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References

Afrika

CHOUDHURY 2020

(Ananyo Choudhury,) Samar K. Kassim, Sally N. Adebamowo, Zané Lombard & Neil A. Hanchard et al., *High-depth African genomes inform human migration and health*. nature **586** (2020), 741–748.

n586-0741-Supplement.pdf

The African continent is regarded as the cradle of modern humans and African genomes contain more genetic variation than those from any other continent, yet only a fraction of the genetic diversity among African individuals has been surveyed1. Here we performed whole-genome sequencing analyses of 426 individuals—comprising 50 ethnolinguistic groups, including previously unsampled populations—to explore the breadth of genomic diversity across Africa. We uncovered more than 3 million previously undescribed variants, most of which were found among individuals from newly sampled ethnolinguistic groups, as well as 62 previously unreported loci that are under strong selection, which were predominantly found in genes that are involved in viral immunity, DNA repair and metabolism. We observed complex patterns of ancestral admixture and putative-damaging and novel variation, both within and between populations, alongside evidence that Zambia was a likely intermediate site along the routes of expansion of Bantu-speaking populations. Pathogenic variants in genes that are currently characterized as medically relevant were uncommon—but in other genes, variants denoted as 'likely pathogenic' in the ClinVar database were commonly observed. Collectively, these findings refine our current understanding of continental migration, identify gene flow and the response to human disease as strong drivers of genome-level population variation, and underscore the scientific imperative for a broader characterization of the genomic diversity of African individuals to understand human ancestry and improve health.

Ananyo Choudhury, Shaun Aron, Laura R. Botigué, Dhriti Sengupta, Gerrit Botha, Taoufik Bensellak, Gordon Wells, Judit Kumuthini, Daniel Shriner, Yasmina J. Fakim, Anisah W. Ghoorah, Eileen Dareng, Trust Odia, Oluwadamilare Falola, Ezekiel Adebiyi, Scott Hazelhurst, Gaston Mazandu, Oscar A. Nyangiri, Mamana Mbiyavanga, Alia Benkahla, Samar K. Kassim, Nicola Mulder, Sally N. Adebamowo, Emile R. Chimusa, Donna Muzny, Ginger Metcalf, Richard A. Gibbs, TrypanoGEN Research Group, Charles Rotimi, Michèle Ramsay, H3Africa Consortium, Adebowale A. Adeyemo, Zané Lombard & Neil A. Hanchard

Aktuell

ASCHWANDEN 2020

Christie Aschwanden, *The False Promise Of Herd Immunity*. nature **587** (2020), 26–28.

Why proposals embraced by Donald Trump's administration and others could bring "untold death and suffering".

Kuwait's low numbers reflected the fact that it was putting in place lots of measures to control the virus, such as establishing local curfews and banning

commercial flights from many countries. If the country stopped those measures, Kwok says, the herd-immunity threshold would go up.

Andersen says. "We have to face reality — never before have we reached herd immunity via natural infection with a novel virus, and SARSCoV2 is unfortunately no different."

Bedford 2020

Trevor Bedford et al., *Cryptic transmission of SARS-CoV-2 in Washington state.* science **370** (2020), 571–575. DOI:10.1126/science.abc0523.
s370-0571-Supplement.pdf

After its emergence in Wuhan, China, in late November or early December 2019, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) virus rapidly spread globally. Genome sequencing of SARS-CoV-2 allows the reconstruction of its transmission history, although this is contingent on sampling. **We analyzed 453 SARS-CoV-2 genomes collected between 20 February and 15 March 2020 from infected patients in Washington state in the United States. We find that most SARS-CoV-2 infections sampled during this time derive from a single introduction in late January or early February 2020, which subsequently spread locally before active community surveillance was implemented.**

Trevor Bedford, Alexander L. Greninger, Pavitra Roychoudhury, Lea M. Starita, Michael Famulare, Meei-Li Huang, Arun Nalla, Gregory Pepper, Adam Reinhardt, Hong Xie, Lasata Shrestha, Truong N. Nguyen, Amanda Adler, Elisabeth Brandstetter, Shari Cho, Danielle Giroux, Peter D. Han, Kairsten Fay, Chris D. Frazar, Misja Ilcisin, Kirsten Lacombe, Jover Lee, Anahita Kiavand, Matthew Richardson, Thomas R. Sibley, Melissa Truong, Caitlin R. Wolf, Deborah A. Nickerson, Mark J. Rieder, Janet A. Englund, The Seattle Flu Study Investigator, James Hadfield, Emma B. Hodcroft, John Huddleston, Louise H. Moncla, Nicola F. Müller, Richard A. Neher, Xianding Deng, Wei Gu, Scot Federman, Charles Chiu, Jeffrey S. Duchin, Romesh Gautom, Geoff Melly, Brian Hiatt, Philip Dykema, Scott Lindquist, Krista Queen, Ying Tao, Anna Uehara, Suxiang Tong, Duncan MacCannell, Gregory L. Armstrong, Geoffrey S. Baird, Helen Y. Chu, Jay Shendure & Keith R. Jerome

Chandrashekhar 2020

Vaishnavi Chandrashekhar,, *Herd immunity? India still has a long way to go, scientists say.* science **370** (2020), 513. DOI:10.1126/science.370.6516.513.

Cohen 2020

Jon Cohen & Kai Kupferschmidt, *'A very, very bad look' for remdesivir, FDA and Europe anointed it as a key therapy just after a major study found it has little value.* science **370** (2020), 642–643. DOI:10.1126/science.370.6517.642.

At best, one large, well-designed study found that remdesivir, which must be infused intravenously, modestly reduced the time to recover from COVID-19 in hospitalized patients with severe illness. A few smaller studies found no impact on the disease whatsoever, and none has found that the antiviral reduces patients' level of SARS-CoV-2, the causative virus.

In August, a Gilead-sponsored study showed patients with moderate pneumonia treated for 5 days with remdesivir improved more quickly than those who received standard care, but oddly, those treated for 10 days did not.

The World Health Organization's (WHO's) giant Solidarity trial showed that remdesivir does not reduce mortality or the time COVID-19 patients take to recover.

K AMPF 2020

Günter Kampf, *Protective effect of mandatory facemasks in the public*, *Relevant variables with likely impact on outcome were not considered.* PNAS **117** (2020), 27076–27077. DOI:10.1073/pnas.2012415117.

K UPFERSCHMIDT 2020

Kai Kupferschmidt, *Europe is locking down again—but its strategy is unclear.* science **370** (2020), 644–645. DOI:10.1126/science.370.6517.644.

Without a plan to eliminate the virus, countries may face shutdowns over and over, scientists warn.

Two months ago, as numbers began to creep up after a blissful summer lull, ...

Instead of using the summer to drive cases down to practically zero, Europe celebrated the holiday season. People seemed to lose their fear of the virus.

Europe's bigger question, however, is what comes next. Osterhaus says the strategy should be to get cases to zero using a hard and long lockdown, combined with strict border controls and quarantines to keep the virus out. That strategy, applied successfully by China, Australia, and New Zealand, may be politically unpalatable, however.

Lauterbach says he favored a longer lockdown in summer to go for elimination. But that would be too hard in winter, he says. "All we can do now is break the wave," he says. "But the water level will remain high."

L AXMINARAYAN 2020

Ramanan Laxminarayan et al., *Epidemiology and transmission dynamics of COVID-19 in two Indian states.* science **370** (2020), 691–697. DOI:10.1126/science.abd7672.

s370-0691-Supplement.pdf

Although most cases of coronavirus disease 2019 (COVID-19) have occurred in low-resource countries, little is known about the epidemiology of the disease in such contexts. Data fromthe Indian states of Tamil Nadu and Andhra Pradesh provide a detailed view into severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission pathways and mortality in a high-incidence setting. Reported cases and deaths have been concentrated in younger cohorts than would be expected from observations in higher-income countries, even after accounting for demographic differences across settings. Among 575,071 individuals exposed to 84,965 confirmed cases, infection probabilities ranged from 4.7 to 10.7 % for low-risk and high-risk contact types, respectively. Same-age contacts were associated with the greatest infection risk. Case fatality ratios spanned 0.05 % at ages of 5 to 17 years to 16.6 % at ages of 85 years or more. Primary data from low-resource countries are urgently needed to guide control measures.

Ramanan Laxminarayan, Brian Wahl, Shankar Reddy Dudala, K. Gopal, Chandra Mohan B, S. Neelima, K. S. Jawahar Reddy, J. Radhakrishnan & Joseph A. Lewnard

L EDFORD 2020

Heidi Ledford, *The Race To Make Covid Antibody Therapies More Potent.* nature **587** (2020), 18.

Antibody injections might prevent mild infections from becoming severe, but the treatments are costly.

Lewis 2020

Dyani Lewis, *Why Schools Probably Aren't Covid Hotspots.* nature **587** (2020), 17.

> Young children are unlikely to spread the virus — but older kids are more at risk, say researchers.

Mallapaty 2020

Smriti Mallapaty, *Why Covid Outbreaks Look Set to Worsen This Winter.* nature **586** (2020), 653.

> It's unclear whether COVID-19 is seasonal like the flu — but out-of-control clusters are likely to grow.

Merow 2020

Cory Merow & Mark C. Urban, *Seasonality and uncertainty in global COVID-19 growth rates.* PNAS **117** (2020), 27456–27464. DOI:10.1073/pnas.2008590117.

> pnas117-27456-Supplement.pdf
>
> The virus causing COVID-19 has spread rapidly worldwide and threatens millions of lives. It remains unknown, as of April 2020, whether summer weather will reduce its spread, thereby alleviating strains on hospitals and providing time for vaccine development. Early insights from laboratory studies and research on related viruses predicted that COVID-19 would decline with higher temperatures, humidity, and ultraviolet (UV) light. Using current, fine-scaled weather data and global reports of infections, we develop a model that explains 36 % of the variation in maximum COVID-19 growth rates based on weather and demography (17 %) and country-specific effects (19 %). UV light is most strongly associated with lower COVID-19 growth. Projections suggest that, without intervention, COVID-19 will decrease temporarily during summer, rebound by autumn, and peak next winter. Validation based on data from May and June 2020 confirms the generality of the climate signal detected. However, uncertainty remains high, and the probability of weekly doubling rates remains >20 % throughout summer in the absence of social interventions. Consequently, aggressive interventions will likely be needed despite seasonal trends.
>
> Keywords: SARS-CoV-2 | climate | pandemic | UV light | humidity
>
> Significance: The virus causing COVID-19 has spread rapidly worldwide. It remains unknown whether summer weather will reduce its spread and justify relaxing political interventions and restarting economic activities. We develop statistical models that predict the maximum potential of COVID-19 worldwide and throughout the year. We find that UV light, in particular, is associated with decreased disease growth rate relative to other analyzed factors. Based on these associations with weather, we predict that COVID-19 will decrease temporarily during summer, rebound by autumn, and peak next winter. However, uncertainty remains high, and many factors besides climate, such as social interventions, will influence transmission. Thus, the world must remain vigilant, and continued interventions will likely be needed until a vaccine becomes available.

Ng 2020

Qin Xiang Ng, Michelle Lee Zhi Qing De Deyn & Wee Song Yeo, *Do face masks help? is not the question.* PNAS **117** (2020), 27078–27079. DOI:10.1073/pnas.2012241117.

S H A M A N 2020

Jeffrey Shaman & Marta Galanti, *Will SARSCoV-2 become endemic?*
science **370** (2020), 527–529. DOI:10.1126/science.abe5960.

Reinfection, seasonality, and viral competition will shape endemic transmission
patterns.

Thus far, the mutation rate of the SARS-CoV-2 genome appears to be slower
than that of influenza viruses. This lower rate may be a consequence of proof-
reading during replication, which is exclusive to coronaviruses among RNA viruses.
Conversely, human coronavirus HCoV) OC43 is highly variable.

W O R O B E Y 2020

Michael Worobey et al., *The emergence of SARS-CoV-2 in
Europe and North America.* science **370** (2020), 564–570.
DOI:10.1126/science.abc8169.

s370-0564-Supplement.pdf

Accurate understanding of the global spread of emerging viruses is critical for
public health responses and for anticipating and preventing future outbreaks. Here
we elucidate when, where, and how the earliest sustained severe acute respiratory
syndrome coronavirus 2 (SARS-CoV-2) transmission networks became established
in Europe and North America. Our results suggest that rapid early interventions
successfully prevented early introductions of the virus from taking hold in Ger-
many and the United States. Other, later introductions of the virus from China
to both Italy and Washington state, United States, founded the earliest sustained
European and North America transmission networks. **Our analyses demon-
strate the effectiveness of public health measures in preventing onward
transmission and show that intensive testing and contact tracing could
have prevented SARS-CoV-2 outbreaks from becoming established in
these regions.**

Michael Worobey, Jonathan Pekar, Brendan B. Larsen, Martha I. Nelson, Verity
Hill, Jeffrey B. Joy, Andrew Rambaut, Marc A. Suchard, Joel O. Wertheim &
Philippe Lemey

Anthropologie

G I B B O N S 2020

Ann Gibbons, *Denisovan DNA found in cave on Tibetan Plateau.*
science **370** (2020), 512–513.

Molecular caving" shows archaic humans visited high-altitude cave over long
period.

M A S S I L A N I 2020

Diyendo Massilani et al., *Denisovan ancestry and population history of
early East Asians.* science **370** (2020), 579–583.

s370-0579-Supplement.pdf

We present analyses of the genome of a ≈34,000-year-old hominin skull cap
discovered in the Salkhit Valley in northeastern Mongolia. We show that this
individual was a female member of a modern human population that, following
the split between East and West Eurasians, experienced substantial gene flow from
West Eurasians. Both she and a 40,000-year-old individual from Tianyuan outside
Beijing carried genomic segments of Denisovan ancestry. These segments derive
from the same Denisovan admixture event(s) that contributed to present-day

mainland Asians but are distinct from the Denisovan DNA segments in present-day Papuans and Aboriginal Australians.

Diyendo Massilani, Laurits Skov, Mateja Hajdinjak, Byambaa Gunchinsuren, Damdinsuren Tseveendorj, Seonbok Yi, Jungeun Lee, Sarah Nagel, Birgit Nickel, Thibaut Devièse, Tom Higham, Matthias Meyer, Janet Kelso, Benjamin M. Peter & Svante Pääbo

Sahlins 1968

Marshall D. Sahlins, *Notes on the Original Affluent Society*. In: Richard B. Lee & Irven DeVore (Hrsg.), *Man the Hunter*. (New York 1968), 85–89.

Sahlins 2009

Marshall Sahlins, *Hunter-gatherers*, *Insights from a golden affluent age*. Pacific Ecologist **2009**, 18, 3–8.

Hunter-gatherers have few possessions and are the lowest energy consumers, reports Marshall Sahlins, yet they are the original affluent society with material needs easily met in a few short hours a week. Paradoxically, in the 21st century's market economy, an era of the greatest technical power, a billion people are starving and people struggle to bridge the gap between unlimited wants and insufficient means. Scarcity and anxiety define our economy, while the hunters' confident trust in nature's abundance signals their success.

Zhang 2020

Dongju Zhang, Bo Li, Zenobia Jacobs, Melinda A. Yang, Svante Pääbo & Qiaomei Fu et al., *Denisovan DNA in Late Pleistocene sediments from Baishiya Karst Cave on the Tibetan Plateau*. science **370** (2020), 584–587.

s370-0584-Supplement.pdf

A late Middle Pleistocene mandible from Baishiya Karst Cave (BKC) on the Tibetan Plateau has been inferred to be from a Denisovan, an Asian hominin related to Neanderthals, on the basis of an amino acid substitution in its collagen. Here we describe the stratigraphy, chronology, and mitochondrial DNA extracted from the sediments in BKC. We recover Denisovan mitochondrial DNA from sediments deposited ≈100 thousand and ≈60 thousand years ago (ka) and possibly as recently as ≈45 ka. The longterm occupation of BKC by Denisovans suggests that they may have adapted to life at high altitudes and may have contributed such adaptations to modern humans on the Tibetan Plateau.

Dongju Zhang, Huan Xia, Fahu Chen, Bo Li, Viviane Slon, Ting Cheng, Ruowei Yang, Zenobia Jacobs, Qingyan Dai, Diyendo Massilani, Xuke Shen, Jian Wang, Xiaotian Feng, Peng Cao, Melinda A. Yang, Juanting Yao, Jishuai Yang, David B. Madsen, Yuanyuan Han, Wanjing Ping, Feng Liu, Charles Perreault, Xiaoshan Chen, Matthias Meyer, Janet Kelso, Svante Pääbo & Qiaomei Fu

Biologie

Bergström 2020

Anders Bergström, Laurent Frantz, Greger Larson & Pontus Skoglund et al., *Origins and genetic legacy of prehistoric dogs*. science **370** (2020), 557–564.

Dogs were the first domestic animal, but little is known about their population history and to what extent it was linked to humans. We sequenced 27 ancient dog genomes and found that all dogs share a common ancestry distinct from present-day wolves, with limited gene flow from wolves since domestication but substantial dog-to-wolf gene flow. By 11,000 years ago, at least five major ancestry lineages had diversified, demonstrating a deep genetic history of dogs during the Paleolithic. Coanalysis with human genomes reveals aspects of dog population history that mirror humans, including Levant-related ancestry in Africa and early agricultural Europe. Other aspects differ, including the impacts of steppe pastoralist expansions in West and East Eurasia and a near-complete turnover of Neolithic European dog ancestry.

Anders Bergström, Laurent Frantz, Ryan Schmidt, Erik Ersmark, Ophelie Lebrasseur, Linus Girdland-Flink, Audrey T. Lin, Jan Storå, Karl-Göran Sjögren, David Anthony, Ekaterina Antipina, Sarieh Amiri, Guy Bar-Oz, Vladimir I. Bazaliiskii, Jelena Bulatović, Dorcas Brown, Alberto Carmagnini, Tom Davy, Sergey Fedorov, Ivana Fiore, Deirdre Fulton, Mietje Germonpré, James Haile, Evan K. Irving-Pease, Alexandra Jamieson, Luc Janssens, Irina Kirillova, Liora Kolska Horwitz, Julka Kuzmanović-Cvetković, Yaroslav Kuzmin, Robert J. Losey, Daria Loßnjak Dizdar, Marjan Mashkour, Mario Novak, Vedat Onar, David Orton, Maja Pasarić, Miljana Radivojević, Dragana Rajković, Benjamin Roberts, Hannah Ryan, Mikhail Sablin, Fedor Shidlovskiy, Ivana Stojanović, Antonio Tagliacozzo, Katerina Trantalidou, Inga Ullén, Aritza Villaluenga, PaulaWapnish, Keith Dobney, Anders Götherström, Anna Linderholm, Love Dalén, Ron Pinhasi, Greger Larson & Pontus Skoglund

Callaway 2020

Ewen Callaway, *Ancient Dog DNA Unveils 11,000 Years of Canine Evolution.* nature **587** (2020), 20.

Genomes trace how the animals moved around the world — often with humans by their side.

Earn 2020

David J. D. Earn, Junling Ma, Hendrik Poinar, Jonathan Dushoff & Benjamin M. Bolker, *Acceleration of plague outbreaks in the second pandemic.* PNAS **117** (2020), 27703–27711.

pnas117-27703-Supplement.pdf

Historical records reveal the temporal patterns of a sequence of plague epidemics in London, United Kingdom, from the 14th to 17th centuries. Analysis of these records shows that later epidemics spread significantly faster ("accelerated"). Between the Black Death of 1348 and the later epidemics that culminated with the Great Plague of 1665, we estimate that the epidemic growth rate increased fourfold. Currently available data do not provide enough information to infer the mode of plague transmission in any given epidemic; nevertheless, order-of-magnitude estimates of epidemic parameters suggest that the observed slow growth rates in the 14th century are inconsistent with direct (pneumonic) transmission. We discuss the potential roles of demographic and ecological factors, such as climate change or human or rat population density, in driving the observed acceleration.

Keywords: plague | London | epidemic growth rate | reproduction number | COVID-19

Significance: Epidemics of plague devastated Europe's population throughout the Medieval and Renaissance periods. Genetic studies of modest numbers of skeletal remains indicate that the causative agent of all these epidemics was the

bacterium Yersinia pestis, but such analyses cannot identify overall patterns of transmission dynamics. Analysis of thousands of archival records from London, United Kingdom, reveals that plague epidemics spread much faster in the 17th century than in the 14th century.

P A V L I D I S 2020

Pavlos Pavlidis & Mehmet Somel, *Of dogs and men, Ancient genomes reveal the common history of human and dog.* science **370** (2020), 522–523.

Islam

G I L L I O T 2011

Claude Gilliot, *Das jüdischchristliche Umfeld bei der Entstehung des Koran und dessen Bedeutung für die islamische Korankommentierung, Christen und Christentum in der frühen islamischen Exegese des Koran.* In: L O T H A R G A L L & D I E T M A R W I L L O W E I T (Hrsg.), *Judaism, Christianity, and Islam in the Course of History, Exchange and Conflicts.* (München 2011), 61–74.

In this paper we intend to show a relative continuity between the narratives of the Koran on Jesus, Mary, and relative topics (materia christiana) and the exegetical traditions of early Muslim exegetes on these matters. The sources of the Koran on them are above all the Diatessaron and the Apocrypha of the New Testament, above all several apocryphal Gospels. It appears that Mohammed and some of those who helped him were in relation with Pre-Nicean Christians or Jewish-Christians and also influenced by Manicheism. It is not surprising because the Koran is a document of Late Antiquity, a period of syncretism. As for the Christians (or the Nazarenes), for the Koran and for the Islamic exegesis the "true Christians" are the Muslims.

Jungpaläolithikum

R I C H T E R 2020

Jürgen Richter, Frank Lehmkuhl, Dirk F. Leder, Andrea Miebach, Florian Sauer & Shumon T. Hussain et al., *Al-Ansab and the Dead Sea, Mid-MIS 3 archaeology and environment of the early Ahmarian population of the Levantine corridor.* PLoS ONE **15** (2020), e239968. DOI:10.1371/journal.pone.0239968.

Our field data from the Upper Palaeolithic site of Al-Ansab 1 (Jordan) and from a pollen sequence in the Dead Sea elucidate the role that changing Steppe landscapes played in facilitating anatomically modern human populations to enter a major expansion and consolidation phase, known as the "Early Ahmarian", several millennia subsequent to their initial Marine Isotope Stage 4/3 migration from Africa, into the Middle East. The Early Ahmarian techno-cultural unit covers a time range between 45 ka–37 ka BP. With so far more than 50 sites found, the Early Ahmarian is the first fully Upper Palaeolithic techno-cultural unit exclusively and undisputedly related to anatomically modern human populations. In order to better understand the potentially attractive features of the Early Ahmarian environmental context that supported its persistence for over 8,000 years,

we carried out a decennial research program in Jordan and in the Dead Sea. This included (1) a geoscientific and archaeological survey program in the Wadi Sabra (Jordan) with a particular focus on excavations at the Early Ahmarian site of Al-Ansab 1 alongside the detailed analysis of Quaternary sediments from the same area and (2) palaeobotanical research based on Quaternary lake deposits from the Dead Sea. Our pollen data from the Dead Sea indicate slow, low frequency vegetational variation with expanding Artemisia steppe, from 60 to 20 ka BP (MIS 3–2). Here, we see a reciprocal assimilation of southern and northern Levantine vegetation zones thereby enhancing a long-lasting south-to-north steppe corridor. The same integration process accelerated about 40 ka ago, when forested areas retreated in the Lebanese Mountains. The process then extended to encompass an area from Southern Lebanon to the Sinai Peninsula. We argue that, at the same time, the carriers of the Early Ahmarian techno-cultural unit extended their habitat from their original Mediterranean biome (in the North) to the Saharo-Arabian biome (to the South). Our excavation of Al-Ansab 1, a campsite at the eastern margins of the Early Ahmarian settlement area, indicates far reaching annual movements of small, highly mobile hunter-gatherer groups. We assume a low degree of settlement complexity, still allowing for habitat extension of the Early Ahmarian into the margins of the Levantine corridor. Due to our radiometric dates, our combined archaeological and environmental record sheds light on an evolved phase of the Early Ahmarian, around 38 ka ago, rather than the starting phase of this techno-cultural unit. Possible application of our model to the starting phase of the Early Ahmarian remains an aspect of future research.

Klima

Lapointe 2020

Francois Lapointe, Raymond S. Bradley, Nicholas L. Balascio, Mark B. Abbott, Joseph S. Stoner & Guillaume St-Onge et al., *Annually resolved Atlantic sea surface temperature variability over the past 2,900 y.* PNAS **117** (2020), 27171–27178.

pnas117-27171-Supplement.pdf

Global warming due to anthropogenic factors can be amplified or dampened by natural climate oscillations, especially those involving sea surface temperatures (SSTs) in the North Atlantic which vary on a multidecadal scale (Atlantic multidecadal variability, AMV). Because the instrumental record of AMV is short, long-term behavior of AMV is unknown, but climatic teleconnections to regions beyond the North Atlantic offer the prospect of reconstructing AMV from high-resolution records elsewhere. Annually resolved titanium from an annually laminated sedimentary record from Ellesmere Island, Canada, shows that the record is strongly influenced by AMV via atmospheric circulation anomalies. Significant correlations between this High-Arctic proxy and other highly resolved Atlantic SST proxies demonstrate that it shares the multidecadal variability seen in the Atlantic. Our record provides a reconstruction of AMV for the past ≈3 millennia at an unprecedented time resolution, indicating North Atlantic SSTs were coldest from ≈1400–1800 CE, while current SSTs are the warmest in the past ≈2,900 y.

Francois Lapointe, Raymond S. Bradley, Pierre Francus, Nicholas L. Balascio, Mark B. Abbott, Joseph S. Stoner, Guillaume St-Onge, Arnaud De Coninck & Thibault Labarre

Significance: Atlantic multidecadal sea surface temperature variability (AMV) strongly influences the Northern Hemisphere's climate, including the Arctic. Here

9

using a well-dated annually laminated lake sediment core, we show that the AMV
exerts a strong influence on High-Arctic climate during the instrumental period
(past ≈150 y) through atmospheric teleconnection. This highly resolved climate
archive is then used to produce the first AMV reconstruction spanning the last
≈3 millennia at unprecedented temporal resolution. Our terrestrial record is sig-
nificantly correlated to several sea surface temperature proxies in the Atlantic,
highlighting the reliability of this record as an annual tracer of the AMV. The
results show that the current warmth in sea surface temperature is unseen in the
context of the past ≈3 millennia.

Kultur

HAAS 2020

Randall Haas et al., *Female hunters of the early Americas.* Science
Advances **6** (2020), eabd0310. DOI:10.1126/sciadv.abd0310.

SciAdv06-eabd0310-Supplement.pdf

Sexual division of labor with females as gatherers and males as hunters is a ma-
jor empirical regularity of huntergatherer ethnography, suggesting an ancestral
behavioral pattern. We present an archeological discovery and meta-analysis that
challenge the man-the-hunter hypothesis. Excavations at the Andean highland site
of Wilamaya Patjxa reveal a 9000-year-old human burial (WMP6) associated with
a hunting toolkit of stone projectile points and animal processing tools. Osteolo-
gical, proteomic, and isotopic analyses indicate that this early hunter was a young
adult female who subsisted on terrestrial plants and animals. Analysis of Late
Pleistocene and Early Holocene burial practices throughout the Americas situate
WMP6 as the earliest and most secure hunter burial in a sample that includes 10
other females in statistical parity with early male hunter burials. The findings are
consistent with nongendered labor practices in which early hunter-gatherer females
were big-game hunters.

Randall Haas, James Watson, Tammy Buonasera, John Southon, Jennifer C.
Chen, Sarah Noe, Kevin Smith, Carlos Viviano Llave, Jelmer Eerkens & Glendon
Parker

ROSENSTOCK 2020

Eva Rosenstock, *Revolute Joints, A Contribution to Prehistoric Ma-
chine Theory.* In: STEPHAN W. E. BLUM, TURAN EFE, TO-
BIAS L. KIENLIN & ERNST PERNICKA (Hrsg.), *From Past to
Present, Studies in Memory of Manfred O. Korfmann.* Studia Troica
Monographien 11 (Bonn 2020), 545–557.

As this paper tries to demonstrate, knowledge of rotary motion is – unlike
claimed in recent textbooks – not coeval with the knowledge of the revolute joint.
Rather, rotary motion attested from at least 14,000 BC onwards in e.g. cordage
is an expression of a cultural capacity that Haidle et al. (2015) have termed com-
plementary. Here, all parts of an implement retain three degrees of freedom. By
contrast, the revolute joint restricted the possible movement to only one, i.e. mere
rotary motion. It appears about 10,000 years after the first indicators of free rotary
motion in several applications around 3000 BC and can plausibly explain why it
took millennia to put animals such as cattle (Masson/Rosenstock 2011) and inan-
imate forces such as the wind to use. Especially in the light of recent evidence for
'informal' cattle traction since the Neolithic (Gaastra/ Greenfield/Vander Linden
2018), the invention of the revolute joint to connect wheels and carriage makes for
a plausible explanation why the wagon was not invented earlier.

Religion

Mayer 1987

Werner R. Mayer, *Ein Mythos von der Erschaffung des Menschen und des Königs.* Orientalia **56** (1987), 55–68.

Inhalt: Zunächst geht es um die Erschaffung des Menschen; nachdem der lullû-Mensch entstanden ist, folgt – ohne spezielle Begründung, jedenfalls nicht im erhaltenen Text – die Bildung des Königs, des māliku-Menschen. Bei der Rolle, die der König in der mesopotamischen Kulturwelt spielte, ist es klar, daß er in besonderer Weise als Geschöpf der Götter angesehen wurde; hier haben wir nun auch einen diesbezüglichen Mythos, der freilich, wenn die Indizien nicht trügen, relativ spät in diese Form gebracht worden ist (Anfang des 1. Jahrtausends?).

Story or Book

Pomeroy 2020

Emma Pomeroy, *The vibrant lives of Neanderthals.* science **370** (2020), 537.

A nuanced portrait of our evolutionary cousins encourages empathy and understanding.

Kindred. Rebecca Wragg Sykes. Bloomsbury Sigma, 2020. 400 pp.

A recurring perspective in Kindred is that diversity can and should be expected in Neanderthal behavior, given their existence over hundreds of thousands of years and their vast geographical range.