peltonen says. Her team linked the lactase gene changes to an ancestral variant that these groups apparently got from intermixing with tribes migrating from the Asian steppes.

The findings support the somewhat controversial theory that nomadic herders known as Kurgans expanded into Europe from the southern Urals 4500 to 3500 years ago, bringing Indo-European languages with them, according to Peltonen.

KIRSANOW 2011

Karola Kirsanow & Joachim Burger, *Ancient human DNA*. [Annals of Anatomy 194 \(2011\), 121–132. DOI:10.1016/j.aanat.2011.11.002.](#)

The contribution of palaeogenetic data to the study of various aspects of hominin biology and evolution has been significant, and has the potential to increase substantially with the widespread implementation of Next Generation Sequencing techniques. Here we discuss the present state-of-the-art of ancient human DNA analysis and the characteristics of hominin aDNA that make sequence validation particularly complex. A brief overview of the development of anthropological palaeogenetic analysis is given to illustrate the technical challenges motivating recent technological advancements.

LACAN 2011A

Marie Lacan et al., *Ancient DNA reveals male diffusion through the Neolithic Mediterranean route*. [PNAS 108 \(2011\), 9788–9791.](#)

[pnas108-09788-Supplement.pdf](#)

Marie Lacan, Christine Keyser, François-Xavier Ricaut, Nicolas Brucato, Francis Duranthon, Jean Guilaine, Eric Crubézy and Bertrand Ludes

The Neolithic is a key period in the history of the European settlement. Although archaeological and present-day genetic data suggest several hypotheses regarding the human migration patterns at this period, validation of these hypotheses with the use of ancient genetic data has been limited. In this context, we studied DNA extracted from 53 individuals buried in a necropolis used by a French local community 5,000 y ago. The relatively good DNA preservation of the samples allowed us to obtain autosomal, Y-chromosomal, and/or mtDNA data for 29 of the 53 samples studied. From these datasets, we established close parental relationships within the necropolis and determined maternal and paternal lineages as well as the absence of an allele associated with lactase persistence, probably carried by Neolithic cultures of central Europe. Our study provides an integrative view of the genetic past in southern France at the end of the Neolithic period. Furthermore, the Y-haplotype lineages characterized and the study of their current repartition in European populations confirm a greater influence of the Mediterranean than the Central European route in the peopling of southern Europe during the Neolithic transition.

LACAN 2011B

Marie Lacan et al., *Ancient DNA suggests the leading role played by men in the Neolithic dissemination*. [PNAS 108 \(2011\), 18255–18259.](#)

Marie Lacan, Christine Keyser, François-Xavier Ricaut, Nicolas Brucato, Josep Tarrús, Angel Bosch, Jean Guilaine, Eric Crubézy, and Bertrand Ludes

The impact of the Neolithic dispersal on the western European populations is subject to continuing debate. To trace and date genetic lineages potentially brought during this transition and so understand the origin of the gene pool of current populations, we studied DNA extracted from human remains excavated in a Spanish funeral cave dating from the beginning of the fifth millennium B.C. Thanks to a

“multimarkers” approach based on the analysis of mitochondrial and nuclear DNA (autosomes and Y-chromosome), we obtained information on the early Neolithic funeral practices and on the biogeographical origin of the inhumed individuals. No close kinship was detected. Maternal haplogroups found are consistent with pre-Neolithic settlement, whereas the Y-chromosomal analyses permitted confirmation of the existence in Spain approximately 7,000 y ago of two haplogroups previously associated with the Neolithic transition: G2a and E1b1b1a1b. These results are highly consistent with those previously found in Neolithic individuals from French Late Neolithic individuals, indicating a surprising temporal genetic homogeneity in these groups. The high frequency of G2a in Neolithic samples in western Europe could suggest, furthermore, that the role of men during Neolithic dispersal could be greater than currently estimated.

LARSON 2005

Greger Larson et al., *Worldwide Phylogeography of Wild Boar Reveals Multiple Centers of Pig Domestication*. *science* **307** (2005), 1618–1621. [s307-1618-Supplement.pdf](#)

Greger Larson, Keith Dobney, Umberto Albarella, Meiyang Fang, Elizabeth Matisoo-Smith, Judith Robins, Stewart Lowden, Heather Finlayson, Tina Brand, Eske Willerslev, Peter Rowley-Conwy, Leif Andersson & Alan Cooper
Mitochondrial DNA (mtDNA) sequences from 686 wild and domestic pig specimens place the origin of wild boar in island Southeast Asia (ISEA), where they dispersed across Eurasia. Previous morphological and genetic evidence suggested pig domestication took place in a limited number of locations (principally the Near East and Far East). In contrast, new genetic data reveal multiple centers of domestication across Eurasia and that European, rather than Near Eastern, wild boar are the principal source of modern European domestic pigs.

LARSON 2007

Greger Larson et al., *Ancient DNA, pig domestication, and the spread of the Neolithic into Europe*. *PNAS* **104** (2007), 15276–15281. [pnas104-15276-Supplement.zip](#)

Greger Larson, Umberto Albarella, Keith Dobney, Peter Rowley-Conwy, Jörg Schibler, Anne Tresset, Jean-Denis Vigne, Ceiridwen J. Edwards, Angela Schlumbaum, Alexandru Dinu, Adrian Bălăşescu, Gaynor Dolman, Antonio Tagliacozzo, Ninna Manaseryan, Preston Miracle, Louise Van Wijngaarden-Bakker, Marco Masseti, Daniel G. Bradley and Alan Cooper

The Neolithic Revolution began 11,000 years ago in the Near East and preceded a westward migration into Europe of distinctive cultural groups and their agricultural economies, including domesticated animals and plants. Despite decades of research, no consensus has emerged about the extent of admixture between the indigenous and exotic populations or the degree to which the appearance of specific components of the “Neolithic cultural package” in Europe reflects truly independent development. Here, through the use of mitochondrial DNA from 323 modern and 221 ancient pig specimens sampled across western Eurasia, we demonstrate that domestic pigs of Near Eastern ancestry were definitely introduced into Europe during the Neolithic (potentially along two separate routes), reaching the Paris Basin by at least the early 4th millennium B.C. Local European wild boar were also domesticated by this time, possibly as a direct consequence of the introduction of Near Eastern domestic pigs. Once domesticated, European pigs rapidly replaced the introduced domestic pigs of Near Eastern origin throughout Europe. Domestic pigs formed a key component of the Neolithic Revolution, and this detailed genetic record of their origins reveals a complex set of interactions and processes during the spread of early farmers into Europe.

LARSON 2010

Greger Larson et al., *Patterns of East Asian pig domestication, migration, and turnover revealed by modern and ancient DNA*. [PNAS 107 \(2010\), 7686–7691](#).

[pnas107-07686-Supplement.pdf](#), [pnas107-07686-Supplement1.xls](#), [pnas107-07686-Supplement2.xls](#), [pnas107-07686-Supplement3.xls](#), [pnas107-07686-Supplement4.xls](#), [pnas107-07686-Supplement5.xls](#)

Greger Larson, Ranran Liu, Xingbo Zhao, Jing Yuan, Dorian Fuller, Loukas Barton, Keith Dobney, Qipeng Fan, Zhiliang Gu, Xiao-Hui Liu, Yunbing Luo, Peng Lv, Leif Andersson and Ning Li

The establishment of agricultural economies based upon domestic animals began independently in many parts of the world and led to both increases in human population size and the migration of people carrying domestic plants and animals. The precise circumstances of the earliest phases of these events remain mysterious given their antiquity and the fact that subsequent waves of migrants have often replaced the first. Through the use of more than 1,500 modern (including 151 previously uncharacterized specimens) and 18 ancient (representing six East Asian archeological sites) pig (*Sus scrofa*) DNA sequences sampled across East Asia, we provide evidence for the long-term genetic continuity between modern and ancient Chinese domestic pigs. Although the Chinese case for independent pig domestication is supported by both genetic and archaeological evidence, we discuss five additional (and possibly) independent domestications of indigenous wild boar populations: one in India, three in peninsular Southeast Asia, and one off the coast of Taiwan. Collectively, we refer to these instances as “cryptic domestication,” given the current lack of corroborating archaeological evidence. In addition, we demonstrate the existence of numerous populations of genetically distinct and widespread wild boar populations that have not contributed maternal genetic material to modern domestic stocks. The overall findings provide the most complete picture yet of pig evolution and domestication in East Asia, and generate testable hypotheses regarding the development and spread of early farmers in the Far East.

MEYER 2014

Matthias Meyer et al., *A mitochondrial genome sequence of a hominin from Sima de los Huesos*. [nature 505 \(2014\), 403–406](#).

Matthias Meyer, Qiaomei Fu, Ayinuer Aximu-Petri, Isabelle Glocke, Birgit Nickel, Juan-Luis Arsuaga, Ignacio Martínez, Ana Gracia, José María Bermúdez de Castro, Eudald Carbonell & Svante Pääbo

Excavations of a complex of caves in the Sierra de Atapuerca in northern Spain have unearthed hominin fossils that range in age from the early Pleistocene to the Holocene¹. One of these sites, the ‘Sima de los Huesos’ (‘pit of bones’), has yielded the world’s largest assemblage of Middle Pleistocene hominin fossils^{2,3}, consisting of at least 28 individuals⁴ dated to over 300,000 years ago⁵. The skeletal remains share a number of morphological features with fossils classified as *Homo heidelbergensis* and also display distinct Neanderthal-derived traits^{6–8}. Here we determine an almost complete mitochondrial genome sequence of a hominin from Sima de los Huesos and show that it is closely related to the lineage leading to mitochondrial genomes of Denisovans^{9,10}, an eastern Eurasian sister group to Neanderthals. Our results pave the way for DNA research on hominins from the Middle Pleistocene.

PINHASI 2012

Ron Pinhasi, Mark G. Thomas, Michael Hofreiter, Mathias Currat & Joachim Burger, *The genetic history of Europeans*. [Trends in Genetics 28 \(2012\), 496–505](#).

The evolutionary history of modern humans is characterized by numerous migrations driven by environmental change, population pressures, and cultural innovations. In Europe, the events most widely considered to have had a major impact on patterns of genetic diversity are the initial colonization of the continent by anatomically modern humans (AMH), the last glacial maximum, and the Neolithic transition. For some decades it was assumed that the geographical structuring of genetic diversity within Europe was mainly the result of gene flow during and soon after the Neolithic transition, but recent advances in next-generation sequencing (NGS) technologies, computer simulation modeling, and ancient DNA (aDNA) analyses are challenging this simplistic view. Here we review the current knowledge on the evolutionary history of humans in Europe based on archaeological and genetic data.

RAGHAVAN 2014

Maanasa Raghavan et al., *Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans*. [nature 505 \(2014\), 87–91](#).
n505-0087-Supplement.pdf

Maanasa Raghavan, Pontus Skoglund, Kelly E. Graf, Mait Metspalu, Anders Albrechtsen, Ida Moltke, Simon Rasmussen, Thomas W. Stafford Jr, Ludovic Orlando, Ene Metspalu, Monika Karmin, Kristiina Tambets, Siiri Rootsi, Reedik Mägi, Paula F. Campos, Elena Balanovska, Oleg Balanovsky, Elza Khusnutdinova, Sergey Litvinov, Ludmila P. Osipova, Sardana A. Fedorova, Mikhail I. Voevoda, Michael DeGiorgio, Thomas Sicheritz-Ponten, Søren Brunak, Svetlana Demeshchenko, Toomas Kivisild, Richard Villems, Rasmus Nielsen, Mattias Jakobsson & Eske Willerslev

The origins of the First Americans remain contentious. Although Native Americans seem to be genetically most closely related to east Asians¹⁻³, there is no consensus with regard to which specific Old World populations they are closest to⁴⁻⁸. Here we sequence the draft genome of an approximately 24,000-year-old individual (MA-1), from Mal'ta in south-central Siberia⁹, to an average depth of 13. To our knowledge this is the oldest anatomically modern human genome reported to date. The MA-1 mitochondrial genome belongs to haplogroup U, which has also been found at high frequency among Upper Palaeolithic and Mesolithic European hunter-gatherers¹⁰⁻¹², and the Y-chromosome of MA-1 is basal to modern-day western Eurasians and near the root of most Native American lineages⁵. Similarly, we find autosomal evidence that MA-1 is basal to modern-day western Eurasians and genetically closely related to modern-day Native Americans, with no close affinity to east Asians. This suggests that populations related to contemporary western Eurasians had a more north-easterly distribution 24,000 years ago than commonly thought. Furthermore, we estimate that 14 to 38% of Native American ancestry may originate through gene flow from this ancient population. This is likely to have occurred after the divergence of Native American ancestors from east Asian ancestors, but before the diversification of Native American populations in the New World. Gene flow from the MA-1 lineage into Native American ancestors could explain why several crania from the First Americans have been reported as bearing morphological characteristics that do not resemble those of east Asians^{2,13}. Sequencing of another south-central Siberian, Afontova Gora-2 dating to approximately 17,000 years ago¹⁴, revealed similar autosomal genetic signatures as MA-1, suggesting that the region was continuously occupied by humans throughout the Last Glacial Maximum. Our findings reveal that western Eurasian genetic signatures in modern-day Native Americans derive not only from post-Columbian admixture, as commonly thought, but also from a mixed ancestry of the First Americans.

RASMUSSEN 2011

Morten Rasmussen et al., *An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia*. [science 334 \(2011\), 94–98](#).

[s334-0094-Supplement.pdf](#)

Morten Rasmussen, Xiaosen Guo, Yong Wang, Kirk E. Lohmueller, Simon Rasmussen, Anders Albrechtsen, Line Skotte, Stinus Lindgreen, Mait Metspalu, Thibaut Jombart, Toomas Kivisild, Weiwei Zhai, Anders Eriksson, Andrea Manica, Ludovic Orlando, Francisco M. De La Vega, Silvana Tridico, Ene Metspalu, Kasper Nielsen, María C. IJvila-Arcos, J. Víctor Moreno-Mayar, Craig Muller, Joe Dortch, M. Thomas P. Gilbert, Ole Lund, Agata Wesolowska, Monika Karmin, Lucy A. Weinert, Bo Wang, Jun Li, Shuaishuai Tai, Fei Xiao, Tsunehiko Hanihara, George van Driem, Aashish R. Jha, François-Xavier Ricaut, Peter de Knijff, Andrea B. Migliano, Irene Gallego Romero, Karsten Kristiansen, David M. Lambert, Søren Brunak, Peter Forster, Bernd Brinkmann, Olaf Nehlich, Michael Bunce, Michael Richards, Ramneek Gupta, Carlos D. Bustamante, Anders Krogh, Robert A. Foley, Marta M. Lahr, Francois Balloux, Thomas Sicheritz-Pontén, Richard Villems, Rasmus Nielsen, Jun Wang, Eske Willerslev

We present an Aboriginal Australian genomic sequence obtained from a 100-year-old lock of hair donated by an Aboriginal man from southern Western Australia in the early 20th century. We detect no evidence of European admixture and estimate contamination levels to be below 0.5%. We show that Aboriginal Australians are descendants of an early human dispersal into eastern Asia, possibly 62,000 to 75,000 years ago. This dispersal is separate from the one that gave rise to modern Asians 25,000 to 38,000 years ago. We also find evidence of gene flow between populations of the two dispersal waves prior to the divergence of Native Americans from modern Asian ancestors. Our findings support the hypothesis that present-day Aboriginal Australians descend from the earliest humans to occupy Australia, likely representing one of the oldest continuous populations outside Africa.

SISTIAGA 2014

A. Sistiaga, F. Berna, R. Laursen & P. Goldberg, *Steroid biomarker analysis of a 14,000 years old putative human coprolite from Paisley Cave, Oregon*. [Journal of Archaeological Science 41 \(2014\), 813–817](#).

Lipid components of a putative human coprolite sample from the Paleoindian site of Paisley Cave, Oregon (12,300 14C yr BP) were analyzed using GC/MS to explore its origin in light of controversial data obtained from mitochondrial DNA, cross-immunoelectrophoresis, trisodium phosphate rehydration, and micromorphology analyses. Results show the predominant presence of 5b-stigmastanol, the biomarker of herbivore fecal matter, supporting micromorphological identification of the coprolite as herbivore. This study highlights the potential of the biomarker approach in coprolite studies devoted to research on the first presence of humans in North America.

Keywords: Coprolite | Fecal biomarkers | Sterols | Coprostanol | 5b-Stigmastanol | Paisley Cave | Pre-Clovis

SMITH 2009

Silvia E. Smith, M. Geoffrey Hayes, Graciela S. Cabana, Chad Huff, Joan Brenner Coltrain & Dennis H. O'Rourke, *Inferring Population Continuity Versus Replacement with aDNA, A Cautionary Tale from the Aleutian Islands*. [Human Biology 81 \(2009\), 407–426](#).

In *The Aleutian and Commander Islands and Their Inhabitants* (Philadelphia: Wistar Institute of Anatomy and Biology, 1945), Hrdlička proposed a population

replacement event in the Aleutian Islands approximately 1,000 years ago based on a perceived temporal shift in cranial morphology. However, the archaeological record indicates cultural, and presumed population, continuity for more than 4,000 years. We use mtDNA haplogroup data in the series of prehistoric eastern Aleutian samples ($n = 86$) studied craniometrically by Hrdlička to test alternative hypotheses regarding population continuity or replacement in the region. This molecular characterization, in conjunction with direct dating of individual specimens, provided increased resolution for hypothesis testing. Results indicate an apparent shift in mtDNA haplogroup frequencies in the eastern Aleutians approximately 1,000 years ago, in concert with changes in mortuary practices and isotopic signatures reflecting resource acquisition strategies. The earliest Aleut populations were characterized by a high frequency of haplogroup A, as are most modern populations of the North American arctic. Later prehistoric peoples in the Aleutians were characterized by a high frequency of haplogroup D and a correspondingly lower frequency of haplogroup A, a pattern typified by modern Aleut populations.

Key Words: ancient DNA, MtDNA haplogroups, replacement, population continuity, Aleutian islands