

References

Aktuell

MALLAPATY 2021

Smriti Mallapaty, *Did the coronavirus jump from animals to people twice?* [nature](#) **597** (2021), 458–459.

An unverified analysis of viral genomes suggests that the pandemic might have multiple animal origins.

WADMAN 2021

Meredith Wadman, *Israel's high case plateau may offer worrisome portent.* [science](#) **373** (2021), 1428–1429. DOI:10.1126/science.acx9161.

Opposing forces keep outside case count steady: school openings, holidays work against boosters.

Amerika

BENNETT 2021

Matthew R. Bennett et al., *Evidence of humans in North America during the Last Glacial Maximum.* [science](#) **373** (2021), 1528–1531.

s373-1528-Supplement.pdf

Archaeologists and researchers in allied fields have long sought to understand human colonization of North America. Questions remain about when and how people migrated, where they originated, and how their arrival affected the established fauna and landscape. Here, we present evidence from excavated surfaces in White Sands National Park (New Mexico, United States), where multiple in situ human footprints are stratigraphically constrained and bracketed by seed layers that yield calibrated radiocarbon ages between ≈ 23 and 21 thousand years ago. These findings confirm the presence of humans in North America during the Last Glacial Maximum, adding evidence to the antiquity of human colonization of the Americas and providing a temporal range extension for the coexistence of early inhabitants and Pleistocene megafauna.

Matthew R. Bennett, David Bustos, Jeffrey S. Pigati, Kathleen B. Springer, Thomas M. Urban, Vance T. Holliday, Sally C. Reynolds, Marcin Budka, Jeffrey S. Honke, Adam M. Hudson, Brendan Fenerty, Clare Connelly, Patrick J. Martinez, Vincent L. Santucci & Daniel Odess

Anthropologie

BEN-DOR 2011

Miki Ben-Dor, Avi Gopher, Israel Hershkovitz & Ran Barkai, *Man the Fat Hunter, The Demise of Homo erectus and the Emergence of a New Hominin Lineage in the Middle Pleistocene (ca. 400 kyr) Levant.* [PLoS ONE](#) **6** (2011), e28689. DOI:10.1371/journal.pone.0028689.

The worldwide association of *H. erectus* with elephants is well documented and so is the preference of humans for fat as a source of energy. We show that

rather than a matter of preference, *H. erectus* in the Levant was dependent on both elephants and fat for his survival. The disappearance of elephants from the Levant some 400 kyr ago coincides with the appearance of a new and innovative local cultural complex – the Levantine Acheulo-Yabrudian and, as is evident from teeth recently found in the Acheulo-Yabrudian 400-200 kyr site of Qesem Cave, the replacement of *H. erectus* by a new hominin. We employ a bio-energetic model to present a hypothesis that the disappearance of the elephants, which created a need to hunt an increased number of smaller and faster animals while maintaining an adequate fat content in the diet, was the evolutionary drive behind the emergence of the lighter, more agile, and cognitively capable hominins. Qesem Cave thus provides a rare opportunity to study the mechanisms that underlie the emergence of our post-*erectus* ancestors, the fat hunters.

Biologie

GYMREK 2021

Melissa Gymrek & Alon Goren, *Missing heritability may be hiding in repeats*. [science](#) **373** (2021), 1440–1441.

Unexplored variable number tandem repeats make a large contribution to complex traits.

MUKAMEL 2021

Ronen E. Mukamel, Robert E. Handsaker, Steven A. McCarroll & Po-Ru Loh et al., *Protein-coding repeat polymorphisms strongly shape diverse human phenotypes*. [science](#) **373** (2021), 1499–1505.

[s373-1499-Supplement.pdf](#)

Many human proteins contain domains that vary in size or copy number because of variable numbers of tandem repeats (VNTRs) in protein-coding exons. However, the relationships of VNTRs to most phenotypes are unknown because of difficulties in measuring such repetitive elements. We developed Methods to estimate VNTR lengths from whole-exome sequencing data and impute VNTR alleles into single-nucleotide polymorphism haplotypes. Analyzing 118 protein-altering VNTRs in 415,280 UK Biobank participants for association with 786 phenotypes identified some of the strongest associations of common variants with human phenotypes, including height, hair morphology, and biomarkers of health. Accounting for large-effect VNTRs further enabled fine-mapping of associations to many more protein-coding mutations in the same genes. These results point to cryptic effects of highly polymorphic common structural variants that have eluded molecular analyses to date.

Ronen E. Mukamel, Robert E. Handsaker, Maxwell A. Sherman, Alison R. Barton, Yiming Zheng, Steven A. McCarroll & Po-Ru Loh

Klima

GERLACH 2012

Renate Gerlach & Eileen Eckmeier, *Prehistoric Land Use and Its Impact on Soil Formation since Early Neolithic, Examples from the Lower Rhine Area*. [eTopoi Journal for Ancient Studies](#) **3** (2012), 11–16.

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The soils of the Central European regions that have been settled since the Early Neolithic, such as the Lower Rhine Region (NW-Germany), have been influenced by agrarian societies for more than 7000 years. This long history of clearing, digging, hoeing, ploughing or fertilizing has had a deep impact on soil formation—beyond the well-known phenomena of soil erosion and colluviation. We will present examples for soil types which were formed as a result of human activities, and which are more archaeological rather than natural features:

- 1.) Luvic Phaeozems, which can be a product of Late Neolithic burning practices,
- 2.) Podzols and hydromorphic soils, which were initialized by forest clearances mainly during the Iron Ages,
- 3.) Cambisols, which are cryptic Plaggen soils built up since the Middle Ages and
- 4.) A ground surface which has been widely destroyed by concealed “micro surface mining” in the Early Modern Period.

LAUER 2014

Franziska Lauer et al., *Organic Fertilization and Sufficient Nutrient Status in Prehistoric Agriculture? – Indications from Multi-Proxy Analyses of A*. *PLoS ONE* **9** (2014), e106244. DOI:10.1371/journal.pone.0106244.

Neolithic and Bronze Age topsoil relicts revealed enhanced extractable phosphorus (P) and plant available inorganic P fractions, thus raising the question whether there was targeted soil amelioration in prehistoric times. This study aimed (i) at assessing the overall nutrient status and the soil organic matter content of these arable topsoil relicts, and (ii) at tracing ancient soil fertilizing practices by respective stable isotope and biomarker analyses. Prehistoric arable topsoils were preserved in archaeological pit fillings, whereas adjacent subsoils served as controls. One Early Weichselian humic zone represented the soil status before the introduction of agriculture. Recent topsoils served as an additional reference. The applied multi-proxy approach comprised total P and micronutrient contents, stable N isotope ratios, amino acid, steroid, and black carbon analyses as well as soil color measurements. Total contents of P and selected micronutrients (I, Cu, Mn, Mo, Se, Zn) of the arable soil relicts were above the limits for which nutrient deficiencies could be assumed. All pit fillings exhibited elevated $\delta^{15}\text{N}$ values close to those of recent topsoils ($\delta^{15}\text{N}$ 6 to 7 ‰), giving first hints for prehistoric organic N input. Ancient legume cultivation as a potential source for N input could not be verified by means of amino acid analysis. In contrast, bile acids as markers for faecal input exhibited larger concentrations in the pit fillings compared with the reference and control soils indicating faeces (i.e. manure) input to Neolithic arable topsoils. Also black carbon contents were elevated, amounting up to 38 % of soil organic carbon, therewith explaining the dark soil color in the pit fillings and pointing to inputs of burned biomass. The combination of different geochemical analyses revealed a sufficient nutrient status of prehistoric arable soils, as well as signs of amelioration (inputs of organic material like charcoal and faeces-containing manure).

Franziska Lauer, Katharina Prost, Renate Gerlach, Stefan Pätzold, Mareike Wolf, Sarah Urmersbach, Eva Lehndorff, Eileen Eckmeier & Wulf Amelung

OSMAN 2021

Matthew B. Osman, Sloan Coats, Sarah B. Das, Joseph R. McConnell & Nathan Chellman, *North Atlantic jet stream projections in the context of the past 1,250 years*. *PNAS* **118** (2021), e2104105118. pnas118-e2104105118-Supplement.pdf

Reconstruction of the North Atlantic jet stream (NAJ) presents a critical, albeit largely unconstrained, paleoclimatic target. Models suggest northward migration

and changing variance of the NAJ under 21st-century warming scenarios, but assessing the significance of such projections is hindered by a lack of long-term observations. Here, we incorporate insights from an ensemble of last-millennium water isotope-enabled climate model simulations and a wide array of mean annual water isotope ($\delta^{18}O$) and annually accumulated snowfall records from Greenland ice cores to reconstruct North Atlantic zonal-mean zonal winds back to the 8th century CE. Using this reconstruction we provide preobservational constraints on both annual mean NAJ position and intensity to show that late 20th- and early 21st-century NAJ variations were likely not unique relative to natural variability. Rather, insights from our 1,250 year reconstruction highlight the overwhelming role of natural variability in thus far masking the response of midlatitude atmospheric dynamics to anthropogenic forcing, consistent with recent large-ensemble transient modeling experiments. This masking is not projected to persist under high greenhouse gas emissions scenarios, however, with model projected annual mean NAJ position emerging as distinct from the range of reconstructed natural variability by as early as 2060 CE.

Keywords: North Atlantic | jet stream | ice core | Greenland | climate change

Significance: The North Atlantic jet stream impacts North American and European societies and is expected to be influenced by ongoing 21st-century warming. To better contextualize recently observed and model-projected jet stream changes, long-term records are required. We use insights from a state-of-the-art water isotope-enabled climate model and a compilation of ice-core records from Greenland to reconstruct mean annual North Atlantic jet stream changes back to the 8th century CE. Our reconstruction suggests that observed jet stream variations are consistent with natural variations, despite dramatic warming across recent decades. Under unabated future warming, however, a progressive migration of the jet stream northward is projected to render it distinct from natural variability by 2060 CE.

PEDERZANI 2021

Sarah Pederzani et al., *Subarctic climate for the earliest Homo sapiens in Europe*. [Science Advances 7 \(2021\), eabi4642](#).
[DOI:10.1126/sciadv.abi4642](#).

[SciAdv07-eabi4642-Supplement.pdf](#)

The expansion of *Homo sapiens* across Eurasia marked a major milestone in human evolution that would eventually lead to our species being found across every continent. Current models propose that these expansions occurred only during episodes of warm climate, based on age correlations between archaeological and climatic records. Here, we obtain direct evidence for the temperatures faced by some of these humans through the oxygen isotope analysis of faunal remains from Bacho Kiro Cave, Bulgaria, the earliest clear record of *H. sapiens* in Europe. The results indicate that humans $\approx 45,000$ years ago experienced subarctic climates with far colder climatic conditions than previously suggested. This demonstrates that the early presence of *H. sapiens* in Europe was not contingent on warm climates. Our results necessitate the revision of key models of human expansion and highlight the need for a less deterministic role of climate in the study of our evolutionary history.

Sarah Pederzani, Kate Britton, Vera Aldeias, Nicolas Bourgon, Helen Fewlass, Tobias Lauer, Shannon P. McPherron, Zeljko Rezek, Nikolay Sirakov, Geoff M. Smith, Rosen Spasov, N.-Han Tran, Tsenka Tsanova & Jean-Jacques Hublin

Metallzeiten

POSTH 2021

Cosimo Posth et al., *The origin and legacy of the Etruscans through a 2000-year archeogenomic time transect*. *Science Advances* **7** (2021), eabi7673. DOI:10.1126/sciadv.abi7673.

SciAdv07-eabi7673-Supplement.pdf

The origin, development, and legacy of the enigmatic Etruscan civilization from the central region of the Italian peninsula known as Etruria have been debated for centuries. Here we report a genomic time transect of 82 individuals spanning almost two millennia (800 BCE to 1000 CE) across Etruria and southern Italy. During the Iron Age, we detect a component of Indo-European-associated steppe ancestry and the lack of recent Anatolian-related admixture among the putative non-Indo-European-speaking Etruscans. Despite comprising diverse individuals of central European, northern African, and Near Eastern ancestry, the local gene pool is largely maintained across the first millennium BCE. This drastically changes during the Roman Imperial period where we report an abrupt population-wide shift to $\approx 50\%$ admixture with eastern Mediterranean ancestry. Last, we identify northern European components appearing in central Italy during the Early Middle Ages, which thus formed the genetic landscape of present-day Italian populations.

Cosimo Posth, Valentina Zaro, Maria A. Spyrou, Stefania Vai, Guido A. Gnechi-Ruscone, Alessandra Modi, Alexander Peltzer, Angela Mötsch, Kathrin Nägele, Ashild J. Vagene, Elizabeth A. Nelson, Rita Radzevièiute, Cäcilia Freund, Lorenzo M. Bondioli, Luca Cappuccini, Hannah Frenzel, Elsa Pacciani, Francesco Boschini, Giulia Capecchi, Ivan Martini, Adriana Moroni, Stefano Ricci, Alessandra Sperduti, Maria Angela Turchetti, Alessandro Riga, Monica Zavattaro, Andrea Zifferero, Henrike O. Heyne, Eva Fernández-Domínguez, Guus J. Kroonen, Michael McCormick, Wolfgang Haak, Martina Lari, Guido Barbujani, Luca Bondioli, Kirsten I. Bos, David Caramelli & Johannes Krause

Ozeanien

IOANNIDIS 2021

Alexander G. Ioannidis et al., *Paths and timings of the peopling of Polynesia inferred from genomic networks*. *nature* **597** (2021), 522–526. n597-0522-Supplement.pdf

Polynesia was settled in a series of extraordinary voyages across an ocean spanning one third of the Earth¹, but the sequences of islands settled remain unknown and their timings disputed. Currently, several centuries separate the dates suggested by different archaeological surveys^{2–4}. Here, using genome-wide data from merely 430 modern individuals from 21 key Pacific island populations and novel ancestry-specific computational analyses, we unravel the detailed genetic history of this vast, dispersed island network. Our reconstruction of the branching Polynesian migration sequence reveals a serial founder expansion, characterized by directional loss of variants, that originated in Samoa and spread first through the Cook Islands (Rarotonga), then to the Society (T_i-taiete m_i) Islands (11th century), the western Austral (Tuha'a Pae) Islands and Tu_imotu Archipelago (12th century), and finally to the widely separated, but genetically connected, megalithic statue-building cultures of the Marquesas (Te Henua 'Enana) Islands in the north, Raivavae in the south, and Easter Island (Rapa Nui), the easternmost of the Polynesian islands, settled in approximately ad 1200 via Mangareva.

Alexander G. Ioannidis, Javier Blanco-Portillo, Karla Sandoval, Erika Hagelberg, Carmina Barberena-Jonas, Adrian V. S. Hill, Juan Esteban Rodríguez-Rodríguez, Keolu Fox, Kathryn Robson, Sonia Haaq-Cardinali, Consuelo D. Quinto-Cortés, Juan Francisco Miquel-Poblete, Kathryn Auckland, Tom Parks, Abdul Salam M. Sofro, María C. Ávila-Arcos, Alexandra Sockell, Julian R. Homburger, Celeste Eng, Scott Huntsman, Esteban G. Burchard, Christopher R. Gignoux, Ricardo A. Verdugo, Mauricio Moraga, Carlos D. Bustamante, Alexander J. Mentzer & Andrés Moreno-Estrada

KIRCH 2021

Patrick V. Kirch, *When early Polynesians migrated eastwards*. [nature](#) **597** (2021), 477–478.

A genome-wide analysis of modern populations in Polynesia suggests the direction and timing of ancient Polynesian migrations. This model bears consistencies and inconsistencies with models based on archaeology and linguistics.