

References

Aktuell

ALTMANN 2021

Daniel M. Altmann, Rosemary J. Boyton & Rupert Beale, *Immunity to SARS-CoV-2 variants of concern*. [science](#) **371** (2021), 1103–1104. DOI:10.1126/science.abg7404.

Variants show variable escape from vaccine immunity, but residual protection may suffice.

CHALLEN 2021

Robert Challen, Ellen Brooks-Pollock, Jonathan M. Read, Louise Dyson, Krasimira Tsaneva-Atanasova & Leon Danon, *Risk of mortality in patients infected with SARS-CoV-2 variant of concern 202012/1, Matched cohort study*. [British Medical Journal](#) **372** (2021), n579. DOI:10.1136/bmj.n579.

The probability that the risk of mortality is increased by infection with VOC-202012/01 is high. If this finding is generalisable to other populations, infection with VOC-202012/1 has the potential to cause substantial additional mortality compared with previously circulating variants. Healthcare capacity planning and national and international control policies are all impacted by this finding, with increased mortality lending weight to the argument that further coordinated and stringent measures are justified to reduce deaths from SARS-CoV-2.

FARIA 2021

Nuno R. Faria et al., *Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil*. [unknown](#) (2021), preprint, 1–44.

Cases of SARS-CoV-2 infection in Manaus, Brazil, resurged in late 2020, despite high levels of previous infection there. Through genome sequencing of viruses sampled in Manaus between November 2020 and January 2021, we identified the emergence and circulation of a novel SARS-CoV-2 variant of concern, lineage P.1, that acquired 17 mutations, including a trio in the spike protein (K417T, E484K and N501Y) associated with increased binding to the human ACE2 receptor. Molecular clock analysis shows that P.1 emergence occurred around early November 2020 and was preceded by a period of faster molecular evolution. Using a two-category dynamical model that integrates genomic and mortality data, we estimate that P.1 may be 1.4–2.2 times more transmissible and able to evade 25–61 % of protective immunity elicited by previous infection with non-P.1 lineages. Enhanced global genomic surveillance of variants of concern, which may exhibit increased transmissibility and/or immune evasion, is critical to accelerate pandemic responsiveness.

One-Sentence Summary: We report the evolution and emergence of a SARS-CoV-2 lineage of concern associated with rapid transmission in Manaus.

KUŚMIERZ 2021

Łukasz Kuśmierz & Taro Toyozumi, *Infection curves on small-world networks are linear only in the vicinity of the critical point*. [PNAS 118 \(2021\), e2024297118](#).

MCCARTHY 2021

Kevin R. McCarthy et al., *Recurrent deletions in the SARS-CoV-2 spike glycoprotein drive antibody escape*. [science 371 \(2021\), 1139–1142](#). DOI:10.1126/science.abf6950.

[s371-1139-Supplement.pdf](#)

Zoonotic pandemics, such as that caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), can follow the spillover of animal viruses into highly susceptible human populations. The descendants of these viruses have adapted to the human host and evolved to evade immune pressure. Coronaviruses acquire substitutions more slowly than other RNA viruses. In the spike glycoprotein, we found that recurrent deletions overcome this slow substitution rate. Deletion variants arise in diverse genetic and geographic backgrounds, transmit efficiently, and are present in novel lineages, including those of current global concern. They frequently occupy recurrent deletion regions (RDRs), which map to defined antibody epitopes. Deletions in RDRs confer resistance to neutralizing antibodies. By altering stretches of amino acids, deletions appear to accelerate SARS-CoV-2 antigenic evolution and may, more generally, drive adaptive evolution.

Kevin R. McCarthy, Linda J. Rennick, Sham Nambulli, Lindsey R. Robinson-McCarthy, William G. Bain, Ghady Haidar & W. Paul Duprex

MALLAPATY 2021

Smriti Mallapaty, *Where Did Covid Come From? Five Mysteries That Remain*. [nature 591 \(2021\), 188–189](#).

In the wake of a World Health Organization investigation, scientists still have questions.

MERZON 2021

Eugene Merzon et al., *The use of aspirin for primary prevention of cardiovascular disease is associated with a lower likelihood of COVID-19 infection*. [FEBS Journal \(2021\), preprint, 1–29](#). DOI:10.1111/FEBS.15784.

Acetylsalicylic acid (aspirin) is commonly used for primary and secondary prevention of cardiovascular diseases. Aspirin use is associated with better outcomes among COVID-19 positive patients. We hypothesized that aspirin use for primary cardiovascular disease prevention might have a protective effect on COVID-19 susceptibility and disease duration. We conducted a retrospective population-based cross-sectional study, utilizing data from the Leumit Health Services database.

The proportion of patients treated with aspirin was significantly lower among the COVID-19-positive group, as compared to the COVID-19-negative group (73 (11.03 %) vs. 1548 (15.77 %); $p=0.001$). Aspirin use was associated with lower likelihood of COVID-19 infection, as compared to non-users (adjusted OR 0.71 (95 % CI, 0.52 to 0.99; $p=0.041$). Aspirin users were older (68.06 ± 12.79 vs. 56.63 ± 12.28 years of age; $p<0.001$), presented a lower BMI (28.77 ± 5.4 vs. 30.37 ± 4.55 ; $p<0.0189$) and showed higher prevalence of hypertension (56, 76.71 %), diabetes (47, 64.38 %) and COPD (11, 15.07 %) than showed the aspirin non-users (151, 25.64 %, $p<0.001$; 130, 22.07 %, $p<0.001$; and 43, 7.3 %, $p=0.023$, respectively).

Moreover, COVID-19 disease duration (considered as the time between the first positive and second negative COVID-19 RT-PCR test results) among aspirin users was significantly shorter, as compared to aspirin non-users (19.8 ± 7.8 vs. 21.9 ± 7.9 $p=0.045$). Among hospitalized COVID-positive patients, a higher proportion of surviving subjects were treated with aspirin (20, 19.05%), as opposed to 1 dead subject (14.29%), although this difference was not significant ($p=0.449$). In conclusion, we observed inverse association between the likelihood of COVID-19 infection, disease duration and mortality and aspirin use for primary prevention.

Keywords: aspirin | COVID-19 | Israeli cohort | disease likelihood

Eugene Merzon, Ilan Green, Shlomo Vinker, Avivit Golan-Cohen, Alessandro Gorohovski, Eva Avramovich, Milana Frenkel-Morgenstern and Eli Magen

MUIK 2021

Alexander Muik et al., *Neutralization of SARS-CoV-2 lineage B.1.1.7 pseudovirus by BNT162b2 vaccine-elicited human sera.* [science 371 \(2021\), 1152–1153. DOI:10.1126/science.abg6105.](#)

[s371-1152-Supplement.pdf](#)

Recently, a new severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) lineage called B.1.1.7 (variant of concern: VOC 202012/01), which is reported to spread more efficiently and faster than other strains, emerged in the United Kingdom. This variant has an unusually large number of mutations, with 10 amino acid changes in the spike (S) protein, raising concerns that its recognition by neutralizing antibodies may be affected. In this study, we tested SARS-CoV-2-S pseudoviruses bearing either the Wuhan reference strain or the B.1.1.7 lineage spike protein with sera of 40 participants who were vaccinated in a previously reported trial with the messenger RNA-based COVID-19 vaccine BNT162b2. The immune sera had slightly reduced but overall largely preserved neutralizing titers against the B.1.1.7 lineage pseudovirus. These data indicate that the B.1.1.7 lineage will not escape BNT162b2-mediated protection.

Alexander Muik, Ann-Kathrin Wallisch, Bianca Sanger, Kena A. Swanson, Julia Muhl, Wei Chen, Hui Cai, Daniel Maurus, Ritu Sarkar, zlem Tureci, Philip R. Dormitzer & Ugur Sahin

TURNER 2021

Stefan Thurner, Peter Klimek & Rudolf Hanel, *A network-based explanation of why most COVID-19 infection curves are linear, Reply to Kuśmierz and Toyozumi.* [PNAS 118 \(2021\), e2100906118.](#)

Anthropologie

PONTZER 2021

Herman Pontzer et al., *Evolution of water conservation in humans.* [Current Biology \(2021\), preprint, 1–24. DOI:10.1016/j.cub.2021.02.045.](#)

To sustain life, humans and other terrestrial animals must maintain a tight balance of water gain and water loss each day.^{1–3} However, the evolution of human water balance physiology is poorly understood due to the absence of comparative measures from other hominoids. While humans drink daily to maintain water balance, rainforest-living great apes typically obtain adequate water from their food and can go days or weeks without drinking^{4–6}. Here, we compare isotope-depletion measures of water turnover (L/d) in zoo- and rainforest-sanctuary-housed apes (chimpanzees, bonobos, gorillas, and orangutans) with 5 diverse human populations, including a hunter-gatherer community in a semi-arid savannah. Across

the entire sample, water turnover was strongly related to total energy expenditure (TEE, kcal/d), physical activity, climate (ambient temperature and humidity), and fat free mass. In analyses controlling for those factors, water turnover was 30 % to 50 % lower in humans than in other apes despite humans' greater sweating capacity. Water turnover in zoo and sanctuary apes was similar to estimated turnover in wild populations, as was the ratio of water intake to dietary energy intake (.2.8 mL/kcal). However, zoo and sanctuary apes ingested a greater ratio of water to dry matter of food, which might contribute to digestive problems in captivity. Compared to apes, humans appear to target a lower ratio of water/energy intake (.1.5 mL/kcal). Water stress due to changes in climate, diet, and behavior apparently led to previously unknown water conservation adaptations in hominin physiology.

Highlights:

- Humans have evolved to use less water per day than other ape species
- Human drinking regulation apparently targets lower water/ dietary energy ratio
- Water-conserving mechanisms in humans are unclear but may include the external nose
- Zoo apes may benefit from diets that match dietary water/ energy ratios in the wild

In brief: Pontzer et al. use isotope depletion to show that humans have evolved to use less water per day. Apes in zoos and sanctuaries adjust their drinking to obtain a similar ratio of dietary water/energy as wild ape diets. Humans across diverse lifestyles, including hunter-gatherers, habitually consume a lower water/energy ratio than apes.

Herman Pontzer, Mary H. Brown, Brian M. Wood, David A. Raichlen, Audax Z. P. Mabulla, Jacob A. Harris, Holly Dunsworth, Brian Hare, Kara Walker, Amy Luke, Lara R. Dugas, Dale Schoeller, Jacob Plange-Rhule, Pascal Bovet, Terrence E. Forrester, Melissa Emery Thompson, Robert W. Shumaker, Jessica M. Rothman, Erin Vogel, Fransiska Sulisty, Shauhin Alavi, Didik Prasetyo, Samuel S. Urlacher & Stephen R. Ross

Archäologie

DORNISCH 2015

Klaus Dornisch, *Sagenhaftes Äthiopien, Archäologie, Geschichte, Religion.* (Darmstadt 2019).

UELSBERG 2020

GABRIELE UELSBERG & MATTHIAS WEMHOFF (Hrsg.), *Germanen, Eine archäologische Bestandsaufnahme.* (Darmstadt 2020).

Biologie

DOLJA 2021

Valerian V. Dolja, *Rapid emergence of virus–host mutualism under stress.* [PNAS 118 \(2021\), e2100936118.](#)

GONZÁLEZ 2021

Rubén González, Anamarija Butković & Santiago F. Elena et al., *Plant virus evolution under strong drought conditions results in a transition from parasitism to mutualism.* [PNAS 118 \(2021\), e2020990118.](#)

pnas118-e2020990118-Supplement.pdf

Environmental conditions are an important factor driving pathogens' evolution. Here, we explore the effects of drought stress in plant virus evolution. We evolved turnip mosaic potyvirus in well-watered and drought conditions in *Arabidopsis thaliana* accessions that differ in their response to virus infection. Virus adaptation occurred in all accessions independently of watering status. Drought-evolved viruses conferred a significantly higher drought tolerance to infected plants. By contrast, nonsignificant increases in tolerance were observed in plants infected with viruses evolved under standard watering. The magnitude of this effect was dependent on the plant accessions. Differences in tolerance were correlated to alterations in the expression of host genes, some involved in regulation of the circadian clock, as well as in deep changes in the balance of phytohormones regulating defense and growth signaling pathways. Our results show that viruses can promote host survival in situations of abiotic stress, with the magnitude of such benefit being a selectable trait.

Keywords: virus evolution | mutualism | experimental evolution | gene expression | hormone signaling

Significance: Viruses are seen as selfish pathogens that harm their hosts to ensure their own survival. However, metagenomic studies are drawing a new picture in which viruses are present everywhere and not always associated to diseases. A classic observation in plant pathology is that the outcome of infection depends on environmental conditions. Here, using experimental evolution, we show that the relationship between a plant virus and its natural host can evolve from pathogenic to mutualistic under severe drought conditions. While viral strains evolved in normal watering conditions increased their virulence, drought-evolved viral strains confer plants with greater resistance to drought. We show that this transition to mutualism depends on a complex reorganization of hormone-induced signaling pathways and changes in gene expression.

Rubén González, Anamarija Butković, Francisco J. Escaray, Javier Martínez-Latorre, Ízan Melero, Enric Pérez-Parets, Aurelio Gómez-Cadenas, Pedro Carrasco & Santiago F. Elena

ROCA 2021

Alfred L. Roca, *A mammoth step back in genomic time.* [nature 591 \(2021\), 208–209.](#)

DNA has been retrieved from mammoth specimens that are more than one million years old. Comparing the genomes of these animals and their descendants provides insights into the changes that occurred as one species evolved into another.

VAN DER VALK 2021

Tom van der Valk, Patrícia Pečnerová, David Díez-del-Molino, Pavel Nikolskiy & Love Dalén et al., *Million-year-old DNA sheds light on the genomic history of mammoths.* [nature 591 \(2021\), 265–269.](#)

n591-0265-Supplement.pdf

Temporal genomic data hold great potential for studying evolutionary processes such as speciation. However, sampling across speciation events would, in many cases, require genomic time series that stretch well back into the Early Pleistocene subepoch. Although theoretical models suggest that DNA should survive on this timescale¹, the oldest genomic data recovered so far are from a horse specimen dated to 780– 560 thousand years ago². Here we report the recovery of genome-wide data from three mammoth specimens dating to the Early and Middle Pleistocene subepochs, two of which are more than one million years old. We find

that two distinct mammoth lineages were present in eastern Siberia during the Early Pleistocene. One of these lineages gave rise to the woolly mammoth and the other represents a previously unrecognized lineage that was ancestral to the first mammoths to colonize North America. Our analyses reveal that the Columbian mammoth of North America traces its ancestry to a Middle Pleistocene hybridization between these two lineages, with roughly equal admixture proportions. Finally, we show that the majority of protein-coding changes associated with cold adaptation in woolly mammoths were already present one million years ago. These findings highlight the potential of deep-time palaeogenomics to expand our understanding of speciation and long-term adaptive evolution.

Tom van der Valk, Patrícia Pečnerová, David Díez-del-Molino, Anders Bergström, Jonas Oppenheimer, Stefanie Hartmann, Georgios Xenikoudakis, Jessica A. Thomas, Marianne Dehasque, Ekin Saglican, Fatma Rabia Fidan, Ian Barnes, Shanlin Liu, Mehmet Somel, Peter D. Heintzman, Pavel Nikolskiy, Beth Shapiro, Pontus Skoglund, Michael Hofreiter, Adrian M. Lister, Anders Götherström & Love Dalén

Datierung

FIACCAVENTO 2014

Chiara Fiaccavento, *Destructions as Historical Markers Towards the End of the 2nd and During the 1st millennium bc in Southern Levant*. In: LORENZO NIGRO (Hrsg.), *Reading Catastrophes: Earthquakes, Floods, Famines, Epidemics between Egypt and Palestine – 3rd–1st millennium BC, Proceedings of the International Conference “Reading Catastrophes”, held in Rome, 3rd–4th December 2012*. ROSAPAT 11 (Rome 2014), 205–259.

Iron Age II saw the emergence of the tribe-based entities of Israel before, and Judah later, along with elements of continuity from the previous period, such as the Phoenician and Philistine towns on the coastal plain, inserted in the vaster mosaic of the rise of the national states all along the Syro-Palestinian strip (in 9th - 8th centuries BC in the north, and in 8th -7th centuries BC in the south). In spite of their cultural vivacity, with important urbanistic and architectural achievements, rich artistic and craft productions, religious and literary creations, the small Levantine entities, from a political point of view, remained always easily to threaten by the giant eastern empires. The threaten became concrete at least three times: to a lesser extent in the 9th century BC in the combat with the Aramaeans of Damascus, but much more with the intervening destructive violence of the Assyrian and Babylonian empires, in the 8th and 7th/6th centuries BC. This normal, yet catastrophic, historic curve found in the deportation of the ruling class of Judah in Babylonia the turning point for a new history, anchored to the past but projected in the preservation, accentuation and reconstruction of the idea of national identity. Defeat and destruction, deportation and subjection are disasters that the sons of Israel [or the God of Israel?] succeeded to overturn through religious ideology and historiography, until to transform it into the secret of their millennial resilience success.

HUBLIN 2021

Jean-Jacques Hublin, *How old are the oldest Homo sapiens in Far East Asia?* PNAS 118 (2021), e2101173118.

Once more, we learn that whenever possible, the direct dating of hominin remains by radiocarbon and now by paleogenetics is essential. Furthermore, if ages established by so-called absolute dating methods seem to have the whole weight of hard science behind them, at the same time all these methods do not offer the same level of reliability and accuracy. Ultimately, in archeology like in other sciences, only coherence of the results obtained by different methods and replication of the observations can guarantee the validity of our models.

Islam

UEBELE 2001

Wolfram Uebele, „Viele Verführer sind in die Welt ausgegangen“, *Die Gegner in den Briefen des Ignatius von Antiochien und in den Johannesbriefen*. (Stuttgart 2001).

Kultur

ESHEL 2021

Tzilla Eshel, Ayelet Gilboa, Naama Yahalom-Mack, Ofir Tirosh & Yigal Erel, *Debasement of silver throughout the Late Bronze – Iron Age transition in the Southern Levant, Analytical and cultural implications*. [Journal of Archaeological Science](#) **125** (2021), 105268, 1–24.

The study of silver, which was an important mean of currency in the Southern Levant during the Bronze and Iron Age periods (≈ 1950 – 586 BCE), revealed an unusual phenomenon. Silver hoards from a specific, yet rather long timespan, ≈ 1200 – 950 BCE, contained mostly silver alloyed with copper. This alloying phenomenon is considered here for the first time, also with respect to previous attempts to provenance the silver using lead isotopes. Eight hoards were studied, from which 86 items were subjected to chemical and isotopic analysis. This is, by far, the largest dataset of sampled silver from this timespan in the Near East. Results show the alloys, despite their silvery sheen, contained high percentages of Cu, reaching up to 80% of the alloy. The Ag–Cu alloys retained a silvery tint using two methods, either by using an enriched silver surface to conceal a copper core, or by adding arsenic and antimony to the alloy. For the question of provenance, we applied a mixing model which simulates the contribution of up to three end members to the isotopic composition of the studied samples. The model demonstrates that for most samples, the more likely combination is that they are alloys of silver from Aegean Anatolian ores, Pb-poor copper, and Pb-rich copper from local copper mines in the Arabah valley (Timna and Faynan). Another, previously suggested possibility, namely that a significant part of the silver originated from the West Mediterranean, cannot be validated analytically. Contextualizing these results, we suggest that the Bronze Age collapse around the Mediterranean led to the termination of silver supply from the Aegean to the Levant in the beginning of the 12th century BCE, causing a shortage of silver. The local administrations initiated sophisticated devaluation methods to compensate for the lack of silver – a suspected forgery. It is further suggested that following the Egyptian withdrawal from Canaan around the mid-12th century BCE, Cu–Ag alloying continued, with the use of copper from Faynan instead of Timna. The revival of long-distance silver trade is evident only in the Iron Age IIA (starting ≈ 950 BCE), when silver was no longer alloyed with copper, and was imported from Anatolia and the West Mediterranean.

Keywords: Silver hoards | Alloys | Lead isotopic analysis | Debasement | Arsenic
| Bronze age collapse | Mediterranean trade

Politik

AGERSNAP 2020

Ole Agersnap, Amalie Jensen & Henrik Kleven, *The Welfare Magnet Hypothesis, Evidence from an Immigrant Welfare Scheme in Denmark*. [American Economic Review: Insights 2 \(2020\), 527–542](#).

We study the effects of welfare generosity on international migration using reforms of immigrant welfare benefits in Denmark. The first reform, implemented in 2002, lowered benefits for non-EU immigrants by about 50 percent, with no changes for natives or EU immigrants. The policy was later repealed and reintroduced. Based on a quasi-experimental research design, we find sizable effects: the benefit reduction reduced the net flow of immigrants by about 5,000 people per year, and the subsequent repeal of the policy reversed the effect almost exactly. The implied elasticity of migration with respect to benefits equals 1.3. This represents some of the first causal evidence on the welfare magnet hypothesis. (JEL F22, H53, I38, J15)

Religion

WAYTZ 2010

Adam Waytz, John Cacioppo & Nicholas Epley, *Who Sees Human? The Stability and Importance of Individual Differences in Anthropomorphism*. [Perspectives on Psychological Science 5 \(2010\), 219–232](#).

Anthropomorphism is a far-reaching phenomenon that incorporates ideas from social psychology, cognitive psychology, developmental psychology, and the neurosciences. Although commonly considered to be a relatively universal phenomenon with only limited importance in modern industrialized societies—more cute than critical—our research suggests precisely the opposite. In particular, we provide a measure of stable individual differences in anthropomorphism that predicts three important consequences for everyday life. This research demonstrates that individual differences in anthropomorphism predict the degree of moral care and concern afforded to an agent, the amount of responsibility and trust placed on an agent, and the extent to which an agent serves as a source of social influence on the self. These consequences have implications for disciplines outside of psychology including human–computer interaction, business (marketing and finance), and law. Concluding discussion addresses how understanding anthropomorphism not only informs the burgeoning study of nonpersons, but how it informs classic issues underlying person perception as well.

Keywords: anthropomorphism | social cognition | individual differences

Sprachlehre

LIPFFERT 1955

Klementine Lipffert, *Symbol-Fibel, Eine Hilfe zum Betrachten und Deuten mittelalterlicher Bildwerke*. (Kassel ⁶1976).

SCHWARZ-WINKLHOFER 1972

I. Schwarz-Winklhofer & H. Biedermann, *Das Buch der Zeichen und Symbole*. (Wiesbaden ⁵2004).