

References

Aktuell

LE CORRE 2020

Valérie Le Corre, Mathieu Siol, Yves Vigouroux, Maud I. Tenaillon & Christophe Délye, *Adaptive introgression from maize has facilitated the establishment of teosinte as a noxious weed in Europe*. [PNAS 117 \(2020\), 25618–25627](#).

[pnas117-25618-Supplement.pdf](#)

Global trade has considerably accelerated biological invasions. The annual tropical teosintes, the closest wild relatives of maize, were recently reported as new agricultural weeds in two European countries, Spain and France. Their prompt settlement under climatic conditions differing drastically from that of their native range indicates rapid genetic evolution. We performed a phenotypic comparison of French and Mexican teosintes under European conditions and showed that only the former could complete their life cycle during maize cropping season. To test the hypothesis that crop-to-wild introgression triggered such rapid adaptation, we used single nucleotide polymorphisms to characterize patterns of genetic variation in French, Spanish, and Mexican teosintes as well as in maize germplasm. We showed that both Spanish and French teosintes originated from *Zea mays* ssp. *mexicana* race “Chalco,” a weedy teosinte from the Mexican highlands. However, introduced teosintes differed markedly from their Mexican source by elevated levels of genetic introgression from the high latitude Dent maize grown in Europe. We identified a clear signature of divergent selection in a region of chromosome 8 introgressed from maize and encompassing *ZCN8*, a major flowering time gene associated with adaptation to high latitudes. Moreover, herbicide assays and sequencing revealed that French teosintes have acquired herbicide resistance via the introgression of a mutant herbicide-target gene (*ACC1*) present in herbicide-resistant maize cultivars. Altogether, our results demonstrate that adaptive crop-to-wild introgression has triggered both rapid adaptation to a new climatic niche and acquisition of herbicide resistance, thereby fostering the establishment of an emerging noxious weed.

Keywords: plant invasion | rapid adaptation | genetic introgression | flowering time | herbicide resistance

Significance: The emergence of noxious weeds poses a serious threat to agricultural production. Understanding their origin and evolution is therefore of major importance. Here we analyzed the intriguing case of teosinte, a wild relative of maize originating from Mexico that recently emerged as an invasive weed in maize fields in Europe. Patterns of genetic variation revealed extensive genetic introgression from maize adapted to temperate latitudes into European teosintes. Introgressed genomic regions harbored a key flowering time gene and an herbicide resistance gene. Our results exemplify how adaptive introgression can drive the evolution of a crop’s wild relative into a weed. Hybridization is an evolutionary force that should not be underestimated when forecasting invasiveness risks.

NETZ 2020

Roland R. Netz & William A. Eaton, *Physics of virus transmission by speaking droplets*. [PNAS 117 \(2020\), 25209–25211](#).

[DOI:10.1073/pnas.2011889117](https://doi.org/10.1073/pnas.2011889117).

To make the physics of person-to-person virus transmission from emitted droplets of oral fluid while speaking easily understood, we present simple and transparent algebraic equations that capture the essential physics of the problem. Calculations with these equations provide a straightforward way of determining whether emitted droplets remain airborne or rapidly fall to the ground, after accounting for the decrease in droplet size from water evaporation. At a relative humidity of 50%, for example, droplets with initial radii larger than about 50 μm rapidly fall to the ground, while smaller, potentially virus-containing droplets shrink in size from water evaporation and remain airborne for many minutes. Estimates of airborne virion emission rates while speaking strongly support the proposal that mouth coverings can help contain the COVID-19 pandemic.

Keywords: COVID-19 | virus transmission | speaking droplets | SARS-CoV-2

SNAPÉ 2020

Matthew D. Snape & Russell M. Viner, *COVID-19 in children and young people*. [science](https://doi.org/10.1126/science.abd6165) **370** (2020), 286–288.
[DOI:10.1126/science.abd6165](https://doi.org/10.1126/science.abd6165).

Children have a low risk of COVID-19 and are disproportionately harmed by precautions.

WU 2020

Xiao Wu, Rachel C. Nethery, M. Benjamin Sabath, Danielle Braun & Francesca Dominici, *Exposure to air pollution and COVID-19 mortality in the United States, A nationwide cross-sectional study*. [medRxiv](https://doi.org/10.1101/2020.04.05.20054502) **2020**, 20054502, 1–36. [DOI:10.1101/2020.04.05.20054502](https://doi.org/10.1101/2020.04.05.20054502).

Objectives: United States government scientists estimate that COVID-19 may kill tens of thousands of Americans. Many of the pre-existing conditions that increase the risk of death in those with COVID-19 are the same diseases that are affected by long-term exposure to air pollution. We investigated whether long-term average exposure to fine particulate matter (PM_{2.5}) is associated with an increased risk of COVID-19 death in the United States.

Design: A nationwide, cross-sectional study using county-level data.

Data sources: COVID-19 death counts were collected for more than 3,000 counties in the United States (representing 98% of the population) up to April 22, 2020 from Johns Hopkins University, Center for Systems Science and Engineering Coronavirus Resource Center.

Main outcome measures: We fit negative binomial mixed models using county-level COVID-19 deaths as the outcome and county-level long-term average of PM_{2.5} as the exposure. In the main analysis, we adjusted by 20 potential confounding factors including population size, age distribution, population density, time since the beginning of the outbreak, time since state’s issuance of stay-at-home order, hospital beds, number of individuals tested, weather, and socioeconomic and behavioral variables such as obesity and smoking. We included a random intercept by state to account for potential correlation in counties within the same state. We conducted more than 68 additional sensitivity analyses.

Results: We found that an increase of only 1 $\mu\text{g}/\text{m}^3$ in PM_{2.5} is associated with an 8% increase in the COVID-19 death rate (95% confidence interval [CI]: 2%, 15%). The results were statistically significant and robust to secondary and sensitivity analyses.

Conclusions: A small increase in long-term exposure to PM_{2.5} leads to a large increase in the COVID-19 death rate. Despite the inherent limitations of the ecological study design, our results underscore the importance of continuing to enforce

existing air pollution regulations to protect human health both during and after the COVID-19 crisis. The data and code are publicly available so our analyses can be updated routinely.

YAM 2020

Kai Chi Yam, Joshua Conrad Jackson, Christopher M. Barnes, Jenson Lau, Xin Qin & Hin Yeung Lee, *The rise of COVID-19 cases is associated with support for world leaders*. *PNAS* **117** (2020), 25429–25433. DOI:10.1073/pnas.2009252117.

[pnas117-25429-Supplement.pdf](#)

COVID-19 has emerged as one of the deadliest and most disruptive events in recent human history. Drawing from political science and psychological theories, we examine the effects of daily confirmed cases in a country on citizens' support for the political leader through the first 120 d of 2020. Using three unique datasets which comprise daily approval ratings of head of government ($n = 1,411,200$) across 11 world leaders (Australia, Brazil, Canada, France, Germany, Hong Kong, India, Japan, Mexico, the United Kingdom, and the United States) and weekly approval ratings of governors across the 50 states in the United States ($n = 912,048$), we find a strong and significant positive association between new daily confirmed and total confirmed COVID-19 cases in the country and support for the heads of government. These analyses show that political leaders received a boost in approval in the early months of the COVID-19 pandemic. Moreover, these findings suggest that the previously documented “rally ‘round the flag’” effect applies beyond just intergroup conflict.

Keywords: COVID-19 | leader support | political support

Significance: Amid the present COVID-19 pandemic, we find that many citizens around the world “rally ‘round the flag’” and increase their support for their respective political leaders. We observe these findings among countries that are culturally and geographically diverse, and even among leaders who are strongly disliked by citizens prior to the pandemic. Our findings could have important voting implications during or immediately after the pandemic. As an example, the Korean ruling party won the most seats in the house by any party since 1960 in an election held during the pandemic in April 2020. COVID-19 might thus serve as a catalyst to help some incumbent governments.

Altpaläolithikum

GAILLARD 2016

Claire Gaillard et al., *The lithic industries on the fossiliferous outcrops of the Late Pliocene Masol Formation, Siwalik Frontal Range, northwestern* *Comptes Rendus Palevol* **15** (2016), 341–357.

The Quranwala zone (QZ) in the sector near Masol (Siwalik Frontal Range, Punjab) has been known since the 1960s for yielding freshwater and terrestrial vertebrates living during the late Pliocene on the sub-Himalayan floodplain. The fossils and quartzite cobbles are constantly unearthed from the core of an anticline. The basal member of QZ is about 130 meters below the Gauss/Matuyama paleomagnetic reversal, i.e., 2.588 Ma. Since 2009 the Indo-French Program of Research ‘Siwaliks’ has surveyed 50 hectares and highlighted a dozen localities on outcrops where artefacts in quartzite occur with fossil bones, of which a few show butchering marks. A few cobble tools and a flake were unearthed from a trial trench opened along the same boundary between silts and sandstones (Masol 2) as the

one that provided a bovid tibia shaft bearing cut marks (Masol 1). Some 250 artefacts were collected mainly from the surface, sometimes in the slopes of outcrops recently eroded. These were mostly heavy-duty tools that comprised a majority of choppers, end choppers rather than side choppers, among which the “simple choppers” (shaped by one single removal) are common. The light-duty tools consist of flakes that are seldom retouched. The cores are very few and the flakes generally result from the shaping of choppers, except the larger flakes that are complemented by split cobbles. The consistency of the lithic assemblages among the localities supports their chronological homogeneity. Their features do not reflect

Claire Gaillard, Mukesh Singh, Anne Dambricourt Malassé, Vipnesh Bhardwaj, Baldev Karir, Amandeep Kaur, Surinder Pal, Anne-Marie Moigne, Cécile Chapon Sao, Salah Abdessadok, Julien Gargani & Alina Tudryn

Keywords: Siwalik Frontal Range | Simple technology | Chopper | Split | Sub-Himalayan floodplain | South Asia

SHCHELINSKY 2016

V. E. Shchelinsky, M. Gurova, A. S. Tesakov, V. V. Titov, P. D. Frolov & A. N. Simakova, *The Early Pleistocene site of Kermek in western Ciscaucasia (southern Russia), Stratigraphy, biotic record and lithic industry (preliminary results)*. [Quaternary International 393 \(2016\), 51–69](#).

The discovery of the Early Pleistocene sites of Bogatyri/Sinyaya Balka and Rodniki 1 on the Taman Peninsula in western Ciscaucasia led to the recognition of a distinctive “Tamanian industry”, with a timerange of 1.6–1.2 Ma, and with characteristics that are transitional between Oldowan and Acheulean (“Archaic Acheulean”). The site of Kermek was discovered by V.E. Shchelinsky in 2008 during investigation of the older Lower Pleistocene sediments exposed in the coastal cliff of the Sea of Azov in the vicinity of previously studied sites.

In this paper, we present preliminary data from a multidisciplinary study of the Early Pleistocene site of Kermek, situated near to the sites of Bogatyri/Sinyaya Balka and Rodniki 1, but which is significantly older. This site is connected with a well-studied Early Pleistocene (late Kujalnikian) fluvial-shallow marine sequence. These reverse magnetized deposits are characterized by freshwater and brackish water mollusks (with *Dreissena theodori*), and by a small mammal fauna (with *Allophaiomys deucalion*), and are dated to the latest Gelasian or early Calabrian ca. 2.1–1.8 Ma. The lithic industry from the site can be attributed to the Classic Oldowan but with distinctive local features that include indications of “advanced technologies” such as the manufacture of large flakes and picks. In this respect, this industry is assumed to have been a genetic precursor of the later Early Pleistocene Tamanian industry, which has a well pronounced Acheulean component.

Keywords: Kermek | Oldowan – Acheulean transition | Early Pleistocene | Upper Kujalnik | Western Ciscaucasia | Southern Russia

Anthropologie

ACKERMANN 2016

Rebecca Rogers Ackermann, Alex Mackay & Michael L. Arnold, *The Hybrid Origin of “Modern” Humans*. [Evolutionary Biology 43 \(2016\), 1–11](#).

Recent genomic research has shown that hybridization between substantially diverged lineages is the rule, not the exception, in human evolution. However,

the importance of hybridization in shaping the genotype and phenotype of *Homo sapiens* remains debated. Here we argue that current evidence for hybridization in human evolution suggests not only that it was important, but that it was an essential creative force in the emergence of our variable, adaptable species. We then extend this argument to a reappraisal of the archaeological record, proposing that the exchange of cultural information between divergent groups may have facilitated the emergence of cultural innovation. We discuss the implications of this Divergence and Hybridization Model for considering the taxonomy of our lineage.

Keywords: Cultural and biological modernity | Hybridization | Frontiers | Neanderthals | Denisovans

CHANG 2014

Belinda S. W. Chang, *Ancient insights into uric acid metabolism in primates*. [PNAS 111 \(2014\), 3657–3658](#).

Why are humans susceptible to certain illnesses but not others? Diseases such as gout and hypertension have plagued us for centuries. The prevalence of gout in the United States has risen to 3.9% in recent years, and a staggering one in three adults have hypertension. It has often been assumed that some of the less than desirable aspects of our physiology are relics of our evolutionary past, but rarely have these ideas been subjected to experimental investigation, and many of these theories have been surprisingly difficult to prove.

DENNELL 2011

Robin W. Dennell, María Martínón-Torres & José M. Bermúdez de Castro, *Hominin variability, climatic instability and population demography in Middle Pleistocene Europe*. [Quaternary Science Reviews 30 \(2011\), 1511–1524](#).

We propose a population model for Middle Pleistocene Europe that is based on demographic “sources” and “sinks”. The former were a small number of “core” or populations in glacial refugia in southern Europe from which hominins expanded northwards in interstadial and interglacial periods; occupation outside glacial refugia would have been restricted to warm or temperate periods, and populations at the northern limit of the Middle Pleistocene range would have been “sink” populations in that they depended upon recruitment from source populations further south. Southwest Asia would also have been a likely source of immigrant, source populations. We argue as an alternative to an “ebb and flow” model in which groups retreated to refugia when conditions worsened that local extinction outside refugia would have been frequent. In extreme situations, Europe may have been a population “sink” (i.e. unpopulated) that was replenished from source populations in Southwest Asia. We suggest that this pattern of repeated colonisation and extinction may help explain the morphological variability of European Middle Pleistocene hominins, particularly *Homo heidelbergensis* and its apparent non-linear evolution towards *Homo neanderthalensis*.

FUSS 2017

Jochen Fuss, Nikolai Spassov, David R. Begun & Madelaine Böhme, *Potential hominin affinities of *Graecopithecus* from the Late Miocene of Europe*. [PLoS ONE 12 \(2017\), e177127](#). [DOI:10.1371/journal.pone.0177127](#).

The split of our own clade from the Panini is undocumented in the fossil record. To fill this gap we investigated the dentognathic morphology of *Graecopithecus freybergi* from Pyrgos Vassilissis (Greece) and cf. *Graecopithecus* sp. from Azmaka

(Bulgaria), using new iCT and 3D reconstructions of the two known specimens. Pyrgos Vassilissis and Azmaka are currently dated to the early Messinian at 7.175 Ma and 7.24 Ma. Mainly based on its external preservation and the previously vague dating, Graecopithecus is often referred to as nomen dubium. The examination of its previously unknown dental root and pulp canal morphology confirms the taxonomic distinction from the significantly older northern Greek hominine Ouranopithecus. Furthermore, it shows features that point to a possible phylogenetic affinity with hominins. *G. freybergi* uniquely shares p4 partial root fusion and a possible canine root reduction with this tribe and therefore, provides intriguing evidence of what could be the oldest known hominin.

FUSS 2018

Jochen Fuss, Gregor Uhlig & Madelaine Böhme, *Earliest evidence of caries lesion in hominids reveal sugar-rich diet for a Middle Miocene dryopithecine from Europe*. *PLoS ONE* **13** (2018), e203307. DOI:10.1371/journal.pone.0203307.

The formation of dental caries is mainly caused by dietary habits and therefore, may contain information for dietary reconstructions of fossil hominids. This study investigates the caries lesion in the 12.5 Ma old type specimen of *Dryopithecus carinthiacus* Mottl 1957 (Primates, Hominidae) from St. Stefan (Austria). Potential food sources are identified on associated palynological data, which allow conclusions about food quality, sugar availability and the hominid metabolism during the Middle Miocene. Using micro computed tomography (iCT) and scanning electron microscopy (SEM) we provide a detailed analysis and characterization of the individuals' caries type. Its lesion is compared with a dataset of 311 wild chimpanzees, indicating morphological and etiological differences in caries formation between both species. The affected molar of *D. carinthiacus* reveals features known from severe dental caries in humans: (1) Cavitation with steep walls and smooth surface; (2) Reparative dentine at the roof of the pulp chamber; (3) Sclerotic dentine below the cavitation; (4) Association with dental calculus and (5) Unilateral usage of the healthy right tooth row. Its advanced primary caries, initiating on the intact enamel surface, indicates a frequent intake of highly cariogenic sugar-rich fruits, which likely exceeds the frugivory of extant chimpanzees. This finding corresponds with the associated palynological record, which infers a habitat with nearly year-round supply (9 ± 10 months/year) of high quality foods ($>$ carbohydrates; $<$ fibers). Our conclusions challenge the model of a step-wise increase in dietary quality during hominid evolution and support the uricase hypothesis, which discusses the hominid autapomorphy of a fructose-based fat accumulation for periods of starvation. This model receives further validation by the identification of soft-tissue preservation, interpreted as fossilized white adipose cells, in the articulated hominid skeleton of *Oreopithecus bamboli* from Italy.

GREGORY 2017

Michael D. Gregory et al., *Neanderthal-Derived Genetic Variation Shapes Modern Human Cranium and Brain*. *Scientific Reports* **7** (2017), 6308. DOI:10.1038/s41598-017-06587-0.

Before their disappearance from the fossil record approximately 40,000 years ago, Neanderthals, the ancient hominin lineage most closely related to modern humans, interbred with ancestors of present-day humans. The legacy of this gene flow persists through Neanderthal-derived variants that survive in modern human DNA; however, the neural implications of this inheritance are uncertain. Here, using MRI in a large cohort of healthy individuals of European-descent, we

show that the amount of Neanderthal-originating polymorphism carried in living humans is related to cranial and brain morphology. First, as a validation of our approach, we demonstrate that a greater load of Neanderthal-derived genetic variants (higher “NeanderScore”) is associated with skull shapes resembling those of known Neanderthal cranial remains, particularly in occipital and parietal bones. Next, we demonstrate convergent NeanderScore-related findings in the brain (measured by gray- and white-matter volume, sulcal depth, and gyrification index) that localize to the visual cortex and intraparietal sulcus. This work provides insights into ancestral human neurobiology and suggests that Neanderthal-derived genetic variation is neurologically functional in the contemporary population.

Michael D. Gregory, J. Shane Kippenhan, Daniel P. Eisenberg, Philip D. Kohn, Dwight Dickinson, Venkata S. Mattay, Qiang Chen, Daniel R. Weinberger, Ziad S. Saad & Karen F. Berman

GUNZ 2019

Philipp Gunz et al., *Neandertal Introgression Sheds Light on Modern Human Endocranial Globularity*. *Current Biology* **29** (2019), 120–127.

In Brief:

Gunz, Tilot et al. combine paleoanthropology, archaic genomics, neuroimaging, and gene expression to study biological foundations of the characteristic modern human endocranial shape. They find introgressed Neandertal alleles that associate with reduced endocranial globularity and affect expression of genes linked to neurogenesis and myelination.

Highlights:

- We use fossil skull data to derive an index of endocranial shape in human MRI scans
- In 4,468 Europeans, we screen introgressed Neandertal SNPs for association with the index
- Lead SNPs consistently associate with reduced globularity in five separate subsamples
- These SNPs affect neural expression of two genes linked to neurogenesis and myelination

One of the features that distinguishes modern humans from our extinct relatives and ancestors is a globular shape of the braincase [1–4]. As the endocranium closely mirrors the outer shape of the brain, these differences might reflect altered neural architecture [4, 5]. However, in the absence of fossil brain tissue, the underlying neuroanatomical changes as well as their genetic bases remain elusive. To better understand the biological foundations of modern human endocranial shape, we turn to our closest extinct relatives: the Neandertals. Interbreeding between modern humans and Neandertals has resulted in introgressed fragments of Neandertal DNA in the genomes of present-day non-Africans [6, 7]. Based on shape analyses of fossil skull endocasts, we derive a measure of endocranial globularity from structural MRI scans of thousands of modern humans and study the effects of introgressed fragments of Neandertal DNA on this phenotype. We find that Neandertal alleles on chromosomes 1 and 18 are associated with reduced endocranial globularity. These alleles influence expression of two nearby genes, *UBR4* and *PHLPP1*, which are involved in neurogenesis and myelination, respectively. Our findings show how integration of fossil skull data with archaic genomics and neuroimaging can suggest developmental mechanisms that may contribute to the unique modern human endocranial shape.

Philipp Gunz, Amanda K. Tilot, Katharina Wittfeld, Alexander Teumer, Chin Yang Shapland, Theo G. M. van Erp, Michael Dannemann, Benjamin Vernot, Simon Neubauer, Tulio Guadalupe, Guillén Fernández, Han G. Brunner, Wolfgang Enard, James Fallon, Norbert Hosten, Uwe Völker, Antonio Profico, Fabio Di

Vincenzo, Giorgio Manzi, Janet Kelso, Beate St. Pourcain, Jean-Jacques Hublin, Barbara Franke, Svante Pääbo, Fabio Macchiardi, Hans J. Grabe & Simon E. Fisher

JACOBS 2019

Guy S. Jacobs, Georgi Hudjashov & Murray P. Cox et al., *Multiple Deeply Divergent Denisovan Ancestries in Papuans*. *Cell* **177** (2019), 1010–1021.

In Brief:

Genome sequences from Island Southeast Asia suggest two independent Denisovan lineages, distinct from the Altai Denisovan, that have contributed to modern Papuan genomes, with one group potentially present east of the Wallace Line and thus capable of crossing geographical barriers.

Highlights:

- A new dataset of 161 genomes covering the understudied Indonesia-New Guinea region
- Introgressing Denisovans comprise at least three genetically divergent groups
- Papuans carry haplotypes from two Denisovan groups, with one unique to Oceania
- Some Denisovan introgression was recent and likely occurred in New Guinea or Wallacea

Genome sequences are known for two archaic hominins—Neanderthals and Denisovans—which interbred with anatomically modern humans as they dispersed out of Africa. We identified high-confidence archaic haplotypes in 161 new genomes spanning 14 island groups in Island Southeast Asia and New Guinea and found large stretches of DNA that are inconsistent with a single introgressing Denisovan origin. Instead, modern Papuans carry hundreds of gene variants from two deeply divergent Denisovan lineages that separated over 350 thousand years ago. Spatial and temporal structure among these lineages suggest that introgression from one of these Denisovan groups predominantly took place east of the Wallace line and continued until near the end of the Pleistocene. A third Denisovan lineage occurs in modern East Asians. This regional mosaic suggests considerable complexity in archaic contact, with modern humans interbreeding with multiple Denisovan groups that were geographically isolated from each other over deep evolutionary time.

Guy S. Jacobs, Georgi Hudjashov, Lauri Saag, Pradiptajati Kusuma, Chelzie C. Darusallam, Daniel J. Lawson, Mayukh Mondal, Luca Pagani, François-Xavier Ricaut, Mark Stoneking, Mait Metspalu, Herawati Sudoyo, J. Stephen Lansing & Murray P. Cox

KRATZER 2014

James T. Kratzer et al., *Evolutionary history and metabolic insights of ancient mammalian uricases*. *PNAS* **111** (2014), 3763–3768.

[pnas111-03763-Supplement.pdf](#)

Uricase is an enzyme involved in purine catabolism and is found in all three domains of life. Curiously, uricase is not functional in some organisms despite its role in converting highly insoluble uric acid into 5-hydroxyisourate. Of particular interest is the observation that apes, including humans, cannot oxidize uric acid, and it appears that multiple, independent evolutionary events led to the silencing or pseudogenization of the uricase gene in ancestral apes. Various arguments have been made to suggest why natural selection would allow the accumulation of uric acid despite the physiological consequences of crystallized monosodium urate acutely causing liver/kidney damage or chronically causing gout. We have applied evolutionary models to understand the history of primate uricases by resurrecting

ancestral mammalian intermediates before the pseudogenization events of this gene family. Resurrected proteins reveal that ancestral uricases have steadily decreased in activity since the last common ancestor of mammals gave rise to descendent primate lineages. We were also able to determine the 3D distribution of amino acid replacements as they accumulated during evolutionary history by crystallizing a mammalian uricase protein. Further, ancient and modern uricases were stably transfected into HepG2 liver cells to test one hypothesis that uricase pseudogenization allowed ancient frugivorous apes to rapidly convert fructose into fat. Finally, pharmacokinetics of an ancient uricase injected in rodents suggest that our integrated approach provides the foundation for an evolutionarily-engineered enzyme capable of treating gout and preventing tumor lysis syndrome in human patients.

Keywords: hyperuricemia | pseudogene | evolution

James T. Kratzer, Miguel A. Lanaspa, Michael N. Murphy, Christina Cicerchi, Christina L. Graves, Peter A. Tipton, Eric A. Ortlund, Richard J. Johnson & Eric A. Gaucher

Significance: Human susceptibility to gout is driven by the fact that we have a pseudogene for uricase that prevents a functional enzyme from being produced. Our inability to convert highly insoluble uric acid into a more soluble molecule makes us vulnerable to disease and other health complications. We have exploited ancestral sequence reconstruction to better understand how and why apes lost this functional enzyme. Our ancient proteins support one hypothesis that the progressive loss of uricase activity allowed our ancestors to readily accumulate fat via the metabolism of fructose from fruits. This adaptation may have provided our ancestors with an advantage when the energy-rich rainforests of Europe and Asia were displaced by temperate forests by the end of the Oligocene.

LORDKIPANIDZE 2005

David Lordkipanidze et al., *The earliest toothless.* [nature](#) **434** (2005), 717–718.

The D3444/D3900 individual apparently survived for a lengthy period without consuming foods that required heavy chewing, possibly by eating soft plant and animal foods and/or by virtue of help from other individuals, which must have exceeded that capable of being offered by non-human primates. The edentulous Dmanisi specimen raises interesting questions regarding social structure, life history and subsistence strategies of early Homo that warrant further investigation.

David Lordkipanidze, Abesalom Vekua, Reid Ferring, G. Philip Rightmire, Jordi Agustí, Gocha Kiladze, Alexander Mouskhelishvili, Medea Nioradze, Marcia S. Ponce de León, Martha Tappen & Christoph P. E. Zollikofer

RACIMO 2016

Fernando Racimo et al., *Archaic Adaptive Introgression in TBX15/WARS2.* [Molecular Biology and Evolution](#) **34** (2016), 509–524.

MolBiolEvol34-0509-Supplement.zip

A recent study conducted the first genome-wide scan for selection in Inuit from Greenland using single nucleotide polymorphism chip data. Here, we report that selection in the region with the second most extreme signal of positive selection in Greenlandic Inuit favored a deeply divergent haplotype that is closely related to the sequence in the Denisovan genome, and was likely introgressed from an archaic population. The region contains two genes, WARS2 and TBX15, and has previously been associated with adipose tissue differentiation and body-fat distribution in humans. We show that the adaptively introgressed allele has been under selection in a much larger geographic region than just Greenland. Furthermore, it is

associated with changes in expression of WARS2 and TBX15 in multiple tissues including the adrenal gland and subcutaneous adipose tissue, and with regional DNA methylation changes in TBX15.

Keywords: adaptive introgression | Denisova | positive selection | Native Americans | methylation | admixture.

Fernando Racimo, David Gokhman, Matteo Fumagalli, Amy Ko, Torben Hansen, Ida Moltke, Anders Albrechtsen, Liran Carmel, Emilia Huerta-Sánchez & Rasmus Nielsen

WANPO 1995

Huang Wanpo, Russell Ciochon, Gu Yumin, Roy Larick, Fang Qiren, Henry Schwarcz, Charles Yonge, John de Vos & William Rink, *Early Homo and associated artefacts from Asia*. *nature* **378** (1995), 275–278.

The site of Longgupo Cave was discovered in 1984 and excavated in 1985–1988 by the Institute of Vertebrate Paleontology and Paleoanthropology (Beijing) and the Chongqing National Museum (Sichuan Province). Important finds include very archaic hominid dental fragments, Gigantopithecus teeth and primitive stone tools. Palaeomagnetic analysis and the presence of Ailuropoda microta (pygmy giant panda) suggested that the hominid-bearing levels dated to the earliest Pleistocene. In 1992, joint Chinese-American-Canadian geochronological research corroborated the age using electron spin resonance (ESR) analysis. We report here that the hominid dentition and stone tools from Longgupo Cave are comparable in age and morphology with early representatives of the genus Homo (*H. habilis* and *H. ergaster*) and the Oldowan technology in East Africa. The Longgupo dentition is demonstrably more primitive than that seen in Asian *Homo erectus*. Longgupo's diverse and well preserved Plio-Pleistocene fauna of 116 species provide a sensitive contextual base for interpreting the early arrival of the genus Homo in Asia.

WEI 2014

Guangbiao Wei, Wanbo Huang, Shaokun Chen, Cunding He, Libo Pang & Yan Wu, *Paleolithic culture of Longgupo and its creators*. *Quaternary International* **354** (2014), 154–161.

Longgupo Site at Wushan (30°51'46.8"N, 109°39'55.8"E), Chongqing Municipality, China was discovered in 1984. The unearthed materials include Hominidae gen. et sp. indet., stone artifacts and a large quantity of vertebrate fossils. More than 1000 stone artifacts with evident human agency such as bipolar hammer, cores, flakes, choppers, points, scrapers, proto-cleavers, drilling tools, proto-picks and proto-hand-axes have been collected from Levels 2–15 successively. Bone accumulations of large amount of limbs of herbivores, indicating human agency, were unearthed from Levels 3–4 and 7–8. All of these early Paleolithic remains are termed "Longgupo culture". The culture signifies that its creators have evolved from tool-using stage to tool-making one in their life style. Who the creators of Longgupo culture were is still a mystery. Three types of highly-evolved primate fossils have been unearthed from Longgupo Site. They are represented by a mandibular fragment with p4-m1, an upper incisor, and 14 isolated teeth of *Gigantopithecus blacki* respectively. All these three types could be the possible creators of Longgupo culture. On the other hand, we cannot exclude a possibility that an ancient human still unknown but similar to *Homo habilis* could be revealed with the forthcoming excavations.

Keywords: Longgupo culture | Stone artifacts | Limb bone accumulations | Human agency

Bibel

BERZBACH 2019

Ulrich Berzbach, “*der nicht ging im Rat von Frevlern*” (*Ps 1,1*), *Lebenslanges Lernen als Weg-Weisung*. [Online 2019, Oct. 31, 151–163](#). .

Als Zurückweisung eines totalitären Machtanspruches erscheint Psalm 1 gut geeignet. Vielleicht war er auch einer jener Texte, die Karl Barth an den Beginn seiner Vorlesungen zu stellen pflegte und die ihm den Rückhalt gegeben haben, sich der rektoralen Anweisung zu widersetzen — und vielleicht war die Erzählung von den Hebammen auch dabei.

HOFFMEIER 1996

James K. Hoffmeier, *Israel in Egypt, The evidence for the authenticity of the Exodus tradition*. (New York 1999).

PETROVICH 2013

Douglas Petrovich, *Amenhotep II and the Historicity of the Exodus-Pharaoh*. [unknown \(2013\), preprint, 1–30](#). .

The goal of the present work was to synchronize Israelite and Egyptian history and to examine the life of the Egyptian monarch who corresponds chronologically to the biography of the exodus-pharaoh, in order to determine whether this historical figure, who turned out to be Amenhotep II, meets these requirements. [...]

These answers prove not only that Amenhotep II is the only legitimate candidate for the exodus-pharaoh, but that the biblical chronology of that era functions as a canon against which Egyptian history may be synchronized precisely with Israelite history.

SCHWALLY 1892

Friedrich Schwally, *Das Leben nach dem Tode nach den Vorstellungen des alten Israel und des Judentums einschliesslich des Volksglaubens im Zeitalter Christi – eine biblisch-theologische Untersuchung*. ([Gießen 1892](#)). Nachdruck von Leopold Classic Library.

Datierung

DEVER 1992

William G. Dever, *The Chronology of Syria-Palestine in the Second Millennium B.C.E. A Review of Current Issues*. [Bulletin of the American Schools of Oriental Research 288 \(1992\), 1–25](#).

The chronology of the Middle Bronze, Late Bronze, and early Iron Ages in Syria-Palestine is in a state of flux, as a result of recently discovered archaeological and textual data. This article reconsiders a number of fundamental issues, both in relative and absolute chronologies, for the second millennium B.C.E. The emphasis is on critical analysis of data, comparative Levantine context, and current scholarship, rather than on definitive solutions of the problems.

WARD 1992

William A. Ward, *The Present Status of Egyptian Chronology*. [Bulletin of the American Schools of Oriental Research 288 \(1992\), 53–66](#).

The current debate on Egyptian chronology is characterized by divergent opinions on the value of the Manethonian tradition, the lengths of reigns of individual Egyptian kings, the existence of coregencies, and the astronomical evidence. In each of these categories, there is little consensus and a wide range of possible solutions; a precise Egyptian chronology is therefore not possible. The present survey of this evidence and the theories derived therefrom emphasizes that modern scholarship wrongly assumes a precision the Egyptians could not achieve, that it is incorrect to speak of astronomical observations made for other than purely local purposes, and that feast days, including the New Year, began on different days at different latitudes along the Nile Valley.

WEINSTEIN 1992

James M. Weinstein, *The Chronology of Palestine in the Early Second Millennium B.C.E.* [Bulletin of the American Schools of Oriental Research](#) **288** (1992), 27–46.

Four major chronological schemes—the ultra-high, high, middle, and low—exist for the early second millennium B.C.E. in Palestine. Those schemes differ primarily in their dating of the MB IIA and transitional MB IIA/B periods. The evidence adduced for the chronology of those periods comes from the excavations at Tell el-Dab’a in Egypt’s eastern Delta, and Egyptian objects (especially scarabs) found at various sites in the Levant.

An analysis of the archaeological and historical data indicates that the MB IIA period began in the early 19th century B.C.E., while the transition from MB IIA to MB IIB probably occurred during the latter years of the 18th century B.C.E. The middle and low chronologies are both possible based on the current evidence for the MB IIA/B transition.

Jungpaläolithikum

HAWS 2020

Jonathan A. Haws, Michael M. Benedetti & Sahra Talamo et al., *The early Aurignacian dispersal of modern humans into westernmost Eurasia.* [PNAS](#) **117** (2020), 25414–25422.

[pnas117-25414-Supplement.pdf](#)

Documenting the first appearance of modern humans in a given region is key to understanding the dispersal process and the replacement or assimilation of indigenous human populations such as the Neanderthals. The Iberian Peninsula was the last refuge of Neanderthal populations as modern humans advanced across Eurasia. Here we present evidence of an early Aurignacian occupation at Lapa do Picareiro in central Portugal. Diagnostic artifacts were found in a sealed stratigraphic layer dated 41.1 to 38.1 ka cal BP, documenting a modern human presence on the western margin of Iberia \approx 5,000 years earlier than previously known. The data indicate a rapid modern human dispersal across southern Europe, reaching the westernmost edge where Neanderthals were thought to persist. The results support the notion of a mosaic process of modern human dispersal and replacement of indigenous Neanderthal populations.

Keywords: Aurignacian | modern human | dispersal | Iberia | Paleolithic

Jonathan A. Haws, Michael M. Benedetti, Sahra Talamo, Nuno Bicho, Joo Cascalheira, M. Grace Ellis, Milena M. Carvalho, Lukas Friedl, Telmo Pereira & Brandon K. Zinsious

Significance: We report the remarkable discovery of an early Aurignacian occupation, \approx 5,000 years older than any Upper Paleolithic site in westernmost Eurasia.

The archaeological and radiocarbon data provide definitive evidence that modern humans were in western Iberia at a time when, if present at all, Neanderthal populations would have been extremely sparse. This discovery has important ramifications for our understanding of the process of modern human dispersal and replacement of Neanderthal populations. The results support a very rapid, unimpeded dispersal of modern humans across western Eurasia and support the notion that climate and environmental change played a significant role in this process.

Klima

KAYA 2018

Ferhat Kaya, Faysal Bibi, Indrė Žliobaitė, Jussi T. Eronen, Tang Hui & Mikael Fortelius, *The rise and fall of the Old World savannah fauna and the origins of the African savannah biome*. [Nature Ecology & Evolution \(2018\), preprint, 1–6. DOI:10.1038/s41559-017-0414-1.](#)

Despite much interest in the ecology and origins of the extensive grassland ecosystems of the modern world, the biogeographic relationships of savannah palaeobiomes of Africa, India and mainland Eurasia have remained unclear. Here we assemble the most recent data from the Neogene mammal fossil record in order to map the biogeographic development of Old World mammalian faunas in relation to palaeoenvironmental conditions. Using genus-level faunal similarity and mean ordinated hypsodonty in combination with palaeoclimate modelling, we show that savannah faunas developed as a spatially and temporally connected entity that we term the Old World savannah palaeobiome. The Old World savannah palaeobiome flourished under the influence of middle and late Miocene global cooling and aridification, which resulted in the spread of open habitats across vast continental areas. This extensive biome fragmented into Eurasian and African branches due to increased aridification in North Africa and Arabia during the late Miocene. Its Eurasian branches had mostly disappeared by the end of the Miocene, but the African branch survived and eventually contributed to the development of Plio–Pleistocene African savannah faunas, including their early hominins. The modern African savannah fauna is thus a continuation of the extensive Old World savannah palaeobiome.

LOUYS 2020

Julien Louys & Patrick Roberts, *Environmental drivers of megafauna and hominin extinction in Southeast Asia*. [nature 586 \(2020\), 402–406. n586-0402-Supplement.xlsx](#)

Southeast Asia has emerged as an important region for understanding hominin and mammalian migrations and extinctions. High-profile discoveries have shown that Southeast Asia has been home to at least five members of the genus *Homo*1–3. Considerable turnover in Pleistocene megafauna has previously been linked with these hominins or with climate change4, although the region is often left out of discussions of megafauna extinctions. In the traditional hominin evolutionary core of Africa, attempts to establish the environmental context of hominin evolution and its association with faunal changes have long been informed by stable isotope methodologies5,6. However, such studies have largely been neglected in Southeast Asia. Here we present a large-scale dataset of stable isotope data for Southeast Asian mammals that spans the Quaternary period. Our results demonstrate that the forests of the Early Pleistocene had given way to savannahs by the Middle Pleistocene, which led to the spread of grazers and extinction of browsers—although geochronological limitations mean that not all samples can be resolved

to glacial or interglacial periods. Savannahs retreated by the Late Pleistocene and had completely disappeared by the Holocene epoch, when they were replaced by highly stratified closed-canopy rainforest. This resulted in the ascendancy of rainforest-adapted species as well as *Homo sapiens*—which has a unique adaptive plasticity among hominins—at the expense of savannah and woodland specialists, including *Homo erectus*. At present, megafauna are restricted to rainforests and are severely threatened by anthropogenic deforestation.

LUDESCHER 2020

Josef Ludescher, Armin Bunde, Ulf Büntgen & Hans Joachim Schellnhuber, *Setting the treering record straight*. [Climate Dynamics \(2020\), preprint, 1–8](#). DOI:10.1007/s00382-020-05433-w.

Tree-ring chronologies are the main source for annually resolved and absolutely dated temperature reconstructions of the last millennia and thus for studying the intriguing problem of climate impacts. Here we focus on central Europe and compare the tree-ring based temperature reconstruction with reconstructions from harvest dates, long meteorological measurements, and historical model data. We find that all data are long-term persistent, but in the tree-ring based reconstruction the strength of the persistence quantified by the Hurst exponent is remarkably larger ($h = 1.02$) than in the other data ($h = 0.52-0.69$), indicating an unrealistic exaggeration of the historical temperature variations. We show how to correct the tree-ring based reconstruction by a mathematical transformation that adjusts the persistence and leads to reduced amplitudes of the warm and cold periods. The new transformed record agrees well with both the observational data and the harvest dates-based reconstructions and allows more realistic studies of climate impacts. It confirms that the present warming is unprecedented.

Keywords: Tree-ring | Temperature reconstructions | Harvest dates | Long-term persistence | Hurst exponent

Metallzeiten

RAINEY 1973

Anson F. Rainey, *Amenhotep II's Campaign to Takhsi*. [Journal of the American Research Center in Egypt 10 \(1973\), 71–75](#).

Furthermore, the partly defaced geographical name in the Memphis stele (Urk. IV, 1301.10) is certainly not t3 Nhsy, “the Nubian Land,” as Helck and Edel have restored it, but Tahsi. The “first campaign” of the Amada stele was directed against the seven princes who were in [...] w n Ta-h-sit “the district of Takhsi” (Urk. IV, 1297.3-4).

Methoden

RAHMSTORF 2017

Lorenz Rahmstorf, *Anglo-Saxons and Sea Peoples, Comparing Similar Approaches for Tracking Ancient Human Migration*. In: PETER M. FISCHER & TERESA BÜRGE (Hrsg.), “Sea Peoples” Up-To-Date – Transformations in the Eastern Mediterranean in the 13th–11th Centuries BCE, *Proceedings of the ESF-Workshop held at the Austrian Academy of Sciences, Vienna, 3–4 November 2014*. Contributions to the Chronology of the Eastern Mediterranean 35 ([Wien 2017](#)), 163–173.

Research on the migrations of Anglo-Saxons and Sea Peoples faces similar general problems in regard to tracking actual migration. Specific archaeological aspects are often comparable in both cases. The Anglo-Saxon migration occurred during the 5th and 6th centuries CE (Early Anglo-Saxon period) from the Continent to Britain, while the migration of the Sea Peoples took place in the early 12th century BCE at the end of the Bronze Age from rather unclear places in the Eastern Mediterranean or even Italy and Southern Europe to the Levantine coast of the Mediterranean. This paper will discuss and compare some of the approaches that have been applied in both archaeological disciplines. These comprise the discussion of the fairly obscure written documentation on the (potential) homeland of the migrants, the recent contribution of methods from the natural sciences to trace migrations, as well as specific archaeological evidence from habitation, burials and specific artefacts. I will specifically compare the archaeological evidence from Early Anglo-Saxon England and the 12th century BCE Southern Levant (Philistia). It is hoped that this will contribute to a more comparative approach and a methodological dissemination of the study of ancient migrations.

SILBERMAN 1998

Neil Asher Silberman, *Whose game is it anyway? The political and social transformations of American Biblical Archaeology*. In: LYNN MESKELL (Hrsg.), *Archaeology Under Fire, Nationalism, politics and heritage in the Eastern Mediterranean and Middle East*. (London 1998), 175–188.

Professor Dever and the others fatally misidentified the ‘game’ that they invented by confusing a process with a particular nationality. Over the decades, the unifying ideal of ASOR’s region-wide scope has withstood the centrifugal force of the rising nationalisms and ethnic suspicions. It has even withstood the seductive appeal of the universalising scientism of New Archaeology. There is no question that an increasing number of ASOR excavation projects are carried out in cooperation (sometimes even as junior partners) with Israeli, Jordanian and Cypriot sponsors. There is no question that the employment prospects of American scholars are affected by the same brutal budgetary cutbacks that have affected all the humanities. But the present transformations of ASOR do not constitute omens of its imminent death.

Ostasien

ZHU 2008

R. X. Zhu, R. Potts, Y. X. Pan, H. T. Yao, L. Q. Lü, X. Zhao, X. Gao, L. W. Chen, F. Gao & C. L. Deng, *Early evidence of the genus Homo in East Asia*. *Journal of Human Evolution* **55** (2008), 1075–1085.

The timing and route of the earliest dispersal from Africa to Eastern Asia are contentious topics in the study of early human evolution because Asian hominin fossil sites with precise age constraints are very limited. Here we report new high-resolution magnetostratigraphic results that place stringent age controls on excavated hominin incisors and stone tools from the Yuanmou Basin, southwest China. The hominin-bearing layer resides in a reverse polarity magnetozone just above the upper boundary of the Olduvai subchron, yielding an estimated age of 1.7 Ma. The finding represents the age of the earliest documented presence of Homo, with affinities to Homo erectus, in mainland East Asia. This age estimate is roughly the same as for H. erectus in island Southeast Asia and immediately prior to the

oldest archaeological evidence in northeast Asia. Mammalian fauna and pollen obtained directly from the hominin site indicate that the Yuanmou hominins lived in a varied habitat of open vegetation with patches of bushland and forest on an alluvial fan close to a lake or swamp. The age and location are consistent with a rapid southern migration route of initial hominin populations into Eastern Asia.

Keywords: Magnetostratigraphy | Yuanmou Basin | Early hominin migration | Geochronology | Paleoenvironment

Politik

STENDERA 2020

Pia Stendera, *Jom Kippur nach dem Attentat in Halle: "Es wird ein nächstes Mal geben"*. [taz.de 2020, Sep. 28](#).

Ich finde es wichtig, auch den Polizeiansatz in Halle zu kritisieren, ohne bestimmte Polizistinnen zu beschuldigen. Ich hoffe, dass es dann beim nächsten Anschlag auf eine Synagoge oder Moschee oder ähnlichem besser laufen wird und die nächsten Überlebenden nicht auch noch zusätzlich durch den Polizeieinsatz traumatisiert werden. Und ja, ich bin der Meinung, dass es ein nächstes Mal geben wird, leider.

STENDERA 2020

Pia Stendera, *Ein Jahr nach dem Attentat von Halle, Menschen stehen zusammen*. [taz.de 2020, Oct. 11](#).

Im letzten Jahr hat Ismet Tekin viel gelernt. Zum Beispiel weiß er sich kämpferisch und doch versöhnlich zu geben. Inzwischen sagt er öffentlich Sätze wie: "Es gibt viel zu tun. Wenn von oben angefangen wird, geht es schneller. Von unten durch Solidarität klappt es auch, aber es dauert länger."

"Nach den Worten der Politiker dachte ich: Es wird schwer, aber durch die Unterstützung von denen, die Ihr Wort gegeben haben, werden wir es hinbekommen. Natürlich kamen die Politiker auch zur Show. Wenn sie trotzdem geholfen hätten, wäre mir das egal", sagt Ismet Tekin heute. Doch es folgten weder Hilfe noch weiterer Dialog. Auch die gesammelten Spenden kamen nie an.

Die Tekins sind nicht die Einzigen, die von staatlicher Seite allein gelassen werden. "Es geht allen Betroffenen so", sagt Ismet Tekin. Adiraxmaan Aftax Ibrahim, der Mann, der in Halle von dem Täter angefahren wurde, findet kaum Erwähnung. Die Frau, die in Wiedersdorf auf der Flucht des Täters angeschossen wurde, sagt heute, die Papierarbeit und die Auseinandersetzungen mit der Krankenkasse seien schlimmer als die Tat selbst gewesen. Zu den zentralen Gedenkveranstaltungen wurden sie und ihr Mann anfangs nicht einmal eingeladen.

Religion

LENCASTRE 2020

Marina Prieto Afonso Lencastre, *Body techniques, religious minds and the social brain, From structural anthropology to evolutionary psychology*. [unknown \(2020\), preprint, 1–14](#).

Traditional religions often dispose of specific body techniques to contact absent realities through trance and hallucinatory activities that are communicated by cultural narration. Complex myths and magic allow for symbolic and practical ways to organize bodily based emotional experiences and social action, stemming from internal urges, affects and insights. Luc de Heusch's structural anthropology

identifies four main religious ideologies – possession, shamanism, mediunism and prophetism – that share specific relationships to these bodily, mental and social experiences. They can be commented upon as the products of the analogic, affective and imaginative social brain and human theory of mind that shaped important aspects of cultural ideation and practices impacting on individual, social and ecological contexts of the evolution of cultural mentalities.

Keywords: body techniques | religious ideologies | evolution | social brain | human theory of mind.