

References

Aktuell

CORNWALL 2020

Warren Cornwall, *Crushing coronavirus means ‘breaking the habits of a lifetime’, Behavior scientists have some tips.* [science 2020, abc2922](#). DOI:10.1126/science.abc2922.

The identity of a trusted messenger depends on the situation. It could be local religious leaders, politicians, sports figures, or celebrities, Gadarian says. [...] In a late March Instagram chat, basketball star Stephen Curry of California’s Golden State Warriors discussed the disease and how to avoid it [...] The video has had nearly half a million views on YouTube.

FORSTER 2020

Peter Forster, Lucy Forster, Colin Renfrew & Michael Forster, *Phylogenetic network analysis of SARS-CoV-2 genomes.* [PNAS 117 \(2020\), 9241–9243](#). DOI:10.1073/pnas.2004999117.

[pnas117-09241-Supplement.pdf](#)

In a phylogenetic network analysis of 160 complete human severe acute respiratory syndrome coronavirus 2 (SARS-Cov-2) genomes, we find three central variants distinguished by amino acid changes, which we have named A, B, and C, with A being the ancestral type according to the bat outgroup coronavirus. The A and C types are found in significant proportions outside East Asia, that is, in Europeans and Americans. In contrast, the B type is the most common type in East Asia, and its ancestral genome appears not to have spread outside East Asia without first mutating into derived B types, pointing to founder effects or immunological or environmental resistance against this type outside Asia. The network faithfully traces routes of infections for documented coronavirus disease 2019 (COVID-19) cases, indicating that phylogenetic networks can likewise be successfully used to help trace undocumented COVID-19 infection sources, which can then be quarantined to prevent recurrent spread of the disease worldwide.

Keywords: SARS-CoV-2 evolution | subtype | ancestral type

Significance: This is a phylogenetic network of SARS-CoV-2 genomes sampled from across the world. These genomes are closely related and under evolutionary selection in their human hosts, sometimes with parallel evolution events, that is, the same virus mutation emerges in two different human hosts. This makes character-based phylogenetic networks the method of choice for reconstructing their evolutionary paths and their ancestral genome in the human host. The network method has been used in around 10,000 phylogenetic studies of diverse organisms, and is mostly known for reconstructing the prehistoric population movements of humans and for ecological studies, but is less commonly employed in the field of virology.

GIESECKE 2020

Johan Giesecke & Edward Stringham, *Lockdown-Free Sweden Had It Right, Says World Health Organization, Interview with Prof. Johan Giesecke.* [American Institute for Economic Research 2020, Apr. 30](#).

<<http://www.aier.org/article/lockdown-free-sweden-had-it-right-says-world-health-organization-interview-with-prof-johan-gieseck>> (2020-05-02).

How long in a democracy do you think it would keep a lock down? How long will it take before people say, “no I’m not taking it”? You can do it in China. In China you can do it: you can tell people to stay at home and you can weld back that door, so they can’t get out. But in a democracy you can’t. And so it will be 3-4 weeks people will say, “Well, I don’t know anyone who had the COVID, and I haven’t met – and I want to go out; I want to go down to the pub.” And so how long do you think you could lock people up like this? Stay in your home, you need a permit to go to the shop.

But it will take a couple of months to climb down, from a lockdown. You can’t climb down from a lock down.

JONES 2020

Terry C. Jones et al., *An analysis of SARS-CoV-2 viral load by patient age*. [unknown \(2020\), preprint, 1–19](#).

Data on viral load, as estimated by real-time RT-PCR threshold cycle values from 3,712 COVID-19 patients were analysed to examine the relationship between patient age and SARS-CoV-2 viral load. Analysis of variance of viral loads in patients of different age categories found no significant difference between any pair of age categories including children. In particular, these data indicate that viral loads in the very young do not differ significantly from those of adults. Based on these results, we have to caution against an unlimited re-opening of schools and kindergartens in the present situation. Children may be as infectious as adults.

Terry C. Jones, Barbara Mühlemann, Talitha Veith, Marta Zuchowski, Jörg Hofmann, Angela Stein, Anke Edelmann, Victor Max Corman & Christian Drosten

KARNAUSKAS 2020

Kristopher B. Karnauskas, Shelly L. Miller & Anna C. Schapiro, *Fossil fuel combustion is driving indoor CO₂ toward levels harmful to human cognition*. [GeoHealth \(2020\), preprint, 1–21](#). DOI:10.1029/2019GH000237.

Human activities are elevating atmospheric carbon dioxide concentrations to levels unprecedented in human history. The majority of anticipated impacts of anthropogenic CO₂ emissions are mediated by climate warming. Recent experimental studies in the fields of indoor air quality and cognitive psychology and neuroscience, however, have revealed significant direct effects of indoor CO₂ levels on cognitive function. Here we shed light on this connection, and estimate the impact of continued fossil fuel emissions on human cognition. We conclude that indoor CO₂ levels may indeed reach levels harmful to cognition by the end of this century, and the best way to prevent this hidden consequence of climate change is to reduce fossil fuel emissions. Finally, we offer recommendations for a broad, interdisciplinary approach to improving such understanding and prediction.

Key Points

- Atmospheric carbon dioxide concentrations are reaching levels never experienced HomoSapiens
- Recent experiments have linked high indoor carbon dioxide concentrations to reduced cognitive function.
- Our models predict that future carbon emissions will increase indoor concentrations to levels harmful to human cognition.

LIU 2020

Yuan Liu et al., *Aerodynamic analysis of SARS-CoV-2 in two Wuhan hospitals*. *nature* (2020), preprint, 1–9. DOI:10.1038/s41586-020-2271-3.

The ongoing COVID-19 outbreak has spread rapidly on a global scale. While the transmission of SARS-CoV-2 via human respiratory droplets and direct contact is clear, the potential for aerosol transmission is poorly understood^{1–3}. This study investigated the aerodynamic nature of SARS-CoV-2 by measuring viral RNA in aerosols in different areas of two Wuhan hospitals during the COVID-19 outbreak in February and March 2020. The concentration of SARS-CoV-2 RNA in aerosols detected in isolation wards and ventilated patient rooms was very low, but it was elevated in the patients' toilet areas. Levels of airborne SARS-CoV-2 RNA in the majority of public areas was undetectable except in two areas prone to crowding, possibly due to infected carriers in the crowd. We found that some medical staff areas initially had high concentrations of viral RNA with aerosol size distributions showing peaks in submicrometre and/or supermicrometre regions, but these levels were reduced to undetectable levels after implementation of rigorous sanitization procedures. Although we have not established the infectivity of the virus detected in these hospital areas, we propose that SARS-CoV-2 may have the potential to be transmitted via aerosols. Our results indicate that room ventilation, open space, sanitization of protective apparel, and proper use and disinfection of toilet areas can effectively limit the concentration of SARS-CoV-2 RNA in aerosols. Future work should explore the infectivity of aerosolized virus.

Yuan Liu, Zhi Ning, Yu Chen, Ming Guo, Yingle Liu, Nirmal Kumar Gali, Li Sun, Yusen Duan, Jing Cai, Dane Westerdahl, Xinjin Liu, Ke Xu, Kin-fai Ho, Haidong Kan, Qingyan Fu & Ke Lan

MALLAPATY 2020

Smriti Mallapaty, *Will Coronavirus Antibody Tests Really Change Everything?* *nature* **580** (2020), 571–572.

The rapidly developed tests have been touted as society's way out of widespread lockdowns, but scientists say it will be a while before they are as useful as hoped.

In an analysis of 9 commercial tests available in Denmark, 3 lab-based tests had sensitivities in the range of 67–93% and specificities of 93–100%. In the same study, 5 out of 6 point-of-care tests had sensitivities ranging from 80% to 93%, and 80–100% specificity, but some kits were tested on fewer than 30 people.

RIVM 2020

Rijksinstituut voor Volksgezondheid, *Kinderen en COVID-19*. [Online 2020, Apr. 28](http://www.rivm.nl/coronavirus-covid-19/kinderen). <<http://www.rivm.nl/coronavirus-covid-19/kinderen>> (2020-05-02).

Wereldwijd zijn er relatief weinig kinderen gemeld met COVID-19, de ziekte die wordt veroorzaakt door het nieuwe coronavirus. Ook de Nederlandse gegevens bevestigen het beeld dat er al was: kinderen spelen een kleine rol in de verspreiding van het nieuwe coronavirus. De meeste verspreiding vindt plaats onder volwassenen en van volwassen familieleden naar kinderen. Verspreiding van COVID-19 onder kinderen of van kinderen naar volwassenen komt minder vaak voor. Omdat het virus nog nieuw is, doen we veel onderzoek om meer over het virus te weten te komen. Dit onderzoek gaat onder andere over de rol van kinderen in de verspreiding van het virus. Lees meer over wat het RIVM doet, hoe we tot deze conclusies komen en wat dit concreet betekent.

WURTZER 2020

Wurtzer S, Marechal V, Mouchel JM & Moulin L, *Time course quantitative detection of SARS-CoV-2 in Parisian wastewaters correlates with COVID-19 confirmed cases*. [medRxiv 2020, 20062679, 1–4](https://doi.org/10.1101/2020.04.12.20062679). DOI:10.1101/2020.04.12.20062679.

As a conclusion, this work demonstrated that a quantitative monitoring of SARS-CoV2 genomes in wastewaters should bring important and additional information for better survey of SARS-CoV2 circulation at the local or regional scale.

Altpaläolithikum

DOMÍNGUEZ-RODRIGO 2009

M. Domínguez-Rodrigo et al., *Unraveling hominin behavior at another anthropogenic site from Olduvai Gorge (Tanzania), New archaeological and taphonomic research at BK, Upper Bed II*. [Journal of Human Evolution 57 \(2009\), 260–283](https://doi.org/10.1098/rstb.2009.0283).

New archaeological excavations and research at BK, Upper Bed II (Olduvai Gorge, Tanzania) have yielded a rich and unbiased collection of fossil bones. These new excavations show that BK is a stratified deposit formed in a riverine setting close to an alluvial plain. The present taphonomic study reveals the second largest collection of hominin-modified bones from Olduvai, with abundant cut marks found on most of the anatomical areas preserved. Meat and marrow exploitation is reconstructed using the taphonomic signatures left on the bones by hominins. Highly cut-marked long limb shafts, especially those of upper limb bones, suggest that hominins at BK were actively engaged in acquiring small and middle-sized animals using strategies other than passive scavenging. The exploitation of large-sized game (Pelorovis) by Lower Pleistocene hominins, as suggested by previous researchers, is supported by the present study.

M. Domínguez-Rodrigo, A. Mabulla, H. T. Bunn, R. Barba, F. Diez-Martín, C. P. Egeland, E. Espílez, A. Egeland, J. Yravedra & P. Sánchez

Keywords: Olduvai Gorge | Meat-eating | Cut marks | Percussion marks | Taphonomy | Lower Pleistocene archaeology | Hunting | Scavenging

Amerika

FITZPATRICK 2020

Scott M. Fitzpatrick, *Ancient aquaculture and the rise of social complexity*. [PNAS 117 \(2020\), 9151–9153](https://doi.org/10.1073/pnas.1911153117).

This interesting case of aquaculture—the scale of which is quite extraordinary—is even more so when one considers that agriculture was nowhere to be found. This places Mound Key and its fish-capturing strategies in a unique position among complex societies and challenges the perceived trajectories that human societies must take to achieve certain milestones. The complexity inherent within the Calusa—documented through multiple lines of archaeological and environmental evidence—clearly shows that scholars have continued to underestimate the adaptive abilities of coastal peoples worldwide.

THOMPSON 2020

Victor D. Thompson et al., *Ancient engineering of fish capture and storage in southwest Florida*. [PNAS 117 \(2020\), 8374–8381](https://doi.org/10.1073/pnas.1911153117).

pnas117-08374-Supplement.pdf

In the 16th century, the Calusa, a fisher-gatherer-hunter society, were the most politically complex polity in Florida, and the archaeological site of Mound Key was their capital. Based on historic documents, the ruling elite at Mound Key controlled surplus production and distribution. The question remains exactly how such surplus pooling occurred and when such traditions were elaborated on and reflected in the built environment. Our work focuses on the “watercourts” and associated areas at Mound Key. These subrectangular constructions of shell and other sediments around centralized inundated areas have been variously interpreted. Here, we detail when these enclosures were constructed and their engineering and function. We argue that these structures were for large surplus capture and storage of aquatic resources that were controlled and managed by corporate groups.

Keywords: archaeology | Calusa | Florida | fisher-gatherer-hunters

Victor D. Thompson, William H. Marquardt, Michael Savarese, Karen J. Walker, Lee A. Newsom, Isabelle Lulewicz, Nathan R. Lawres, Amanda D. Roberts Thompson, Allan R. Bacon & Christoph A. Walser

Significance: Fish were captured and stored by Native Americans of southwestern Florida in complex walled structures called watercourts, constructed of shell and other sediments. These structures were engineered with knowledge of tidal systems, hydrology, and the biology of species to be stored in these courts. This work documents the considerable ability of the Calusa, a nonagricultural society, to engineer systems that significantly alter their natural environment. These structures are associated with an ever-growing population and complex system of governance among the Calusa of Florida.

Biologie

STOKSTAD 2020

Erik Stokstad, *Heat-protected plants offer cool surprise—greater yields, Engineered rice grows better at normal temperatures.* [science](#) **368** (2020), 355.

Chloroplasts, the organelles that host photosynthesis, have their own DNA, including a gene for D1, and most biologists assumed the protein had to be made there. But the chloroplast genome is much harder to tweak than genes in a plant cell’s nucleus.

Guo and colleagues tested the idea in the mustard *Arabidopsis thaliana*. They took its chloroplast gene for D1, coupled it to a stretch of DNA that turns on during heat stress, and moved it to the nucleus.

Datierung

GRÜN 1991

R. Grün & C. B. Stringer, *Electron Spin Resonance Dating and the Evolution of Modern Humans.* [Archaeometry](#) **33** (1991), 153–199.

An ESR signal used for dating should have the following properties.

- (i) A zeroing effect deletes all previously stored ESR intensity in the sample at the event which is to be dated.
- (ii) The signal intensity grows in proportion to the dose received.
- (iii) The signals must have a stability which is at least one order of magnitude higher than the age of the sample.

- (iv) The number of traps is constant or changes in a predictable manner. Recrystallization, crystal growth or phase transitions must not have occurred.
- (v) The ESR signal is not influenced by sample preparation (grinding, exposure to laboratory light) or anomalous fading.

Judentum

MILLER 2018

Shem Miller, *The Role of Performance and the Performance of Role, Cultural Memory in the Hodayot*. [Journal of Biblical Literature 137 \(2018\), 359–382](#).

In this article, I explore how the Hodayot—an anthology of thanksgiving hymns—were experienced through oral performance and used for identity formation in the sectarian communities associated with the Dead Sea Scrolls. In particular, I describe the impact of the Hodayot’s oral performance for both community members and a community leader, the Maskil. I begin with a survey of internal evidence that establishes public praise as a plausible sociolinguistic setting for the Hodayot. On the basis of performance criticism, I focus on the impact of the Hodayot as spoken words (speech) that appear in oral performance (reading). The Hodayot embodied the sectarian movement’s cultural memory, and the manner in which the Hodayot represent the “self “ enables speakers to imagine, or “re-member,” themselves through oral performance. On the one hand, the membership’s oral performance of the Hodayot functioned to produce collective identity, transform personal identity, and socialize members through narration of shared stories. On the other hand, the leadership utilized oral performance to self-identify with the pedagogical leadership, special knowledge, and institutional authority of the Maskil. Through oral performance, ordinary members could reimagine their identity as model sectarians, and a qualified leader could appropriate the Maskil’s office.

Methoden

HERMANN 2020

Raphael Hermann, Andrea Dolfini, Rachel J. Crellin, Quanyu Wang & Marion Uckelmann, *Bronze Age Swordsmanship, New Insights from Experiments and Wear Analysis*. [Journal of Archaeological Method and Theory \(2020\), preprint, 1–44](#). DOI:10.1007/s10816-020-09451-0.

JArchMethTheo2020.04-Hermann-Supplement.docx

The article presents a new picture of sword fighting in Middle and Late Bronze Age Europe developed through the Bronze Age Combat Project. The project investigated the uses of Bronze Age swords, shields, and spears by combining integrated experimental archaeology and metalwork wear analysis. The research is grounded in an explicit and replicable methodology providing a blueprint for future experimentation with, and wear analysis of, prehistoric copper-alloy weapons. We present a four-step experimental methodology including both controlled and actualistic experiments. The experimental results informed the wear analysis of 110 Middle and Late Bronze Age swords from Britain and Italy. The research has generated new understandings of prehistoric combat, including diagnostic and undiagnostic combat marks and how to interpret them; how to hold and use a Bronze Age sword; the degree of skill and training required for proficient combat; the realities of Bronze Age swordplay including the frequency of blade-on-blade contact;

the body parts and areas targeted by prehistoric sword fencers; and the evolution of fighting styles in Britain and Italy from the late 2nd to the early 1st millennia BC.

Keywords: European Bronze Age | Experimental archaeology. Metalworkwear analysis | Warfare and violence | Combat archaeology

Ozeanien

HARRIS 2020

Daniel N. Harris et al., *Evolutionary history of modern Samoans.*

[PNAS 117 \(2020\), 9458–9465.](#)

[pnas117-09458-Supplement1.pdf](#), [pnas117-09458-Supplement2.pdf](#)

Archaeological studies estimate the initial settlement of Samoa at 2,750 to 2,880 y ago and identify only limited settlement and human modification to the landscape until about 1,000 to 1,500 y ago. At this point, a complex history of migration is thought to have begun with the arrival of people sharing ancestry with Near Oceanic groups (i.e., Austronesian-speaking and Papuan-speaking groups), and was then followed by the arrival of non-Oceanic groups during European colonialism. However, the specifics of this peopling are not entirely clear from the archaeological and anthropological records, and is therefore a focus of continued debate. To shed additional light on the Samoan population history that this peopling reflects, we employ a population genetic approach to analyze 1,197 Samoan high-coverage whole genomes. We identify population splits between the major Samoan islands and detect asymmetrical gene flow to the capital city. We also find an extreme bottleneck until about 1,000 y ago, which is followed by distinct expansions across the islands and subsequent bottlenecks consistent with European colonization. These results provide for an increased understanding of Samoan population history and the dynamics that inform it, and also demonstrate how rapid demographic processes can shape modern genomes.

Keywords: genetically understudied populations | Oceania | Austronesian | rare variants | fine-scale population structure

Daniel N. Harris, Michael D. Kessler, Amol C. Shetty, Daniel E. Weeks, Ryan L. Minster, Sharon Browning, Ethan E. Cochrane, Ranjan Deka, Nicola L. Hawley, Muagututi'a Sefuiva Reupena, Take Naseri, Trans-Omics for Precision Medicine Consortium, TOPMed Population Genetics Working Group, Stephen T. McGarvey & Timothy D. O'Connor

Significance: There are multiple archaeological debates regarding early Samoan population history. Here, we add genetic data to this discussion, which supports an initial small population size at the founding of the Samoan islands. We also indicate a major demographic change approximately 1,000 y ago that mirrors the archaeological record. In addition, we demonstrate the utility of rare genetic variants in identifying sparse population structure. These genetic results help establish a detailed demographic model for the Samoan population, which will aid in future studies of Oceanic populations for both history and disease.