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References

Aktuell

LAI 2020

Shengjie Lai et al., *Effect of non-pharmaceutical interventions to contain COVID-19 in China.* nature **585** (2020), 410–413. DOI:10.1038/s41586-020-2293-x.

n585-0410-Supplement1.pdf, n585-0410-Supplement2.xlsx, n585-0410-Supplement3.xlsx

On 11 March 2020, the World Health Organization (WHO) declared coronavirus disease 2019 (COVID-19) a pandemic1. The strategies based on non-pharmaceutical interventions that were used to contain the outbreak in China appear to be effective2, but quantitative research is still needed to assess the efficacy of non-pharmaceutical interventions and their timings3. Here, using epidemiological data on COVID-19 and anonymized data on human movement4,5, we develop a modelling framework that uses daily travel networks to simulate different outbreak and intervention scenarios across China. We estimate that there were a total of 114,325 cases of COVID-19 (interquartile range 76,776–164,576) in mainland China as of 29 February 2020. Without non-pharmaceutical interventions, we predict that the number of cases would have been 67-fold higher (interquartile range 44–94-fold) by 29 February 2020, and we find that the effectiveness of different interventions varied. We estimate that early detection and isolation of cases prevented more infections than did travel restrictions and contact reductions, but that a combination of non-pharmaceutical interventions achieved the strongest and most rapid effect. According to our model, the lifting of travel restrictions from 17 February 2020 does not lead to an increase in cases across China if social distancing interventions can be maintained, even at a limited level of an on average 25 % reduction in contact between individuals that continues until late April. These findings improve our understanding of the effects of non-pharmaceutical interventions on COVID-19, and will inform response efforts across the world.

Shengjie Lai, Nick W. Ruktanonchai, Liangcai Zhou, Olivia Prosper, Wei Luo, Jessica R. Floyd, Amy Wesolowski, Mauricio Santillana, Chi Zhang, Xiangjun Du, Hongjie Yu & Andrew J. Tatem

MAJIYA 2020

Majiya H. et al., *Seroprevalence of COVID-19 in Niger State.* medRxiv **2020**, 20168112, 1–24. DOI:10.1101/2020.08.04.20168112.

Coronavirus Disease 2019 (COVID-19) Pandemic is ongoing, and to know how far the virus has spread in Niger State, Nigeria, a pilot study was carried out to determine the COVID-19 seroprevalence, patterns, dynamics, and risk factors in the state. A cross sectional study design and clustered-stratified-Random sampling strategy were used. COVID-19 IgG and IgM Rapid Test Kits (Colloidal gold immunochromatography lateral flow system) were used to determine the presence or absence of antibodies to SARS-CoV-2 in the blood of sampled participants across Niger State as from 26th June 2020 to 30th June 2020. The test kits were validated using the blood samples of some of the NCDC confirmed positive and negative COVID-19 cases in the State. COVID-19 IgG and IgM Test results were entered into the EPIINFO questionnaire administered simultaneously with each test. EPIINFO was then used for both the descriptive and inferential statistical analyses of the data generated. The seroprevalence of COVID-19 in Niger State was found to be 25.41 % and 2.16 % for the positive IgG and IgM respectively. Seroprevalence among age groups, gender and by occupation varied widely. A seroprevalence of 37.21 % was recorded among health care workers in Niger State. Among age groups, COVID-19 seroprevalence was found to be in order of 30-41 years (33.33 %) > 42-53 years (32.42 %) > 54-65 years (30 %) > 66 years and above (25 %) > 6-17 years (19.20 %) > 18-29 years (17.65 %) > 5 years and below (6.66 %). A seroprevalence of 27.18 % was recorded for males and 23.17 % for females in the state. COVID-19 asymptomatic rate in the state was found to be 46.81 %. The risk analyses showed that the chances of infection are almost the same for both urban and rural dwellers in the state. However, health care workers and those that have had contact with person (s) that travelled out of Nigeria in the last six (6) months are twice (2 times) at risk of being infected with the virus. More than half (54.59 %) of the participants in this study did not practice social distancing at any time since the pandemic started. Discussions about knowledge, practice and attitude of the participants are included. The observed Niger State COVID-19 seroprevalence means that the herd immunity for COVID-19 is yet to be achieved and the population is still susceptible for more infection and transmission of the virus. If the prevalence stays as reported here, the population will definitely need COVID-19 vaccines when they become available. Niger State should fully enforce the use of face/nose masks and observation of social/physical distancing in gatherings including religious gatherings in order to stop or slow the spread of the virus.

OJAL 2020

John Ojal et al., *Revealing the extent of the COVID-19 pandemic in Kenya based on serological and PCR-test data.* medRxiv **2020**, 20186817, 1–32. DOI:10.1101/2020.09.02.20186817.

Policy makers in Africa need robust estimates of the current and future spread of SARS-CoV-2. Data suitable for this purpose are scant. We used national surveillance PCR test, serological survey and mobility data to develop and fit a county-specific transmission model for Kenya. We estimate that the SARS-CoV-2 pandemic peaked before the end of July 2020 in the major urban counties, with 34 – 41 % of residents infected, and will peak elsewhere in the country within 2-3 months. Despite this penetration, reported severe cases and deaths are low. Our analysis suggests the COVID-19 disease burden in Kenya may be far less than initially feared. A similar scenario across sub-Saharan Africa would have implications for balancing the consequences of restrictions with those of COVID-19.

PASTOR-BARRIUSO 2020

Roberto Pastor-Barriuso et al., *SARS-CoV-2 infection fatality risk in a nationwide seroepidemiological study.* medRxiv **2020**, 20169722, 1–14. DOI:10.1101/2020.08.06.20169722.

The magnitude of the infection fatality risk (IFR) of SARS-CoV-2 remains under debate. Because the IFR is the number of deaths divided by the number of infected, serological studies are needed to identify asymptomatic and mild cases. Also, because ascertainment of deaths attributable to COVID19 is often incomplete, the calculation of the IFR needs to be complemented with data on excess mortality. We used data from a nation-wide seroepidemiological study and two sources of mortality information—deaths among laboratory-confirmed COVID-19 cases and excess deaths—to estimate the range of IFR, both overall and by age and sex, in Spain.

The overall IFR ranged between 1.1 % and 1.4 % in men and 0.58 % to 0.77 % in women. The IFR increased sharply after age 50, ranging between 11.6 % and 16.4 % in men ≥80 years and between 4.6 % and 6.5 % in women ≥80 years. Our IFR estimates for SARS-CoV-2 are substantially greater than IFR estimators for seasonal influenza, justifying the implementation of special public health measures.

THURNER 2020

Stefan Thurner, Peter Klimek & Rudolf Hanel, *A network-based explanation of why most COVID-19 infection curves are linear.* PNAS **117** (2020), 22684–22689. DOI:10.1073/pnas.2010398117.

pnas117-22684-Supplement.pdf

Many countries have passed their first COVID-19 epidemic peak. Traditional epidemiological models describe this as a result of nonpharmaceutical interventions pushing the growth rate below the recovery rate. In this phase of the pandemic many countries showed an almost linear growth of confirmed cases for extended time periods. This new containment regime is hard to explain by traditional models where either infection numbers grow explosively until herd immunity is reached or the epidemic is completely suppressed. Here we offer an explanation of this puzzling observation based on the structure of contact networks. We show that for any given transmission rate there exists a critical number of social contacts, Dc , below which linear growth and low infection prevalence must occur. Above Dc traditional epidemiological dynamics take place, e.g., as in susceptible–infected–recovered (SIR) models. When calibrating our model to empirical estimates of the transmission rate and the number of days being contagious, we find Dc .7:2. Assuming realistic contact networks with a degree of about 5, and assuming that lockdown measures would reduce that to household size (about 2.5), we reproduce actual infection curves with remarkable precision, without fitting or fine-tuning of parameters. In particular, we compare the United States and Austria, as examples for one country that initially did not impose measures and one that responded with a severe lockdown early on. Our findings question the applicability of standard compartmental models to describe the COVID-19 containment phase. The probability to observe linear growth in these is practically zero.

Keywords: compartmental epidemiological model | mean-field (well mixed) approximation | social contact networks | network theory | COVID-19

Significance: For many countries a plain-eye inspection of the COVID-19 infection curves reveals a remarkable linear growth over extended time periods. This observation is practically impossible to understand with traditional epidemiological models. These, to make them expressible in compact mathematical form, typically ignore the structure of real contact networks that are essential in the characteristic spreading dynamics of COVID-19. Here we show that by properly taking some relevant network features into account, linear growth can be naturally explained. Further, the effect of nonpharmaceutical interventions (NPIs), like national lockdowns, can be modeled with a remarkable degree of precision without fitting or fine-tuning of parameters.

UYOGA 2020

Sophie Uyoga et al., *Seroprevalence of anti-SARS-CoV-2 IgG antibodies in Kenyan blood donors.* medRxiv **2020**, 20162693, 1–29. DOI:10.1101/2020.07.27.20162693.

Background: There are no data on SARS-CoV-2 seroprevalence in Africa though the COVID-19 epidemic curve and reported mortality differ from patterns seen elsewhere. We estimated the anti-SARS-CoV-2 antibody prevalence among blood donors in Kenya.

Methods: We measured anti-SARS-CoV-2 spike IgG prevalence by ELISA on residual blood donor samples obtained between April 30 and June 16, 2020. Assay sensitivity and specificity were 83 % (95 % CI 59-96 %) and 99.0 % (95 % CI 98.1-99.5 %), respectively. National seroprevalence was estimated using Bayesian multilevel regression and post-stratification to account for non-random sampling with respect to age, sex and region, adjusted for assay performance.

Results: Complete data were available for 3098 of 3174 donors, aged 15-64 years. By comparison with the Kenyan population, the sample over- represented males (82 % versus 49 %), adults aged 25-34 years (40 % versus 27 %) and residents of coastal Counties (49 % versus 9 %). Crude overall seroprevalence was 5.6 % (174/3098). Population-weighted, test- adjusted national seroprevalence was 5.2 % (95 % CI 3.7– 7.1 %). Seroprevalence was highest in the 3 largest urban Counties – Mombasa (9.3 % [95 % CI 6.4-13.2 %)], Nairobi (8.5 % [95 % CI 4.9-13.5 %]) and Kisumu (6.5 % [95 % CI 3.3-11.2 %]).

Conclusions: We estimate that 1 in 20 adults in Kenya had SARS-CoV-2 antibodies during the study period. By the median date of our survey, only 2093 COVID-19 cases and 71 deaths had been reported through the national screening system. This contrasts, by several orders of magnitude, with the numbers of cases and deaths reported in parts of Europe and America when seroprevalence was similar.

Ward 2020

Ward H. et al., *Antibody prevalence for SARS-CoV-2 following the peak of the pandemic in England*, *REACT2 study in 100,000 adults.* unknown (2020), preprint, 1–20.

Background: England, UK has experienced a large outbreak of SARS-CoV-2 infection. As in USA and elsewhere, disadvantaged communities have been disproportionately affected.

Methods: National REal-time Assessment of Community Transmission-2 (REACT-2) seroprevalence study using self-administered lateral flow immunoassay (LFIA) test for IgG among a random population sample of 100,000 adults over 18 years in England, 20 June to 13 July 2020.

Results: Completed questionnaires were available for 109,076 participants, yielding 5,544 IgG positive results and adjusted (for test performance), re-weighted (for sampling) prevalence of 6.0 % (95 % CI: 5.8, 6.1). Highest prevalence was in London (13.0 % [12.3, 13.6]), among people of Black or Asian (mainly South Asian) ethnicity (17.3 % [15.8, 19.1] and 11.9 % [11.0, 12.8] respectively) and those aged 18-24 years (7.9 % [7.3, 8.5]). Care home workers with client-facing roles had adjusted odds ratio of 3.1 (2.5, 3.8) compared with non-essential workers. One third (32.2 %, [31.0-33.4]) of antibody positive individuals reported no symptoms. Among symptomatic cases, the majority (78.8 %) reported symptoms during the peak of the epidemic in England in March (31.3 %) and April (47.5 %) 2020. We estimate that 3.36 million (3.21, 3.51) people have been infected with SARS-CoV-2 in England to end June 2020, with an overall infection fatality ratio of 0.90 % (0.86, 0.94).

Conclusion: The pandemic of SARS-CoV-2 infection in England disproportionately affected ethnic minority groups and health and care home workers. The higher risk of infection in these groups may explain, at least in part, their increased risk of hospitalisation and mortality from COVID-19.

Metallzeiten

GUIMARAES 2020

Silvia Guimaraes, Benjamin S. Arbuckle, Thierry Grange & Eva-Maria Geigl et al., *Ancient DNA shows domestic horses were introduced in the southern Caucasus and Anatolia during the Bronze Age.* Science Advances **6** (2020), eabb0030. DOI:10.1126/sciadv.abb0030.

SciAdv06-eabb0030-Supplement.pdf

Despite the important roles that horses have played in human history, particularly in the spread of languages and cultures, and correspondingly intensive research on this topic, the origin of domestic horses remains elusive. Several domestication centers have been hypothesized, but most of these have been invalidated through recent paleogenetic studies. Anatolia is a region with an extended history of horse exploitation that has been considered a candidate for the origins of domestic horses but has never been subject to detailed investigation. Our paleogenetic study of pre- and protohistoric horses in Anatolia and the Caucasus, based on a diachronic sample from the early Neolithic to the Iron Age (≈8000 to ≈1000 BCE) that encompasses the presumed transition from wild to domestic horses (4000 to 3000 BCE), shows the rapid and large-scale introduction of domestic horses at the end of the third millennium BCE. Thus, our results argue strongly against autochthonous independent domestication of horses in Anatolia.

Silvia Guimaraes, Benjamin S. Arbuckle, Joris Peters, Sarah E. Adcock, Hijlke Buitenhuis, Hannah Chazin, Ninna Manaseryan, Hans-Peter Uerpmann, Thierry Grange & Eva-Maria Geigl

Methoden

FETAYA 2020

Ethan Fetaya, Yonatan Lifshitz, Elad Aaron & Shai Gordin, *Restoration of fragmentary Babylonian texts using recurrent neural networks.* PNAS **117** (2020), 22743–22751.

pnas117-22743-Supplement0.pdf, pnas117-22743-Supplement1.txt, pnas117-22743-Supplement2.txt, pnas117-22743-Supplement3.txt, pnas117-22743-Supplement4.txt, pnas117-22743-Supplement5.csv, pnas117-22743-Supplement6.csv

The main sources of information regarding ancient Mesopotamian history and culture are clay cuneiform tablets. Many of these tablets are damaged, leading to missing information. Currently, the missing text is manually reconstructed by experts. We investigate the possibility of assisting scholars, by modeling the language using recurrent neural networks and automatically completing the breaks in ancient Akkadian texts from Achaemenid period Babylonia.

Keywords: Babylonian heritage | cuneiform script | Late Babylonian dialect | Achaemenid empire | neural networks

Significance: The documentary sources for the political, economic, and social history of ancient Mesopotamia constitute hundreds of thousands of clay tablets inscribed in the cuneiform script. Most tablets are damaged, leaving gaps in the texts written on them, and the missing portions must be restored by experts. This paper uses available digitized texts for training advanced machine-learning algorithms to restore daily economic and administrative documents from the Persian empire (sixth to fourth centuries BCE). As the amount of digitized texts grows, the model can be trained to restore damaged texts belonging to other genres, such as scientific or literary texts. Therefore, this is a first step for a large-scale reconstruction of a lost ancient heritage.

Mittelalter

Curry 2020

Andrew Curry, *Ancient DNA tracks Vikings across Europe.* science **369** (2020), 1416–1417.

Massive sequencing effort shows people of diverse genetic backgrounds adopted Viking culture.

“The big story is in line with what’s told by archaeologists and historians,” says Erika Hagelberg, an ancient DNA expert at the University of Oslo who was not part of the research team. “It’s the small details of particular sites that are really compelling.”

“We can follow the patterns of contact suggested by written sources, but disputed by historians for decades,” says co-author Søren Sindbæk, an archaeologist at Aarhus University.

Margaryan 2020

Ashot Margaryan et al., *Population genomics of the Viking world.* nature **585** (2020), 390–396.

n585-0390-Supplement1.pdf, n585-0390-Supplement2.xlsx

The maritime expansion of Scandinavian populations during the Viking Age (about ad 750–1050) was a far-flung transformation in world history1,2. Here we sequenced the genomes of 442 humans from archaeological sites across Europe and Greenland (to a median depth of about 1×) to understand the global influence of this expansion. We find the Viking period involved gene flow into Scandinavia from the south and east. We observe genetic structure within Scandinavia, with diversity hotspots in the south and restricted gene flow within Scandinavia. We find evidence for a major influx of Danish ancestry into England; a Swedish influx into the Baltic; and Norwegian influx into Ireland, Iceland and Greenland. Additionally, we see substantial ancestry from elsewhere in Europe entering Scandinavia during the Viking Age. Our ancient DNA analysis also revealed that a Viking expedition included close family members. By comparing with modern populations, we find that pigmentation-associated loci have undergone strong population differentiation during the past millennium, and trace positively selected loci—including the lactase-persistence allele of LCT and alleles of ANKA that are associated with the immune response—in detail. We conclude that the Viking diaspora was characterized by substantial transregional engagement: distinct populations influenced the genomic makeup of different regions of Europe, and Scandinavia experienced increased contact with the rest of the continent.

Ashot Margaryan, Daniel J. Lawson, Martin Sikora, Fernando Racimo, Simon Rasmussen, Ida Moltke, Lara M. Cassidy, Emil Jorsboe, Andrés Ingason, Mikkel W. Pedersen, Thorfinn Korneliussen, Helene Wilhelmson, Magdalena M. Buœ, Peter de Barros Damgaard, Rui Martiniano, Gabriel Renaud, Claude Bhérer, J. Víctor Moreno-Mayar, Anna K. Fotakis, Marie Allen, Raili Allmäe, Martyna Molak, Enrico Cappellini, Gabriele Scorrano, Hugh McColl, Alexandra Buzhilova, Allison Fox, Anders Albrechtsen, Berit Schütz, Birgitte Skar, Caroline Arcini, Ceri Falys, Charlotte Hedenstierna Jonson, Dariusz Błaszczyk, Denis Pezhemsky, Gordon Turner-Walker, Hildur Gestsdóttir, Inge Lundstrom, Ingrid Gustin, Ingrid Mainland, Inna Potekhina, Italo M. Muntoni, Jade Cheng, Jesper Stenderup, Jilong Ma, Julie Gibson, Jüri Peets, Jörgen Gustafsson, Katrine H. Iversen, Linzi Simpson, Lisa Strand, Louise Loe, Maeve Sikora, Marek Florek, Maria Vretemark, Mark Redknap, Monika Bajka, Tamara Pushkina, Morten Sovso, Natalia Grigoreva, Tom Christensen, Ole Kastholm, Otto Uldum, Pasquale Favia, Per Holck, Sabine Sten, Símun V. Arge, Sturla Ellingvag, Vayacheslav Moiseyev, Wiesław Bogdanowicz, Yvonne Magnusson, Ludovic Orlando, Peter Pentz, Mads Dengso Jessen, Anne Pedersen, Mark Collard, Daniel G. Bradley, Marie Louise Jorkov, Jette Arneborg, Niels Lynnerup, Neil Price, M. Thomas P. Gilbert, Morten E. Allentoft, Jan Bill, Soren M. Sindbak, Lotte Hedeager, Kristian Kristiansen, Rasmus Nielsen, Thomas Werge & Eske Willerslev

Story or Book

GROSJEAN 2020

Pauline Grosjean, *Why the West is WEIRD.* science **369** (2020), 1438.

Catholicism's policy forbidding cousins to wed may have led to the distinctive characteristics of Western society.

The WEIRDest People in the World. Joseph Henrich. Farrar, Straus and Giroux, 2020. 704 pp.

He does, however, suggest that the Europeans' propensity for late marriage was a consequence of the Church's marriage prohibitions. This is inconsistent with the evidence that there has been much variation over time in the age at marriage and also the fact that it dropped sharply when 19th-century Europeans migrated to the colonies of the United States or Australia, where land was much more abundant.