

References

Aktuell

CAI 2021

Yongfei Cai, Jun Zhang, Tianshu Xiao & Bing Chen et al., *Structural basis for enhanced infectivity and immune evasion of SARS-CoV-2 variants*. *science* **373** (2021), 642–648. DOI:10.1126/science.abi9745. s373-0642-Supplement.pdf

Several fast-spreading variants of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have become the dominant circulating strains in the COVID-19 pandemic. We report here cryo-electron microscopy structures of the full-length spike (S) trimers of the B.1.1.7 and B.1.351 variants, as well as their biochemical and antigenic properties. Amino acid substitutions in the B.1.1.7 protein increase both the accessibility of its receptor binding domain and the binding affinity for receptor angiotensin-converting enzyme 2 (ACE2). The enhanced receptor engagement may account for the increased transmissibility. The B.1.351 variant has evolved to reshape antigenic surfaces of the major neutralizing sites on the S protein, making it resistant to some potent neutralizing antibodies. These findings provide structural details on how SARS-CoV-2 has evolved to enhance viral fitness and immune evasion.

Yongfei Cai, Jun Zhang, Tianshu Xiao, Christy L. Lavine, Shaun Rawson, Hanqin Peng, Haisun Zhu, Krishna Anand, Pei Tong, Avneesh Gautam, Shen Lu, Sarah M. Sterling, Richard M. Walsh Jr., Sophia Rits-Volloch, Jianming Lu, Duane R. Wesemann, Wei Yang, Michael S. Seaman & Bing Chen

GOBEIL 2021

Sophie M.-C. Gobeil, Rory Henderson & Priyamvada Acharya et al., *Effect of natural mutations of SARS-CoV-2 on spike structure, conformation, and antigenicity*. *science* **373** (2021), eabi6226. DOI:10.1126/science.abi6226.

s373-eabi6226-Supplement.pdf

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants with multiple spike mutations enable increased transmission and antibody resistance. We combined cryo-electron microscopy (cryo-EM), binding, and computational analyses to study variant spikes, including one that was involved in transmission between minks and humans, and others that originated and spread in human populations. All variants showed increased angiotensin-converting enzyme 2 (ACE2) receptor binding and increased propensity for receptor binding domain (RBD)-up states. While adaptation to mink resulted in spike destabilization, the B.1.1.7 (UK) spike balanced stabilizing and destabilizing mutations. A local destabilizing effect of the RBD E484K mutation was implicated in resistance of the B.1.1.28/P.1 (Brazil) and B.1.351 (South Africa) variants to neutralizing antibodies. Our studies revealed allosteric effects of mutations and mechanistic differences that drive either interspecies transmission or escape from antibody neutralization.

Sophie M.-C. Gobeil, Katarzyna Janowska, Shana McDowell, Katayoun Mansouri, Robert Parks, Victoria Stalls, Megan F. Kopp, Kartik Manne, Dapeng Li, Kevin Wiehe, Kevin O. Saunders, Robert J. Edwards, Bette Korber, Barton F. Haynes, Rory Henderson & Priyamvada Acharya

IRONS 2021

Nicholas J. Irons & Adrian E. Raftery, *Estimating SARS-CoV-2 infections from deaths, confirmed cases, tests, and random surveys*.

[PNAS 118 \(2021\), e2103272118](#). DOI:10.1073/pnas.2103272118.

[pnas118-e2103272118-Supplement.pdf](#)

There are multiple sources of data giving information about the number of SARS-CoV-2 infections in the population, but all have major drawbacks, including biases and delayed reporting. For example, the number of confirmed cases largely underestimates the number of infections, and deaths lag infections substantially, while test positivity rates tend to greatly overestimate prevalence. Representative random prevalence surveys, the only putatively unbiased source, are sparse in time and space, and the Results can come with big delays. Reliable estimates of population prevalence are necessary for understanding the spread of the virus and the effectiveness of mitigation strategies. We develop a simple Bayesian framework to estimate viral prevalence by combining several of the main available data sources. It is based on a discrete-time Susceptible–Infected–Removed (SIR) model with time-varying reproductive parameter. Our model includes likelihood components that incorporate data on deaths due to the virus, confirmed cases, and the number of tests administered on each day. We anchor our inference with data from randomsample testing surveys in Indiana and Ohio. We use the results from these two states to calibrate the model on positive test counts and proceed to estimate the infection fatality rate and the number of new infections on each day in each state in the United States. We estimate the extent to which reported COVID cases have underestimated true infection counts, which was large, especially in the first months of the pandemic. We explore the implications of our results for progress toward herd immunity.

Keywords: SARS-CoV-2 incidence | coronavirus infections | Bayesian estimation | United States COVID data

Significance: The novel coronavirus SARS-CoV-2 has infected over 33 million people in the United States. Nationwide, over 600,000 have died in the COVID-19 pandemic, which has necessitated shutdowns of schools and sectors of the economy. The extent of the virus' spread remains uncertain due to biases in test data. We combine multiple data sources to estimate the true number of infections in all US states. These data include representative random testing surveys from Indiana and Ohio, which provide potentially unbiased prevalence estimates. We find that approximately 60% of infections have gone unreported. Even so, only about 20% of the United States had been infected as of early March 2021, suggesting that the country was far from herd immunity at that point.

KARLINSKY 2021

Ariel Karlinsky & Dmitry Kobak, *Tracking excess mortality across countries during the COVID-19 pandemic with the World Mortality Dataset*. [eLife 10 \(2021\), e69336](#). DOI:10.7554/eLife.69336.

Comparing the impact of the COVID-19 pandemic between countries or across time is difficult because the reported numbers of cases and deaths can be strongly affected by testing capacity and reporting policy. Excess mortality, defined as the increase in all-cause mortality relative to the expected mortality, is widely considered as a more objective indicator of the COVID19 death toll. However, there has been no global, frequently updated repository of the all-cause mortality data across countries. To fill this gap, we have collected weekly, monthly, or quarterly allcause mortality data from 103 countries and territories, openly available as the regularly updated World Mortality Dataset. We used this dataset to compute the excess mortality in each country during the COVID-19 pandemic. We found that

in several worst-affected countries (Peru, Ecuador, Bolivia, Mexico) the excess mortality was above 50% of the expected annual mortality (Peru, Ecuador, Bolivia, Mexico) or above 400 excess deaths per 100,000 population (Peru, Bulgaria, North Macedonia, Serbia). At the same time, in several other countries (e.g. Australia and New Zealand) mortality during the pandemic was below the usual level, presumably due to social distancing measures decreasing the non-COVID infectious mortality. Furthermore, we found that while many countries have been reporting the COVID-19 deaths very accurately, some countries have been substantially underreporting their COVID-19 deaths (e.g. Nicaragua, Russia, Uzbekistan), by up to two orders of magnitude (Tajikistan). Our results highlight the importance of open and rapid all-cause mortality reporting for pandemic monitoring.

KLEIN 2021

Richard G. Klein, *Middle Stone Age marine resource exploitation at Ysterfontein 1 rockshelter, South Africa*. [PNAS 118 \(2021\), e2107978118](#).

Regarding coastal resource exploitation, the rate at which deposits accumulated inside a shelter does not measure exploitation intensity outside. Average shell size in intertidal gastropod species does. Gastropods are sessile, and collectors will naturally take the largest individuals first. If they continue to collect, they will drive down average size.

The rate at which deposits may have accumulated at a site does not inform on this. The deposits at Ysterfontein 1 are mostly aeolian sands whose rate of accumulation depended primarily on wind velocity and direction.

MCCALLUM 2021

Matthew McCallum et al., *SARS-CoV-2 immune evasion by the B.1.427/B.1.429 variant of concern*. [science 373 \(2021\), 648–654](#).
[DOI:10.1126/science.abi7994](#).

[s373-0648-Supplement.pdf](#)

A novel variant of concern (VOC) named CAL.20C (B.1.427/B.1.429), which was originally detected in California, carries spike glycoprotein mutations S13I in the signal peptide, W152C in the N-terminal domain (NTD), and L452R in the receptor-binding domain (RBD). Plasma from individuals vaccinated with a Wuhan-1 isolate-based messenger RNA vaccine or from convalescent individuals exhibited neutralizing titers that were reduced 2- to 3.5-fold against the B.1.427/B.1.429 variant relative to wild-type pseudoviruses. The L452R mutation reduced neutralizing activity in 14 of 34 RBD-specific monoclonal antibodies (mAbs). The S13I and W152C mutations resulted in total loss of neutralization for 10 of 10 NTD-specific mAbs because the NTD antigenic supersite was remodeled by a shift of the signal peptide cleavage site and the formation of a new disulfide bond, as revealed by mass spectrometry and structural studies.

Matthew McCallum, Jessica Bassi, Anna De Marco, Alex Chen, Alexandra C. Walls, Julia Di Iulio, M. Alejandra Tortorici, Mary-Jane Navarro, Chiara Silacci-Fregni, Christian Saliba, Kaitlin R. Sprouse, Maria Agostini, Dora Pinto, Katja Culap, Siro Bianchi, Stefano Jaconi, Elisabetta Cameroni, John E. Bowen, Sasha W. Tilles, Matteo Samuele Pizzuto, Sonja Bernasconi Guastalla, Giovanni Bona, Alessandra Franzetti Pellanda, Christian Garzoni, Wesley C. Van Voorhis, Laura E. Rosen, Gyorgy Snell, Amalio Telenti, Herbert W. Virgin, Luca Piccoli, Davide Corti & David Veasley

MALLAPATY 2021

Smriti Mallapaty, *Covid vaccines slash viral spread – but Delta is an unknown*. [nature 596 \(2021\), 17–18](#).

Studies show that vaccines reduce the spread of some variants of SARS-CoV-2 by more than 80 %.

NIESPOLO 2021

Elizabeth M. Niespolo, Warren D. Sharp, Graham Avery & Todd E. Dawson, *Ysterfontein 1 shellmidden (South Africa) and the antiquity of coastal adaptation, Reply to Klein*. [PNAS 118 \(2021\), e2108794118](#).

We stand by our conclusions that YFT1 is currently the oldest well-dated true shell midden and that at times it was intensively occupied by humans, documenting an early example of coastal adaptation.

Altpaläolithikum

MACDONALD 2021

Katharine MacDonald, Fulco Scherjon, Eva van Veen, Krist Vaesen & Wil Roebroeks, *Middle Pleistocene fire use, The first signal of widespread cultural diffusion in human evolution*. [PNAS 118 \(2021\), e2101108118](#).

Control of fire is one of the most important technological innovations within the evolution of humankind. The archaeological signal of fire use becomes very visible from around 400,000 y ago onward. Interestingly, this occurs at a geologically similar time over major parts of the Old World, in Africa, as well as in western Eurasia, and in different subpopulations of the wider hominin metapopulation. We interpret this spatiotemporal pattern as the result of cultural diffusion, and as representing the earliest clear-cut case of widespread cultural change resulting from diffusion in human evolution. This fire-use pattern is followed slightly later by a similar spatiotemporal distribution of Levallois technology, at the beginning of the African Middle Stone Age and the western Eurasian Middle Paleolithic. These archaeological data, as well as studies of ancient genomes, lead us to hypothesize that at the latest by 400,000 y ago, hominin subpopulations encountered one another often enough and were sufficiently tolerant toward one another to transmit ideas and techniques over large regions within relatively short time periods. Furthermore, it is likely that the large-scale social networks necessary to transmit complicated skills were also in place. Most importantly, this suggests a form of cultural behavior significantly more similar to that of extant *Homo sapiens* than to our great ape relatives.

Keywords: fire use | cultural behavior | Middle Pleistocene | Middle Stone Age | Middle Paleolithic

Anthropologie

CONDE-VALVERDE 2021

Mercedes Conde-Valverde, Ignacio Martínez, Rolf M. Quam & Manuel Rosa et al., *Neanderthals and *Homo sapiens* had similar auditory and speech capacities*. [Nature Ecology & Evolution 5 \(2021\), 609–615](#).

NatEcoEvo05-0609-Supplement.pdf

The study of audition in fossil hominins is of great interest given its relationship with intraspecific vocal communication. While the auditory capacities have been studied in early hominins and in the Middle Pleistocene Sima de los Huesos hominins, less is known about the hearing abilities of the Neanderthals. Here, we provide

a detailed approach to their auditory capacities. Relying on computerized tomography scans and a comprehensive model from the field of auditory bioengineering, we have established sound power transmission through the outer and middle ear and calculated the occupied bandwidth in Neanderthals. The occupied bandwidth is directly related to the efficiency of the vocal communication system of a species. Our results show that the occupied bandwidth of Neanderthals was greater than the Sima de los Huesos hominins and similar to extant humans, implying that Neanderthals evolved the auditory capacities to support a vocal communication system as efficient as modern human speech.

Mercedes Conde-Valverde, Ignacio Martínez, Rolf M. Quam, Manuel Rosa, Alex D. Velez, Carlos Lorenzo, Pilar Jarabo, José María Bermúdez de Castro, Eudald Carbonell & Juan Luis Arsuaga

LALUEZA-FOX 2021

Carles Lalueza-Fox, *Neanderthal assimilation?* [Nature Ecology & Evolution](#) **5** (2021), 711–712.

Four new Late Pleistocene European modern human genomes had Neanderthal ancestors in their immediate family history, suggesting that interbreeding with the last Neanderthals was common.

The finding that Late Pleistocene modern humans systematically bear evidence of recent Neanderthal ancestry suggests that this pattern of interbreeding was not an exception, but a rule. Overall, the new genomic evidence suggests that the later Neanderthals were perhaps not replaced by incoming modern humans, but absorbed by them, and their Neanderthal genomic signal was diluted from the Upper Palaeolithic gene pool by differential demography and later by successive population replacements with lower Neanderthal ancestry.

PRÜFER 2021

Kay Prüfer, Cosimo Posth & Johannes Krause et al., *A genome sequence from a modern human skull over 45,000 years old from Zlatý kůň in Czechia.* [Nature Ecology & Evolution](#) **5** (2021), 820–825.

NatEcoEvo05-0820-Supplement.pdf

Modern humans expanded into Eurasia more than 40,000 years ago following their dispersal out of Africa. These Eurasians carried $\approx 2\text{--}3\%$ Neanderthal ancestry in their genomes, originating from admixture with Neanderthals that took place sometime between 50,000 and 60,000 years ago, probably in the Middle East. In Europe, the modern human expansion preceded the disappearance of Neanderthals from the fossil record by 3,000–5,000 years. The genetic makeup of the first Europeans who colonized the continent more than 40,000 years ago remains poorly understood since few specimens have been studied. Here, we analyse a genome generated from the skull of a female individual from Zlatý kůň, Czechia. We found that she belonged to a population that appears to have contributed genetically neither to later Europeans nor to Asians. Her genome carries $\approx 3\%$ Neanderthal ancestry, similar to those of other Upper Palaeolithic hunter-gatherers. However, the lengths of the Neanderthal segments are longer than those observed in the currently oldest modern human genome of the $\approx 45,000$ -year-old Ust'-Ishim individual from Siberia, suggesting that this individual from Zlatý kůň is one of the earliest Eurasian inhabitants following the expansion out of Africa.

Kay Prüfer, Cosimo Posth, He Yu, Alexander Stoessel, Maria A. Spyrou, Thibaut Deviese, Marco Mattonai, Erika Ribechini, Thomas Higham, Petr Velemínský, Jaroslav Brůžek & Johannes Krause

PÜSCHEL 2021

Hans P. Püschel, Ornella C. Bertrand, Joseph E. O'Reilly, René Bobe & Thomas A. Püschel, *Divergence-time estimates for hominins provide insight into encephalization and body mass trends in human evolution*. [Nature Ecology & Evolution 5 \(2021\), 808–819](#).

[NatEcoEvo05-0808-Supplement.pdf](#)

Quantifying speciation times during human evolution is fundamental as it provides a timescale to test for the correlation between key evolutionary transitions and extrinsic factors such as climatic or environmental change. Here, we applied a total evidence dating approach to a hominin phylogeny to estimate divergence times under different topological hypotheses. The time-scaled phylogenies were subsequently used to perform ancestral state reconstructions of body mass and phylogenetic encephalization quotient (PEQ). Our divergence-time estimates are consistent with other recent studies that analysed extant species. We show that the origin of the genus *Homo* probably occurred between 4.30 and 2.56 million years ago. The ancestral state reconstructions show a general trend towards a smaller body mass before the emergence of *Homo*, followed by a trend towards a greater body mass. PEQ estimations display a general trend of gradual but accelerating encephalization evolution. The obtained results provide a rigorous temporal framework for human evolution.

SCARDIA 2021

Giancarlo Scardia, Walter A. Neves, Ian Tattersall & Lukas Blumrich, *What kind of hominin first left Africa?* [Evolutionary Anthropology 30 \(2021\), 122–127](#).

Recent discoveries of stone tools from Jordan (2.5 Ma) and China (2.1 Ma) document hominin presence in Asia at the beginning of the Pleistocene, well before the conventional Dmanisi datum at 1.8 Ma. Although no fossil hominins documenting this earliest Out of Africa phase have been found, on chronological grounds a pre-*Homo erectus* hominin must be considered the most likely maker of those artifacts. If so, this sheds new light on at least two disputed subjects in paleo-anthropology, namely the remarkable variation among the five Dmanisi skulls, and the ancestry of *Homo floresiensis*.

Keywords: early Pleistocene | *Homo floresiensis* | *Homo georgicus* | Out of Africa

TEIXEIRA 2021

João C. Teixeira et al., *Widespread Denisovan ancestry in Island Southeast Asia but no evidence of substantial super-archaic hominin admixture*. [Nature Ecology & Evolution 5 \(2021\), 616–624](#).

[NatEcoEvo05-0616-Supplement.pdf](#)

The hominin fossil record of Island Southeast Asia (ISEA) indicates that at least two endemic ‘super-archaic’ species—*Homo luzonensis* and *H. floresiensis*—were present around the time anatomically modern humans arrived in the region >50,000 years ago. Intriguingly, contemporary human populations across ISEA carry distinct genomic traces of ancient interbreeding events with Denisovans—a separate hominin lineage that currently lacks a fossil record in ISEA. To query this apparent disparity between fossil and genetic evidence, we performed a comprehensive search for super-archaic introgression in >400 modern human genomes, including >200 from ISEA. Our results corroborate widespread Denisovan ancestry in ISEA populations, but fail to detect any substantial super-archaic admixture signals compatible with the endemic fossil record of ISEA. We discuss the implications of our findings for the understanding of hominin history in ISEA, including

future research directions that might help to unlock more details about the prehistory of the enigmatic Denisovans.

João C. Teixeira, Guy S. Jacobs, Chris Stringer, Jonathan Tuke, Georgi Hudjashov, Gludhug A. Purnomo, Herawati Sudoyo, Murray P. Cox, Raymond Tobler, Chris S. M. Turney, Alan Cooper & Kristofer M. Helgen

VAESEN 2021

Krist Vaesen & Wybo Houkes, *Is Human Culture Cumulative?* [Current Anthropology](#) **62** (2021), 218–238.

It has been claimed that a unique feature of human culture is that it accumulates beneficial modifications over time. On the basis of a couple of methodological considerations, we here argue that, perhaps surprisingly, there is insufficient evidence for a proper test of this claim. And we indicate what further research would be needed to firmly establish the cumulateness of human culture.

Krist Vaesen & Wybo Houkes, Christine A. Caldwell et al., Paloma de la Peña, Miriam Noël Haidle & Oliver Schlaudt, Alex Mesoudi, Antoine Muller, Bruce Rawlings et al., Ceri Shipton, Dietrich Stout, Claudio Tennie

Bibel

REGEV 2020

Johanna Regev, Joe Uziel, Tehillah Lieberman, Avi Solomon, Yuval Gadot, Doron Ben-Ami, Lior Regev & Elisabetta Boaretto, *Radiocarbon dating and microarchaeology untangle the history of Jerusalem’s Temple Mount, A view from Wilson’s Arch.* [PLoS ONE](#) **15** (2020), e233307. DOI:10.1371/journal.pone.0233307.

Radiocarbon dating is rarely applied in Classical and Post-Classical periods in the Eastern Mediterranean, as it is not considered precise enough to solve specific chronological questions, often causing the attribution of historic monuments to be based on circumstantial evidence. This research, applied in Jerusalem, presents a novel approach to solve this problem. Integrating fieldwork, stratigraphy, and microarchaeology analyses with intense radiocarbon dating of charred remains in building materials beneath Wilson’s Arch, we absolutely dated monumental structures to very narrow windows of time—even to specific rulers. Wilson’s Arch was initiated by Herod the Great and enlarged during the Roman Procurators, such as Pontius Pilatus, in a range of 70 years, rather than 700 years, as previously discussed by scholars. The theater-like structure is dated to the days of Emperor Hadrian and left unfinished before 132–136 AD. Through this approach, it is possible to solve archaeological riddles in intensely urban environments in the historical periods.

Klima

JONGMAN 2021

Brenden Jongman, *Fraction of population at risk of floods is growing.* [nature](#) **596** (2021), 37–38.

Satellite imaging combined with population data shows that, globally, the number of people living in flood-prone areas is growing faster than is the number living on higher ground—greatly increasing the potential impact of floods.

LAZAGABASTER 2021

Ignacio A. Lazagabaster et al., *Rare crested rat subfossils unveil Afro-Eurasian ecological corridors synchronous with early human dispersals*. *PNAS* **118** (2021), e2105719118.

pnas118-e2105719118-Supplement.pdf

Biotic interactions between Africa and Eurasia across the Levant have invoked particular attention among scientists aiming to unravel early human dispersals. However, it remains unclear whether behavioral capacities enabled early modern humans to surpass the Saharo-Arabian deserts or if climatic changes triggered punctuated dispersals out of Africa. Here, we report an unusual subfossil assemblage discovered in a Judean Desert’s cliff cave near the Dead Sea and dated to between $\approx 42,000$ and at least $103,000$ y ago. Paleogenomic and morphological comparisons indicate that the specimens belong to an extinct subspecies of the eastern African crested rat, *Lophiomys imhausi maremortum subspecies nova*, which diverged from the modern eastern African populations in the late Middle Pleistocene $\approx 226,000$ to $165,000$ y ago. The reported paleomitogenome is the oldest so far in the Levant, opening the door for future paleo-DNA analyses in the region. Species distribution modeling points to the presence of continuous habitat corridors connecting eastern Africa with the Levant during the Last Interglacial $\approx 129,000$ to $116,000$ y ago, providing further evidence of the northern ingression of African biomes into Eurasia and reinforcing previous suggestions of the critical role of climate change in Late Pleistocene intercontinental biogeography. Furthermore, our study complements other paleoenvironmental proxies with local—instead of interregional—paleoenvironmental data, opening an unprecedented window into the Dead Sea rift paleolandscape.

Keywords: paleogenetics | geometric morphometrics | rodent | paleoenvironment | ecological models

Ignacio A. Lazagabaster, Valentina Rovelli, Pierre-Henri Fabre, Roi Porat, Micka Ullman, Uri Davidovich, Tal Lavi, Amir Ganor, Eitan Klein, Keren Weiss, Perach Nuriel, Meirav Meiri & Nimrod Marom

Significance: The extent and timing of paleoenvironmental connections between Africa and Eurasia during the last glacial and interglacial periods are key issues in relation to early dispersals of *Homo sapiens* out of Africa. However, direct evidence of synchronous faunal dispersals is sparse. We report the discovery near the Dead Sea of subfossils belonging to an ancient relative of the eastern African crested rat dated to between $\approx 42,000$ and at least $103,000$ y ago. Morphological comparisons, ancient DNA, and ecological modeling suggest that the Judean Desert was greener in the past and that continuous habitat corridors connected eastern Africa with the Levant. This finding strengthens the hypothesis that early human dispersals were prompted by climatic changes and Late Pleistocene intercontinental connectivity.

TELLMAN 2021

B. Tellman et al., *Satellite imaging reveals increased proportion of population exposed to floods*. *nature* **596** (2021), 80–86.

n596-0080-Supplement.pdf

Flooding affects more people than any other environmental hazard and hinders sustainable development^{1,2}. Investing in flood adaptation strategies may reduce the loss of life and livelihood caused by floods³. Where and how floods occur and who is exposed are changing as a result of rapid urbanization⁴, flood mitigation infrastructure⁵ and increasing settlements in floodplains⁶. Previous estimates of the global flood-exposed population have been limited by a lack of observational data, relying instead on models, which have high uncertainty^{3,7–11}. Here we use daily

satellite imagery at 250-metre resolution to estimate flood extent and population exposure for 913 large flood events from 2000 to 2018. We determine a total inundation area of 2.23 million square kilometres, with 255–290 million people directly affected by floods. We estimate that the total population in locations with satellite-observed inundation grew by 58–86 million from 2000 to 2015. This represents an increase of 20 to 24 per cent in the proportion of the global population exposed to floods, ten times higher than previous estimates⁷. Climate change projections for 2030 indicate that the proportion of the population exposed to floods will increase further. The high spatial and temporal resolution of the satellite observations will improve our understanding of where floods are changing and how best to adapt. The global flood database generated from these observations will help to improve vulnerability assessments, the accuracy of global and local flood models, the efficacy of adaptation interventions and our understanding of the interactions between landcover change, climate and floods.

B. Tellman, J. A. Sullivan, C. Kuhn, A. J. Kettner, C. S. Doyle, G. R. Brakenridge, T. A. Erickson & D. A. Slayback

Kultur

GROUCUTT 2021

Huw S. Groucutt & W. Christopher Carleton, *Mass-kill hunting and Late Quaternary ecology, New insights into the ‘desert kite’ phenomenon in Arabia*. [Journal of Archaeological Science: Reports](#) **37** (2021), 102995, 1–10.

JASRep037-a102995-Supplement1.pdf, JASRep037-a102995-Supplement2.xlsx

Over 6,000 ‘desert kites’—mass-kill stone hunting traps constructed at various times over the last 10,000 years—have been identified from northern Arabia to western central Asia. It has been proposed that kites had a significant impact on animal demography, leading to changes in ecology and human societies. While there has been considerable discussion regarding the function and chronology of kites, their spatial distribution is poorly understood. Here we report over 300 desert kites from several areas of the Arabian Peninsula, including \approx 500 km further south than previously suggested. Using satellite imagery, we studied their super-imposition revealing an extended chronology of kite-construction, including multiple phases of rebuilding in some cases and kites built relatively recently. This shows that desert kites were significantly more spatially and temporally widespread than previously believed, suggesting that they played a role in transforming Late Quaternary ecosystems and offering insights into the behaviour of human societies in challenging environments.

Keywords: Stone structures | Hunting | GIS | Remote sensing | Archaeology

Mathematik Klima

BOERS 2021

Niklas Boers, *Observation-based early-warning signals for a collapse of the Atlantic Meridional Overturning Circulation*. [Nature Climate Change](#) **11** (2021), 680–688.

NatClimCh11-680-Supplement.pdf

The Atlantic Meridional Overturning Circulation (AMOC), a major ocean current system transporting warm surface waters toward the northern Atlantic, has

been suggested to exhibit two distinct modes of operation. A collapse from the currently attained strong to the weak mode would have severe impacts on the global climate system and further multi-stable Earth system components. Observations and recently suggested fingerprints of AMOC variability indicate a gradual weakening during the last decades, but estimates of the critical transition point remain uncertain. Here, a robust and general early-warning indicator for forthcoming critical transitions is introduced. Significant early-warning signals are found in eight independent AMOC indices, based on observational sea-surface temperature and salinity data from across the Atlantic Ocean basin. These results reveal spatially consistent empirical evidence that, in the course of the last century, the AMOC may have evolved from relatively stable conditions to a point close to a critical transition.

Ostasien

DAI 2021

Jinqi Dai, Xipeng Cai, Jianhui Jin, Wei Ge, Yunming Huang, Wei Wu, Taoqin Xia, Fusheng Li & Xinxin Zuo, *Earliest arrival of millet in the South China coast dating back to 5,500 years ago*. [Journal of Archaeological Science](#) **129** (2021), 105356, 1–9.

[JAS129-a105356-Supplement.pdf](#)

Crop dispersal has long been recognised as an important topic in agricultural archaeology and food globalisation. The southern coastal region of China, including Fujian Province, is of particular interest as a key junction for crop dispersal into Taiwan and the Pacific islands from mainland China. However, due to poor preservation of macroplant fossils caused by the acidic soil condition, questions about when and where millet first arrived in this region remain a topic of debate. Our study focused on the millet phytoliths remains from three Neolithic sites in southeast coastal Fujian. Multiple dating methods, including charred carbon dating, phytolith carbon dating, and optically stimulated luminescence were used to construct the chronologies of the sites. The results reveal that the earliest millet phytoliths emerged in the Lower Tanshishan cultural layer of the Baitoushan site, which was initially occupied at 5.5 ka BP. After ca. 5.0 ka BP, common millet phytoliths were found in the Tanshishan cultural layers of all three sites. The microfossil of millet examined in this study was likely the earliest millet remains found in Fujian, indicating that millet may have arrived in the southern coast of China at least 5,500 years ago. These findings not only provide new insights to millet dispersal routes in China, but also have significant implications for crop communications between Taiwan and mainland China during the Neolithic age.

Keywords: Phytolith | Millet agriculture | Fujian | Lower Tanshishan culture | OSL dating