

References

Aktuell

ADAM 2020

Dillon C. Adam et al., *Clustering and superspreading potential of severe acute respiratory coronavirus 2 (SARS-CoV-2) infections in Hong Kong*. [unknown \(2020\), preprint, 1–27](#). .

Superspreading events have characterised previous epidemics of severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) infections. Using contact tracing data, we identified and characterized SARS-CoV-2 clusters in Hong Kong. Given a superspreading threshold of 6-8 secondary cases, we identified 5-7 probable superspreading events and evidence of substantial overdispersion in transmissibility, and estimated that 20% of cases were responsible for 80% of local transmission. Among terminal cluster cases, 27% (45/167) ended in quarantine. Social exposures produced a greater number of secondary cases compared to family or work exposures ($p < 0.001$) while delays between symptom onset and isolation did not reliably predict the number of individual secondary cases or resulting cluster sizes. Public health authorities should focus on rapid tracing and quarantine of contacts, along with physical distancing to prevent superspreading events in high-risk social environments.

Keywords: coronavirus | COVID-19 | superspreading | transmission | public health

Dillon C. Adam, Peng Wu, Jessica Y. Wong, Eric H. Y. Lau, Tim K. Tsang, Simon Cauchemez, Gabriel M. Leung & Benjamin J. Cowling

ALTHOUSE 2020

Benjamin M. Althouse et al., *Stochasticity and heterogeneity in the transmission dynamics of SARS-CoV-2*. [Online 2020, May 29](#).

SARS-CoV-2 causing COVID-19 disease has moved rapidly around the globe, infecting millions and killing hundreds of thousands. The basic reproduction number, which has been widely used and misused to characterize the transmissibility of the virus, hides the fact that transmission is stochastic, is dominated by a small number of individuals, and is driven by super-spreading events (SSEs). The distinct transmission features, such as high stochasticity under low prevalence, and the central role played by SSEs on transmission dynamics, should not be overlooked. Many explosive SSEs have occurred in indoor settings stoking the pandemic and shaping its spread, such as long-term care facilities, prisons, meat-packing plants, fish factories, cruise ships, family gatherings, parties and night clubs. These SSEs demonstrate the urgent need to understand routes of transmission, while posing an opportunity that outbreak can be effectively contained with targeted interventions to eliminate SSEs. Here, we describe the potential types of SSEs, how they influence transmission, and give recommendations for control of SARS-CoV-2.

Keywords: SARS-CoV-2 | COVID-19 | basic reproduction number | super-spreading events

Benjamin M. Althouse, Edward A. Wenger, Joel C. Miller, Samuel V. Scarpino, Antoine Allard, Laurent Hébert-Dufresne & Hao Hu

BAKER 2020

Rachel E. Baker, Wenchang Yang, Gabriel A. Vecchi, C. Jessica E. Metcalf & Bryan T. Grenfell, *Susceptible supply limits the role of climate in the early SARS-CoV-2 pandemic*. [science \(2020\), preprint, 1–9](#). DOI:10.1126/science.abc2535.

Preliminary evidence suggests that climate may modulate the transmission of SARS-CoV-2. Yet it remains unclear whether seasonal and geographic variations in climate can substantially alter the pandemic trajectory, given high susceptibility is a core driver. Here, we use a climate-dependent epidemic model to simulate the SARS-CoV-2 pandemic probing different scenarios based on known coronavirus biology. We find that while variations in weather may be important for endemic infections, during the pandemic stage of an emerging pathogen the climate drives only modest changes to pandemic size. A preliminary analysis of non-pharmaceutical control measures indicates that they may moderate the pandemic-climate interaction via susceptible depletion. Our findings suggest, without effective control measures, strong outbreaks are likely in more humid climates and summer weather will not substantially limit pandemic growth.

BALL 2020

Philip Ball & Amy Maxmen, *Battling the Infodemic*. [nature 581 \(2020\), 371–374](#).

Researchers are analysing false rumours and disinformation about COVID-19 in hopes of curbing their spread.

DEHNING 2020

Jonas Dehning et al., *Inferring change points in the spread of COVID-19 reveals the effectiveness of interventions*. [science \(2020\), preprint, 1–14](#). DOI:10.1126/science.abb9789.

As COVID-19 is rapidly spreading across the globe, short-term modeling forecasts provide time-critical information for decisions on containment and mitigation strategies. A major challenge for short-term forecasts is the assessment of key epidemiological parameters and how they change when first interventions show an effect. By combining an established epidemiological model with Bayesian inference, we analyze the time dependence of the effective growth rate of new infections. Focusing on COVID-19 spread in Germany, we detect change points in the effective growth rate that correlate well with the times of publicly announced interventions. Thereby, we can quantify the effect of interventions, and we can incorporate the corresponding change points into forecasts of future scenarios and case numbers. Our code is freely available and can be readily adapted to any country or region.

Jonas Dehning, Johannes Zierenberg, F. Paul Spitzner, Michael Wibral, Joao Pinheiro Neto, Michael Wilczek and Viola Priesemann

EDITORIAL 2020

Coronavirus misinformation needs researchers to respond. [nature 581 \(2020\), 355–356](#). DOI:10.1038/d41586-020-01550-y.

Researchers must be transparent and acknowledge what is known and what isn't.

For low-income countries, and in those without universal health care, a key obstacle is ensuring that vaccines are available and affordable. For certain higher-income countries — for example some in Europe — the challenge for coronavirus will be to overcome scepticism about vaccines, which is being fuelled by false information.

For consumers, it can be a double whammy — they are paying, and also being misinformed or misled.

Condence was highest in low-income countries — notably Bangladesh and Rwanda — where public-awareness campaigns against infectious diseases such as malaria, typhoid and hepatitis are common.

ENDO 2020

Akira Endo, COVID-19 Working Group, Sam Abbott, Adam J. Kucharski & Sebastian Funk, *Estimating the overdispersion in COVID-19 transmission using outbreak sizes outside China*. Wellcome Open Research 2020, May 28. DOI:10.12688/wellcomeopenres.15842.1.

Background: A novel coronavirus disease (COVID-19) outbreak has now spread to a number of countries worldwide. While sustained transmission chains of human-to-human transmission suggest high basic reproduction number, variation in the number of secondary transmissions (often R characterised by so-called superspreading events) may be large as some countries have observed fewer local transmissions than others.

Methods: We quantified individual-level variation in COVID-19 transmission by applying a mathematical model to observed outbreak sizes in affected countries. We extracted the number of imported and local cases in the affected countries from the World Health Organization situation report and applied a branching process model where the number of secondary transmissions was assumed to follow a negative-binomial distribution.

Results: Our model suggested a high degree of individual-level variation in the transmission of COVID-19. Within the current consensus range of R (2-3), the overdispersion parameter of a negative-binomial distribution k was estimated to be around 0.1 (median estimate 0.1; 95% CrI: 0.05-0.2 for $R_0 = 2.5$), suggesting that 80% of secondary transmissions may have been caused by a small fraction of infectious individuals ($\approx 10\%$). A joint estimation yielded likely ranges for k and R (95% CrIs: 1.4-12; R k R k 0.04-0.2); however, the upper bound of k was not well informed by the R model and data, which did not notably differ from that of the prior distribution.

Conclusions: Our finding of a highly-overdispersed offspring distribution highlights a potential benefit to focusing intervention efforts on superspreading. As most infected individuals do not contribute to the expansion of an epidemic, the effective reproduction number could be drastically reduced by preventing relatively rare superspreading events.

GRONENBORN 2020

Detlef Gronenborn, *Wer gewinnt den Wettlauf um die Globalisierung? Gedanken aus einer historischen Langfristperspektive*. Online 2020, May 20. <<http://archaeologik.blogspot.com/2020/05/wer-gewinnt-den-wettlauf-um-die.html>> (2020-05-29).

HAUSHOFER 2020

Johannes Haushofer & C. Jessica E. Metcalf, *Which interventions work best in a pandemic?* science (2020), preprint, 1–4. DOI:10.1126/science.abb6144.

We can exploit randomized controlled trials, compartmental models, and spillovers

KUPFERSCHMIDT 2020

Kai Kupferschmidt, *Why do some COVID-19 patients infect many others, whereas most don't spread the virus at all?* [science 2020, abc8931](#). DOI:10.1126/science.abc8931.

Countries that have beaten back the virus to low levels need to be especially vigilant for superspreading events, because they can easily undo hard-won gains.

Privacy is another concern. Untangling the links between patients can reveal who was at the origin of a cluster or expose information about people's private lives. In its report about the chorus, CDC left out a seating map that could show who brought the virus to the practice. Some clubs involved in the new South Korean cluster were gay venues, which resulted in an antigay backlash and made contact tracing harder.

LLOYD-SMITH 2005

J. O. Lloyd-Smith, S. J. Schreiber, P. E. Kopp & W. M. Getz, *Superspreading and the effect of individual variation on disease emergence*. [nature 438 \(2005\), 355–359](#).

Population-level analyses often use average quantities to describe heterogeneous systems, particularly when variation does not arise from identifiable groups^{1,2}. A prominent example, central to our current understanding of epidemic spread, is the basic reproductive number, R_0 , which is defined as the mean number of infections caused by an infected individual in a susceptible population^{3,4}. Population estimates of R_0 can obscure considerable individual variation in infectiousness, as highlighted during the global emergence of severe acute respiratory syndrome (SARS) by numerous 'superspreading events' in which certain individuals infected unusually large numbers of secondary cases^{5–10}. For diseases transmitted by non-sexual direct contacts, such as SARS or smallpox, individual variation is difficult to measure empirically, and thus its importance for outbreak dynamics has been unclear^{2,10,11}. Here we present an integrated theoretical and statistical analysis of the influence of individual variation in infectiousness on disease emergence. Using contact tracing data from eight directly transmitted diseases, we show that the distribution of individual infectiousness around R_0 is often highly skewed. Model predictions accounting for this variation differ sharply from average-based approaches, with disease extinction more likely and outbreaks rarer but more explosive. Using these models, we explore implications for outbreak control, showing that individual-specific control measures outperform population-wide measures. Moreover, the dramatic improvements achieved through targeted control policies emphasize the need to identify predictive correlates of higher infectiousness. Our findings indicate that superspreading is a normal feature of disease spread, and to frame ongoing discussion we propose a rigorous definition for superspreading events and a method to predict their frequency.

PRATHER 2020

Kimberly A. Prather, Chia C. Wang & Robert T. Schooley, *Reducing transmission of SARS-CoV-2*. [science \(2020\), preprint, 1–4](#). DOI:10.1126/science.abc6197.

Masks and testing are necessary to combat asymptomatic spread in aerosols and droplets

RIOU 2020

Julien Riou & Christian L. Althaus, *Pattern of early human-to-human transmission of Wuhan 2019 novel coronavirus (2019-nCoV)*,

December 2019 to January 2020. *Euro Surveill* **2020**, Jan. 30. DOI:10.2807/1560-7917.ES.2020.25.4.2000058.

Since December 2019, China has been experiencing a large outbreak of a novel coronavirus (2019-nCoV) which can cause respiratory disease and severe pneumonia. We estimated the basic reproduction number R_0 of 2019-nCoV to be around 2.2 (90% high density interval: 1.4–3.8), indicating the potential for sustained human-to-human transmission. Transmission characteristics appear to be of similar magnitude to severe acute respiratory syndrome-related coronavirus (SARS-CoV) and pandemic influenza, indicating a risk of global spread.

WÖLFEL 2020

Roman Wölfel et al., *Virological assessment of hospitalized patients with COVID-2019*. *nature* **581** (2020), 465–469. DOI:10.1038/s41586-020-2196-x.

n581-0465-Supplement.pdf

Coronavirus disease 2019 (COVID-19) is an acute infection of the respiratory tract that emerged in late 2019^{1,2}. Initial outbreaks in China involved 13.8% of cases with severe courses, and 6.1% of cases with critical courses³. This severe presentation may result from the virus using a virus receptor that is expressed predominantly in the lung^{2,4}; the same receptor tropism is thought to have determined the pathogenicity—but also aided in the control—of severe acute respiratory syndrome (SARS) in 2003⁵. However, there are reports of cases of COVID-19 in which the patient shows mild upper respiratory tract symptoms, which suggests the potential for pre- or oligosymptomatic transmission^{6–8}. There is an urgent need for information on virus replication, immunity and infectivity in specific sites of the body. Here we report a detailed virological analysis of nine cases of COVID-19 that provides proof of active virus replication in tissues of the upper respiratory tract. Pharyngeal virus shedding was very high during the first week of symptoms, with a peak at 7.11×10^8 RNA copies per throat swab on day 4. Infectious virus was readily isolated from samples derived from the throat or lung, but not from stool samples—in spite of high concentrations of virus RNA. Blood and urine samples never yielded virus. Active replication in the throat was confirmed by the presence of viral replicative RNA intermediates in the throat samples. We consistently detected sequence-distinct virus populations in throat and lung samples from one patient, proving independent replication. The shedding of viral RNA from sputum outlasted the end of symptoms. Seroconversion occurred after 7 days in 50% of patients (and by day 14 in all patients), but was not followed by a rapid decline in viral load. COVID-19 can present as a mild illness of the upper respiratory tract. The confirmation of active virus replication in the upper respiratory tract has implications for the containment of COVID-19.

Roman Wölfel, Victor M. Corman, Wolfgang Guggemos, Michael Seilmaier, Sabine Zange, Marcel A. Müller, Daniela Niemeyer, Terry C. Jones, Patrick Vollmar, Camilla Rothe, Michael Hoelscher, Tobias Bleicker, Sebastian Brünink, Julia Schneider, Rosina Ehmann, Katrin Zwirgmaier, Christian Drosten & Clemens Wendtner

Anthropologie

WALLACE 2020

Ian J. Wallace, M. Loring Burgess & Biren A. Patel, *Phalangeal curvature in a chimpanzee raised like a human, Implications for inferring arboreality in fossil hominins*. *PNAS* **117** (2020), 11223–11225.

Arboreal primates such as chimpanzees exhibit pronounced curvature in their hand and foot phalanges, which is assumed to develop throughout life in response to mechanical loads produced by grasping and hanging from branches. Intriguingly, ancient fossil hominins also exhibit substantial phalangeal curvature, which, too, has been interpreted as a direct result of habitual arboreality during life. Here, we describe the phalangeal curvature of a chimpanzee who was raised during the 1930s in New York City to live much like a human, including by having very few opportunities to engage in arboreal activities. We show that the degree of hand and foot phalangeal curvature in this individual is indistinguishable from that of wild chimpanzees and distinct from humans. Thus, rather than being a direct effect of mechanical loads produced by lifetime arboreal activities, phalangeal curvature appears to be shaped largely by genetic factors. An important implication of this finding is that phalangeal curvature among fossil hominins is evidently best interpreted as a primitive trait inherited from an arboreal ancestral species rather than proof of engagement in arboreal activities during life.

Keywords: human evolution | locomotion | suspension | climbing | bone curvature

Bibel

NA'AMAN 2018

Nadav Na'aman, *The Battle of Gibeah Reconsidered (Judges 20:29-48)*. *Vetus Testamentum* **68** (2018), 102–110.

In this article I discuss the episode of the Israelite-Benjaminite battle at Gibeah (Judges 20:29-48). The battle account suffers from many inconsistencies, and to date no satisfactory solution was suggested for its composition. I posit that the battle story has a unified framework (vv. 29-31a and 47-48), and this framework embraces two complete alternative accounts of the battle, each describing a different version of the event (vv. 31b-36a and 36b-46). Following a translation of the two accounts, I analyze each account seeking to show how it describes the related event. I then examine the diachronic and synchronic solutions offered for the way the text has emerged, seeking to clarify how it might have reached its garbled final form.

Keywords: Battle of Gibeah | Benjaminites | Israelites | strategy | synchronic and diachronic solutions

NA'AMAN 2019

Nadav Na'aman, *Hiram of Tyre in the Book of Kings and in the Tyrian Records*. *Journal of Near Eastern Studies* **78** (2019), 75–85.

In light of the prominence of Hiram I in the early history of Tyre, I suggest that oral stories of his Golden Age and his outstanding accomplishments reached the court of Jerusalem. The author of the “Acts of Solomon” was aware of these stories and selected Hiram to play the partner of Solomon in his major building projects, and in obtaining gold by maritime missions to Ophir. Details of the two kings’ correspondence as related in the Book of Kings, the agreement they reached, the participation of the Tyrians and Gebalites in the supply of trees and the building operations in Jerusalem, the maritime expedition to Ophir, and the way Solomon repaid his debt to Hiram—all these details were born in the creative mind of the author. In this creative manner, he tied together the histories of the two kings, each of them memorialized in his respective kingdom as representative of the Golden Age of its history.

NA'AMAN 2019

Nadav Na'aman, *The Jacob Story, Between Oral and Written Modes. Scandinavian Journal of the Old Testament* **33** (2019), 136–158.

In this article I examine the relations between Jacob's putative oral story and the pre-Priestly narrative. I argue that Hosea's prophecy presents the version of Jacob's oral story related in his time and antedated by many years the composition of the story-cycle in its written form. Comparison of Hosea's prophecy and Jacob's narrative indicates the thorough way in which the exilic author worked the oral story he received in order to fit it to his ideological messages and religious concepts. To further examine the relations between the oral and written modes, I discuss the episode of the treaty between Laban and Jacob (Gen 31,45-54) in light of a Mari letter (A.3592). Comparison of the two episodes indicates that part of the biblical narrative rests on the oral story and other part was written by the late author. Evidently, the long process of oral transmission, the growth of the narratives in its course, and the creative reworking of the author make it impossible to either isolate the early oral layer within the present story-cycle or to date the stages of its growth in the oral process of transmission.

Keywords: Jacob's story | Hosea's prophecy | oral story | Haran | Idrimi | Mari | Synchronistic History | exilic author

NA'AMAN 2019

Nadav Na'aman, *The Isaac Story (Genesis 26) and the Land of Gerar. Semitica* **61** (2019), 59–88.

This article suggests that the identification of Gerar at Tell Jemmeh and the elucidation of the Assyrian operations on the empire's border with Egypt are the keys to the interpretation and dating of the original Isaac story (Genesis 26). The story reflects the time of the establishment of Gerar as centre of an Assyrian estate that developed in the Naal Besor region. Although the story is wholly legendary, it reflects the political and social reality of the time in which it was composed and should be dated to the mid-seventh century BCE.

Biologie

GLOBUS 2020

Noemie Globus & Roger D. Blandford, *The Chiral Puzzle of Life. The Astrophysical Journal Letters* **895** (2020), L11.

Biological molecules chose one of two structurally chiral systems which are related by reflection in a mirror. It is proposed that this choice was made, causally, by cosmic rays, which are known to play a major role in mutagenesis. It is shown that magnetically polarized cosmic rays that dominate at ground level today can impose a small, but persistent, chiral bias in the rate at which they induce structural changes in simple, chiral monomers that are the building blocks of biopolymers. A much larger effect should be present with helical biopolymers, in particular, those that may have been the progenitors of ribonucleic acid and deoxyribonucleic acid. It is shown that the interaction can be both electrostatic, just involving the molecular electric field, and electromagnetic, also involving a magnetic field. It is argued that this bias can lead to the emergence of a single, chiral life form over an evolutionary timescale. If this mechanism dominates, then the handedness of living systems should be universal. Experiments are proposed to assess the efficacy of this process.

Datierung

GIMATZIDIS 2020

Stefanos Gimatzidis & Bernhard Weninger, *Radiocarbon dating the Greek Protogeometric and Geometric periods, The evidence of Sindos*. [PLoS ONE 15 \(2020\), e232906](#).

Mediterranean Early Iron Age chronology was mainly constructed by means of Greek Protogeometric and Geometric ceramic wares, which are widely used for chronological correlations with the Aegean. However, Greek Early Iron Age chronology that is exclusively based on historical evidence in the eastern Mediterranean as well as in the contexts of Greek colonisation in Sicily has not yet been tested by extended series of radiocarbon dates from welldated stratified contexts in the Aegean. Due to the high chronological resolution that is only achievable by (metric-scale) stratigraphic ^{14}C -age-depth modelling, the analysis of 21 ^{14}C AMS dates on stratified animal bones from Sindos (northern Greece) shows results that immediately challenge the conventional Greek chronology. Based on pottery-style comparisons with other sites, the new dates for Sindos not only indicate a generally higher Aegean Early Iron Age chronology, but also imply the need for a revised understanding of the Greek periodisation system that will foreseeably have a major impact on our understanding of Greek and Mediterranean history.

Kultur

POUW 2020

Wim Pouw, Alexandra Paxton, Steven J. Harrison & James A. Dixon, *Acoustic information about upper limb movement in voicing*. [PNAS 117 \(2020\), 11364–11367](#).

We show that the human voice has complex acoustic qualities that are directly coupled to peripheral musculoskeletal tensioning of the body, such as subtle wrist movements. In this study, human vocalizers produced a steady-state vocalization while rhythmically moving the wrist or the arm at different tempos. Although listeners could only hear and not see the vocalizer, they were able to completely synchronize their own rhythmic wrist or arm movement with the movement of the vocalizer which they perceived in the voice acoustics. This study corroborates recent evidence suggesting that the human voice is constrained by bodily tensioning affecting the respiratory–vocal system. The current results show that the human voice contains a bodily imprint that is directly informative for the interpersonal perception of another’s dynamic physical states.

Keywords: vocalization acoustics | hand gesture | interpersonal synchrony | motion tracking

Significance: We show that the human voice carries an acoustic signature of muscle tensioning during upper limb movements which can be detected by listeners. Specifically, we find that human listeners can synchronize their own movements to very subtle wrist movements of a vocalizer only by listening to their vocalizations and without any visual contact. This study shows that the human voice contains information about dynamic bodily states, breaking ground for our understanding of the evolution of spoken language and nonverbal communication. The current findings are in line with other research on nonhuman animals, showing that vocalizations carry information about bodily states and capacities.