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References

Aktuell

BARBI 2018

Elisabetta Barbi, Francesco Lagona, Marco Marsili, James W. Vaupel & Kenneth W. Wachter, *The plateau of human mortality*, *Demography of longevity pioneers*. science **360** (2018), 1459–1461.

s360-1459-Supplement.pdf

Theories about biological limits to life span and evolutionary shaping of human longevity depend on facts about mortality at extreme ages, but these facts have remained a matter of debate. Do hazard curves typically level out into high plateaus eventually, as seen in other species, or do exponential increases persist? In this study, we estimated hazard rates from data on all inhabitants of Italy aged 105 and older between 2009 and 2015 (born 1896–1910), a total of 3836 documented cases. We observed level hazard curves, which were essentially constant beyond age 105. Our estimates are free from artifacts of aggregation that limited earlier studies and provide the best evidence to date for the existence of extreme-age mortality plateaus in humans.

EINAV 2018

Liran Einav, Amy Finkelstein, Sendhil Mullainathan & Ziad Obermeyer, *Predictive modeling of U.S. health care spending in late life.* science **360** (2018), 1462–1465.

s360-1462-Supplement.pdf

That one-quarter of Medicare spending in the United States occurs in the last year of life is commonly interpreted as waste. But this interpretation presumes knowledge of who will die and when. Here we analyze how spending is distributed by predicted mortality, based on a machine-learning model of annual mortality risk built using Medicare claims. Death is highly unpredictable. Less than 5 % of spending is accounted for by individuals with predicted mortality above 50 %. The simple fact that we spend more on the sick—both on those who recover and those who die—accounts for 30 to 50 % of the concentration of spending on the dead. Our results suggest that spending on the ex post dead does not necessarily mean that we spend on the ex ante “hopeless.”

GARCIN 2018

Yannick Garcin et al., *No evidence for climate variability during the late Holocene rainforest crisis in Western Central Africa*, *Reply to Giresse et al.* PNAS **115** (2018), E6674–E6675.

Yannick Garcin, Pierre Deschamps, Guillemette Ménot, Geoffroy de Saulieu, Enno Schefuß, David Sebag, Lydie M. Dupont, Richard Oslisly, Brian Brademann, Kevin G. Mbusnum, Jean-Michel Onana, Andrew A. Ako, Laura S. Epp, Rik Tjallingii, Manfred R. Strecker, Achim Brauer & Dirk Sachse

Evergreen and subtropical deciduous trees produce leaf waxes over much longer timescales—their dD (dDwax) values have been shown to capture environmental variability on even seasonal timescales.

Giresse 2018

P. Giresse, J. Maley, C. Doumenge, N. Philippon, G. Mahé, A. Chepstow-Lusty, J. Aleman, M. Lokonda & H. Elenga, *Paleoclimatic changes are the most probable causes of the rainforest crises 2,600 y ago in Central Africa*. PNAS **115** (2018), E6672–E6673.

No archaeological remains were found, notably pottery shards and charcoal in the topsoil, providing evidence against anthropic settlements. On the other hand, it can be stressed that, during the 20th century, the population largely increased in south Cameroon to the north of the Yaound' – region without preventing a marked expansion of tropical rainforest (ref. 8, their figure 5).

Jones 2018

Laura K. Jones, Bonnie Mowinski Jennings, Melinda K. Higgins & Frans B. M. de Waal, *Ethological observations of social behavior in the operating room*. PNAS **115** (2018), 7575–7580.

pnas115-07575-Supplement.pdf

Operating rooms (ORs) are inhabited by hierarchical, mixedgender clinical teams that are often prone to conflict. In evolutionary terms, one expects more within- than between-gender rivalries, especially since the OR is a place where all sorts of social interactions occur, not merely technical communications. To document the full range of behavior, the present study used ethological observation techniques, recording live all social behavior by the team. Using an ethogram, 6,348 spontaneous social interactions and nontechnical communications were timestamped during 200 surgical procedures. Cooperation sequences (59.0 %) were more frequent than conflict sequences (2.8 %), which ranged from constructive differences of opinion to discord and distraction that could jeopardize patient safety. Behavior varied by clinical role and with the gender composition in the OR. Conflict was initiated mostly down the hierarchy between individuals several ranks apart. Cooperation tended to increase with a rising proportion of females in the OR, but themost pronounced effect concerned the interaction between both genders. If the attending surgeon's gender differed from that of the majority of other personnel in the OR, cooperation was significantly more common.

Keywords: medical | human behavior | gender | operating room | conflict

Significance: Hierarchy and gender composition affect the balance of cooperation and conflict on surgical teams. In this investigation, behavior was quantified with methods traditionally used to study nonhuman primate groups. Observers used an ethogram to timestamp 6,348 spontaneous social interactions from 200 surgical procedures. Conflict and cooperation in the operating room showed a significant interaction effect with regard to professional roles (e.g., conflict was initiated mostly down the hierarchy between individuals several ranks apart) and by gender interaction (e.g., cooperation was better if the attending surgeon's gender differed from that of the team majority). These findings may inform ongoing and future interventions designed to improve team performance and patient safety.

Kikis 2018

Elise A. Kikis, *The cost of a career*. science **360** (2018), 1478.

“Are you really going to cross the picket line?” my mother asked. She had called after reading that the clerical union workers were on strike, and she could hear in the background the tell-tale honking horns and ringing bells of the picket line. “Yes,” I responded. Despite her impassioned pleas, I was not going to boycott my first day of graduate school. A few weeks later, I said no when asked to join the graduate student union. Why would I, a paid student, need union representation?

If only I had known then what I know now, 16 years later, this is what I would have told myself.

SMITH 2018

Michael L. Smith, *Dinner without reservations*. science **360** (2018), 1370.

When my Ph.D. adviser recommended that I organize the dinner for a visiting speaker, I enthusiastically agreed. I was thinking of asking this scientist to be my postdoc adviser, and hosting would be a good way to get to know him. But restaurant dinners—the norm for visiting speakers—had always felt stuffy and overly formal to me. I couldn't hear beyond my immediate neighbors, I couldn't mingle, and I couldn't linger for postdinner discussion. So I proposed an alternative: hosting dinner at my home. I reasoned that I could do the cooking and accommodate a larger group. Best of all, we would not have to worry about restaurant constraints. I had a month to prepare. Easy peasy.

TREAL TAYLOR 2018

William Timothy Treal Taylor et al., *Origins of equine dentistry*. PNAS **115** (2018), E6707–E6715.

pnas115-E06707-Supplement.pdf

William Timothy Treal Taylor, Jamsranjav Bayarsaikhan, Tumurbaatar Tuvshinjargal, Scott Bender, Monica Tromp, Julia Clark, K. Bryce Lowry, Jean-Luc Houle, Dimitri Staszewski, Jocelyn Whitworth, William Fitzhugh & Nicole Boivin

From the American West to the steppes of Eurasia, the domestic horse transformed human societies, providing rapid transport, communication, and military power, and serving as an important subsistence animal. Because of the importance of oral equipment for horse riding, dentistry is an essential component of modern horse care. In the open grasslands of northeast Asia, horses remain the primary form of transport for many herders. Although freerange grazing on gritty forage mitigates many equine dental issues, contemporary Mongolian horsemen nonetheless practice some forms of dentistry, including the removal of problematic deciduous teeth and the vestigial first premolar ("wolf tooth"). Here, we present archaezoological data from equine skeletal remains spanning the past 3,200 y, indicating that nomadic dental practices have great antiquity. Anthropogenic modifications to malerupted deciduous central incisors in young horses from the Late Bronze Age demonstrate their attempted removal, coinciding with the local innovation or adoption of horseback riding and the florescence of Mongolian pastoral society. Horse specimens from this period show no evidence of first premolar removal, which we first identify in specimens dating to ca. 750 BCE. The onset of premolar extraction parallels the archaeological appearance of jointed bronze and iron bits, suggesting that this technological shift prompted innovations in dentistry that improved horse health and horse control. These discoveries provide the earliest directly dated evidence for veterinary dentistry, and suggest that innovations in equine care by nomadic peoples ca. 1150 BCE enabled the use of horses for increasingly sophisticated mounted riding and warfare.

Keywords: horses | veterinary care | horseback riding | domestication | Mongolia

Significance: The domestication of horses and adoption of horse riding were critical processes that culminated in the emergence of mounted warriors and nomadic empires that shaped world history. The constraints of horse biology and riding equipment meant that equine veterinary care, particularly of teeth, was a core component of the success of the human–horse relationship. We report the earliest evidence of equine dentistry, from the Mongolian Steppe, at 1150 BCE. Key shifts in equine dentistry practice through time can be linked first to the emergence of horseback riding and later to the use of metal bits that enabled better control of horses. The maintenance of horse health through dentistry underwrote the key role of horses in cultures and economies around the world.

Anthropologie

de Barros Damgaard 2018

Peter de Barros Damgaard et al., *The first horse herders and the impact of early Bronze Age steppe expansions into Asia*. science **360** (2018), 1422.

s360-1422-Supplement.pdf

Peter de Barros Damgaard, Rui Martiniano, Jack Kamm, J. Víctor Moreno-Mayar, Guus Kroonen, Michaël Peyrot, Gojko Barjamovic, Simon Rasmussen, Claus Zacho, Nurbol Baimukhanov, Victor Zaibert, Victor Merz, Arjun Biddanda, Ilja Merz, Valeriy Loman, Valeriy Evdokimov, Emma Usmanova, Brian Hemphill, Andaine Seguin-Orlando, Fulya Eylem Yediay, Inam Ullah, Karl-Göran Sjögren, Katrine Højholt Iversen, Jeremy Choin, Constanza de la Fuente, Melissa Ilardo, Hannes Schroeder, Vyacheslav Moiseyev, Andrey Gromov, Andrei Polyakov, Sachihiro Omura, Süleyman Yücel Senyurt, Habib Ahmad, Catriona McKenzie, Ashot Margaryan, Abdul Hameed, Abdul Samad, Nazish Gul, Muhammad Hassan Khokhar, O. I. Goriunova, Vladimir I. Bazaliiskii, John Novembre, Andrzej W. Weber, Ludovic Orlando, Morten E. Allentoft, Rasmus Nielsen, Kristian Kristiansen, Martin Sikora, Alan K. Outram, Richard Durbin & Eske Willerslev

The Yamnaya expansions from the western steppe into Europe and Asia during the Early Bronze Age (≈3000 BCE) are believed to have brought with them Indo-European languages and possibly horse husbandry. We analyzed 74 ancient whole-genome sequences from across Inner Asia and Anatolia and show that the Botai people associated with the earliest horse husbandry derived from a hunter-gatherer population deeply diverged from the Yamnaya. Our results also suggest distinct migrations bringing West Eurasian ancestry into South Asia before and after, but not at the time of, Yamnaya culture. We find no evidence of steppe ancestry in Bronze Age Anatolia from when Indo-European languages are attested there. Thus, in contrast to Europe, Early Bronze Age Yamnaya-related migrations had limited direct genetic impact in Asia.

Conclusion: Our findings reveal that the early spread of Yamnaya Bronze Age pastoralists had limited genetic impact in Anatolia as well as Central and South Asia. As such, the Asian story of Early Bronze Age expansions differs from that of Europe. Intriguingly, we find that direct descendants of Upper Paleolithic hunter-gatherers of Central Asia, now extinct as a separate lineage, survived well into the Bronze Age. These groups likely engaged in early horse domestication as a preyroute transition from hunting to herding, as otherwise seen for reindeer. Our findings further suggest that West Eurasian ancestry entered South Asia before and after, rather than during, the initial expansion of western steppe pastoralists, with the later event consistent with a Late Bronze Age entry of IE languages into South Asia. Finally, the lack of steppe ancestry in samples from Anatolia indicates that the spread of the earliest branch of IE languages into that region was not associated with a major population migration from the steppe.

Cohen 2018

Jon Cohen, *Neanderthal brain organoids come to life*. science **360** (2018), 1284.

Human "minibrains" with gene from our extinct relative have intriguing differences.

Several of these differences mirror what Muotri has found studying neuronal development in the brains of children with autism. "I don't want families to conclude that I'm comparing autistic kids to Neanderthals, but it's an important observation," says Muotri, who has a stepson with autism. "In modern humans, these types of changes are linked to defects in brain development that are needed for socialization. If we believe that's one of our advantages over Neanderthals, it's relevant."

Galway-Witham 2018

Julia Galway-Witham & Chris Stringer, *How did Homo sapiens evolve?* science **360** (2018), 1296–1298.

Genetic and fossil evidence challenges current models of modern human evolution.

With only a few dissenters, the strictest versions of both RAO (which denies interbreeding with other lineages or species) and multiregionalism (which argues for an interbreeding network of one species over the past ≈1.8 million years) are now generally regarded as falsified. Instead, two intermediate theories best accommodate the complex interactions between hominin taxa ≈40,000 to 100,000 years ago: RAO with hybridization (RAOWH) and the assimilation model (AM).

The two theories differ in their reconstructions of the processes by which the DNA of dispersing H. sapiens populations mixed with those of other populations outside of Africa. AM emphasizes demic diffusion, in which populations of African-derived H. sapiens and Eurasian Neandertals and Denisovans would have mixed over wide areas. Genes would have flowed gradually between these regional populations, catalyzing genetic and anatomical changes and leading to the spread of modern traits. In contrast, RAOWH envisages H. sapiens genes as largely entering and traversing Eurasia within the bodies of dispersing humans of African origin. Along the way there were successful hybridization events with indigenous populations, but these were effectively absorbing fragmented populations of indigenes in a relatively rapid replacement process, where they overlapped.

Scerri 2018

Eleanor M. L. Scerri et al., *Did Our Species Evolve in Subdivided Populations across Africa, and Why Does It Matter?* Trends in Ecology & Evolution (2018), preprint, 1–13. DOI:10.1016/j.tree.2018.05.005.

Eleanor M. L. Scerri, Mark G. Thomas, Andrea Manica, Philipp Gunz, Jay T. Stock, Chris Stringer, Matt Grove, Huw S. Groucutt, Axel Timmermann, G. Philip Rightmire, Francesco d'Errico, Christian A. Tryon, Nick A. Drake, Alison S. Brooks, Robin W. Dennell, Richard Durbin, Brenna M. Henn, Julia Lee-Thorp, Peter deMenocal, Michael D. Petraglia, Jessica C. Thompson, Aylwyn Scally & Lounès Chikhi

We challenge the view that our species, Homo sapiens, evolved within a single population and/or region of Africa. The chronology and physical diversity of Pleistocene human fossils suggest that morphologically varied populations pertaining to the H. sapiens clade lived throughout Africa. Similarly, the African archaeological record demonstrates the polycentric origin and persistence of regionally distinct Pleistocene material culture in a variety of paleoecological settings. Genetic studies also indicate that present-day population structure within Africa extends to deep times, paralleling a paleoenvironmental record of shifting and fractured habitable zones. We argue that these fields support an emerging view of a highly structured

African prehistory that should be considered in human evolutionary inferences, prompting new interpretations, questions, and interdisciplinary research directions.

Highlights:

- The view that Homo sapiens evolved from a single region/population within Africa has been given primacy in studies of human evolution.
- However, developments across multiple fields show that relevant data are no longer consistent with this view.
- We argue instead that Homo sapiens evolved within a set of interlinked groups living across Africa, whose connectivity changed through time.
- Genetic models therefore need to incorporate a more complex view of ancient migration and divergence in Africa.
- We summarize this new framework emphasizing population structure, outline how this changes our understanding of human evolution, and identify new research directions.

Bibel

JOOSTEN 2018

Jan Joosten, *A New Interpretation of Lev 18:22 (par. Lev 20:13) and its Ethical Implications*. unknown (2018), preprint, 1–8.

The blanket condemnation of male-male intercourse is a Fremdkörper in the Hebrew Bible and the Ancient Near East. In contrast, the “protection” of the union of man and wife as the paradigmatic form of human relationships is ubiquitous in the Hebrew Bible. The prohibition of adultery is reiterated many times and in many forms. On the new interpretation, Lev 18:22 participates in this protection. One could say it comes to close a legal loophole. The law is formulated in a male-centred perspective: sex with a married woman is forbidden. But what about sex with a married man? This is not covered by the prohibition of adultery. But it is covered in our verses.

The moral value of the laws in Leviticus 18 and 20 is easier to embrace on this new reading. Nevertheless, the laws still stand at some distance from modern mentalities. [. . .] Homosexual relations are relegated to the realm beyond marriage. Non-married men, it seems, are free to lie with one another in any way they choose. Perhaps David and Jonathan were lovers in their youth, and nobody cared.

This view of human sexuality falls short of contemporary demands for equal rights for same-sex relationships. One will admit, however—whether or not my interpretation of Lev 18:22 par. is the right one—that the paradigmatic value of monogamous male-female relationships dominates biblical discourse in general. From the creation stories in Genesis 1 and 2 to the prophetic parables presenting Israel as Gods wife, the monogamous heterosexual couple is the universal norm. This is true too for the incest laws in Lev 18 and 20, which revolve around the notion that the Israelite addressed in the law would have parents, a wife, and married children—even if the distinction between offspring “born at home or born abroad” and other indications show that the law was not wholly naïve about the actual vicissitudes of married couples.

KLEIMAN 2018

Assaf Kleiman & Israel Finkelstein, *The Date of Building 338 at Megiddo, Eppur Si Muove!* Israel Exploration Journal **68** (2018), 50–55.

This is a response to David Ussishkin’s rejoinder to our article on Building 338 at Megiddo. None of Ussishkin’s arguments, aimed at maintaining his affiliation of the building with Stratum VA–IVB, withstands scrutiny. Building 338 belongs to Stratum IVA, in the first half of the eighth century BCE.

Biologie

CATALA 2018

Rafael Catalá & Julio Salinas, *Tailoring crop nutrition to fight weeds.* PNAS **115** (2018), 7456–7458.

As stressed by authors in their work, a highly remarkable asset of this technology is the low probability that Phi-resistant weeds could develop since that would imply the acquisition of completely new enzymatic activity to metabolize Phi, which would require several mutations in preexisting dehydrogenases. Moreover, in contrast to Pi, Phi can be obtained from different sources, such as from the recycling of waste products from industrial processes in which sodium hypophosphite is employed to reduce metal ions in chemical plating (i.e., nickel plating for decorative purposes). Finally, it is worth mentioning that Phi does not represent any risk for human or animal health and is already being used extensively as an effective fungicide in agriculture.

MÜHLEMANN 2018

Barbara Mühlemann et al., *Ancient human parvovirus B19 in Eurasia reveals its long-term association with humans.* PNAS **115** (2018), 7557–7562.

pnas115-07557-Supplement.pdf

Barbara Mühlemann, Ashot Margaryan, Peter de Barros Damgaard, Morten E. Allentoft, Lasse Vinner, Anders J. Hansen, Andrzej Weber, Vladimir I. Bazaliiskii, Martyna Molak, Jette Arneborg, Wieslaw Bogdanowicz, Ceri Falys, Mikhail Sablin, Václav Smr¡cka, Sabine Sten, Kadicha Tashbaeva, Niels Lynnerup, Martin Sikora, Derek J. Smith, Ron A. M. Fouchier, Christian Drosten, Karl-Göran Sjögren, Kristian Kristiansen, Eske Willerslev & Terry C. Jones

Human parvovirus B19 (B19V) is a ubiquitous human pathogen associated with a number of conditions, such as fifth disease in children and arthritis and arthralgias in adults. B19V is thought to evolve exceptionally rapidly among DNA viruses, with substitution rates previously estimated to be closer to those typical of RNA viruses. On the basis of genetic sequences up to ≈70 years of age, the most recent common ancestor of all B19V has been dated to the early 1800s, and it has been suggested that genotype 1, the most common B19V genotype, only started circulating in the 1960s. Here we present 10 genomes (63.9–99.7 % genome coverage) of B19V from dental and skeletal remains of individuals who lived in Eurasia and Greenland from ≈0.5 to ≈6.9 thousand years ago (kya). In a phylogenetic analysis, five of the ancient B19V sequences fall within or basal to the modern genotype 1, and five fall basal to genotype 2, showing a long-term association of B19V with humans. The most recent common ancestor of all B19V is placed ≈12.6 kya, and we find a substitution rate that is an order of magnitude lower than inferred previously. Further, we are able to date the recombination event between genotypes 1 and 3 that formed genotype 2 to ≈5.0–6.8 kya. This study emphasizes the importance of ancient viral sequences for our understanding of virus evolution and phylogenetics.

Keywords: parvovirus B19 | ancient DNA | virus evolution | paleo virology | virology

Significance: The majority of viral genomic sequences available today are fewer than 50 years old. Parvovirus B19 (B19V) is a ubiquitous human pathogen causing fifth disease in children, as well as other conditions. By isolating B19V DNA from human remains between ≈0.5 and 6.9 thousand years old, we show that B19V has been associated with humans for thousands of years, which is significantly longer than previously thought. We also show that the virus has been evolving at a rate an order of magnitude lower than estimated previously. Access to viral sequences isolated from individuals living thousands of years ago greatly improves our understanding of the timescales of virus evolution, spatiotemporal distribution, and their substitution rates, and can uncover genetic diversity that is now extinct.

PANDEYA 2018

Devendra Pandeya et al., *Selective fertilization with phosphite allows unhindered growth of cotton plants expressing the ptxD gene while suppressing weeds.* PNAS **115** (2018), E6946–E6955.

pnas115-E06946-Supplement.pdf

Devendra Pandeya, Damar L. López-Arredondo, Madhusudhana R. Janga, LeAnne M. Campbell, Priscila Estrella-Hernández, Muthukumar V. Bagavathiannan, Luis Herrera-Estrella & Keerti S. Rathore

Weeds, which have been the bane of agriculture since the beginning of civilization, are managed manually, mechanically, and, more recently, by chemicals. However, chemical control options are rapidly shrinking due to the recent rise in the number of herbicide-resistant weeds in crop fields, with few alternatives on the horizon. Therefore, there is an urgent need for alternative weed suppression systems to sustain crop productivity while reducing our dependence on herbicides and tillage. Such a development will also allay some of the negative perceptions associated with the use of herbicide-resistance genes and heavy dependence on herbicides. Transgenic plants expressing the bacterial phosphite dehydrogenase (ptxD) gene gain an ability to convert phosphite (Phi) into orthophosphate [Pi, the metabolizable form of phosphorus (P)]. Such plants allow for a selective fertilization scheme, based on Phi as the sole source of P for the crop, while offering an effective alternative for suppressing weed growth. Here, we show that, when P is supplied in the form of Phi, ptxD-expressing cotton (Gossypium hirsutum L.) plants outcompete, in both artificial substrates and natural soils from agricultural fields, three different monocot and dicot weed species intentionally introduced in the experiments, as well as weeds naturally present in the tested soils. Importantly, the ptxD/Phi system proved highly efficacious in inhibiting the growth of glyphosate-resistant Palmer amaranth. With over 250 weed species resistant to currently available herbicides, ptxD-transgenic plants fertilized with Phi could provide an effective alternative to suppressing the growth of these weeds while providing adequate nutrition to the crop.

Keywords: weed suppression | phosphite | phosphite dehydrogenase | herbicide-resistant weeds | cotton

Significance: An increasing number of herbicide-resistant weeds are being reported in the United States, Argentina, and Brazil. This is becoming a global challenge for the production of several major crops, such as cotton, maize, and soybean. New strategies for weed control are required to sustain agricultural production while reducing our dependence on herbicides. Here, we report that selective fertilization of transgenic cotton, expressing a bacterial phosphite dehydrogenase (PTXD), with phosphite provides an effective way to suppress weed growth. Importantly, we show that the ptxD-transgenic cotton plants successfully outcompete a highly aggressive glyphosate-resistant weed. The ptxD/phosphite system represents one of the most promising technologies of recent times with potential to solve many of the agricultural and environmental problems that we encounter currently.

SCALLY 2018

Aylwyn Scally, *Newfound differences between great apes.* nature **559** (2018), 336–338.

High-quality genome sequences for some of the great apes have been assembled using state-of-the-art sequencing tools. The assemblies provide an unbiased comparison between humans and their closest evolutionary relatives.

Datierung

NALAWADE-CHAVAN 2013

Shweta Nalawade-Chavan et al., *Compound-Specific Radiocarbon Dating of Essential and Nonessential Amino Acids, Towards Determination of Dietary Reservoir Effects in Humans.* Radiocarbon **55** (2013), 709–719.

Shweta Nalawade-Chavan, James McCullagh, Robert Hedges, Clive Bonsall, Adina Boronean, Christopher Bronk Ramsey & Thomas Higham

When humans consume foods from different radiocarbon reservoirs offset in age to the atmosphere, inaccuracies in the 14C date of bone collagen can occur. Mesolithic human skeletons from the Iron Gates section of the Lower Danube Valley have yielded reservoir offsets of up to ≈500 yr. This has been demonstrated through direct dating of bulk collagen from human bones and the remains of ungulate bone projectile points that were found embedded in them (Cook et al. 2001). We present improvements to a novel HPLC method for the detection and separation of underivatized amino acids using a wateronly mobile phase free of organic or inorganic modifiers, ensuring very low carbon backgrounds. Our hypothesis is that direct 14C dating of single essential and non-essential amino acids might allow an improvement in the dating accuracy for reservoiraffected human bones. The method facilitates separation of less polar amino acids (mostly "essential"), currently not possible in the recently published protocol. We discuss methodological developments, demonstrate carbon backgrounds, and present analytical approaches to minimize their effects. We validate the precision and accuracy of the method by accelerator mass spectrometry (AMS) dating relatively modern and 14C-dead, known-age bone standards. Finally, we apply the method to the dating of single amino acids from bone samples with a proven ≈500-yr carbon reservoir effect from Mesolithic burials at the Iron Gates sites. We investigate whether differences can be found in AMS dates for essential and non-essential amino acids since, although contemporaneous, these are expected to derive from dietary sources with differing 14C reservoirs.

Grabung

MAIXNER 2018

Frank Maixner et al., *The Iceman's Last Meal Consisted of Fat, Wild Meat, and Cereals.* Current Biology (2018), preprint, 1–8. DOI:10.1016/j.cub.2018.05.067.

Frank Maixner, Dmitrij Turaev, Amaury Cazenave-Gassiot, Marek Janko, Ben Krause-Kyora, Michael R. Hoopmann, Ulrike Kusebauch, Mark Sartain, Gea Guerriero, Niall O'Sullivan, Matthew Teasdale, Giovanna Cipollini, Alice Paladin, Valeria Mattiangeli, Marco Samadelli, Umberto Tecchiati, Andreas Putzer, Mine Palazoglu, John Meissen, Sandra Lösch, Philipp Rausch, John F. Baines, Bum

Jin Kim, Hyun-Joo An, Paul Gostner, Eduard Egarter-Vigl, Peter Malfertheiner, Andreas Keller, Robert W. Stark, Markus Wenk, David Bishop, Daniel G. Bradley, Oliver Fiehn, Lars Engstrand, Robert L. Moritz, Philip Doble, Andre Franke, Almut Nebel, Klaus Oeggl, Thomas Rattei, Rudolf Grimm & Albert Zink

The history of humankind is marked by the constant adoption of new dietary habits affecting human physiology, metabolism, and even the development of nutrition-related disorders. Despite clear archaeological evidence for the shift from hunter-gatherer lifestyle to agriculture in Neolithic Europe [1], very little information exists on the daily dietary habits of our ancestors. By undertaking a complementary -omics approach combined with microscopy, we analyzed the stomach content of the Iceman, a 5,300-yearold European glacier mummy [2, 3]. He seems to have had a remarkably high proportion of fat in his diet, supplemented with fresh or dried wild meat, cereals, and traces of toxic bracken. Our multipronged approach provides unprecedented analytical depth, deciphering the nutritional habit, meal composition, and food-processing methods of this Copper Age individual.

Highlights:

- The last meal of the Iceman, a European Copper Agemummy, was reconstructed
- Our multipronged approach deciphers the meal composition and food processing
- His high-fat diet was supplemented with wild meat and cereals

In Brief: Maixner et al. report the dietary reconstruction of the Iceman's last meal using a combined multi-omics approach. The stomach content analysis of the 5,300-year-old glacier mummy shows that the Iceman's diet preceding his death was a mix of carbohydrates, proteins, and lipids, well adjusted to the energetic requirements of his high-altitude trekking.

Islam

Rassoul 1986

Die ungefähre Bedeutung des Al Qur'ān Al Karīm in deutscher Sprache, Aus dem Arabischen von Abu-r-Riḍā' Muhammad ibn Ahmad ibn Rassoul. (Köln ^{9}2013).

Koran

Klima

Chen 2018

Xianyao Chen & Ka-Kit Tung, *Global surface warming enhanced by weak Atlantic overturning circulation.* nature **559** (2018), 387–391.

Evidence from palaeoclimatology suggests that abrupt Northern Hemisphere cold events are linked to weakening of the Atlantic Meridional Overturning Circulation (AMOC)1, potentially by excess inputs of fresh water2. But these insights—often derived from model runs under preindustrial conditions—may not apply to the modern era with our rapid emissions of greenhouse gases. If they do, then a weakened AMOC, as in 1975–1998, should have led to Northern Hemisphere cooling. Here we show that, instead, the AMOC minimum was a period of rapid surface warming. More generally, in the presence of greenhouse-gas heating, the AMOC's dominant role changed from transporting surface heat northwards, warming Europe and North America, to storing heat in the deeper Atlantic, buffering surface warming for the planet as a whole. During an accelerating phase from the mid-1990s to the early 2000s, the AMOC stored about half of excess heat globally, contributing to the global-warming slowdown. By contrast, since mooring observations began3–5 in 2004, the AMOC and oceanic heat uptake have weakened. Our results, based on several independent indices, show that AMOC changes since the 1940s are best explained by multidecadal variability6, rather than an anthropogenically forced trend. Leading indicators in the subpolar North Atlantic today suggest that the current AMOC decline is ending. We expect a prolonged AMOC minimum, probably lasting about two decades. If prior patterns hold, the resulting low levels of oceanic heat uptake will manifest as a period of rapid global surface warming.

FELIS 2018

Thomas Felis, Monica Ionita, Norel Rimbu, Gerrit Lohmann & Martin Kölling, *Mild and Arid Climate in the Eastern Sahara-Arabian Desert During the Late Little Ice Age*. Geophysical Research Letters (2018), preprint, 1–15. DOI:10.1029/2018GL078617.

GeoResLet2018.07-Supplement.pdf

Key Points:

- Coral Sr/Ca and oxygen isotope records of the northern Red Sea provide annual reconstructions of temperature and aridity back to 1750.
- The eastern Sahara-Arabian Desert region did not experience pronounced cooling during the late Little Ice Age (≈1750-1850).
- The late Little Ice Age climate of the eastern Sahara-Arabian Desert was even more arid than today, and ended abruptly around 1850

The climate of the Sahara and Arabian deserts during the Little Ice Age is not well known, due to a lack of annually resolved natural and documentary archives. We present an annual reconstruction of temperature and aridity derived from Sr/Ca and oxygen isotopes in a coral of the desert-surrounded northern Red Sea. Our data indicate that the eastern Sahara and Arabian Desert did not experience pronounced cooling during the late Little Ice Age (≈1750-1850), but suggest an even more arid mean climate than in the following ≈150 years. The mild temperatures are broadly in line with predominantly negative phases of the NorthAtlantic Oscillation during the Little Ice Age. The more arid climate is best explained by meridional advection of dry continental air from Eurasia. We find evidence for an abrupt termination of the more arid climate after 1850, coincident with a reorganization of the atmospheric circulation over Europe.

Plain Language Summary The Little Ice Age (≈1450-1850) is thought to have been characterized by generally cold conditions in many regions of the globe with little similarities regarding the hydroclimate.The climate of the Sahara and Arabian deserts during the Little Ice Age is not well known, due to a lack of annually resolved sedimentary, tree-ring, speleothem and documentary archives in these uninhabited arid regions. We present an annual reconstruction of temperature and aridity derived from Sr/Ca and oxygen isotopes in a coral of northern Red Sea, a narrow ocean basin bounded by the eastern Sahara and Arabian Desert. Our data indicate these desert areas did not experience pronounced cooling during the late Little IceAge (≈1750-1850), but suggest an even more arid mean climate than today. The mild temperatures and more arid climate are attributed to a changed atmospheric circulation at that time. We find an abrupt termination of the more arid climate after 1850, coincident with a reorganization of the atmospheric circulation over Europe at the end of the Little Ice Age. Our study highlights the need for temperature and aridity reconstructions from the global deserts to detect the full range of climate change over the Common Era.

Kultur

Stanish 2018

Charles Stanish, Henry Tantaleán & Kelly Knudson, *Feasting and the evolution of cooperative social organizations circa 2300 B.P. in Paracas culture, southern Peru.* PNAS **115** (2018), E6716–E6721.

Recent theoretical innovations in cultural evolutionary theory emphasize the role of cooperative social organizations that unite diverse groups as a key step in the evolution of social complexity. A principal mechanism identified by this theory is feasting, a strategy that reinforces norms of cooperation. Feasts occur throughout the premodern world, and the intensification of feasting is empirically correlated to increased social complexity. A critical factor in assessing the evolutionary significance of this practice is the scale and range of the feast from that focused on a single community to ones that draw from a large region or catchment zone. This work addresses the degree to which hosts draw on a local area vs. a regional one in initial prehistoric feasting. We report on excavations at a locus of intensive feasting—a ceremonial sunken court—in a fifth- to third-century BCE Paracas site on the south coast of Peru. We selected 39 organic objects from the court placed as offerings during major feasting episodes. We analyzed the radiogenic strontium isotope (87Sr/86Sr) values to determine the geographical origin of each object. The 87Sr/86Sr data plus additional archaeological data support a hypothesis that the catchment of the court was quite extensive. The initial strategy of political and economic alliance building was macroregional in scope. These data indicate that the most effective initial strategy in early state formation in this case study was to build wide alliances at the outset, as opposed to first consolidating local ones that subsequently expand.

Keywords: cultural evolution | feasting | 87Sr/86Sr | cooperation | Paracas

Significance: A key process in cultural evolution is the development of cooperative organizations that confront the collective action problems inherent in human social interactions. We demonstrate that one classic ethnographic mechanism of cooperative social organization, the hosting of feasts, was used in an early complex, nonstate society in the south coast of Peru ≈2300 B.P. We likewise demonstrate that the catchment zone of the people and goods that participated in the feast was extensive. These data support a cultural evolutionary model of early state formation as one of a network strategy. That is, key areas across a large landscape were initially integrated into a cooperative group as opposed to a strategy of local consolidation and subsequent aggregative growth.

Religion

Mureddu 2018

Nicola Mureddu, *A Dark Dionysus*, *The transformation of a Greek god between the Bronze and Iron Age.* Rosetta **22** (2018), 90–111.

Dionysus was thought until recently to be a foreign god in the Greek pantheon; a result of trade contacts with Thrace and Phrygia, a late acquirement connected with the renewed prosperity of Greece after the “Dark Age.” According to the classical myth, he was just another illicit son of Zeus. He presided over frenzy, drunkenness, wilderness and everything concerning the chaotic forces of nature. But why was his name already in the Mycenaean pantheon? Why did the Orphics know a completely different myth and his name was found accompanying the dead? New studies seem to challenge the classical image of a tipsy Bacchus and lead us to a different, darker and more ancient scenario, helping us to shed some light on a still unclear prehistory of Greek religion.

WADE 2018

Lizzie Wade, *Feeding the Gods.* science **360** (2018), 1288–1292.

Hundreds of skulls testify to the monumental scale of human sacrifice in the Aztec capital.

Subject peoples in the Mexica Empire were also sometimes required to send individuals as tribute. “The killing of captives, even in a ritual context, is a strong political statement,” Verano says. “It’s a way to demonstrate power and political influence—and, some people have said, it’s a way to control your own population.”

Story or Book

DINNENY 2018

José R. Dinneny, *Getting it right on GMOs.* science **360** (2018), 1407.

A protester’s change of heart sheds light on the public’s reservations about genetic engineering.

Seeds of Science. Why We Got It So Wrong on GMOs. Mark Lynas. Bloomsbury Sigma, 2018. 304 pp.

But then Lynas comes face to face with evidence that contradicts what he thought he knew about GM technology. “Certainly it was very worrying if real scientists—not to mention the scientific community in general—were on the other side from me on this issue,” he writes. By the end of chapter 7, science has won the debate.

So what went wrong? Lynas argues that applying GM technology first to herbicideresistant crops was a mistake that aligned the chemical manufacturing industry—which was already regarded with skepticism—with the burgeoning technology. If pest-resistant crops that allowed farmers to apply fewer chemical pesticides had been introduced first, the narrative might have been different.