

References

Aktuell

AZIMI 2021

Parham Azimi, Zahra Keshavarz, Jose Guillermo Cedeno Laurent, Brent Stephens & Joseph G. Allen, *Mechanistic transmission modeling of COVID-19 on the Diamond Princess cruise ship demonstrates the importance of aerosol transmission*. *PNAS* **118** (2021), e2015482118. DOI:10.1073/pnas.2015482118.

[pnas118-e2015482118-Supplement.pdf](#)

Several lines of existing evidence support the possibility of airborne transmission of coronavirus disease 2019 (COVID-19). However, quantitative information on the relative importance of transmission pathways of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) remains limited. To evaluate the relative importance of multiple transmission routes for SARS-CoV-2, we developed a modeling framework and leveraged detailed information available from the Diamond Princess cruise ship outbreak that occurred in early 2020. We modeled 21,600 scenarios to generate a matrix of solutions across a full range of assumptions for eight unknown or uncertain epidemic and mechanistic transmission factors. A total of 132 model iterations met acceptability criteria ($R^2 > 0.95$ for modeled vs. reported cumulative daily cases and $R^2 > 0$ for daily cases). Analyzing only these successful model iterations quantifies the likely contributions of each defined mode of transmission. Mean estimates of the contributions of short-range, longrange, and fomite transmission modes to infected cases across the entire simulation period were 35 %, 35 %, and 30 %, respectively. Mean estimates of the contributions of larger respiratory droplets and smaller respiratory aerosols were 41 % and 59 %, respectively. Our results demonstrate that aerosol inhalation was likely the dominant contributor to COVID-19 transmission among the passengers, even considering a conservative assumption of high ventilation rates and no air recirculation conditions for the cruise ship. Moreover, close-range and long-range transmission likely contributed similarly to disease progression aboard the ship, with fomite transmission playing a smaller role. The passenger quarantine also affected the importance of each mode, demonstrating the impacts of the interventions.

Keywords: COVID-19 | transmission risk model | aerosol transmission | Diamond Princess Cruise Ship | built environment

Significance: We find that airborne transmission likely accounted for >50 % of disease transmission on the Diamond Princess cruise ship, which includes inhalation of aerosols during close contact as well as longer range. These findings underscore the importance of implementing public health measures that target the control of inhalation of aerosols in addition to ongoing measures targeting control of large-droplet and fomite transmission, not only aboard cruise ships but in other indoor environments as well. Guidance from health organizations should include a greater emphasis on controls for reducing spread by airborne transmission. Last, although our work is based on a cruise ship outbreak of COVID-19, the model approach can be applied to other indoor environments and other infectious diseases.

LEWIS 2021

Dyani Lewis, *The Superspreading Problem*. *nature* **590** (2021), 544–546.

Uneven transmission of the SARS-CoV-2 coronavirus has had tragic consequences — but also offers clues for how best to target control measures.

NÉANT 2021

Nadège Néant et al., *Modeling SARS-CoV-2 viral kinetics and association with mortality in hospitalized patients from the French COVID cohort*. *PNAS* **118** (2021), e2017962118. DOI:10.1073/pnas.2017962118.

The characterization of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) viral kinetics in hospitalized patients and its association with mortality is unknown. We analyzed death and nasopharyngeal viral kinetics in 655 hospitalized patients from the prospective French COVID cohort. The model predicted a median peak viral load that coincided with symptom onset. Patients with age ≥ 65 y had a smaller loss rate of infected cells, leading to a delayed median time to viral clearance occurring 16 d after symptom onset as compared to 13 d in younger patients ($P < 10^{-4}$). In multivariate analysis, the risk factors associated with mortality were age ≥ 65 y, male gender, and presence of chronic pulmonary disease (hazard ratio [HR] > 2.0). Using a joint model, viral dynamics after hospital admission was an independent predictor of mortality (HR = 1.31, $P < 10^{-3}$). Finally, we used our model to simulate the effects of effective pharmacological interventions on time to viral clearance and mortality. A treatment able to reduce viral production by 90% upon hospital admission would shorten the time to viral clearance by 2.0 and 2.9 d in patients of age < 65 y and ≥ 65 y, respectively. Assuming that the association between viral dynamics and mortality would remain similar to that observed in our population, this could translate into a reduction of mortality from 19 to 14% in patients of age ≥ 65 y with risk factors. Our results show that viral dynamics is associated with mortality in hospitalized patients. Strategies aiming to reduce viral load could have an effect on mortality rate in this population.

Keywords: SARS-CoV-2 | viral dynamics | mortality

Significance: A detailed characterization of viral load kinetics and its association with disease evolution is key to understand the virus pathogenesis, identify high-risk patients, and design better treatment strategies. We here analyze the mortality and the virological information collected in 655 hospitalized patients, including 284 with longitudinal measurements, and we build a mathematical model of virus dynamics and survival. We predict that peak viral load occurs 1 d before symptom onset, on average, and that dynamics of decline after peak is slower in older patients. Viral load dynamics after hospital admission is an independent predictor of the risk of death, suggesting that prolonged viral shedding of high quantities of virus is associated with poor outcome in this population.

WIESENDANGER 2021

Roland Wiesendanger, *Ursprung der Coronavirus-Pandemie*. *Online* **2021**, Feb. 14. DOI:10.13140/RG.2.2.31754.80323.

Bis heute gibt es keine wissenschaftlich basierten strikten Beweise für eine der beiden genannten Theorien. In einer solchen Situation sollten Wissenschaftler – unabhängig von der jeweiligen Fachrichtung – eine neutrale Haltung einnehmen und eine ergebnisoffene Diskussion bis zur endgültigen Klärung der entscheidenden Frage nach dem Ursprung der Pandemie führen. Gleichwohl haben sich einige namhafte Virologen sehr frühzeitig auf die erste Theorie, also eine Zoonose, in öffentlichen Stellungnahmen festgelegt.

In den Medien wurde sehr frühzeitig im Zusammenhang mit der These des Laborursprungs der Coronavirus-Pandemie von einer “Verschwörungstheorie” gesprochen, ohne allerdings zu begründen, warum die wissenschaftlich durchaus plausible Annahme bezüglich des Ursprungs der Pandemie den Charakter einer “Verschwörung” hat.

YAMEY 2021

Gavin Yamey, *Rich countries should tithe their vaccines*. [nature](#) **590** (2021), 529.

Game theory suggests that donating doses can help nations of all income levels.

Biologie

CALLAWAY 2021

Ewen Callaway, *Mammoth Genomes Shatter Record for Oldest Ancient DNA*. [nature](#) **590** (2021), 537–538.

Permafrost-preserved teeth, up to 1.65 million years old, identify a new kind of mammoth in Siberia.

WYCKELSMA 2021

Victoria L. Wyckelsma, Tomas Venckunas, Marius Brazaitis & Håkan Westerblad et al., *Loss of a-actinin-3 during human evolution provides superior cold resilience and muscle heat generation*. [American Journal of Human Genetics](#) (2021), preprint, 1–19. DOI:10.1016/j.ajhg.2021.01.013.

The protein a-actinin-3 expressed in fast-twitch skeletal muscle fiber is absent in 1.5 billion people worldwide due to homozygosity for a nonsense polymorphism in ACTN3 (R577X). The prevalence of the 577X allele increased as modern humans moved to colder climates, suggesting a link between a-actinin-3 deficiency and improved cold tolerance. Here, we show that humans lacking a-actinin3 (XX) are superior in maintaining core body temperature during cold-water immersion due to changes in skeletal muscle thermogenesis. Muscles of XX individuals displayed a shift toward more slow-twitch isoforms of myosin heavy chain (MyHC) and sarcoplasmic reticulum (SR) proteins, accompanied by altered neuronal muscle activation resulting in increased tone rather than overt shivering. Experiments on Actn3 knockout mice showed no alterations in brown adipose tissue (BAT) properties that could explain the improved cold tolerance in XX individuals. Thus, this study provides a mechanism for the positive selection of the ACTN3 X-allele in cold climates and supports a key thermogenic role of skeletal muscle during cold exposure in humans.

Victoria L. Wyckelsma, Tomas Venckunas, Peter J. Houweling, Maja Schlittler, Volker M. Lauschke, Chrystal F. Tiong, Harrison D. Wood, Niklas Ivarsson, Henrikas Paulauskas, Nerijus Eimantas, Daniel C. Andersson, Kathryn N. North, Marius Brazaitis & Håkan Westerblad

Klima

THALER 2021

Evan A. Thaler, Isaac J. Larsen & Qian Yu, *The extent of soil loss across the US Corn Belt*. [PNAS](#) **118** (2021), e1922375118.

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Soil erosion in agricultural landscapes reduces crop yields, leads to loss of ecosystem services, and influences the global carbon cycle. Despite decades of soil erosion research, the magnitude of historical soil loss remains poorly quantified across large agricultural regions because preagricultural soil data are rare, and it is challenging to extrapolate local-scale erosion observations across time and space. Here we focus on the Corn Belt of the midwestern United States and use a remote-sensing method to map areas in agricultural fields that have no remaining organic carbon-rich A-horizon. We use satellite and LiDAR data to develop a relationship between A-horizon loss and topographic curvature and then use topographic data to scale-up soil loss predictions across 3.9×10^5 km² of the Corn Belt. Our results indicate that 35 ± 11 % of the cultivated area has lost A-horizon soil and that prior estimates of soil degradation from soil survey-based methods have significantly underestimated A-horizon soil loss. Convex hilltops throughout the region are often completely denuded of A-horizon soil. The association between soil loss and convex topography indicates that tillage-induced erosion is an important driver of soil loss, yet tillage erosion is not simulated in models used to assess nationwide soil loss trends in the United States. We estimate that A-horizon loss decreases crop yields by 6 ± 2 %, causing $\$2.8 \pm \0.9 billion in annual economic losses. Regionally, we estimate 1.4 ± 0.5 Pg of carbon have been removed from hillslopes by erosion of the A-horizon, much of which likely remains buried in depositional areas within the fields.

Keywords: soil erosion | remote sensing | soil organic carbon | agricultural productivity

Significance: Conventional agricultural practices erode carbon-rich soils that are the foundation of agriculture. However, the magnitude of A-horizon soil loss across agricultural regions is poorly constrained, hindering the ability to assess soil degradation. Using a remote-sensing method for quantifying the absence of A-horizon soils and the relationship between soil loss and topography, we find that A-horizon soil has been eroded from roughly one-third of the midwestern US Corn Belt, whereas prior estimates indicated none of the Corn Belt region has lost A-horizon soils. The loss of A-horizon soil has removed 1.4 ± 0.5 Pg of carbon from hillslopes, reducing crop yields in the study area by ≈ 6 % and resulting in $\$2.8$ – $\$0.9$ billion in annual economic losses.

Ostasien

SUN 2021

Xue-feng Sun, Shao-qing Wen, Darren Curnoe & Hua-yu Lu et al., *Ancient DNA and multimethod dating confirm the late arrival of anatomically modern humans in southern China*. [PNAS 118 \(2021\), e2019158118](#).

pnas118-e2019158118-Supplement.pdf

The expansion of anatomically modern humans (AMHs) from Africa around 65,000 to 45,000 y ago (ca. 65 to 45 ka) led to the establishment of present-day non-African populations. Some paleoanthropologists have argued that fossil discoveries from Huanglong, Zhiren, Luna, and Fuyan caves in southern China indicate one or more prior dispersals, perhaps as early as ca. 120 ka. We investigated the age of the human remains from three of these localities and two additional early AMH sites (Yangjiapo and Sanyou caves, Hubei) by combining ancient DNA (aDNA) analysis with a multimethod geological dating strategy. Although U–Th dating of capping flowstones suggested they lie within the range ca. 168 to 70 ka,

analyses of aDNA and direct AMS 14C dating on human teeth from Fuyan and Yangjiapo caves showed they derive from the Holocene. OSL dating of sediments and AMS 14C analysis of mammal teeth and charcoal also demonstrated major discrepancies from the flowstone ages; the difference between them being an order of magnitude or more at most of these localities. Our work Highlights the surprisingly complex depositional history recorded at these subtropical caves which involved one or more episodes of erosion and redeposition or intrusion as recently as the late Holocene. In light of our findings, the first appearance datum for AMHs in southern China should probably lie within the timeframe set by molecular data of ca. 50 to 45 ka.

Keywords: anatomically modern humans | Late Pleistocene | East Asia | ancient DNA | dating

Xue-feng Sun, Shao-qing Wen, Cheng-qiu Lu, Bo-yan Zhou, Darren Curnoe, Hua-yu Lu, Hong-chun Li, Wei Wang, Hai Cheng, Shuang-wen Yi, Xin Jia, Pan-xin Du, Xing-hua Xu, Yi-ming Lu, Ying Lu, Hong-xiang Zheng, Hong Zhang, Chang Sun, Lan-hai Wei, Fei Han, Juan Huang, R. Lawrence Edwards, Li Jin & Hui Li

Significance: Genetic studies show the founders of all living non-African populations expanded from Africa ca. 65 to 45 ka. This “late dispersal” model has been challenged by the discovery of isolated AMHs at caves in southern China suggested as early as ca. 120 ka. We assessed the age of early AMH fossils from five caves in this region using ancient DNA analysis and a multimethod geological dating strategy. We found they were much younger than previously suggested, with some remains dating to the Holocene owing to the complex depositional history at these subtropical caves. Current evidence shows AMHs settled southern China within the timeframe set by molecular data of less than ca. 50 to 45 ka and no earlier.