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References

Aktuell

ANNAVAJHALA 2021

Medini K. Annavajhala et al., *Emergence and expansion of SARS-CoV-2 B.1.526 after identification in New York*. nature **597** (2021), 703–708. DOI:10.1038/s41586-021-03908-2.

SARS-CoV-2 infections have surged across the globe in recent months, concomitant with considerable viral evolution1–3. Extensive mutations in the spike protein may threaten the efficacy of vaccines and therapeutic monoclonal antibodies4. Two signature spike mutations of concern are E484K, which has a crucial role in the loss of neutralizing activity of antibodies, and N501Y, a driver of rapid worldwide transmission of the B.1.1.7 lineage. Here we report the emergence of the variant lineage B.1.526 (also known as the Iota variant5), which contains E484K, and its rise to dominance in New York City in early 2021. This variant is partially or completely resistant to two therapeutic monoclonal antibodies that are in clinical use and is less susceptible to neutralization by plasma from individuals who had recovered from SARS-CoV-2 infection or serum from vaccinated individuals, posing a modest antigenic challenge. The presence of the B.1.526 lineage has now been reported in all 50 states in the United States and in many other countries. B.1.526 rapidly replaced earlier lineages in New York, with an estimated transmission advantage of 35 %. These transmission dynamics, together with the relative antibody resistance of its E484K sub-lineage, are likely to have contributed to the sharp rise and rapid spread of B.1.526. Although SARS-CoV-2 B.1.526 initially outpaced B.1.1.7 in the region, its growth subsequently slowed concurrently with the rise of B.1.1.7 and ensuing variants.

Medini K. Annavajhala, Hiroshi Mohri, Pengfei Wang, Manoj Nair, Jason E. Zucker, Zizhang Sheng, Angela Gomez-Simmonds, Anne L. Kelley, Maya Tagliavia, Yaoxing Huang, Trevor Bedford, David D. Ho & Anne-Catrin Uhlemann

CRONIN 2021

Christopher J. Cronin & William N. Evans, *Excess mortality from COVID and non-COVID causes in minority populations*. PNAS **118** (2021), e2101386118. DOI:10.1073/pnas.2101386118.

pnas118-e2101386118-Supplement.pdf

The 2020 US mortality totaled 2.8 million after early March, which is 17.3 % higher than age-population–weighted mortality over the same time interval in 2017 to 2019, for a total excess death count of 413,592. We use data on weekly death counts by cause, as well as life tables, to quantify excess mortality and life years lost from both COVID-19 and non–COVID-19 causes by race/ethnicity, age, and gender/sex. Excess mortality from non–COVID-19 causes is substantial and much more heavily concentrated among males and minorities, especially Black, non-Hispanicmales, than COVID-19 deaths. Thirty-four percent of the excess life years lost for males is from non–COVID-19 causes. While minorities represent 36 % of COVID-19 deaths, they represent 70 % of non–COVID-19 related excess deaths and 58 % of non–COVID-19 excess life years lost. Black, non-Hispanic males represent only 6.9 %of the population, but they are responsible for 8.9 % of COVID-19 deaths and 28 % of 2020 excess deaths from non–COVID-19 causes. For this group, nearly half of the excess life years lost in 2020 are due to non–COVID-19 causes.

Keywords: excess mortality | COVID-19 | racial disparities

Significance: Research has documented the heavy cost COVID-19 mortality has placed on minorities. There is, however, less discussion of the inordinate burden that non–COVID-19 excess mortality i.e., pandemic-era non–COVID-19 deaths in excess of the historical average) has exacted on this same group. Our analysis shows that minorities, particularly Black, non-Hispanic men, represent a disproportionate share of excess mortality and life years lost from non–COVID-19 causes. Early evidence suggests combination of factors, including deaths of despair, murders, uninfected Alzheimer's patients, reduced health care use, and economic dislocation. Moving forward, the challenge for the public health community is to understand the etiology of non–COVID-19 excess mortality and attack it with the same zeal as it attacks the virus.

DOLGIN 2021

Elie Dolgin, *COVID vaccine immunity is waning—how much does that matter?* nature **597** (2021), 606–607.

As debates about booster shots heat up, knowledge about the duration of vaccine-based immunity is still evolving.

Amerika

CALLAWAY 2021

Ewen Callaway, *Ancient footprints could be oldest traces of humans in the Americas.* nature **597** (2021), 601–602.

Children left tracks in New Mexico around 22,500 years ago — thousands of years before most scientists thought humans settled in North America.

Bibel

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JOOSTEN 2021

Jan Joosten, *Text and Versions – Old Testament.* unknown (2021), preprint, 1–26. .

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Biologie

BARBIERI 2021

Rémi Barbieri, *Origin, transmission, and evolution of plague over 400 y in Europe.* PNAS **118** (2021), e2114241118.

FEUERBORN 2021

Tatiana R. Feuerborn, Alberto Carmagnini, Anders J. Hansen, Mikkel-Holger S. Sinding & Laurent Frantz et al., *Modern Siberian dog ancestry was shaped by several thousand years of Eurasian-wide trade and human dispersal*. PNAS **118** (2021), e2100338118.

pnas118-e2100338118-Supplement.pdf

Dogs have been essential to life in the Siberian Arctic for over 9,500 y, and this tight link between people and dogs continues in Siberian communities. Although Arctic Siberian groups such as the Nenets received limited gene flow from neighboring groups, archaeological evidence suggests that metallurgy and new subsistence strategies emerged in Northwest Siberia around 2,000 y ago. It is unclear if the Siberian Arctic dog population was as continuous as the people of the region or if instead admixture occurred, possibly in relation to the influx of material culture from other parts of Eurasia. To address this question, we sequenced and analyzed the genomes of 20 ancient and historical Siberian and Eurasian Steppe dogs. Our analyses indicate that while Siberian dogs were genetically homogenous between 9,500 to 7,000 y ago, later introduction of dogs from the Eurasian Steppe and Europe led to substantial admixture. This is clearly the case in the Iamal-Nenets region (Northwestern Siberia) where dogs from the Iron Age period (≈2,000 y ago) possess substantially less ancestry related to European and Steppe dogs than dogs from the medieval period (≈1,000 y ago). Combined with findings of nonlocal materials recovered from these archaeological sites, including glass beads and metal items, these results indicate that Northwest Siberian communities were connected to a larger trade network through which they acquired genetically distinctive dogs from other regions. These exchanges were part of a series of major societal changes, including the rise of large-scale reindeer pastoralism ≈800 y ago.

Keywords: dogs | palaeogenomics | Arctic | population genetics

Tatiana R. Feuerborn, Alberto Carmagnini, Robert J. Losey, Tatiana Nomokonova, Arthur Askeyev, Igor Askeyev, Oleg Askeyev, Ekaterina E. Antipina, Martin Appelt, Olga P. Bachura, Fiona Beglane, Daniel G. Bradley, Kevin G. Daly, Shyam Gopalakrishnan, Kristian Murphy Gregersen, Chunxue Guo, Andrei V. Gusev, Carleton Jones, Pavel A. Kosintsev, Yaroslav V. Kuzmin, Valeria Mattiangeli, Angela R. Perri, Andrei V. Plekhanov, Jazmín Ramos-Madrigal, Anne Lisbeth Schmidt, Dilyara Shaymuratova, Oliver Smith, Lilia V. Yavorskaya, Guojie Zhang, Eske Willerslev, Morten Meldgaard, M. Thomas P. Gilbert, Greger Larson, Love Dalén, Anders J. Hansen, Mikkel-Holger S. Sinding & Laurent Frantz

Significance: The Siberian Arctic has witnessed numerous societal changes since the first known appearance of dogs in the region ≈10,000 years ago. These changes include the introduction of ironworking ≈2,000 years ago and the emergence of reindeer pastoralism ≈800 years ago. The analysis of 49 ancient dog genomes reveals that the ancestry of Arctic Siberia dogs shifted over the last 2,000 years due to an influx of dogs from the Eurasian Steppe and Europe. Combined with genomic data from humans and archaeological evidence, our results suggest that though the ancestry of human populations in Arctic Siberia did not change over this period, people there participated in trade with distant communities that involved both dogs and material culture.

Methoden

WENDT 2009

Karl Peter Wendt & Andreas Zimmermann, *Transforming Archaeological Data Between Different Geographical Scales*, *A GIS application* *for the estimation of population density.* In: Alexandra Velho & Hans Kamermans (Hrsg.), *Technology and Methodology for Archaeological Practice – Practical applications for the past reconstruction*, *International Union for Prehistoric and Protohistoric Sciences – XV World Congress (Lisbon, 4-9 September 2006).* BAR International Series 2029 (Oxford 2009), 49–59.

Within the Rhine-LUCIFS project, a bundle of GIS-based methods is developed with the objective to determine and visualize population densities from different sources and time periods. It is based on a hierarchical scale model with standardised steps of upscaling. At the small scale level of key areas the number of houses per km^2 is estimated. At the scale of large distribution maps isolines circumscribing settlement areas are constructed. The density of features in key ares are upscaled to settlement areas. In this paper an introduction to the methods is presented and for two periods their application is demonstrated (the Early Neolithic Bandkeramik and the Roman period of the 2nd century AD).

Keywords: GIS application | estimation of population density | hierarchical scale model | Bandkeramik | Roman Period

Zimmermann 2009

Andreas Zimmermann & Karl Peter Wendt, *Environmental suitability and land use*, *A diachronic comparison.* In: Alexandra Velho & Hans Kamermans (Hrsg.), *Technology and Methodology for Archaeological Practice – Practical applications for the past reconstruction*, *International Union for Prehistoric and Protohistoric Sciences – XV World Congress (Lisbon, 4-9 September 2006).* BAR International Series 2029 (Oxford 2009), 101–110.

The last applications of site catchment analysis and recent predictive modelling analysed culture-environment-relations typically at a scale of 1:25.000. The analysis presented here uses large scale maps covering Germany in total, due to the aims of the Rhine-LUCIFS research group projects, which consider the whole Rhine-catchment or at least large parts of it. Soil maps of Germany (BÜK 1000, scale 1:1 million) are combined with settlement areas deduced from isolines of site density (same volume). Using a chi-square index of preferred and not preferred soil classes, a model of suitability with three classes is created. Because of the regional and qualitative differences between the analysed time horizons, this approach is a good instrument for crosschronological studies. Efficiency studies show the predictive character of this method. Additionally, data of precipitation could be visualized on the resulting maps to support the analysis of the factor soil.

Keywords: culture | environment | relationship | cross-chronological analysis | chi-square index