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References

Aktuell

Alwan 2021

Nisreen A. Alwan, *The road to addressing Long Covid.* science **373** (2021), 491–493. DOI:10.1126/science.abg7113.

Reporting, recognizing, and researching the chronic effects of COVID-19 will help those affected.

Hodcroft 2021

Emma B. Hodcroft et al., *Spread of a SARS-CoV-2 variant through Europe in the summer of 2020.* nature **595** (2021), 707–712. DOI:10.1038/s41586-021-03677-y.

n595-0707-Supplement.pdf

Following its emergence in late 2019, the spread of SARS-CoV-21,2 has been tracked by phylogenetic analysis of viral genome sequences in unprecedented detail3–5. Although the virus spread globally in early 2020 before borders closed, intercontinental travel has since been greatly reduced. However, travel within Europe resumed in the summer of 2020. Here we report on a SARS-CoV-2 variant, 20E (EU1), that was identified in Spain in early summer 2020 and subsequently spread across Europe. We find no evidence that this variant has increased transmissibility, but instead demonstrate how rising incidence in Spain, resumption of travel, and lack of effective screening and containment may explain the variant's success. Despite travel restrictions, we estimate that 20E (EU1) was introduced hundreds of times to European countries by summertime travellers, which is likely to have undermined local efforts to minimize infection with SARS-CoV-2. Our results illustrate how a variant can rapidly become dominant even in the absence of a substantial transmission advantage in favourable epidemiological settings. Genomic surveillance is critical for understanding how travel can affect transmission of SARS-CoV-2, and thus for informing future containment strategies as travel resumes.

Emma B. Hodcroft, Moira Zuber, Sarah Nadeau, Timothy G. Vaughan, Katharine H. D. Crawford, Christian L. Althaus, Martina L. Reichmuth, John E. Bowen, Alexandra C. Walls, Davide Corti, Jesse D. Bloom, David Veesler, David Mateo, Alberto Hernando, Iñaki Comas, Fernando González-Candelas, SeqCOVID-SPAIN consortium, Tanja Stadler & Richard A. Neher

Ledford 2021

Heidi Ledford, *Should children get COVID vaccines? What the science says.* nature **595** (2021), 638–639.

Lemey 2021

Philippe Lemey et al., *Untangling introductions and persistence in COVID-19 resurgence in Europe.* nature **595** (2021), 713–717. DOI:10.1038/s41586-021-03754-2.

n595-0713-Supplement.pdf

After the first wave of SARS-CoV-2 infections in spring 2020, Europe experienced a resurgence of the virus starting in late summer 2020 that was deadlier and more difficult to contain1. Relaxed intervention measures and summer travel have been implicated as drivers of the second wave2. Here we build a phylogeographical model to evaluate how newly introduced lineages, as opposed to the rekindling of persistent lineages, contributed to the resurgence of COVID-19 in Europe. We inform this model using genomic, mobility and epidemiological data from 10 European countries and estimate that in many countries more than half of the lineages circulating in late summer resulted from new introductions since 15 June 2020. The success in onward transmission of newly introduced lineages was negatively associated with the local incidence of COVID-19 during this period. The pervasive spread of variants in summer 2020 Highlights the threat of viral dissemination when restrictions are lifted, and this needs to be carefully considered in strategies to control the current spread of variants that are more transmissible and/or evade immunity. Our findings indicate that more effective and coordinated measures are required to contain the spread through cross-border travel even as vaccination is reducing disease burden.

Philippe Lemey, Nick Ruktanonchai, Samuel L. Hong, Vittoria Colizza, Chiara Poletto, Frederik Van den Broeck, Mandev S. Gill, Xiang Ji, Anthony Levasseur, Bas B. Oude Munnink, Marion Koopmans, Adam Sadilek, Shengjie Lai, Andrew J. Tatem, Guy Baele, Marc A. Suchard & Simon Dellicour

SCUDELLARI 2021

Megan Scudellari, *How the Coronavirus Infects Our Cells.* nature **595** (2021), 640–644.

WADMAN 2021

Meredith Wadman, *The overlooked superpower of mRNA vaccines.* science **373** (2021), 479. DOI:10.1126/science.373.6554.479.

Growing literature shows the vaccines are shutting down even asymptomatic viral invasion.

Anthropologie

HENSHILWOOD 2011

CHRISTOPHER S. HENSHILWOOD & FRANCESCO D'ERRICO (Hrsg.), *Homo Symbolicus*, *The dawn of language, imagination and spirituality.* (Amsterdam 2011).

Bibel

BERLIN 2009

Adele Berlin, *Sex and the Single Girl in Deuteronomy 22.* In: NILI SACHER FOX, DAVID A. GLATT-GILAD & MICHAEL J. WILLIAMS (Hrsg.), *Mishneh Todah*, *Studies in Deuteronomy and Its Cultural Environment in Honor of Jeffrey H. Tigay.* (Winona Lake 2009), 131–148.

Hays 2019

Christopher B. Hays, *'Make Peace With Me', The Josianic Origins of Isaiah 24–27*. Interpretation **73** (2019), 143–157.

Isaiah 24-27 has been an enduring mystery for scholars of the book. Contrary to theories that it is the latest part of the book, it is not apocalyptic; its imagery of divine feasting and conquering death have very ancient cognates; and its Hebrew language does not indicate lateness. The passage celebrates the receding of Assyrian power from Judah, and especially from the citadel at Ramat Rahel near Jerusalem, in the late seventh century. This was the time of King Josiah and his scribes, who saw a political opportunity and issued an overture to the former northern kingdom: "Make Peace With Me!"

Keywords: Isaiah (24-27) | Josiah | scribalism | Assyria | 7th century | resurrection | Judah | Israel/Northern Kingdom

Richelle 2021

Matthieu Richelle, *A re-examination of the reading bt dwd ("house of David") on the Mesha stele*. In: Shmuel Aḥituv, Hannah Cotton & Matthew Morgenstern (Hrsg.), *Ada Yardeni Volume*. Eretz-Israel 34 (Jerusalem 2021), 152–159.

What seems to be sure, in the end, is that it is very difficult to read anything in this part of the inscription. So for the time being, I would side with Parker (2018) and abstain from proposing a reading between B and W. the reading bt dwd is possible, but not required by the evidence; there exist many other possibilities.

Wilson 2021

Jake Wilson, יְהֹוָה *– Pronounced As It Is Written? The True Pronunciation Of YHWH According To Kabbalists (And Other Fools)*. Online **2021**, July 28.

The erroneous notion of Yehovah being the divine name has been disseminated since the Dark Ages, and advertising it as a new discovery seems at best misplaced. Both papal and rabbinic idolatries such as Trinitarianism or Kabbalah reach back to the mystery religions of Bavel, and it doesn't surprise that a gibberish name is primarily pushed by Rome. At the same time, Yehovah's revival appears symptomatic of man's unprecedented depravity which will fortunately soon be concluded by the Parousia.

Biologie

Ren 2021

Guangpeng Ren & Luca Fumagalli et al., *Large-scale whole-genome resequencing unravels the domestication history of Cannabis sativa*. Science Advances **7** (2021), eabg2286. DOI:10.1126/sciadv.abg2286.

Cannabis sativa has long been an important source of fiber extracted from hemp and both medicinal and recreational drugs based on cannabinoid compounds. Here, we investigated its poorly known domestication history using whole-genome resequencing of 110 accessions from worldwide origins. We show that C. sativa was first domesticated in early Neolithic times in East Asia and that all current hemp and drug cultivars diverged from an ancestral gene pool currently represented by feral plants and landraces in China. We identified candidate genes associated with traits differentiating hemp and drug cultivars, including branching pattern and cellulose/ lignin biosynthesis. We also found evidence for loss of function of genes involved in the synthesis of the two major biochemically competing cannabinoids during selection for increased fiber production or psychoactive properties. Our results provide a unique global view of the domestication of C. sativa and offer valuable genomic resources for ongoing functional and molecular breeding research.

Guangpeng Ren, Xu Zhang, Ying Li, Kate Ridout, Martha L. Serrano-Serrano, Yongzhi Yang, Ai Liu, Gudasalamani Ravikanth, Muhammad Ali Nawaz, Abdul Samad Mumtaz, Nicolas Salamin & Luca Fumagalli

Judentum

KOHLER 2021

Noa Sophie Kohler, *Negotiating Jewishness through genetic testing in the State of Israel*. Journal for Technology Assessment in Theory and Practice **30** (2021), ii, 36–40.

In Israel, several hundred thousand citizens form a minority group that wishes to be acknowledged as Jewish by the state authorities. Most of them immigrated from the former Soviet Union and cannot provide sufficient evidence of their maternal ancestors' affiliation with a Jewish community. This has a direct impact on their civil rights. Based on a scientific research article on matrilineal genetic markers among Eastern and Central European Jews, the rabbinical dean of an institute for advanced Jewish studies in Jerusalem proposed to accept, under certain conditions, the presence of specific genetic markers as legal proof of "Jewishness." Genetic testing here is meant to become a tool for empowerment and (re)claiming Jewish status. This case raises many questions concerning a biological understanding of Judaism and shows how genetic ancestry testing could be used to uphold the religious orthodox narrative.

Keywords: genetic ancestry testing | Jewishness | essentialism | citizenship

In Israel gehören mehrere hunderttausend Bürger einer Minderheit an, die von den staatlichen Behörden als jüdisch anerkannt werden möchte. Die meisten von ihnen stammen aus der ehemaligen Sowjetunion und können keine ausreichenden Beweise für die Zugehörigkeit ihrer Vorfahren mütterlicherseits zu einer jüdischen Gemeinde vorlegen. Das hat direkte Auswirkungen auf ihre Bürgerrechte. Auf der Grundlage eines wissenschaftlichen Forschungsartikels über matrilineare genetische Marker bei ost- und mitteleuropäischen Juden schlug der rabbinische Dekan eines Instituts für jüdische Studien in Jerusalem vor, unter bestimmten Bedingungen das Vorhandensein spezifischer genetischer Marker als rechtlichen Beweis für "Jüdischsein" zu akzeptieren. Gentests sollen hier als Instrument für Empowerment und die (Wieder-)Erlangung des jüdischen Status dienen. Dieser Fall wirft viele Fragen bezüglich eines biologischen Verständnisses von Judentum auf und zeigt, wie genetische Abstammungstests eingesetzt werden könnten, um das religiös-orthodoxe Narrativ aufrechtzuerhalten.

Klima

BERENGUER 2021

Erika Berenguer, Gareth D. Lennox & Jos Barlow et al., *Tracking the impacts of El Niño drought and fire in human-modified Amazonian forests*. PNAS **118** (2021), e2019377118.

pnas118-e2019377118-Supplement.pdf

With humanity facing an unprecedented climate crisis, the conservation of tropical forests has never been so important – their vast terrestrial carbon stocks can be turned into emissions by climatic and human disturbances. However, the duration of these effects is poorly understood, and it is unclear whether impacts are amplified in forests with a history of previous human disturbance. Here,we focus on the Amazonian epicenter of the 2015–16 El Niño, a region that encompasses 1.2 % of the Brazilian Amazon. We quantify, at high temporal resolution, the impacts of an extreme El Niño (EN) drought and extensive forest fires on plant mortality and carbon loss in undisturbed and human-modified forests. Mortality remained higher than pre-El Niño levels for 36 mo in EN-drought–affected forests and for 30 mo in EN-fire–affected forests. In EN-fire–affected forests, human disturbance significantly increased plant mortality. Our investigation of the ecological and physiological predictors of tree mortality showed that trees with lower wood density, bark thickness and leaf nitrogen content, as well as those that experienced greater fire intensity, were more vulnerable. Across the region, the 2015–16 El Niño led to the death of an estimated 2.5 ± 0.3 billion stems, resulting in emissions of 495 ± 94 Tg CO2. Three years after the El Niño, plant growth and recruitment had offset only 37 % of emissions. Our results show that limiting forest disturbance will not only help maintain carbon stocks, but will also maximize the resistance of Amazonian forests if fires do occur.*

Keywords: Amazon | degradation | El Niño | forest fires | logging

Erika Berenguer, Gareth D. Lennox, Joice Ferreira, Yadvinder Malhi, Luiz E. O. C. Arago, Julia Rodrigues Barreto, Fernando Del Bon Esprito-Santo, Axa Emanuelle S. Figueiredo, Filipe Frana, Toby Alan Gardner, Carlos A. Joly, Alessandro F. Palmeira, Carlos Alberto Quesada, Liana Chesini Rossi, Marina Maria Moraes de Seixas, Charlotte C. Smith, Kieran Withey & Jos Barlow

Significance: Amazonia is experiencing an increase in the frequency of extreme droughts and wildfires. However, the duration of their impacts on plant mortality and carbon stocks are poorly known, and it is unclear whether impacts are amplified in forests with a history of previous human disturbance. We show that plant mortality rates remain above baseline levels for over 3 y in forests affected by drought and 2.5 y in forests affected by both drought and fire. A history of human disturbance led to greater plant mortality in forests simultaneously affected by drought and fire. Our assessment of an area covering 1.2 % of the Brazilian Amazon shows that regional drought and fires can have globally relevant impacts on the world's carbon balance.

YANG 2021

Bao Yang et al., *Long-term decrease in Asian monsoon rainfall and abrupt climate change events over the past 6,700 years.* PNAS **118** (2021), e2102007118.

pnas118-e2102007118-Supplement.pdf

Asian summer monsoon (ASM) variability and its long-term ecological and societal impacts extending back to Neolithic times are poorly understood due to a lack of high-resolution climate proxy data. Here, we present a precisely dated and well-calibrated treering stable isotope chronology from the Tibetan Plateau with 1- to 5-y resolution that reflects high- to low-frequency ASM variability from 4680 BCE to 2011 CE. Superimposed on a persistent drying trend since the mid-Holocene, a rapid decrease in moisture availability between ≈2000 and ≈1500 BCE caused a dry hydroclimatic regime from ≈1675 to ≈1185 BCE, with mean precipitation estimated at 42 ± % and 5 ± 2 % lower than during themid-Holocene and the instrumental period, respectively. This second-millennium–BCE megadrought marks the mid-to late Holocene transition, during which regional forests declined

and enhanced aeolian activity affected northern Chinese ecosystems. We argue that this abrupt aridification starting ≈2000 BCE contributed to the shift of Neolithic cultures in northern China and likely triggered human migration and societal transformation.

Keywords: tree rings | stable isotopes | climate variability | megadrought | Asian summer monsoon

Bao Yang, Chun Qin, Achim Bräuning, Timothy J. Osborn, Valerie Trouet, Fredrik Charpentier Ljungqvist, Jan Esper, Lea Schneider, Jussi Grießinger, Ulf Büntgen, Sergio Rossi, Guanghui Dong, Mi Yan, Liang Ning, Jianglin Wang, Xiaofeng Wang, Suming Wang, Jürg Luterbacher, Edward R. Cook & Nils Chr. Stenseth

Significance: The variability of the Asian summer monsoon (ASM) is important for the functioning of ecological and societal systems at regional to continental scales, but the long-term evolution and interannual variability of this system is not well understood. Here, we present a stable isotope–based reconstruction of ASM variability covering 4680 BCE to 2011 CE. Superimposed on a gradual drying trend, a rapid drop in mean annual precipitation (>40 %) toward persistently drier conditions occurred in ≈1675 BCE. This megadrought caused regional forest deterioration and enhanced aeolian activity affecting Chinese ecosystems. We argue that this abrupt aridification starting ≈2000 BCE triggered waves of human migration and societal transformation in northern China, which contributed to the alteration of spatial pattern of ancient civilizations.

Kultur

VANDKILDE 2021

Helle Vandkilde, *Trading and weighing metals in Bronze Age Western Eurasia*. PNAS **118** (2021), e2110552118.

The stability of weight systems reflects directional knowledge transfer over two millennia (1). Transmissions of ideas likely also comprised new possibilities that could be acted upon, not least regarding metals. This commentary has looked deeper into the three geographical weight zones. Scientific and quantitative analyses in nexus with theoretical thinking provide the way forward, as the weighing article (1) demonstrates in a distinguished manner.

Mathematik

VOOSEN 2021

Paul Voosen, *Climate panel confronts implausibly hot models*. science **373** (2021), 474–475.

Major IPCC report likely to curb near-term projections with measured warming trend.

Last year, a landmark paper that largely eschewed models and instead used documented factors including ongoing warming trends calculated a likely climate sensitivity of between 2.6°C and 3.9°C (Science, 24 July 2020, p. 354). But many of the new models from leading centers showed warming of more than 5°C—uncomfortably outside these bounds.

The models were also out of step with records of past climate. For example, scientists used the new model from NCAR to simulate the coldest point of the most recent ice age, 20,000 years ago. Extensive paleoclimate records suggest Earth cooled nearly 6°C compared with preindustrial times, but the model, fed with low ice age CO2 levels, had temperatures plummeting by nearly twice that much, suggesting it was far too sensitive to the ups and downs of CO2. “That is clearly outside the range of what the geological data indicate.”

Methoden

Burmeister 2021

Stefan Burmeister, *Does the concept of genetic ancestry reinforce racism? A commentary on the discourse practice of archaeogenetics.* Journal for Technology Assessment in Theory and Practice **30** (2021), ii, 41–46.

Genetic ancestry is seen as an alternative to the problematic concept of race and is positioned against abusive racist and nationalist perspectives. The concept of genetic ancestry is nevertheless not free of racial categorizations. Increasingly, it is becoming an integral part of identity politics. Genetic ancestry is promoted as a way to give identity and visibility to marginalized groups but is also rejected as a form of biocolonialism. In xenophobic and racist discourses of right-wing groups, the concept has found fertile ground. The field of genetics is partly to blame for this since it opens the door to problematic identity discourses through a careless use of archaeological, ethnic, and genetic categories.

Keywords: ancestry | genetics | migration | race | racism

Genetische Abstammung wird als Gegenentwurf zum überkommenen Konzept der Rasse gesehen und gegen missbräuchliche rassistische und nationalistische Perspektiven in Stellung gebracht. Das genetische Abstammungskonzept ist dennoch nicht frei von rassischen Kategorisierungen. Zunehmend wird es zum integralen Bestandteil von Identitätspolitik. Genetische Abstammung wird als Möglichkeit propagiert, marginalisierten Gruppen Identität und Sichtbarkeit zu verschaffen, wird aber auch als eine Form des Biokolonialismus zurückgewiesen. In den xenophoben und rassistischen Diskursen rechter Gruppen hat das Konzept Konjunktur. Daran trägt die Genetik eine Mitschuld, da sie durch leichtfertigen Umgang mit archäologischen, ethnischen und genetischen Kategorien problematischen Identitätsdiskursen die Tür öffnet.